

**METHODS FOR TREATING HEMATOLOGICAL CANCERS AND THE USE OF
BIOMARKERS AS A PREDICTOR OF CLINICAL SENSITIVITY TO
IMMUNOMODULATORY THERAPIES**

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of priority to U.S. Serial No. 61/913,046 filed December 6, 2013, which is herein incorporated by reference in its entirety.

1. FIELD

[0001] Provided herein are biomarkers for use in predicting the clinical sensitivity of hematologic cancers, such as non-Hodgkin's lymphoma, and a patient's response to treatment with an immunomodulatory agent, such as 3-(4-amino-1-oxo-1,3-dihydro-isoindol-2-yl)-piperidine-2,6-dione, which is also known as lenalidomide or Revlimid®. In one aspect, provided herein are methods of treating or managing non-Hodgkin's lymphomas, including but not limited to, diffuse large B-cell lymphoma (DLBCL), using prognostic factors.

2. BACKGROUND

2.1 Pathobiology of Cancer

[0002] Cancer is characterized primarily by an increase in the number of abnormal cells derived from a given normal tissue, invasion of adjacent tissues by these abnormal cells, or lymphatic or blood-borne spread of malignant cells to regional lymph nodes and to distant sites (metastasis). Clinical data and molecular biologic studies indicate that cancer is a multistep process that begins with minor pre-neoplastic changes, which may under certain conditions progress to neoplasia. The neoplastic lesion may evolve clonally and develop an increasing capacity for invasion, growth, metastasis, and heterogeneity, especially under conditions in which the neoplastic cells escape the host's immune surveillance. Roitt, I., Brostoff, J and Kale, D., Immunology, 17.1-17.12 (3rd ed., Mosby, St. Louis, Mo., 1993).

[0003] There is an enormous variety of cancers which are described in detail in the medical literature. Examples include cancers of the lung, colon, rectum, prostate, breast, brain, blood and intestine. The incidence of cancer continues to climb as the general population ages, as new cancers develop, and as susceptible populations (e.g., people infected with AIDS or excessively exposed to sunlight) grow. However, options for the treatment of cancer are limited. For example, in the case

of blood cancers (*e.g.*, multiple myeloma), few treatment options are available, especially when conventional chemotherapy fails and bone-marrow transplantation is not an option. A tremendous demand therefore exists for new methods and compositions that can be used to treat patients with cancer.

[0004] Many types of cancers are associated with new blood vessel formation, a process known as angiogenesis. Several of the mechanisms involved in tumor-induced angiogenesis have been elucidated. The most direct of these mechanisms is the secretion by the tumor cells of cytokines with angiogenic properties. Examples of these cytokines include acidic and basic fibroblastic growth factor (a,b-FGF), angiogenin, vascular endothelial growth factor (VEGF), and TNF- α . Alternatively, tumor cells can release angiogenic peptides through the production of proteases and the subsequent breakdown of the extracellular matrix where some cytokines are stored (*e.g.*, b-FGF). Angiogenesis can also be induced indirectly through the recruitment of inflammatory cells (particularly macrophages) and their subsequent release of angiogenic cytokines (*e.g.*, TNF- α , b-FGF).

[0005] Lymphoma refers to cancers that originate in the lymphatic system. Lymphoma is characterized by malignant neoplasms of lymphocytes—B lymphocytes and T lymphocytes (*i.e.*, B-cells and T-cells). Lymphoma generally starts in lymph nodes or collections of lymphatic tissue in organs including, but not limited to, the stomach or intestines. Lymphoma may involve the marrow and the blood in some cases. Lymphoma may spread from one site to other parts of the body.

[0006] The treatment of various forms of lymphomas are described, for example, in U.S. patent no. 7,468,363, the entirety of which is incorporated herein by reference. Such lymphomas include, but are not limited to, Hodgkin's lymphoma, non-Hodgkin's lymphoma, cutaneous B-cell lymphoma, activated B-cell lymphoma, DLBCL, mantle cell lymphoma (MCL), follicular center lymphoma, transformed lymphoma, lymphocytic lymphoma of intermediate differentiation, intermediate lymphocytic lymphoma (ILL), diffuse poorly differentiated lymphocytic lymphoma (PDL), centrocytic lymphoma, diffuse small-cleaved cell lymphoma (DSCCL), peripheral T-cell lymphomas (PTCL), cutaneous T-Cell lymphoma and mantle zone lymphoma and low grade follicular lymphoma.

[0007] The non-Hodgkin lymphomas (NHLs) are a diverse group of blood cancers that include any kind of lymphoma except Hodgkin's lymphomas. Types of NHL vary significantly in their severity, from indolent to very aggressive. Less aggressive non-Hodgkin lymphomas are compatible with a long survival while more aggressive non-Hodgkin lymphomas can be rapidly fatal without

treatment, they can be formed from either B-cells or T-cells. B-cell non-Hodgkin lymphomas include Burkitt lymphoma, chronic lymphocytic leukemia/small lymphocytic lymphoma (CLL/SLL), diffuse large B-cell lymphoma, follicular lymphoma, immunoblastic large cell lymphoma, precursor B-lymphoblastic lymphoma, and mantle cell lymphoma. T-cell non-Hodgkin lymphomas include mycosis fungoides, anaplastic large cell lymphoma, and precursor T-lymphoblastic lymphoma. Prognosis and treatment depend on the stage and type of disease.

[0008] Diffuse large B-cell lymphoma (DLBCL) accounts for approximately one-third of non-Hodgkin's lymphomas. While some DLBCL patients are cured with traditional chemotherapy, the remainder die from the disease. Anticancer drugs cause rapid and persistent depletion of lymphocytes, possibly by direct apoptosis induction in mature T and B cells. *See* K. Stahnke, *et al.*, *Blood* 2001, 98:3066-3073. Absolute lymphocyte count (ALC) has been shown to be a prognostic factor in follicular non-Hodgkin's lymphoma and recent results have suggested that ALC at diagnosis is an important prognostic factor in diffuse large B-cell lymphoma.

[0009] The diffuse large-B-cell lymphomas (DLBCL) can be divided into distinct molecular subtypes according to their gene profiling patterns: germinal-center B-cell-like DLBCL (GCB-DLBCL), activated B-cell-like DLBCL (ABC-DLBCL), and primary mediastinal B-cell lymphoma (PMBL) or unclassified type. These subtypes are characterized by distinct differences in survival, chemo-responsiveness, and signaling pathway dependence, particularly the NF- κ B pathway. *See* D. Kim *et al.*, *Journal of Clinical Oncology*, 2007 ASCO Annual Meeting Proceedings Part I. Vol 25, No. 18S (June 20 Supplement), 2007: 8082. *See* Bea S, *et al.*, *Blood* 2005; 106: 3183-90; Ngo V.N. *et al.*, *Nature* 2011; 470: 115-9. Such differences have prompted the search for more effective and subtype-specific treatment strategies in DLBCL.

[0010] Leukemia refers to malignant neoplasms of the blood-forming tissues. Various forms of leukemias are described, for example, in U.S. patent no. 7,393,862 and U.S. provisional patent application no. 60/380,842, filed May 17, 2002, the entireties of which are incorporated herein by reference. Although viruses reportedly cause several forms of leukemia in animals, causes of leukemia in humans are to a large extent unknown. *The Merck Manual*, 944-952 (17th ed. 1999). Transformation to malignancy typically occurs in a single cell through two or more steps with subsequent proliferation and clonal expansion. In some leukemias, specific chromosomal translocations have been identified with consistent leukemic cell morphology and special clinical features (*e.g.*, translocations of 9 and 22 in chronic myelocytic leukemia, and of 15 and 17 in acute

promyelocytic leukemia). Acute leukemias are predominantly undifferentiated cell populations and chronic leukemias more mature cell forms.

[0011] Acute leukemias are divided into lymphoblastic (ALL) and non-lymphoblastic (ANLL) types. *The Merck Manual*, 946-949 (17th ed. 1999). They may be further subdivided by their morphologic and cytochemical appearance according to the French-American-British (FAB) classification or according to their type and degree of differentiation. The use of specific B- and T-cell and myeloid-antigen monoclonal antibodies are most helpful for classification. ALL is predominantly a childhood disease which is established by laboratory findings and bone marrow examination. ANLL, also known as acute myelogenous leukemia or acute myeloid leukemia (AML), occurs at all ages and is the more common acute leukemia among adults; it is the form usually associated with irradiation as a causative agent.

[0012] Chronic leukemias are described as being lymphocytic (CLL) or myelocytic (CML). *The Merck Manual*, 949-952 (17th ed. 1999). CLL is characterized by the appearance of mature lymphocytes in blood, bone marrow, and lymphoid organs. The hallmark of CLL is sustained, absolute lymphocytosis ($> 5,000/\mu\text{L}$) and an increase of lymphocytes in the bone marrow. Most CLL patients also have clonal expansion of lymphocytes with B-cell characteristics. CLL is a disease of middle or old age. In CML, the characteristic feature is the predominance of granulocytic cells of all stages of differentiation in blood, bone marrow, liver, spleen, and other organs. In the symptomatic patient at diagnosis, the total white blood cell (WBC) count is usually about $200,000/\mu\text{L}$, but may reach $1,000,000/\mu\text{L}$. CML is relatively easy to diagnose because of the presence of the Philadelphia chromosome.

[0013] Bone marrow stromal cells are well known to support CLL disease progression and resistance to chemotherapy. Disrupting the interactions between CLL cells and stromal cells is an additional target of CLL chemotherapy.

[0014] In addition to the acute and chronic categorization, neoplasms are also categorized based upon the cells giving rise to such disorder into precursor or peripheral. *See e.g.*, U.S. patent publication no. 2008/0051379, the disclosure of which is incorporated herein by reference in its entirety. Precursor neoplasms include ALLs and lymphoblastic lymphomas and occur in lymphocytes before they have differentiated into either a T- or B-cell. Peripheral neoplasms are those that occur in lymphocytes that have differentiated into either T- or B-cells. Such peripheral neoplasms include, but are not limited to, B-cell CLL, B-cell prolymphocytic leukemia, lymphoplasmacytic lymphoma, mantle cell lymphoma, follicular lymphoma, extranodal marginal

zone B-cell lymphoma of mucosa-associated lymphoid tissue, nodal marginal zone lymphoma, splenic marginal zone lymphoma, hairy cell leukemia, plasmacytoma, diffuse large B-cell lymphoma and Burkitt lymphoma. In over 95 percent of CLL cases, the clonal expansion is of a B cell lineage. *See Cancer: Principles & Practice of Oncology* (3rd Edition) (1989) (pp. 1843-1847). In less than 5 percent of CLL cases, the tumor cells have a T-cell phenotype. Notwithstanding these classifications, however, the pathological impairment of normal hematopoiesis is the hallmark of all leukemias.

[0015] Multiple myeloma (MM) is a cancer of plasma cells in the bone marrow. Normally, plasma cells produce antibodies and play a key role in immune function. However, uncontrolled growth of these cells leads to bone pain and fractures, anemia, infections, and other complications. Multiple myeloma is the second most common hematological malignancy, although the exact causes of multiple myeloma remain unknown. Multiple myeloma causes high levels of proteins in the blood, urine, and organs, including but not limited to M-protein and other immunoglobulins (antibodies), albumin, and beta-2-microglobulin. M-protein, short for monoclonal protein, also known as paraprotein, is a particularly abnormal protein produced by the myeloma plasma cells and can be found in the blood or urine of almost all patients with multiple myeloma.

[0016] Skeletal symptoms, including bone pain, are among the most clinically significant symptoms of multiple myeloma. Malignant plasma cells release osteoclast stimulating factors (including IL-1, IL-6 and TNF) which cause calcium to be leached from bones causing lytic lesions; hypercalcemia is another symptom. The osteoclast stimulating factors, also referred to as cytokines, may prevent apoptosis, or death of myeloma cells. Fifty percent of patients have radiologically detectable myeloma-related skeletal lesions at diagnosis. Other common clinical symptoms for multiple myeloma include polyneuropathy, anemia, hyperviscosity, infections, and renal insufficiency.

[0017] Bone marrow stromal cells are well known to support multiple myeloma disease progression and resistance to chemotherapy. Disrupting the interactions between multiple myeloma cells and stromal cells is an additional target of multiple myeloma chemotherapy.

[0018] Further, rituximab is known to deplete normal host B cells. M. Aklilu et al., *Annals of Oncology* 15:1109-1114, 2004. The long-term immunologic effects of B cell depletion with rituximab and the characteristics of the reconstituting B cell pool in lymphoma patients are not well defined, despite the widespread usage of this therapy. *See Jennifer H. Anolik et al., Clinical Immunology*, vol. 122, issue 2, February 2007, pages 139-145.

[0019] The approach for patients with relapsed or refractory disease relies heavily on experimental treatments followed by stem cell transplantation, which may not be appropriate for patients with a poor performance status or advanced age. Therefore, a tremendous demand exists for new methods that can be used to treat patients with NHL.

[0020] The incidence of cancer continues to climb as the general population ages, as new cancers develop, and as susceptible populations (e.g., people infected with AIDS or excessively exposed to sunlight) grow. A tremendous demand therefore exists for new methods and compositions that can be used to treat patients with cancer including NHL.

2.2. Methods of Treatment

[0001] Current cancer therapy may involve surgery, chemotherapy, hormonal therapy and/or radiation treatment to eradicate neoplastic cells in a patient (see, for example, Stockdale, 1998, *Medicine*, vol. 3, Rubenstein and Federman, eds., Chapter 12, Section IV). Recently, cancer therapy could also involve biological therapy or immunotherapy. All of these approaches pose significant drawbacks for the patient. Surgery, for example, may be contraindicated due to the health of a patient or may be unacceptable to the patient. Additionally, surgery may not completely remove neoplastic tissue. Radiation therapy is only effective when the neoplastic tissue exhibits a higher sensitivity to radiation than normal tissue. Radiation therapy can also often elicit serious side effects. Hormonal therapy is rarely given as a single agent. Although hormonal therapy can be effective, it is often used to prevent or delay recurrence of cancer after other treatments have removed the majority of cancer cells. Biological therapies and immunotherapies are limited in number and may produce side effects such as rashes or swellings, flu-like symptoms, including fever, chills and fatigue, digestive tract problems or allergic reactions.

[0002] With respect to chemotherapy, there are a variety of chemotherapeutic agents available for treatment of cancer. A majority of cancer chemotherapeutics act by inhibiting DNA synthesis, either directly, or indirectly by inhibiting the biosynthesis of deoxyribonucleotide triphosphate precursors, to prevent DNA replication and concomitant cell division. Gilman et al., *Goodman and Gilman's: The Pharmacological Basis of Therapeutics*, Tenth Ed. (McGraw Hill, New York).

[0003] Despite availability of a variety of chemotherapeutic agents, chemotherapy has many drawbacks. Stockdale, *Medicine*, vol. 3, Rubenstein and Federman, eds., ch. 12, sect. 10, 1998. Almost all chemotherapeutic agents are toxic, and chemotherapy causes significant, and often

dangerous side effects including severe nausea, bone marrow depression, and immunosuppression. Additionally, even with administration of combinations of chemotherapeutic agents, many tumor cells are resistant or develop resistance to the chemotherapeutic agents. In fact, those cells resistant to the particular chemotherapeutic agents used in the treatment protocol often prove to be resistant to other drugs, even if those agents act by different mechanism from those of the drugs used in the specific treatment. This phenomenon is referred to as pleiotropic drug or multidrug resistance. Because of the drug resistance, many cancers prove refractory to standard chemotherapeutic treatment protocols.

[0004] Still, there is a significant need for safe and effective methods of treating, preventing and managing cancer, particularly for tumors that are refractory to standard treatments, such as surgery, radiation therapy, chemotherapy and hormonal therapy, while reducing or avoiding the toxicities and/or side effects associated with the conventional therapies. Moreover, there remains a need for the ability to predict and monitor response to cancer therapy in order to increase the quality of care for cancer patients, avoid unnecessary treatment and to increase the success rate in cancer therapy in clinical practice.

3. SUMMARY

[0021] The present invention is based, in part, on the finding that certain genes are differentially expressed in DLBCL patients responsive to the immunomodulatory therapy lenalidomide (Revlimid®) relative to DLBCL patients unresponsive to lenalidomide. In addition, the present invention is based, in part, on the finding that the cellular composition (*e.g.*, immune cell composition) of the tumor of a DLBCL patient may be indicative of whether the patient tumor will respond to an immunomodulatory therapy, such as lenalidomide, including its pharmaceutically acceptable salts, solvates or isomers.

[0022] In one aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 3, *infra*, (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 3 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having the same type of hematological cancer as the first

patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and wherein the differential expression of the one, two, three, four, five or more of the genes in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0023] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 4, *infra*, (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 4 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and wherein the differential expression of the one, two, three, four, five or more of the genes in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an

immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0024] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 1, *infra*, and (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 1 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to the immunomodulatory therapy, and wherein a higher level of expression of the one, two, three, four, five or more of the genes in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is refractory relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0025] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 2, *infra*, and (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in

Table 2 in the first biological sample with the level of expression of the same genes in a second biological sample is from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to the immunomodulatory therapy, and wherein a lower level of expression of the one, two, three, four, five or more of the genes in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0026] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 1, *infra*, and measuring the level of expression one, two, three, four, five or more of the genes identified in Table 2, *infra*, and (c) comparing the level of expression of the genes identified in Tables 1 and 2 in the first biological sample with the level of expression of the same genes in a second biological sample is from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to the immunomodulatory therapy, and wherein (i) a higher level of expression of the one, two, three, four, five or more of the genes identified in Table 1 in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample, and (ii) a lower level of expression of the one, two, three, four, five or more of the genes identified in Table 2 in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample, indicates that the hematological cancer in the first patient

will be clinical sensitive to treatment with the immunomodulatory therapy. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0027] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 1, 2, 3 or 4, or any combination thereof in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the genes or subset of genes in the first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy, and a gene expression profile for the genes or subset of genes in first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy indicates that the hematological cancer of the first patient will be clinically insensitive to the treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 1, 2, 3 or 4, or any combination thereof. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 1, 2, 3 or 4, or any combination thereof. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-

cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0028] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of dendritic cells in the first tumor sample, and (c) comparing the proportion of dendritic cells in the first tumor sample with the proportion of dendritic cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with the immunomodulatory therapy, and wherein a higher proportion of dendritic cells in the first tumor sample relative the proportion of dendritic cells in the second tumor sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0029] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of plasma cells in the first tumor sample, and (c) comparing the proportion of plasma cells in the first tumor sample with the proportion of plasma cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with the immunomodulatory therapy, and

wherein a higher proportion of plasma cells in the first tumor sample relative the proportion of plasma cells in the second tumor sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0030] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of dendritic cells and plasma cells in the first tumor sample, and (c) comparing the proportion of dendritic cells and plasma cells in the first tumor sample with the proportion of dendritic cells and plasma cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with the immunomodulatory therapy, and wherein a higher proportion of dendritic cells and plasma cells in the first tumor sample relative the proportion of dendritic cells and plasma cells in the second tumor sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0031] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having a hematological cancer, (b) measuring the proportion of immune cells in the tumor sample, and (c) comparing the proportion of the immune cells in the first tumor sample to (i) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a proportion of the immune cells in the first tumor sample similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy, and a proportion of the immune cells in the first tumor sample similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical insensitive to treatment with the immunomodulatory therapy. In some embodiments, the immune cells are subset of immune cells, such as subset of B cells. In certain embodiments, the immune cells are dendritic cells. In some embodiments, the immune cells are plasma cells. In certain embodiments, the immune cells are monocytes. In some embodiments, the immune cells are tumor infiltrating immune cells. In certain embodiments, the immune cells are T cells. In some embodiments, the immune cells are B cells. In certain embodiments, the immune cells are NK cells. In some embodiments, the immune cells are two, three or more subsets of immune cells, such as two more types of T cells (*e.g.*, CD4+ and CD8+ T cells). In some embodiments, the proportion of different populations of immune cells in the first tumor sample are compared to (i) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like

subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0032] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 3, *infra*, (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 3 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the one, two, three, four, five or more of the genes in the first biological sample are differentially expressed relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0033] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 4, *infra*, (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 4 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having the same

type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the one, two, three, four, five or more of the genes in the first biological sample are differentially expressed relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0034] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 1, *infra*, (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 1 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a higher level of expression of the one, two, three, four, five or more of the genes in the first biological sample is measured relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise

lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0035] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 2, *infra*, (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 2 in the first biological sample with the level of expression of the same genes in a second biological sample is from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a lower level of expression of the one, two, three, four, five or more of the genes in the first biological sample is measured relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample. In certain embodiments, the immunomodulatory therapy is not administered or additional assays are conducted if the level of expression of one, two, three, four, five or more of the genes are not lower in the first biological sample than in the second biological sample. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0036] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 1, *infra*, and measuring the level of expression one, two, three, four, five or more of the genes identified in Table 2, *supra*, (c) comparing the level of expression of the genes identified in Tables 1 and 2 in the first biological sample with the level of expression of the same genes in a second biological sample is from a second patient having the same type of

hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and (d) administering the immunomodulatory to the first patient if (i) a higher level of expression of the one, two, three, four, five or more of the genes identified in Table 1 in the first biological sample is measured relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample, and (ii) a lower level of expression of the one, two, three, four, five or more of the genes identified in Table 2 in the first biological sample is measured relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0037] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of a certain subset of genes set forth in Table 1, 2, 3 or 4, or any combination thereof in the first biological sample, and (c) comparing the gene expression profile of the subset of genes in the first biological sample to (i) the gene expression profile of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if: (i) the gene expression profile for the subset of genes in the first biological sample is similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the gene expression profile for the subset of genes in first biological sample is not similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically

insensitive to the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 1, 2, 3 or 4, or any combination thereof. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 1, 2, 3 or 4, or any combination thereof. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0038] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of dendritic cells in the first tumor sample, (c) comparing the proportion of dendritic cells in the first tumor sample with the proportion of dendritic cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a higher proportion of dendritic cells in the first tumor sample is measured relative the proportion of dendritic cells in the second tumor sample. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0039] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of plasma cells in the first tumor sample, (c) comparing the proportion of plasma cells in the first tumor sample with the proportion of plasma cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the

second patient's hematological cancer is clinically insensitive to treatment with an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a higher proportion of plasma cells in the first tumor sample is measured relative the proportion of plasma cells in the second tumor sample. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0040] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of dendritic cells and plasma cells in the first tumor sample, (c) comparing the proportion of dendritic cells and plasma cells in the first tumor sample with the proportion of dendritic cells and plasma cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a higher proportion of dendritic cells and plasma cells in the first tumor sample is measured relative the proportion of dendritic cells and plasma cells in the second tumor sample. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0041] In another aspect, provided herein are for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having a hematological cancer, (b) measuring the proportion of immune cells in the first tumor sample, and (c) comparing the proportion of the immune cells in the first tumor sample to (i) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the proportion of the immune cells in the first tumor sample is (i) similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy, and (ii) not similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy. In some embodiments, the immune cells are subset of immune cells, such as subset of B cells. In certain embodiments, the immune cells are dendritic cells. In some embodiments, the immune cells are plasma cells. In certain embodiments, the immune cells are monocytes. In some embodiments, the immune cells are tumor infiltrating immune cells. In certain embodiments, the immune cells are T cells. In some embodiments, the immune cells are B cells. In certain embodiments, the immune cells are NK cells. In some embodiments, the immune cells are two, three or more subsets of immune cells, such as two more types of T cells (*e.g.*, CD4+ and CD8+ T cells). In some embodiments, the proportion of different populations of immune cells in the first tumor sample are compared to (i) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy. In a specific embodiment, the hematological cancer is DLBCL. In certain embodiments, the DLBCL is refractory to certain therapies, such as chemotherapy. In some embodiments, the DLBCL is relapsed in a patient. In a specific embodiment, the DLBCL is an activated B-cell-like subtype. In another specific embodiment, the DLBCL is a germinal center B-cell-like subtype. The immunomodulatory therapy can comprise the administration of an immunomodulatory compound, such as lenalidomide, or its pharmaceutically acceptable salts, solvates or isomers. An

immunomodulatory therapy of the embodiments of the methods provided herein can comprise lenalidomide as immunomodulatory compound, or its pharmaceutically acceptable salts, solvates or isomers. In another specific embodiment, the immunomodulatory therapy is lenalidomide.

[0042] In accordance with the methods described herein, the biological sample can be any sample obtained from the patient. In certain embodiments, the biological sample is a cell sample. In other embodiments, the biological sample is whole blood sample, peripheral blood mononuclear cell sample, or tissue sample. In specific embodiments, the biological sample is a tumor sample. See Section 5.8, *infra*, regarding biological samples.

[0043] In accordance with the methods described herein, the level of expression of one, two, three, four, five or more of the genes in Table 1 and/or Table 2 and/or Table 3 and/or Table 4, *infra*, can be measured at the RNA and/or protein levels. In certain embodiments, the level of expression of the genes are measured at the RNA (*e.g.*, mRNA) level. In other embodiments, the level of expression of the genes are measured at the protein level.

[0044] In another aspect, provided herein are kits useful for predicting the likelihood of an effective patient tumor response. In certain embodiments, the kit comprises a solid support, and a means for detecting the protein expression of at least one biomarker in a biological sample. Such a kit may employ, for example, a dipstick, a membrane, a chip, a disk, a test strip, a filter, a microsphere, a slide, a multiwell plate, or an optical fiber. The solid support of the kit can be, for example, a plastic, silicon, a metal, a resin, glass, a membrane, a particle, a precipitate, a gel, a polymer, a sheet, a sphere, a polysaccharide, a capillary, a film, a plate, or a slide. In some embodiments, the kit comprises a solid support, nucleic acids contacting the support, where the nucleic acids are complementary to at least 20, 50, 100, 200, 350, or more bases of mRNA, and a means for detecting the expression of the mRNA in a biological sample.

[0045] In certain embodiments, the kits provided herein employ means for detecting the expression of a biomarker by quantitative real-time PCR (QRT-PCR), microarray, flow cytometry or immunofluorescence. In other embodiments, the expression of the biomarker is measured by ELISA-based methodologies or other similar methods known in the art.

4. BRIEF DESCRIPTION OF THE FIGURES

[0046] **FIG. 1:** Hierarchical clustering (Euclidean distance; Ward linkage) of relative gene expression across 21 lenalidomide/Revlimid®-arm FF profiles, as represented by A. 1018 genes deemed significantly differentially regulated at FDR5%, and B. A subset of those genes deemed

significantly differentially regulated at FDR1%, between discrete best-response categories. Gene expressions standardized to zero mean and unit standard variance across all profiles. Bars below dendrogram display: DLBCL cell of origin sub-type {GCB (white), ABC/Other (black), as determined by IHC at screen}; Investigator defined best response of patients in the Revlimid arm, {CR,PR,SD} (black) vs. {PD,Death} (white).

[0047] **FIG. 2:** Decomposition of 21 lenalidomide/Revlimid®-arm profiles derived from FF samples. Each boxplot represents estimated proportion (y-axis) of corresponding cell phenotype (x-axis) across two discrete Investigator defined best-response categories, {CR,PR,SD} (grey) and {PD,death} (white). Cell-types on the x-axis are: T-helper cells (Th); Activated T-helper cells (Th act); T-cells (Tc); Activated T-cells (Tc act); B-cells (B); Activated B-cells (B act); BCR-ligated B-cells (B aIgM); IgG Memory B-cells (Mem IgG); IgM Memory B-cells (Mem IgM); Plasma cells (PC); Natural Killer cells (NK); Activated Natural Killer cells (NK act); Monocytes (mono); Activated Monocytes (mono act); Dendritic Cells (DC); Activated Dendritic cells (DC act); Neutrophils (neutro). Phenotypic cell types defined in (Abbas et al., PLoS One, 2009).

[0048] **FIG. 3:** Summed estimated proportion of resting and activated dendritic cells (y-axis, left) across 21 lenalidomide/Revlimid®-arm profiles derived from FF samples (x-axis; triangles, ordered by descending PFS). PFS (y-axis, right; unit weeks) overlaid as line-connected points, with censor events denoted by a cross.

[0049] **FIG. 4:** Summed estimated proportion of BCR-ligated B-cells (y-axis, left) across 21 lenalidomide/Revlimid®-arm profiles derived from FF samples (x-axis; triangles, ordered by descending PFS). PFS (y-axis, right; unit weeks) overlaid as line-connected points, with censor events denoted by a cross.

[0050] **FIG. 5:** Bar plot of difference in estimated proportion of BCR-ligated B-cells and plasma cells (y-axis, left), derived from lenalidomide/Revlimid®-arm FF profiles (one profile per bar, x-axis; sorted in order of increasing difference between BCR-ligated B-cell/plasma-cell proportions. PFS (y-axis, right; unit weeks) overlaid as line-connected points, with censor events denoted by a cross. Dashed line represents median PFS in the two groups defined by estimated BCR-ligated B-cell proportion being greater or less than estimated plasma cell proportion.

5. DETAILED DESCRIPTION

5.1 Terminology

[0051] As used herein, and unless otherwise specified, the terms “treat,” “treating” and “treatment” refer to an action that occurs while a patient is suffering from the specified cancer, which includes the reduction in the severity of the cancer, reduces tumor size, or retards or slows the progression of the cancer.

[0052] The term “sensitivity” and “sensitive” when made in reference to treatment with compound is a relative term which refers to the degree of effectiveness of the compound in lessening or decreasing the progress of a tumor or the disease being treated.

[0053] As used herein, and unless otherwise specified, the term “effective amount” of a compound is an amount sufficient to provide a therapeutic benefit in the treatment or management of a cancer, or to delay or minimize one or more symptoms associated with the presence of the cancer. An effective amount of a compound means an amount of therapeutic agent, alone or in combination with other therapies, which provides a therapeutic benefit in the treatment or management of the cancer. The term “effective amount” can encompass an amount that improves overall therapy, reduces or avoids symptoms or causes of cancer, or enhances the therapeutic efficacy of another therapeutic agent.

[0054] As used herein, an “effective patient tumor response” refers to any increase in the therapeutic benefit to the patient. An “effective patient tumor response” can be, for example, a 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% decrease in the rate of progress of the tumor. An “effective patient tumor response” can be, for example, a 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% decrease in the physical symptoms of a cancer. An “effective patient tumor response” can be, for example, a 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% decrease in the size of a tumor. An “effective patient tumor response” can be, for example, a 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% decrease in the physical symptoms of a cancer. An “effective patient tumor response” can also be, for example, a 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100% , or 200%, or more increase in the response of the patient, as measured by any suitable means, such as gene expression, cell counts, assay results, *etc.*

[0055] The term “likelihood” generally refers to an increase in the probability of an event. The term “likelihood” when used in reference to the effectiveness of a patient tumor response generally

contemplates an increased probability that the rate of tumor progress or tumor cell growth will decrease. The term “likelihood” when used in reference to the effectiveness of a patient tumor response can also generally mean the increase of indicators, such as mRNA or protein expression, that may evidence an increase in the progress in treating the tumor.

[0056] The term “predict” generally means to determine or tell in advance. When used to “predict” the effectiveness of a cancer treatment, for example, the term “predict” can mean that the likelihood of the outcome of the cancer treatment can be determined at the outset, before the treatment has begun, or before the treatment period has progressed substantially.

[0057] An improvement in the cancer or cancer-related disease can be characterized as a complete or partial response. “Complete response” refers to an essential absence (or absence) of clinically detectable disease with normalization of any previously abnormal radiographic studies, bone marrow, and cerebrospinal fluid (CSF) or abnormal monoclonal protein measurements. “Partial response” refers to at least about a 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% decrease in all measurable tumor burden (*i.e.*, the number of malignant cells present in the subject, or the measured bulk of tumor masses or the quantity of abnormal monoclonal protein) in the absence of new lesions. The term “treatment” contemplates both a complete and a partial response.

[0058] “Tumor,” as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues. “Neoplastic,” as used herein, refers to any form of dysregulated or unregulated cell growth, whether malignant or benign, resulting in abnormal tissue growth. Thus, “neoplastic cells” include malignant and benign cells having dysregulated or unregulated cell growth.

[0059] The terms “cancer” and “cancerous” refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, blood-borne tumors (*e.g.*, multiple myeloma, lymphoma and leukemia), and solid tumors.

[0060] The term “refractory or resistant” refers to a circumstance where patients, even after intensive treatment, have residual cancer cells (*e.g.*, leukemia or lymphoma cells) in their lymphatic system, blood and/or blood forming tissues (*e.g.*, marrow).

[0061] As used herein the terms “polypeptide” and “protein” as used interchangeably herein, refer to a polymer of amino acids of three or more amino acids in a serial array, linked through peptide bonds. The term “polypeptide” includes proteins, protein fragments, protein analogues,

oligopeptides and the like. The term polypeptide as used herein can also refer to a peptide. The amino acids making up the polypeptide may be naturally derived, or may be synthetic. The polypeptide can be purified from a biological sample.

[0062] An mRNA that is “upregulated” is generally increased upon a given treatment or condition. An mRNA that is “downregulated” generally refers to a decrease in the level of expression of the mRNA in response to a given treatment or condition. In some situations, the mRNA level can remain unchanged upon a given treatment or condition.

[0063] An mRNA from a patient sample can be “upregulated” when treated with an immunomodulatory therapy, as compared to a control. This upregulation can be, for example, an increase of about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 90%, 100%, 200%, 300%, 500%, 600%, 700%, 800%, 900%, 1,000%, 1,500%, 2,000%, 2,500%, 3,00%, 3,500%, 4,000%, 4,500%, 5,000% or more of the comparative control mRNA level.

[0064] Alternatively, an mRNA can be “downregulated”, or expressed at a lower level, in response to administration of certain immunomodulatory therapies or other therapies. A downregulated mRNA can be, for example, present at a level of about 99%, 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, 3%, 1% or less of the comparative control mRNA level.

[0065] Similarly, the level of a polypeptide or protein biomarker from a patient sample can be increased when treated with an immunomodulatory therapy, as compared to a non-treated control. This increase can be about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 200%, 300%, 400%, 500%, 700%, 1,000%, 1,500%, 2,000%, 2,500%, 3,000%, 3,500%, 4,000%, 4,500%, 5,000% or more of the comparative control protein level.

[0066] Alternatively, the level of a protein biomarker can be decreased in response to administration of certain immunomodulatory therapies or other agents. This decrease can be, for example, present at a level of about 99%, 95%, 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 10%, 5%, 3%, 1% or less of the comparative control protein level.

[0067] The terms “determining”, “measuring”, “evaluating”, “assessing” and “assaying” as used herein generally refer to any form of measurement, and include determining if an element is present or not. These terms include both quantitative and/or qualitative determinations. Assessing may be relative or absolute. “Assessing the presence of” can include determining the amount of something present, as well as determining whether it is present or absent.

[0068] The terms “nucleic acid” and “polynucleotide” are used interchangeably herein to describe a polymer of any length composed of nucleotides, *e.g.*, deoxyribonucleotides or ribonucleotides, or compounds produced synthetically, which can hybridize with naturally occurring nucleic acids in a sequence specific manner analogous to that of two naturally occurring nucleic acids, *e.g.*, can participate in Watson-Crick base pairing interactions. As used herein in the context of a polynucleotide sequence, the term “bases” (or “base”) is synonymous with “nucleotides” (or “nucleotide”), *i.e.*, the monomer subunit of a polynucleotide. The terms “nucleoside” and “nucleotide” are intended to include those moieties that contain not only the known purine and pyrimidine bases, but also other heterocyclic bases that have been modified. Such modifications include methylated purines or pyrimidines, acylated purines or pyrimidines, alkylated riboses or other heterocycles. In addition, the terms “nucleoside” and “nucleotide” include those moieties that contain not only conventional ribose and deoxyribose sugars, but other sugars as well. Modified nucleosides or nucleotides also include modifications on the sugar moiety, *e.g.*, wherein one or more of the hydroxyl groups are replaced with halogen atoms or aliphatic groups, or are functionalized as ethers, amines, or the like. “Analogues” refer to molecules having structural features that are recognized in the literature as being mimetics, derivatives, having analogous structures, or other like terms, and include, for example, polynucleotides incorporating non-natural nucleotides, nucleotide mimetics such as 2'-modified nucleosides, peptide nucleic acids, oligomeric nucleoside phosphonates, and any polynucleotide that has added substituent groups, such as protecting groups or linking moieties.

[0069] The terms “isolated” and “purified” refer to isolation of a substance (such as mRNA or protein) such that the substance comprises a substantial portion of the sample in which it resides, *i.e.* greater than the substance is typically found in its natural or un-isolated state. Typically, a substantial portion of the sample comprises, *e.g.*, greater than 1%, greater than 2%, greater than 5%, greater than 10%, greater than 20%, greater than 30%, greater than 50%, or more, usually up to about 90%-100% of the sample. For example, a sample of isolated mRNA can typically comprise at least about 1% total mRNA. Techniques for purifying polynucleotides are well known in the art and include, for example, gel electrophoresis, ion-exchange chromatography, affinity chromatography, flow sorting, and sedimentation according to density.

[0070] The term “sample” as used herein relates to a material or mixture of materials, typically, although not necessarily, in fluid form, containing one or more components of interest.

[0071] “Biological sample” as used herein refers to a sample obtained from a biological subject, including sample of biological tissue or fluid origin, obtained, reached, or collected *in vivo* or *in situ*. A biological sample also includes samples from a region of a biological subject containing precancerous or cancer cells or tissues. Such samples can be, but are not limited to, organs, tissues, fractions and cells isolated from a subject. Exemplary biological samples include but are not limited to cell lysate, a cell culture, a cell line, a tissue, oral tissue, gastrointestinal tissue, an organ, an organelle, a biological fluid, a blood sample, a urine sample, a skin sample, and the like. Preferred biological samples include but are not limited to whole blood, partially purified blood, PBMCs, tissue biopsies, and the like.

[0072] As used herein, the terms “patient” and “subject” refer to an animal, such as a mammal. In a specific embodiment, the patient is a human. In other embodiments, the patient is a non-human animal, such as a dog, cat, farm animal (*e.g.*, horse, pig, or donkey), chimpanzee, or monkey.

[0073] A biological marker or “biomarker” is a substance whose detection indicates a particular biological state, such as, for example, the presence of cancer. In some embodiments, biomarkers can either be determined individually, or several biomarkers can be measured simultaneously.

[0074] A “biomarker” can indicate a change in the level of mRNA expression that may correlate with the risk or progression of a disease, or with the susceptibility of the disease to a given treatment. In some embodiments, the biomarker is a nucleic acid, such as a mRNA or cDNA.

[0075] A “biomarker” can also indicate a change in the level of polypeptide or protein expression that may correlate with the risk, susceptibility to treatment, or progression of a disease. The biomarker can be a polypeptide or protein, or a fragment thereof. The relative level of specific proteins can be determined by methods known in the art. For example, antibody based methods, such as an immunoblot, enzyme-linked immunosorbent assay (ELISA), or other methods can be used.

[0076] As used herein and unless otherwise indicated, the term “pharmaceutically acceptable salt” encompasses non-toxic acid and base addition salts of the compound to which the term refers. Acceptable non-toxic acid addition salts include those derived from organic and inorganic acids or bases known in the art, which include, for example, hydrochloric acid, hydrobromic acid, phosphoric acid, sulfuric acid, methanesulphonic acid, acetic acid, tartaric acid, lactic acid, succinic acid, citric acid, malic acid, maleic acid, sorbic acid, aconitic acid, salicylic acid, phthalic acid, embolic acid, enanthic acid, and the like.

[0077] Compounds that are acidic in nature are capable of forming salts with various pharmaceutically acceptable bases. The bases that can be used to prepare pharmaceutically acceptable base addition salts of such acidic compounds are those that form non-toxic base addition salts, *i.e.*, salts containing pharmacologically acceptable cations such as, but not limited to, alkali metal or alkaline earth metal salts and the calcium, magnesium, sodium or potassium salts in particular. Suitable organic bases include, but are not limited to, N,N-dibenzylethylenediamine, chlorprocaine, choline, diethanolamine, ethylenediamine, meglumine (N-methylglucamine), lysine, and procaine.

[0078] As used herein and unless otherwise indicated, the term “solvate” means a compound provided herein or a salt thereof, that further includes a stoichiometric or non-stoichiometric amount of solvent bound by non-covalent intermolecular forces. Where the solvent is water, the solvate is a hydrate.

[0079] As used herein and unless otherwise indicated, the term “stereomerically pure” means a composition that comprises one stereoisomer of a compound and is substantially free of other stereoisomers of that compound. For example, a stereomerically pure composition of a compound having one chiral center will be substantially free of the opposite enantiomer of the compound. A stereomerically pure composition of a compound having two chiral centers will be substantially free of other diastereomers of the compound. A typical stereomerically pure compound comprises greater than about 80% by weight of one stereoisomer of the compound and less than about 20% by weight of other stereoisomers of the compound, more preferably greater than about 90% by weight of one stereoisomer of the compound and less than about 10% by weight of the other stereoisomers of the compound, even more preferably greater than about 95% by weight of one stereoisomer of the compound and less than about 5% by weight of the other stereoisomers of the compound, and most preferably greater than about 97% by weight of one stereoisomer of the compound and less than about 3% by weight of the other stereoisomers of the compound. As used herein and unless otherwise indicated, the term “stereomerically enriched” means a composition that comprises greater than about 60% by weight of one stereoisomer of a compound, preferably greater than about 70% by weight, more preferably greater than about 80% by weight of one stereoisomer of a compound. As used herein and unless otherwise indicated, the term “enantiomerically pure” means a stereomerically pure composition of a compound having one chiral center. Similarly, the term “stereomerically enriched” means a stereomerically enriched composition of a compound having one chiral center.

[0080] It should be noted that if there is a discrepancy between a depicted structure and a name given that structure, the depicted structure is to be accorded more weight. In addition, if the stereochemistry of a structure or a portion of a structure is not indicated with, for example, bold or dashed lines, the structure or portion of the structure is to be interpreted as encompassing all stereoisomers of it.

[0081] The practice of the embodiments provided herein will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, and immunology, which are within the skill of those working in the art. Such techniques are explained fully in the literature. Examples of particularly suitable texts for consultation include the following: Sambrook *et al.* (1989) *Molecular Cloning; A Laboratory Manual* (2d ed.); D.N. Glover, ed. (1985) *DNA Cloning*, Volumes I and II; M.J. Gait, ed. (1984) *Oligonucleotide Synthesis*; B.D. Hames & S.J. Higgins, eds. (1984) *Nucleic Acid Hybridization*; B.D. Hames & S.J. Higgins, eds. (1984) *Transcription and Translation*; R.I. Freshney, ed. (1986) *Animal Cell Culture; Immobilized Cells and Enzymes* (IRL Press, 1986); *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes (1987) *Protein Purification: Principles and Practice* (2d ed.; Springer Verlag, N.Y.); and D.M. Weir and C. C. Blackwell, eds. (1986) *Handbook of Experimental Immunology*, Volumes I-IV.

5.2 Methods for Predicting Clinical Sensitivity of a Hematological Cancer By Measuring Gene Expression

[0082] In one aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 3 or 4, *infra*, (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 3 or 4 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and wherein the differential expression of the one, two, three, four, five or more of the genes in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample indicates that the

hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy.

[0083] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 1, *infra*, and (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 1 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to the immunomodulatory therapy, and wherein a higher level of expression of the one, two, three, four, five or more of the genes in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy.

[0084] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 2, *infra*, and (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 2 in the first biological sample with the level of expression of the same genes in a second biological sample is from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to the immunomodulatory therapy, and wherein a lower level of expression of the one, two, three, four, five or more of the genes in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy.

[0085] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 1, *infra*, and

measuring the level of expression one, two, three, four, five or more of the genes identified in Table 2, *infra*, and (c) comparing the level of expression of the genes identified in Tables 1 and 2 in the first biological sample with the level of expression of the same genes in a second biological sample is from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to the immunomodulatory therapy, and wherein (i) a higher level of expression of the one, two, three, four, five or more of the genes identified in Table 1 in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample, and (ii) a lower level of expression of the one, two, three, four, five or more of the genes identified in Table 2 in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample, indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy.

[0086] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining biological samples from patients having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 3, *infra*, (c) assessing expression levels of the selected genes, either individually, conjointly, or via a functional transformation thereof, and (d) using of the expression levels to predict patients as sensitive or insensitive to an immunomodulatory therapy, via similarity to expression phenotypes displayed across the same genes by patients with the same indication and already known to be sensitive or insensitive to that therapy.

[0087] In one aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining biological samples from patients having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 4, *infra*, (c) assessing expression levels of the selected genes, either individually, conjointly, or via a functional transformation thereof, and (d) using of the expression levels to predict patients as sensitive or insensitive to an immunomodulatory therapy, via similarity to expression phenotypes displayed across the same genes by patients with the same indication and already known to be sensitive or insensitive to that therapy.

[0088] In one aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining

biological samples from patients having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 1, *infra*, (c) assessing expression levels of the selected genes, either individually, conjointly, or via a functional transformation thereof, and (d) using of the expression levels to predict patients as sensitive or insensitive to an immunomodulatory therapy, via similarity to expression phenotypes displayed across the same genes by patients with the same indication and already known to be sensitive or insensitive to that therapy.

[0089] In one aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining biological samples from patients having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 2, *infra*, (c) assessing expression levels of the selected genes, either individually, conjointly, or via a functional transformation thereof, and (d) using of the expression levels to predict patients as sensitive or insensitive to an immunomodulatory therapy, via similarity to expression phenotypes displayed across the same genes by patients with the same indication and already known to be sensitive or insensitive to that therapy.

[0090] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of a certain subset of genes set forth in Table 3 in the first biological sample, and (c) comparing the gene expression profile of the subset of genes in the first biological sample to (i) the gene expression profile of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the subset of genes in the first biological sample similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy, and a gene expression profile for the subset of genes in first biological sample similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the

immunomodulatory therapy indicates that the hematological cancer of the first patient will be clinically insensitive to the treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 3. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 3.

[0091] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of a certain subset of genes set forth in Table 3 in the first biological sample, and (c) comparing the gene expression profile of the subset of genes in the first biological sample to (i) the gene expression profile of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the subset of genes in the first biological sample similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 3. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 3.

[0092] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of a certain subset of genes set forth in Table 3 in the first biological sample, and (c) comparing the gene expression profile of the subset of genes in the first biological sample to (i) the gene expression profile of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the subset of genes in first biological sample similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of

hematological cancer which are clinically insensitive to the immunomodulatory therapy indicates that the hematological cancer of the first patient will be clinically insensitive to the treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 3. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 3.

[0093] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 4 in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in Table 4 in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the genes or subset of genes in the first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy, and a gene expression profile for the subset of genes in first biological sample similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy indicates that the hematological cancer of the first patient will be clinically insensitive to the treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 4. In some embodiments, the subset of genes comprises 2-5, 5-10, or 10-15 of the genes in Table 4.

[0094] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 4 in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples

from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in Table 4 in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the genes or subset of genes in the first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 4. In some embodiments, the subset of genes comprises 2-5, 5-10, or 10-15 of the genes in Table 4.

[0095] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 4 in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in Table 4 in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the subset of genes in first biological sample similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy indicates that the hematological cancer of the first patient will be clinically insensitive to the treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 4. In some embodiments, the subset of genes comprises 2-5, 5-10, or 10-15 of the genes in Table 4.

[0096] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 1 in the first biological

sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the genes or subset of genes in the first biological sample similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy, and a gene expression profile for the genes or subset of genes in first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy indicates that the hematological cancer of the first patient will be clinically insensitive to the treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 1. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 1.

[0097] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 1 in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the genes or subset of genes in the first biological sample similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In certain

embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 1. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 1.

[0098] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 1 in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the genes or subset of genes in first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy indicates that the hematological cancer of the first patient will be clinically insensitive to the treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 1. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 1.

[0099] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 2 in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the genes or subset of genes in the first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are

clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy, and a gene expression profile for the genes or subset of genes in first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy indicates that the hematological cancer of the first patient will be clinically insensitive to the treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 2. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 2.

[00100] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 2 in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the genes or subset of genes in the first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 2. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 2.

[00101] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 2 in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first

biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a gene expression profile for the genes or subset of genes in first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy indicates that the hematological cancer of the first patient will be clinically insensitive to the treatment with the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 2. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 2.

[00102] In accordance with the methods described herein, the biological sample can be any sample obtained from the patient. In certain embodiments, the biological sample is a cell sample. In other embodiments, the biological sample is whole blood sample, peripheral blood mononuclear cell sample, or tissue sample. In specific embodiments, the biological sample is a tumor sample. *See* Section 5.8, *infra*, regarding biological samples.

[00103] In accordance with the methods described herein, the hematological cancer can be any hematological cancer. Examples of hematological cancers can be found in Section 5.5, *infra*. In a specific embodiment, the hematological cancer is a lymphoma. In another specific embodiment, the hematological cancer is a non-Hodgkin's lymphoma. In yet another embodiment, the hematological cancer is a diffuse large B-cell lymphoma (DLBCL). In certain embodiments, the DLBCL is a germinal center B-cell-like DLBCL. In other embodiments, the DLBCL is an activated B-cell-like DLBCL.

[00104] In accordance with the methods described herein, the level of expression of one, two, three, four, five or more of the genes in Table 1, Table 2, Table 3, and/or Table 4, *infra*, can be measured at the RNA and/or protein levels. In certain embodiments, the level of expression of the genes are measured at the RNA (*e.g.*, mRNA) level. In other embodiments, the level of expression of the genes are measured at the protein level.

[00105] Techniques known to one skilled in the art may be used to measure the amount of an RNA transcript(s). In some embodiments, the amount of one, two, three, four, five or more RNA transcripts is measured using deep sequencing, such as ILLUMINA® RNASeq, ILLUMINA® next

generation sequencing (NGS), ION TORRENT™ RNA next generation sequencing, 454™ pyrosequencing, or Sequencing by Oligo Ligation Detection (SOLID™). In other embodiments, the amount of multiple RNA transcripts is measured using a microarray and/or gene chip, such as described in Section 6, *infra*. In certain embodiments, the amount of one, two, three or more RNA transcripts is determined by RT-PCR. In other embodiments, the amount of one, two, three or more RNA transcripts is measured by RT-qPCR. Techniques for conducting these assays are known to one skilled in the art. *See* Section 5.9, *infra*, for examples of assays to measure RNA transcripts.

[00106] In some embodiments, a statistical analysis or other analysis is performed on data from the assay utilized to measure an RNA transcript or protein. In certain specific embodiments, p value of those RNA transcripts or proteins differentially expressed is 0.1, 0.5, 0.4, 0.3, 0.2, 0.01, 0.05, 0.001, 0.005, or 0.0001. In specific embodiments, a false discovery rate (FDR) of 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1% or less is selected.

[00107] Techniques known to one skilled in the art may be used to measure the amount of a protein. For example, flow cytometry, immunofluorescence, enzyme-linked immunosorbent assay-based methodologies (ELISA) and similar assays known in the art. *See* Section 5.10, *infra*, for examples of assays to measure protein.

[00108] In accordance with the methods described herein, the immunomodulatory therapy can be any therapy that modulates the immune system or immune response. Examples of immunomodulatory therapies are provided in Section 5.6, *infra*. In a specific embodiment, the immunomodulatory therapy is lenalidomide (Revlimid®).

5.3 Methods for Predicting Clinical Sensitivity of a Hematological Cancer By Measuring Proportion of Cells

[00109] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of dendritic cells in the first tumor sample, and (c) comparing the proportion of dendritic cells in the first tumor sample with the proportion of dendritic cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with the immunomodulatory therapy, and wherein a higher proportion of dendritic cells in the first tumor sample relative the proportion of

dendritic cells in the second tumor sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy.

[00110] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of plasma cells in the first tumor sample, and (c) comparing the proportion of plasma cells in the first tumor sample with the proportion of plasma cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with the immunomodulatory therapy, and wherein a higher proportion of plasma cells in the first tumor sample relative the proportion of plasma cells in the second tumor sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy.

[00111] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of dendritic cells and plasma cells in the first tumor sample, and (c) comparing the proportion of dendritic cells and plasma cells in the first tumor sample with the proportion of dendritic cells and plasma cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with the immunomodulatory therapy, and wherein a higher proportion of dendritic cells and plasma cells in the first tumor sample relative the proportion of dendritic cells and plasma cells in the second tumor sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy.

[00112] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of B cells in the first tumor sample, and (c) comparing the proportion of B cells in the first tumor sample with the proportion of B cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with the immunomodulatory therapy, and wherein a decreased proportion of B cells in the first tumor sample relative the proportion of B cells in the second tumor

sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy.

[00113] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of Natural Killer (NK) cells in the first tumor sample, and (c) comparing the proportion of NK cells in the first tumor sample with the proportion of NK cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with the immunomodulatory therapy, and wherein a higher proportion of NK cells in the first tumor sample relative the proportion of NK cells in the second tumor sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy.

[00114] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of tumor infiltrating immune cells in the first tumor sample, and (c) comparing the proportion of tumor infiltrating immune cells in the first tumor sample with the proportion of tumor infiltrating immune cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with the immunomodulatory therapy, and wherein a higher proportion of tumor infiltrating immune cells in the first tumor sample relative the proportion of tumor infiltrating immune cells in the second tumor sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy.

[00115] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of monocytes in the first tumor sample, and (c) comparing the proportion of NK cells in the first tumor sample with the proportion of monocytes in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with the immunomodulatory therapy, and wherein a higher proportion of monocytes in the first tumor sample relative the proportion of monocytes in the

second tumor sample indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy.

[00116] In certain embodiments of the foregoing paragraphs in this section, the second patient is a single patient. In other embodiments of the foregoing paragraphs in this section, the second patient is a population of patients. In specific embodiments, the population comprises 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 200, 225, 250, 300 or more patients.

[00117] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having a hematological cancer, (b) measuring the proportion of immune cells in the tumor sample, and (c) comparing the proportion of the immune cells in the first tumor sample to (i) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a proportion of the immune cells in the first tumor sample similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient will be clinical sensitive to treatment with the immunomodulatory therapy. In some embodiments, the immune cells are subset of immune cells, such as subset of B cells. In certain embodiments, the immune cells are dendritic cells. In some embodiments, the immune cells are plasma cells. In certain embodiments, the immune cells are monocytes. In some embodiments, the immune cells are tumor infiltrating immune cells. In certain embodiments, the immune cells are T cells. In some embodiments, the immune cells are B cells. In certain embodiments, the immune cells are NK cells. In some embodiments, the immune cells are two, three or more subsets of immune cells, such as two more types of T cells (*e.g.*, CD4+ and CD8+ T cells). In some embodiments, the proportion of different populations of immune cells in the first tumor sample are compared to (i) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy.

[00118] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having a hematological cancer, (b) measuring the proportion of immune cells in the tumor sample, and (c) comparing the proportion of the immune cells in the first tumor sample to (i) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a proportion of the immune cells in the first tumor sample similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy indicates that the hematological cancer of the first patient will be clinically insensitive to the treatment with the immunomodulatory therapy. In some embodiments, the immune cells are subset of immune cells, such as subset of B cells. In certain embodiments, the immune cells are dendritic cells. In some embodiments, the immune cells are plasma cells. In certain embodiments, the immune cells are monocytes. In some embodiments, the immune cells are tumor infiltrating immune cells. In certain embodiments, the immune cells are T cells. In some embodiments, the immune cells are B cells. In certain embodiments, the immune cells are NK cells. In some embodiments, the immune cells are two, three or more subsets of immune cells, such as two more types of T cells (*e.g.*, CD4+ and CD8+ T cells). In some embodiments, the proportion of different populations of immune cells in the first tumor sample are compared to (i) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy.

[00119] In another aspect, provided herein are methods for predicting the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy comprising: (a) obtaining a first tumor sample from a first patient having a hematological cancer, (b) measuring the proportion of immune cells in the tumor sample, and (c) comparing the proportion of the immune cells in the first tumor sample to (i) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an

immunomodulatory therapy and (ii) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, wherein a proportion of the immune cells in the first tumor sample similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy indicates that the hematological cancer in the first patient, and a proportion of the immune cells in the first tumor sample similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy indicates that the hematological cancer of the first patient will be clinically insensitive to the treatment with the immunomodulatory therapy. In some embodiments, the immune cells are subset of immune cells, such as subset of B cells. In certain embodiments, the immune cells are dendritic cells. In some embodiments, the immune cells are plasma cells. In certain embodiments, the immune cells are monocytes. In some embodiments, the immune cells are tumor infiltrating immune cells. In certain embodiments, the immune cells are T cells. In some embodiments, the immune cells are B cells. In certain embodiments, the immune cells are NK cells. In some embodiments, the immune cells are two, three or more subsets of immune cells, such as two more types of T cells (*e.g.*, CD4+ and CD8+ T cells). In some embodiments, the proportion of different populations of immune cells in the first tumor sample are compared to (i) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy.

[00120] In addition to measuring the cells (*e.g.*, dendritic cells, plasma cells, B cells, monocytes, and infiltrating immune cells) in a tumor sample from a patient, levels of expression of genes (*e.g.*, one, two, three, four, five or more of the genes in Table 1 and/or Table 2) may be assessed. In specific embodiments, the methods set forth in Section 5.1, *supra*, are combined with the methods set forth in this Section 5.2 to predict the clinical sensitivity of a hematological cancer to treatment with an immunomodulatory therapy.

[00121] Techniques known to one skilled in the art may be used to measure the proportion of cells in a tumor sample. In certain embodiments, the proportion of cells is measured by flow cytometry, immunofluorescence, enzyme-linked immunosorbent assay-based methodologies

(ELISA) and similar assays known in the art. *See* Section 5.8, *infra*, regarding techniques for measuring and distinguishing cell types. In other embodiments, the proportion of cells is measured by inference from gene expression profiles.

[00122] In accordance with the methods described herein, the hematological cancer can be any hematological cancer. Examples of hematological cancers can be found in Section 5.5, *infra*. In a specific embodiment, the hematological cancer is a lymphoma. In another specific embodiment, the hematological cancer is a non-Hodgkin's lymphoma. In yet another embodiment, the hematological cancer is a diffuse large B-cell lymphoma (DLBCL). In certain embodiments, the DLBCL is a germinal center B-cell-like DLBCL. In other embodiments, the DLBCL is an activated B-cell-like DLBCL.

[00123] In accordance with the methods described herein, the immunomodulatory therapy can be any therapy that modulates the immune system or immune response. Examples of immunomodulatory therapies are provided in Section 5.6, *infra*. In a specific embodiment, the immunomodulatory therapy is lenalidomide (Revlimid®).

5.4 Methods for Managing and Treating Hematological Cancer

[00124] In one aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 3 or 4, *infra*, (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 3 or 4 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the one, two, three, four, five or more of the genes in the first biological sample are differentially expressed relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample. In certain embodiments, the immunomodulatory therapy is not administered or additional assays are conducted if the level of expression of one, two, three, four, five or more of the genes are not higher in the first biological sample than in the second biological sample.

[00125] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a

hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 1, *infra*, (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 1 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a higher level of expression of the one, two, three, four, five or more of the genes in the first biological sample is measured relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample. In certain embodiments, the immunomodulatory therapy is not administered or additional assays are conducted if the level of expression of one, two, three, four, five or more of the genes are not higher in the first biological sample than in the second biological sample.

[00126] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 2, *infra*, (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 2 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a lower level of expression of the one, two, three, four, five or more of the genes in the first biological sample is measured relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample. In certain embodiments, the immunomodulatory therapy is not administered or additional assays are conducted if the level of expression of one, two, three, four, five or more of the genes are not lower in the first biological sample than in the second biological sample. In certain embodiments, the immunomodulatory therapy is not administered or additional assays are conducted if the level of expression of one, two, three, four, five or more of the genes are not higher in the first biological sample than in the second biological sample.

[00127] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the level of expression of one, two, three, four, five or more of

the genes identified in Table 1, *infra*, and measuring the level of expression one, two, three, four, five or more of the genes identified in Table 2, *infra*, (c) comparing the level of expression of the genes identified in Tables 1 and 2 in the first biological sample with the level of expression of the same genes in a second biological sample is from a second patient having the same type of hematological cancer as the first patient, wherein the hematological cancer in the second patient is clinically insensitive to an immunomodulatory therapy, and (d) administering the immunomodulatory to the first patient if (i) a higher level of expression of the one, two, three, four, five or more of the genes identified in Table 1 in the first biological sample is measured relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample, and (ii) a lower level of expression of the one, two, three, four, five or more of the genes identified in Table 2 in the first biological sample is measured relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample. In certain embodiments, the immunomodulatory therapy is not administered or additional assays are conducted if the level of expression of one, two, three, four, five or more of the genes are not higher in the first biological sample than in the second biological sample.

[00128] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of a certain subset of genes set forth in Table 3, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the subset of genes in the first biological sample to (i) the gene expression profile of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the gene expression profile for the subset of genes in the first biological sample is similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 3. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 3.

[00129] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a

hematological cancer, (b) measuring the expression of a certain subset of genes set forth in Table 3, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the subset of genes in the first biological sample to (i) the gene expression profile of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the gene expression profile for the subset of genes in the first biological sample is not similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 3. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 3.

[00130] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of a certain subset of genes set forth in Table 3, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the subset of genes in the first biological sample to (i) the gene expression profile of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if: (i) the gene expression profile for the subset of genes in the first biological sample is similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the gene expression profile for the subset of genes in first biological sample is not similar to the gene expression profile for the subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 3. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 3.

[00131] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 4, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the genes or a subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the gene expression profile for the genes or subset of genes in the first biological sample is similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 4. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 4.

[00132] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 4, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the gene expression profile for the genes or subset of genes in the first biological sample is not similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 4. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 4.

[00133] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 4, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if: (i) the gene expression profile for the genes or subset of genes in the first biological sample is similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the gene expression profile for the genes or subset of genes in first biological sample is not similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 4. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 4.

[00134] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 1, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the genes or a subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the gene expression profile for the genes or subset of genes in the first biological sample is similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy. In certain

embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 1. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 1.

[00135] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 1, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes *i* in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the gene expression profile for the genes or subset of genes in the first biological sample is not similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 1. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 1.

[00136] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 1, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if: (i) the gene expression profile for the genes or subset of genes in the first biological sample is similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the

gene expression profile for the genes or subset of genes in first biological sample is not similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 1. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 1.

[00137] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 2, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the genes or a subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the gene expression profile for the genes or subset of genes in the first biological sample is similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 2. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 2.

[00138] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 2, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the gene expression profile for

the genes or subset of genes in the first biological sample is not similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 2. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 2.

[00139] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first biological sample from a first patient having a hematological cancer, (b) measuring the expression of the genes or a certain subset of genes set forth in Table 2, *infra*, in the first biological sample, and (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if: (i) the gene expression profile for the genes or subset of genes in the first biological sample is similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the gene expression profile for the genes or subset of genes in first biological sample is not similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory. In certain embodiments, the subset of genes comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15 or more of the genes in Table 2. In some embodiments, the subset of genes comprises 2-5, 5-10, 10-15, 15-20, 20-25 or 25-30 of the genes in Table 2.

[00140] In accordance with the methods described herein, the biological sample can be any sample obtained from the patient. In certain embodiments, the biological sample is a cell sample. In other embodiments, the biological sample is whole blood sample, peripheral blood mononuclear cell sample, or tissue sample. In specific embodiments, the biological sample is a tumor sample. *See* Section 5.8, *infra*, regarding biological samples.

[00141] In accordance with the methods described herein, the level of expression of one, two, three, four, five or more of the genes in Table 1 and/or Table 2 and/or Table 3 and/or Table 4, *infra*,

can be measured at the RNA and/or protein levels. In certain embodiments, the level of expression of the genes are measured at the RNA (*e.g.*, mRNA) level. In other embodiments, the level of expression of the genes are measured at the protein level.

[00142] Techniques known to one skilled in the art may be used to measure the amount of an RNA transcript(s). In some embodiments, the amount of one, two, three, four, five or more RNA transcripts is measured using deep sequencing, such as ILLUMINA® RNASeq, ILLUMINA® next generation sequencing (NGS), ION TORRENT™ RNA next generation sequencing, 454™ pyrosequencing, or Sequencing by Oligo Ligation Detection (SOLID™). In other embodiments, the amount of multiple RNA transcripts is measured using a microarray and/or gene chip, such as described in Section 6, *infra*. In certain embodiments, the amount of one, two, three or more RNA transcripts is determined by RT-PCR. In other embodiments, the amount of one, two, three or more RNA transcripts is measured by RT-qPCR. Techniques for conducting these assays are known to one skilled in the art. *See* Section 5.9, *infra*, for examples of assays for measuring RNA transcripts.

[00143] In some embodiments, a statistical analysis or other analysis is performed on data from the assay utilized to measure an RNA transcript or protein. In some specific embodiments, p value of those RNA transcripts or proteins differentially expressed is 0.1, 0.5, 0.4, 0.3, 0.2, 0.01, 0.05, 0.001, or 0.0001. In specific embodiments, a false discovery rate (FDR) of 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2% 1% or less is selected.

[00144] Techniques known to one skilled in the art may be used to measure the amount of a protein. For example, flow cytometry, immunofluorescence, enzyme-linked immunosorbent assay-based methodologies (ELISA) and similar assays known in the art. *See* Section 5.9, *infra*, for examples of assays for measuring RNA transcripts.

[00145] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of dendritic cells in the first tumor sample, (c) comparing the proportion of dendritic cells in the first tumor sample with the proportion of dendritic cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a higher proportion of dendritic cells in the first tumor sample is measured relative the proportion of dendritic cells in the second tumor sample.

[00146] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of plasma cells in the first tumor sample, (c) comparing the proportion of plasma cells in the first tumor sample with the proportion of plasma cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a higher proportion of plasma cells in the first tumor sample is measured relative the proportion of plasma cells in the second tumor sample.

[00147] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of dendritic cells and plasma cells in the first tumor sample, (c) comparing the proportion of dendritic cells and plasma cells in the first tumor sample with the proportion of dendritic cells and plasma cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a higher proportion of dendritic cells and plasma cells in the first tumor sample is measured relative the proportion of dendritic cells and plasma cells in the second tumor sample.

[00148] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of B cells in the first tumor sample, (c) comparing the proportion of B cells in the first tumor sample with the proportion of B cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a decreased proportion of B cells in the first tumor sample is measured relative the proportion of B cells in the second tumor sample.

[00149] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of tumor infiltrating immune cells in the first tumor sample, (c) comparing the proportion of tumor infiltrating immune cells in the first tumor sample with the

proportion of tumor infiltrating immune cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a higher proportion of tumor infiltrating immune cells in the first tumor sample is measured relative the proportion of tumor infiltrating immune cells in the second tumor sample.

[00150] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of NK cells in the first tumor sample, (c) comparing the proportion of NK cells in the first tumor sample with the proportion of NK cells in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a higher proportion of NK cells in the first tumor sample is measured relative the proportion of NK cells in the second tumor sample.

[00151] In another aspect, provided herein are methods for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having the hematological cancer, (b) measuring the proportion of monocytes in the first tumor sample, (c) comparing the proportion of monocytes in the first tumor sample with the proportion of monocytes in a second tumor sample from a second patient having the same type of hematological cancer, wherein the second patient's hematological cancer is clinically insensitive to treatment with an immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if a higher proportion of monocytes in the first tumor sample is measured relative the proportion of monocytes in the second tumor sample.

[00152] In certain embodiments of the foregoing paragraphs in this section, the second patient is a single patient. In other embodiments of the foregoing paragraphs in this section, the second patient is a population of patients. In specific embodiments, the population comprises 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 200, 225, 250, 300 or more patients.

[00153] In another aspect, provided herein are for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having a hematological cancer, (b) measuring the proportion of immune cells in the first tumor sample, and (c) comparing the

proportion of the immune cells in the first tumor sample to (i) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the proportion of the immune cells in the first tumor sample is similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy. In some embodiments, the immune cells are subset of immune cells, such as subset of B cells. In certain embodiments, the immune cells are dendritic cells. In some embodiments, the immune cells are plasma cells. In certain embodiments, the immune cells are monocytes. In some embodiments, the immune cells are tumor infiltrating immune cells. In certain embodiments, the immune cells are T cells. In some embodiments, the immune cells are B cells. In certain embodiments, the immune cells are NK cells. In some embodiments, the immune cells are two, three or more subsets of immune cells, such as two more types of T cells (*e.g.*, CD4+ and CD8+ T cells). In some embodiments, the proportion of different populations of immune cells in the first tumor sample are compared to (i) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy.

[00154] In another aspect, provided herein are for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having a hematological cancer, (b) measuring the proportion of immune cells in the first tumor sample, and (c) comparing the proportion of the immune cells in the first tumor sample to (i) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the proportion of the immune cells in the first tumor sample is not similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the

immunomodulatory therapy. In some embodiments, the immune cells are subset of immune cells, such as subset of B cells. In certain embodiments, the immune cells are dendritic cells. In some embodiments, the immune cells are plasma cells. In certain embodiments, the immune cells are monocytes. In some embodiments, the immune cells are tumor infiltrating immune cells. In certain embodiments, the immune cells are T cells. In some embodiments, the immune cells are B cells. In certain embodiments, the immune cells are NK cells. In some embodiments, the immune cells are two, three or more subsets of immune cells, such as two more types of T cells (*e.g.*, CD4+ and CD8+ T cells). In some embodiments, the proportion of different populations of immune cells in the first tumor sample are compared to (i) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy.

[00155] In another aspect, provided herein are for managing or treating a hematological cancer comprising: (a) obtaining a first tumor sample from a first patient having a hematological cancer, (b) measuring the proportion of immune cells in the first tumor sample, and (c) comparing the proportion of the immune cells in the first tumor sample to (i) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to an immunomodulatory therapy and (ii) the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy, and (d) administering the immunomodulatory therapy to the first patient if the proportion of the immune cells in the first tumor sample is (i) similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy, and (ii) not similar to the proportion of the same immune cells in tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy. In some embodiments, the immune cells are subset of immune cells, such as subset of B cells. In certain embodiments, the immune cells are dendritic cells. In some embodiments, the immune cells are plasma cells. In certain embodiments, the immune cells are monocytes. In some embodiments, the immune cells are tumor infiltrating immune cells. In certain embodiments, the immune cells are T cells. In some embodiments, the immune cells are B cells. In certain embodiments, the immune cells are NK cells. In some

embodiments, the immune cells are two, three or more subsets of immune cells, such as two more types of T cells (*e.g.*, CD4+ and CD8+ T cells). In some embodiments, the proportion of different populations of immune cells in the first tumor sample are compared to (i) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically sensitive to the immunomodulatory therapy and (ii) the proportion of the same populations of immune cells in the tumor samples from patients having the same type of hematological cancer which are clinically insensitive to the immunomodulatory therapy.

[00156] In addition to measuring the cells (*e.g.*, dendritic cells and plasma cells) in a tumor sample from a patient, levels of expression of genes (*e.g.*, one, two, three, four, five or more of the genes in Table 1 and/or Table 2 and/or Table 3 and/or Table 4) may be assessed. In specific embodiments, the methods set forth for measuring gene expression *supra*, are combined with the methods set forth for measuring a proportion of cells to determine if an immunomodulatory therapy is to be administered to a patient with a hematological cancer.

[00157] Techniques known to one skilled in the art may be used to measure the proportion of cells in a tumor sample. In certain embodiments, the proportion of cells is measured by flow cytometry, immunofluorescence, enzyme-linked immunosorbent assay-based methodologies (ELISA) and similar assays known in the art. In other embodiments, the proportion of cells is measured by inference from gene expression profiles.

[00158] In accordance with the methods described herein, the immunomodulatory therapy can be any therapy that modulates the immune system or immune response. Examples of immunomodulatory therapies are provided in Section 5.6, *infra*. In a specific embodiment, the immunomodulatory therapy is lenalidomide (Revlimid®).

[00159] In specific embodiments, an immunomodulatory therapy is administered to a hematological cancer patient in the form of a pharmaceutical composition. In a specific embodiment, a pharmaceutical composition administered to a hematological cancer patient comprising an immunomodulatory therapy and a pharmaceutically acceptable carrier or excipient. In certain embodiments, the pharmaceutical composition may comprise an additional therapy, such as described in Section 5.7, *infra*. The dosage form of the pharmaceutical composition will vary depending upon the route of administration. The immunomodulatory therapy or a pharmaceutical composition thereof may be administered by any route of administration, such as oral, mucosal, parenteral (*e.g.*, subcutaneous, intravenous, bolus injection, intramuscular), topical, transdermal, or

transcutaneous. In a specific embodiment, the immunomodulatory therapy or a pharmaceutical composition thereof is orally administered to a hematological cancer patient.

[00160] [00160] In accordance with the methods described herein, the dose of an immunomodulatory therapy administered to a patient varies depending on a variety of factors, such as the health and age of the patient. In certain embodiments, in accordance with the methods described herein the patient is administered a dose of 0.01 mg to 1000 mg of an immunomodulatory therapy. In certain embodiments, in accordance with the methods described herein the patient is administered a dose of 0.01 mg to 500 mg of an immunomodulatory therapy. In certain embodiments, in accordance with the methods described herein the patient is administered a dose of 0.01 mg to 100 mg of an immunomodulatory therapy. In some embodiments, in accordance with the methods described herein the patient is administered a dose of 0.1 mg to 500 mg of an immunomodulatory therapy. . In some embodiments, in accordance with the methods described herein the patient is administered a dose of 0.01 mg to 500 mg of an immunomodulatory therapy. In some embodiments, in accordance with the methods described herein the patient is administered a dose of 1 mg to 500 mg of an immunomodulatory therapy. In certain embodiments, in accordance with the methods described herein the patient is administered a dose of 0.1 mg to 100 mg of an immunomodulatory therapy. In certain embodiments, in accordance with the methods described herein the patient is administered a dose of 1 mg to 100 mg of an immunomodulatory therapy. In some embodiments, in accordance with the methods described herein the patient is administered a dose of 1 mg to 50 mg of an immunomodulatory therapy. In some embodiments, in accordance with the methods described herein the patient is administered a dose of 1 mg to 100 mg of an immunomodulatory therapy. In some embodiments, in accordance with the methods described herein the patient is administered a dose of 1 mg to 500 mg of an immunomodulatory therapy. In some embodiments, in accordance with the methods described herein the patient is administered a dose of 1 mg to 1000 mg of an immunomodulatory therapy. The dose of the immunomodulatory therapy can be administered once, twice or three times per day. The dose of the immunomodulatory therapy can be administered every other day, every two days, every three days, every four days, every five days, every six days, or once per week. Specific doses per day include 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 mg per day. The dose of the immunomodulatory therapy is administered in accordance with the label for the therapy. The immunomodulatory therapy can be lenalidomide (Revlimid®), or its pharmaceutically acceptable

salt, solvate, hydrate or stereoisomer, and it is administered at a dose of 1 to 50 mg per day, or anything in between, or 25 mg per day.

[00161] In accordance with the methods described herein, the hematological cancer can be any hematological cancer. Examples of hematological cancers can be found in Section 5.5, *infra*. In a specific embodiment, the hematological cancer is a lymphoma. In another specific embodiment, the hematological cancer is a non-Hodgkin's lymphoma. In yet another embodiment, the hematological cancer is a diffuse large B-cell lymphoma (DLBCL). In certain embodiments, the DLBCL is a germinal center B-cell-like DLBCL. In other embodiments, the DLBCL is an activated B-cell-like DLBCL.

[00162] In certain embodiments, the methods of managing or treating a hematological cancer involve the administration of another therapy. In some embodiments, the other therapy is to alleviate pain or one or more other symptoms associated with the hematological cancer. Examples of other therapies that may be used in combination with an immunomodulatory therapy are disclosed in Section 5.7, *infra*. In certain embodiments, one or more of the following additional active ingredients are administered in combination with an immunomodulatory therapy in accordance with the methods described herein: oblimersen, melphalan, G-CSF, GM-CSF, EPO, a cox-2 inhibitor, topotecan, pentoxifylline, ciprofloxacin, taxotere, iritotecan, dexamethasone, doxorubicin, vincristine, IL 2, IFN, dacarbazine, Ara-C, vinorelbine and/or isotretinoin. In a specific embodiment, chemotherapeutic agents, such as cyclohexamide, hydroxydaunorubicin, oncovin, and prednisone (CHOP), are used in combination with an immunomodulatory therapy, such as lenalidomide, in accordance with the methods described herein. In another specific embodiment, rituximab is used in combination with an immunomodulatory therapy, such as lenalidomide.. In another specific embodiment, CHOP and rituximab are used in combination with an immunomodulatory therapy, such as lenalidomide.

5.5 Hematological Cancers

[00163] In some embodiments, the hematological cancer is a lymphoma. In other embodiments, the hematological cancer is a leukemia. In one embodiment, the hematological cancer is multiple myeloma. In another embodiment, the hematological cancer is chronic lymphocytic leukemia (CLL). In another embodiment, the hematological cancer is myelodysplastic syndrome, an acute leukemia, *e.g.*, acute T cell leukemia, acute myelogenous leukemia (AML), acute promyelocytic leukemia, acute myeloblastic leukemia, acute megakaryoblastic leukemia, precursor B acute lymphoblastic leukemia, precursor T acute lymphoblastic leukemia, Burkitt's leukemia (Burkitt's

lymphoma), or acute biphenotypic leukemia; a chronic leukemia, *e.g.*, chronic myeloid lymphoma, chronic myelogenous leukemia (CML), chronic monocytic leukemia, small lymphocytic lymphoma, or B-cell prolymphocytic leukemia; hairy cell lymphoma; T-cell prolymphocytic leukemia; or a lymphoma, *e.g.*, histiocytic lymphoma, lymphoplasmacytic lymphoma (*e.g.*, Waldenström macroglobulinemia), splenic marginal zone lymphoma, plasma cell neoplasm (*e.g.*, plasma cell myeloma, plasmacytoma, a monoclonal immunoglobulin deposition disease, or a heavy chain disease), extranodal marginal zone B cell lymphoma (MALT lymphoma), nodal marginal zone B cell lymphoma (NMZL), follicular lymphoma, mantle cell lymphoma, diffuse large B cell lymphoma, mediastinal (thymic) large B cell lymphoma, intravascular large B cell lymphoma, primary effusion lymphoma, T cell large granular lymphocytic leukemia, aggressive NK cell leukemia, adult T cell leukemia/lymphoma, extranodal NK/T cell lymphoma, nasal type, enteropathy-type T cell lymphoma, hepatosplenic T cell lymphoma, blastic NK cell lymphoma, mycosis fungoides (Sezary syndrome), a primary cutaneous CD30-positive T cell lymphoproliferative disorder (*e.g.*, primary cutaneous anaplastic large cell lymphoma or lymphomatoid papulosis), angioimmunoblastic T cell lymphoma, peripheral T cell lymphoma, unspecified, anaplastic large cell lymphoma, a Hodgkin's lymphoma or a nodular lymphocyte-predominant Hodgkin's lymphoma.

[00164] In a specific embodiment, the hematological cancer is DLBCL. In another specific embodiment, the hematological cancer is an activated B-cell-like DLBCL. In another specific embodiment, the hematological cancer is a germinal center B-cell-like DLBCL.

5.6 Immunomodulatory Therapies

[00165] Immunomodulatory therapies described in the methods provided herein include compounds known as "IMiDs[®]" (Celgene Corporation), a group of compounds that can be useful to treat several types of human diseases, including certain cancers.

[00166] As used herein and unless otherwise indicated, the terms "immunomodulatory compound", "immunomodulatory agent" and "immunomodulatory therapy" are used interchangeably, and can encompass certain small organic molecules that inhibit LPS induced monocyte TNF- α , IL-1 β , IL-12, IL-6, MIP-1 α , MCP-1, GM-CSF, G-CSF, and COX-2 production. These compounds can be prepared synthetically, or can be obtained commercially.

[00167] Exemplary immunomodulating compounds include but are not limited to N-([2-(2,6-dioxo(3-piperidyl)-1,3-dioxoisindolin-4-yl)methyl]cyclopropyl-carboxamide; 3-[2-(2,6-dioxo-

piperidin-3-yl)-1,3-dioxo-2,3-dihydro-1H-isoindol-4-ylmethyl]-1,1-dimethyl-urea; (-)-3-(3,4-Dimethoxy-phenyl)-3-(1-oxo-1,3-dihydro-isoindol-2-yl)-propionamide; (+)-3-(3,4-Dimethoxy-phenyl)-3-(1-oxo-1,3-dihydro-isoindol-2-yl)-propionamide; (-)-{2-[1-(3-ethoxy-4-methoxyphenyl)-2-methylsulfonylethyl]-4-acetylaminisoindoline-1,3-dione}; (+)-{2-[1-(3-ethoxy-4-methoxyphenyl)-2-methylsulfonylethyl]-4-acetylaminisoindoline-1,3-dione}; Difluoro-methoxy SelCIDs; 1-phthalimido-1-(3,4-diethoxyphenyl)ethane; 3-(3,4-dimethoxyphenyl)-3-(3,5-dimethoxyphenyl)acrylo nitrile; 1-oxo-2-(2,6-dioxopiperidin-3-yl)-4-aminoisoindoline; 1,3-dioxo-2-(2,6-dioxopiperidin-3-yl)-4-aminoisoindoline; 4-amino-2-(3-methyl-2,6-dioxo-piperidine-3-yl)-isoindole-1,3-dione; 3-(3-acetoamidophthalimido)-3-(3-ethoxy-4-methoxyphenyl)-N-hydroxypropionamide; 1-oxo-2-(2,6-dioxopiperidin-3-yl)-4-methylisoindoline; Cyclopropyl-N-{2-[(1S)-1-(3-ethoxy-4-methoxyphenyl)-2-(methylsulfonyl)ethyl]-3-oxoisoindoline-4-yl} carboxamide; Substituted 2-(3-hydroxy-2,6- dioxopiperidin-5-yl) isoindoline; N-[2-(2,6-Dioxo-piperidin-3-yl)-1,3-dioxo-2,3-dihydro-1H-isoindol-5-ylmethyl]-4-trifluoromethoxybenzamide; (S)-4-chloro-N-((2-(3-methyl-2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-5-yl)methyl) benzamide; Pyridine-2-carboxylic acid [2-[(3S)-3-methyl-2,6-dioxo-piperidin-3-yl]-1,3-dioxo-2,3-dihydro-1H-isoindol-5-ylmethyl]-amide; (S)-N-((2-(3-methyl-2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-5-yl)methyl)-4-(trifluoromethyl)benzamide; 3-(2,5-dimethyl-4-oxo-4*H*-quinazolin-3-yl)-piperidine-2,6-dione, and the like. In a specific embodiment, the immunomodulatory compound is 3-(4-amino-1-oxo-1,3-dihydro-isoindol-2-yl)-piperidine-2,6-dione, or a salt, solvate or hydrate thereof.

[00168] Immunomodulatory compounds disclosed herein may enhance the degradation of TNF- α mRNA. Immunomodulatory compounds disclosed herein may also be potent co-stimulators of T cells and increase cell proliferation dramatically in a dose dependent manner. Immunomodulatory compounds disclosed herein may also have a greater co-stimulatory effect on the CD8⁺ T cell subset than on the CD4⁺ T cell subset. Immunomodulatory compounds disclosed herein may be capable of acting both indirectly through cytokine activation and directly on Natural Killer (“NK”) cells and Natural Killer T (“NKT”) cells, and increase the NK cells’ ability to produce beneficial cytokines such as, but not limited to, IFN- γ , and to enhance NK and NKT cell cytotoxic activity.

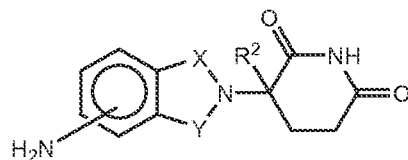
[00169] Specific examples of immunomodulatory compounds include cyano and carboxy derivatives of substituted styrenes such as those disclosed in U.S. patent no. 5,929,117; 1-oxo-2-(2,6-dioxo-3-fluoropiperidin-3-yl) isoindolines and 1,3-dioxo-2-(2,6-dioxo-3-fluoropiperidine-3-yl) isoindolines such as those described in U.S. patent nos. 5,874,448 and 5,955,476; the tetra substituted 2-(2,6-dioxopiperdin-3-yl)-1-oxoisoindolines described in U.S. patent no. 5,798,368; 1-

oxo and 1,3-dioxo-2-(2,6-dioxopiperidin-3-yl) isoindolines (e.g., 4-methyl derivatives of thalidomide), substituted 2-(2,6-dioxopiperidin-3-yl) phthalimides and substituted 2-(2,6-dioxopiperidin-3-yl)-1-oxoisoindoles including, but not limited to, those disclosed in U.S. patent nos. 5,635,517, 6,281,230, 6,316,471, 6,403,613, 6,476,052 and 6,555,554; 1-oxo and 1,3-dioxoisoindolines substituted in the 4- or 5-position of the indoline ring (e.g., 4-(4-amino-1,3-dioxoisoindoline-2-yl)-4-carbamoylbutanoic acid) described in U.S. patent no. 6,380,239; isoindoline-1-one and isoindoline-1,3-dione substituted in the 2-position with 2,6-dioxo-3-hydroxypiperidin-5-yl (e.g., 2-(2,6-dioxo-3-hydroxy-5-fluoropiperidin-5-yl)-4-aminoisoindolin-1-one) described in U.S. patent no. 6,458,810; a class of non-polypeptide cyclic amides disclosed in U.S. patent nos. 5,698,579 and 5,877,200; and isoindole-imide compounds such as those described in U.S. patent publication no. 2003/0045552 published on March 6, 2003, U.S. patent publication no. 2003/0096841 published on May 22, 2003, and International Application No. PCT/US01/50401 (International Publication No. WO 02/059106). US patent publication no. 2006/0205787 describes 4-amino-2-(3-methyl-2,6-dioxopiperidin-3-yl)-isoindole-1,3-dione compositions. US patent publication no. 2007/0049618 describes isoindole-imide compounds. The entireties of each of the patents and patent applications identified herein are incorporated by reference. In one embodiment, immunomodulatory compounds do not include thalidomide.

[00170] Various immunomodulatory compounds disclosed herein contain one or more chiral centers, and can exist as racemic mixtures of enantiomers or mixtures of diastereomers. Thus, also provided herein is the use of stereomerically pure forms of such compounds, as well as the use of mixtures of those forms. For example, mixtures comprising equal or unequal amounts of the enantiomers of a particular immunomodulatory compounds may be used. These isomers may be asymmetrically synthesized or resolved using standard techniques such as chiral columns or chiral resolving agents. See, e.g., Jacques, J., *et al.*, *Enantiomers, Racemates and Resolutions* (Wiley-Interscience, New York, 1981); Wilen, S. H., *et al.*, *Tetrahedron* 33:2725 (1977); Eliel, E. L., *Stereochemistry of Carbon Compounds* (McGraw-Hill, NY, 1962); and Wilen, S. H., *Tables of Resolving Agents and Optical Resolutions* p. 268 (E.L. Eliel, Ed., Univ. of Notre Dame Press, Notre Dame, IN, 1972).

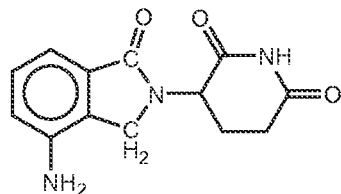
[00171] Immunomodulatory compounds provided herein include, but are not limited to, 1-oxo- and 1,3 dioxo-2-(2,6-dioxopiperidin-3-yl) isoindolines substituted with amino in the benzo ring as described in U.S. Patent no. 5,635,517 which is incorporated herein by reference.

[00172] These compounds have the structure I:

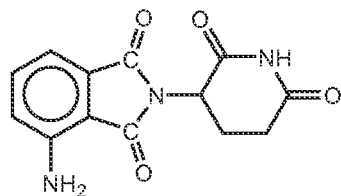


I

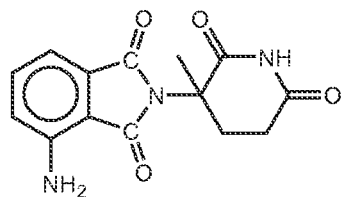
in which one of X and Y is C=O, the other of X and Y is C=O or CH₂, and R² is hydrogen or lower alkyl, in particular methyl. Specific immunomodulatory compounds include, but are not limited to:



1-oxo-2-(2,6-dioxopiperidin-3-yl)-4-aminoisoindoline;



1,3-dioxo-2-(2,6-dioxopiperidin-3-yl)-4-aminoisoindoline; and

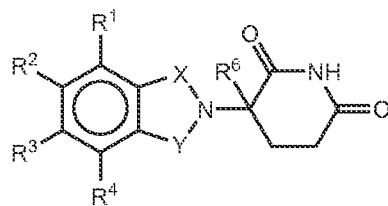


1,3-dioxo-2-(3-methyl-2,6-dioxopiperidin-3-yl)-4-aminoisoindole, and

optically pure isomers thereof.

[00173] The compounds can be obtained via standard, synthetic methods (*see e.g.*, United States Patent No. 5,635,517, incorporated herein by reference). The compounds are also available from Celgene Corporation, Warren, NJ.

[00174] Other specific immunomodulatory compounds belong to a class of substituted 2-(2,6-dioxopiperidin-3-yl) phthalimides and substituted 2-(2,6-dioxopiperidin-3-yl)-1-oxoisoindoles, such as those described in U.S. patent nos. 6,281,230; 6,316,471; 6,335,349; and 6,476,052, and International Patent Application No. PCT/US97/13375 (International Publication No. WO 98/03502), each of which is incorporated herein by reference. Representative compounds are of formula:



in which:

one of X and Y is C=O and the other of X and Y is C=O or CH₂;

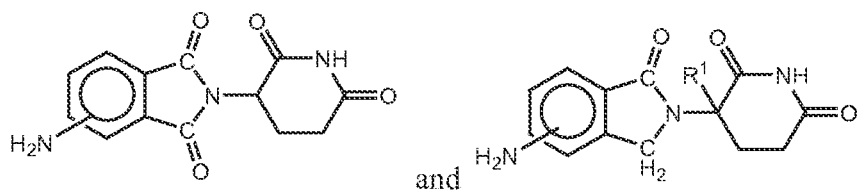
(i) each of R¹, R², R³, and R⁴, independently of the others, is halo, alkyl of 1 to 4 carbon atoms, or alkoxy of 1 to 4 carbon atoms or (ii) one of R¹, R², R³, and R⁴ is -NHR⁵ and the remaining of R¹, R², R³, and R⁴ are hydrogen;

R⁵ is hydrogen or alkyl of 1 to 8 carbon atoms;

R⁶ is hydrogen, alkyl of 1 to 8 carbon atoms, benzyl, or halo;

provided that R⁶ is other than hydrogen if X and Y are C=O and (i) each of R¹, R², R³, and R⁴ is fluoro or (ii) one of R¹, R², R³, or R⁴ is amino.

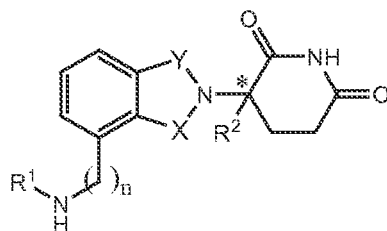
[00175] Compounds representative of this class are of the formulas:



wherein R¹ is hydrogen or methyl. In a separate embodiment, provided herein is the use of enantiomerically pure forms (*e.g.* optically pure (R) or (S) enantiomers) of these compounds.

[00176] Still other specific immunomodulatory compounds disclosed herein belong to a class of isoindole-imides disclosed in U.S. Patent No. 7,091,353, U.S. Patent Publication No.

2003/0045552, and International Application No. PCT/US01/50401 (International Publication No. WO 02/059106), each of which are incorporated herein by reference. Representative compounds are of formula II:



II

and pharmaceutically acceptable salts, hydrates, solvates, clathrates, enantiomers, diastereomers, racemates, and mixtures of stereoisomers thereof, wherein:

one of X and Y is C=O and the other is CH₂ or C=O;

R¹ is H, (C₁-C₈)alkyl, (C₃-C₇)cycloalkyl, (C₂-C₈)alkenyl, (C₂-C₈)alkynyl, benzyl, aryl, (C₀-C₄)alkyl-(C₁-C₆)heterocycloalkyl, (C₀-C₄)alkyl-(C₂-C₅)heteroaryl, C(O)R³, C(S)R³, C(O)OR⁴, (C₁-C₈)alkyl-N(R⁶)₂, (C₁-C₈)alkyl-OR⁵, (C₁-C₈)alkyl-C(O)OR⁵, C(O)NHR³, C(S)NHR³, C(O)NR³R^{3'}, C(S)NR³R^{3'}, or (C₁-C₈)alkyl-O(CO)R⁵;

R² is H, F, benzyl, (C₁-C₈)alkyl, (C₂-C₈)alkenyl, or (C₂-C₈)alkynyl;

R³ and R^{3'} are independently (C₁-C₈)alkyl, (C₃-C₇)cycloalkyl, (C₂-C₈)alkenyl, (C₂-C₈)alkynyl, benzyl, aryl, (C₀-C₄)alkyl-(C₁-C₆)heterocycloalkyl, (C₀-C₄)alkyl-(C₂-C₅)heteroaryl, (C₀-C₈)alkyl-N(R⁶)₂, (C₁-C₈)alkyl-OR⁵, (C₁-C₈)alkyl-C(O)OR⁵, (C₁-C₈)alkyl-O(CO)R⁵, or C(O)OR⁵;

R⁴ is (C₁-C₈)alkyl, (C₂-C₈)alkenyl, (C₂-C₈)alkynyl, (C₁-C₄)alkyl-OR⁵, benzyl, aryl, (C₀-C₄)alkyl-(C₁-C₆)heterocycloalkyl, or (C₀-C₄)alkyl-(C₂-C₅)heteroaryl;

R⁵ is (C₁-C₈)alkyl, (C₂-C₈)alkenyl, (C₂-C₈)alkynyl, benzyl, aryl, or (C₂-C₅)heteroaryl;

each occurrence of R⁶ is independently H, (C₁-C₈)alkyl, (C₂-C₈)alkenyl, (C₂-C₈)alkynyl, benzyl, aryl, (C₂-C₅)heteroaryl, or (C₀-C₈)alkyl-C(O)O-R⁵ or the R⁶ groups can join to form a heterocycloalkyl group;

n is 0 or 1; and

* represents a chiral-carbon center.

[00177] In specific compounds of formula II, when n is 0 then R¹ is (C₃-C₇)cycloalkyl, (C₂-C₈)alkenyl, (C₂-C₈)alkynyl, benzyl, aryl, (C₀-C₄)alkyl-(C₁-C₆)heterocycloalkyl, (C₀-C₄)alkyl-(C₂-C₅)heteroaryl, C(O)R³, C(O)OR⁴, (C₁-C₈)alkyl-N(R⁶)₂, (C₁-C₈)alkyl-OR⁵, (C₁-C₈)alkyl-C(O)OR⁵, C(S)NHR³, or (C₁-C₈)alkyl-O(CO)R⁵;

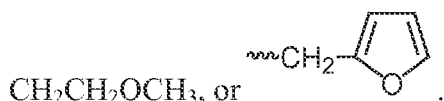
R² is H or (C₁-C₈)alkyl; and

R³ is (C₁-C₈)alkyl, (C₃-C₇)cycloalkyl, (C₂-C₈)alkenyl, (C₂-C₈)alkynyl, benzyl, aryl, (C₀-C₄)alkyl-(C₁-C₆)heterocycloalkyl, (C₀-C₄)alkyl-(C₂-C₅)heteroaryl, (C₅-C₈)alkyl-N(R⁶)₂; (C₀-C₈)alkyl-NH-C(O)O-R⁵; (C₁-C₈)alkyl-OR⁵, (C₁-C₈)alkyl-C(O)OR⁵, (C₁-C₈)alkyl-O(CO)R⁵, or C(O)OR⁵; and the other variables have the same definitions.

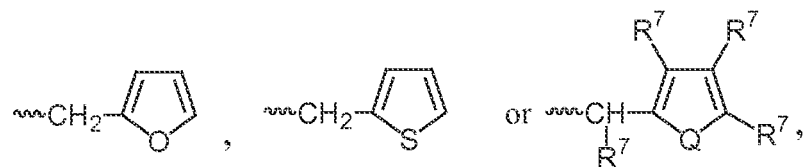
[00178] In other specific compounds of formula II, R² is H or (C₁-C₄)alkyl.

[00179] In other specific compounds of formula II, R¹ is (C₁-C₈)alkyl or benzyl.

[00180] In other specific compounds of formula II, R¹ is H, (C₁-C₈)alkyl, benzyl, CH₂OCH₃,



[00181] In another embodiment of the compounds of formula II, R¹ is



wherein Q is O or S, and each occurrence of R⁷ is independently H, (C₁-C₈)alkyl, (C₃-C₇)cycloalkyl, (C₂-C₈)alkenyl, (C₂-C₈)alkynyl, benzyl, aryl, halogen, (C₀-C₄)alkyl-(C₁-C₆)heterocycloalkyl, (C₀-C₄)alkyl-(C₂-C₅)heteroaryl, (C₀-C₈)alkyl-N(R⁶)₂, (C₁-C₈)alkyl-OR⁵, (C₁-C₈)alkyl-C(O)OR⁵, (C₁-C₈)alkyl-O(CO)R⁵, or C(O)OR⁵, or adjacent occurrences of R⁷ can be taken together to form a bicyclic alkyl or aryl ring.

[00182] In other specific compounds of formula II, R¹ is C(O)R³.

[00183] In other specific compounds of formula II, R³ is (C₀-C₄)alkyl-(C₂-C₅)heteroaryl, (C₁-C₈)alkyl, aryl, or (C₀-C₄)alkyl-OR⁵.

[00184] In other specific compounds of formula II, heteroaryl is pyridyl, furyl, or thienyl.

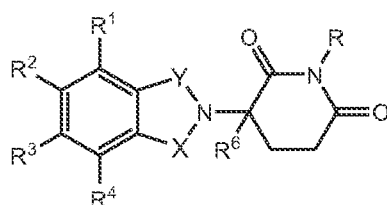
[00185] In other specific compounds of formula II, R¹ is C(O)OR⁴.

[00186] In other specific compounds of formula II, the H of C(O)NHC(O) can be replaced with (C₁-C₄)alkyl, aryl, or benzyl.

[00187] Further examples of the compounds in this class include, but are not limited to: [2-(2,6-dioxo-piperidin-3-yl)-1,3-dioxo-2,3-dihydro-1H-isoindol-4-ylmethyl]-amide; (2-(2,6-dioxo-piperidin-3-yl)-1,3-dioxo-2,3-dihydro-1H-isoindol-4-ylmethyl)-carbamic acid *tert*-butyl ester; 4-(aminomethyl)-2-(2,6-dioxo(3-piperidyl))-isoindoline-1,3-dione; *N*-(2-(2,6-dioxo-piperidin-3-yl)-1,3-dioxo-2,3-dihydro-1H-isoindol-4-ylmethyl)-acetamide; *N*-{(2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl)methyl} cyclopropyl-carboxamide; 2-chloro-*N*-{(2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl)methyl}acetamide; *N*-(2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl)-3-pyridylcarboxamide; 3-{1-oxo-4-(benzylamino)isoindolin-2-yl}piperidine-2,6-dione; 2-(2,6-dioxo(3-piperidyl))-4-(benzylamino)isoindoline-1,3-dione; *N*-{(2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl)methyl}propanamide; *N*-{(2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl)methyl}-3-pyridylcarboxamide; *N*-{(2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl)methyl}heptanamide; *N*-{(2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl)methyl}-2-furylcarboxamide; {*N*-(2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl)carbonyl}methyl

acetate; *N*-(2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl)pentanamide; *N*-(2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl)-2-thienylcarboxamide; *N*-{[2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl] methyl}(butylamino)carboxamide; *N*-{[2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl] methyl}(octylamino)carboxamide; and *N*-{[2-(2,6-dioxo(3-piperidyl))-1,3-dioxoisindolin-4-yl] methyl}(benzylamino)carboxamide.

[00188] Still other specific immunomodulatory compounds disclosed herein belong to a class of isoindole-imides disclosed in U.S. Patent Application Publication Nos. US 2002/0045643, International Publication No. WO 98/54170, and United States Patent No. 6,395,754, each of which is incorporated herein by reference. Representative compounds are of formula III:



III

and pharmaceutically acceptable salts, hydrates, solvates, clathrates, enantiomers, diastereomers, racemates, and mixtures of stereoisomers thereof, wherein:

one of X and Y is C=O and the other is CH₂ or C=O;

R is H or CH₂OCOR';

(i) each of R¹, R², R³, or R⁴, independently of the others, is halo, alkyl of 1 to 4 carbon atoms, or alkoxy of 1 to 4 carbon atoms or (ii) one of R¹, R², R³, or R⁴ is nitro or -NHR⁵ and the remaining of R¹, R², R³, or R⁴ are hydrogen;

R⁵ is hydrogen or alkyl of 1 to 8 carbons

R⁶ hydrogen, alkyl of 1 to 8 carbon atoms, benzo, chloro, or fluoro;

R' is R⁷-CHR¹⁰-N(R⁸R⁹);

R⁷ is m-phenylene or p-phenylene or -(CnH2n)- in which n has a value of 0 to 4;

each of R⁸ and R⁹ taken independently of the other is hydrogen or alkyl of 1 to 8 carbon atoms, or

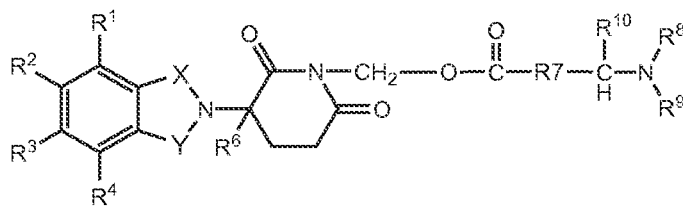
R⁸ and R⁹ taken together are tetramethylene, pentamethylene, hexamethylene,

or -CH₂CH₂X¹CH₂CH₂- in which X¹ is -O-, -S-, or -NH-;

R¹⁰ is hydrogen, alkyl of to 8 carbon atoms, or phenyl; and

* represents a chiral-carbon center.

[00189] Other representative compounds are of formula:



wherein:

one of X and Y is C=O and the other of X and Y is C=O or CH₂;

(i) each of R^1 , R^2 , R^3 , or R^4 , independently of the others, is halo, alkyl of 1 to 4 carbon atoms, or alkoxy of 1 to 4 carbon atoms or (ii) one of R^1 , R^2 , R^3 , and R^4 is $-NHR^5$ and the remaining of R^1 , R^2 , R^3 , and R^4 are hydrogen;

R⁵ is hydrogen or alkyl of 1 to 8 carbon atoms;

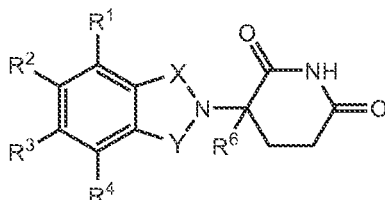
R⁶ is hydrogen, alkyl of 1 to 8 carbon atoms, benzo, chloro, or fluoro;

R^7 is m-phenylene or p-phenylene or $-(C_nH_{2n})-$ in which n has a value of 0 to 4;

each of R⁸ and R⁹ taken independently of the other is hydrogen or alkyl of 1 to 8 carbon atoms, or R⁸ and R⁹ taken together are tetramethylene, pentamethylene, hexamethylene, or -CH₂CH₂X¹CH₂CH₂- in which X¹ is -O-, -S-, or -NH-; and

R¹⁰ is hydrogen, alkyl of to 8 carbon atoms, or phenyl.

[00190] Other representative compounds are of formula:



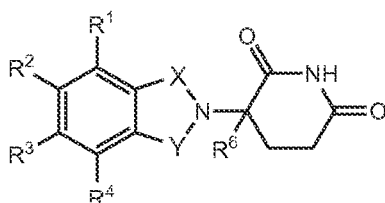
in which

one of X and Y is C=O and the other of X and Y is C=O or CH₂;

each of R¹, R², R³, and R⁴, independently of the others, is halo, alkyl of 1 to 4 carbon atoms, or alkoxy of 1 to 4 carbon atoms or (ii) one of R¹, R², R³, and R⁴ is nitro or protected amino and the remaining of R¹, R², R³, and R⁴ are hydrogen; and

R⁶ is hydrogen, alkyl of 1 to 8 carbon atoms, benzo, chloro, or fluoro.

[00191] Other representative compounds are of formula:



in which:

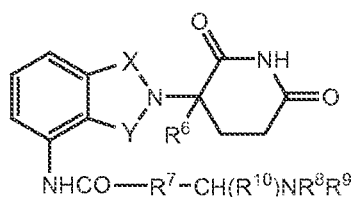
one of X and Y is C=O and the other of X and Y is C=O or CH₂;

(i) each of R¹, R², R³, and R⁴, independently of the others, is halo, alkyl of 1 to 4 carbon atoms, or alkoxy of 1 to 4 carbon atoms or (ii) one of R¹, R², R³, and R⁴ is -NHR⁵ and the remaining of R¹, R², R³, and R⁴ are hydrogen;

R⁵ is hydrogen, alkyl of 1 to 8 carbon atoms, or CO-R⁷-CH(R¹⁰)NR⁸R⁹ in which each of R⁷, R⁸, R⁹, and R¹⁰ is as herein defined; and

R⁶ is alkyl of 1 to 8 carbon atoms, benzo, chloro, or fluoro.

[00192] Specific examples of the compounds are of formula:



in which:

one of X and Y is C=O and the other of X and Y is C=O or CH₂;

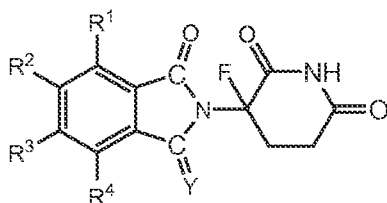
R⁶ is hydrogen, alkyl of 1 to 8 carbon atoms, benzyl, chloro, or fluoro;

R⁷ is m-phenylene, p-phenylene or -(CnH2n)- in which n has a value of 0 to 4;

each of R⁸ and R⁹ taken independently of the other is hydrogen or alkyl of 1 to 8 carbon atoms, or R⁸ and R⁹ taken together are tetramethylene, pentamethylene, hexamethylene, or -CH₂CH₂X¹CH₂CH₂- in which X¹ is -O-, -S- or -NH-; and

R¹⁰ is hydrogen, alkyl of 1 to 8 carbon atoms, or phenyl.

[00193] Other specific immunomodulatory compounds are 1-oxo-2-(2,6-dioxo-3-fluoropiperidin-3-yl) isoindolines and 1,3-dioxo-2-(2,6-dioxo-3-fluoropiperidine-3-yl) isoindolines such as those described in U.S. patent nos. 5,874,448 and 5,955,476, each of which is incorporated herein by reference. Representative compounds are of formula:

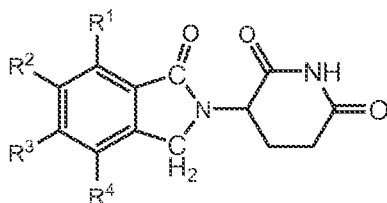


wherein:

Y is oxygen or H₂ and

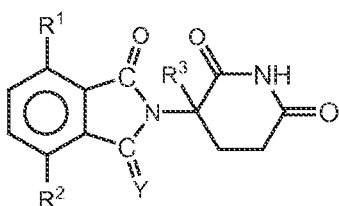
each of R^1 , R^2 , R^3 , and R^4 , independently of the others, is hydrogen, halo, alkyl of 1 to 4 carbon atoms, alkoxy of 1 to 4 carbon atoms, or amino.

[00194] Other specific immunomodulatory compounds are the tetra substituted 2-(2,6-dioxopiperidin-3-yl)-1-oxoisindolines described in U.S. patent no. 5,798,368, which is incorporated herein by reference. Representative compounds are of formula:



wherein each of R^1 , R^2 , R^3 , and R^4 , independently of the others, is halo, alkyl of 1 to 4 carbon atoms, or alkoxy of 1 to 4 carbon atoms.

[00195] Other specific immunomodulatory compounds are 1-oxo and 1,3-dioxo-2-(2,6-dioxopiperidin-3-yl) isoindolines disclosed in U.S. patent no. 6,403,613, which is incorporated herein by reference. Representative compounds are of formula:



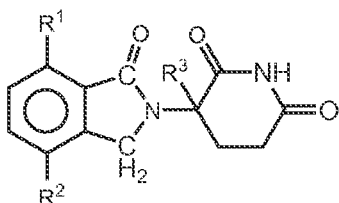
in which

Y is oxygen or H_2 ,

a first of R^1 and R^2 is halo, alkyl, alkoxy, alkylamino, dialkylamino, cyano, or carbamoyl, the second of R^1 and R^2 , independently of the first, is hydrogen, halo, alkyl, alkoxy, alkylamino, dialkylamino, cyano, or carbamoyl, and

R^3 is hydrogen, alkyl, or benzyl.

[00196] Specific examples of the compounds are of formula:

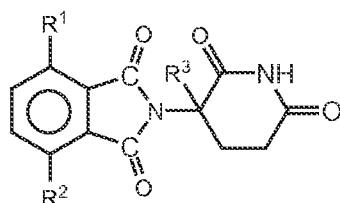


wherein

a first of R^1 and R^2 is halo, alkyl of from 1 to 4 carbon atoms, alkoxy of from 1 to 4 carbon atoms, dialkylamino in which each alkyl is of from 1 to 4 carbon atoms, cyano, or carbamoyl;

the second of R^1 and R^2 , independently of the first, is hydrogen, halo, alkyl of from 1 to 4 carbon atoms, alkoxy of from 1 to 4 carbon atoms, alkylamino in which alkyl is of from 1 to 4 carbon atoms, dialkylamino in which each alkyl is of from 1 to 4 carbon atoms, cyano, or carbamoyl; and R^3 is hydrogen, alkyl of from 1 to 4 carbon atoms, or benzyl. Specific examples include, but are not limited to, 1-oxo-2-(2,6-dioxopiperidin-3-yl)-4-methylisoindoline.

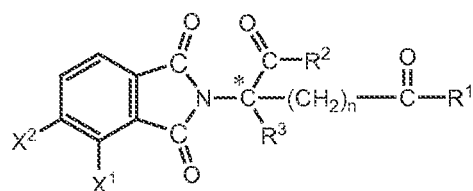
[00197] Other representative compounds are of formula:



wherein:

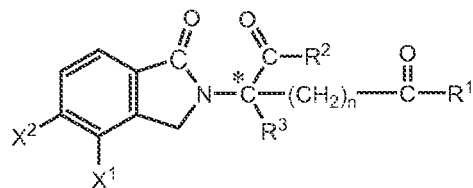
a first of R^1 and R^2 is halo, alkyl of from 1 to 4 carbon atoms, alkoxy of from 1 to 4 carbon atoms, dialkylamino in which each alkyl is of from 1 to 4 carbon atoms, cyano, or carbamoyl; the second of R^1 and R^2 , independently of the first, is hydrogen, halo, alkyl of from 1 to 4 carbon atoms, alkoxy of from 1 to 4 carbon atoms, alkylamino in which alkyl is of from 1 to 4 carbon atoms, dialkylamino in which each alkyl is of from 1 to 4 carbon atoms, cyano, or carbamoyl; and R^3 is hydrogen, alkyl of from 1 to 4 carbon atoms, or benzyl.

[00198] Other specific immunomodulatory compounds disclosed herein are 1-oxo and 1,3-dioxoisindolines substituted in the 4- or 5-position of the indoline ring described in U.S. Patent No. 6,380,239 and U.S. Patent No. 7,244,759, both of which are incorporated herein by reference. Representative compounds are of formula:



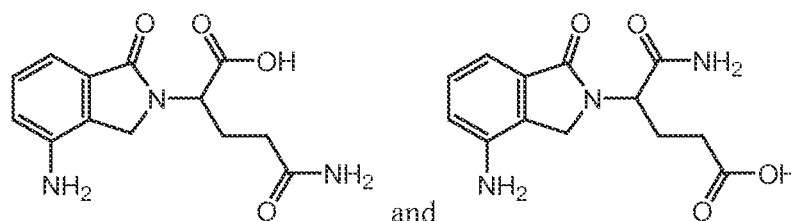
in which the carbon atom designated C* constitutes a center of chirality (when n is not zero and R^1 is not the same as R^2); one of X^1 and X^2 is amino, nitro, alkyl of one to six carbons, or NH-Z, and the other of X^1 or X^2 is hydrogen; each of R^1 and R^2 independent of the other, is hydroxy or NH-Z; R^3 is hydrogen, alkyl of one to six carbons, halo, or haloalkyl; Z is hydrogen, aryl, alkyl of one to six carbons, formyl, or acyl of one to six carbons; and n has a value of 0, 1, or 2; provided that if X^1 is amino, and n is 1 or 2, then R^1 and R^2 are not both hydroxy; and the salts thereof.

[00199] Further representative compounds are of formula:

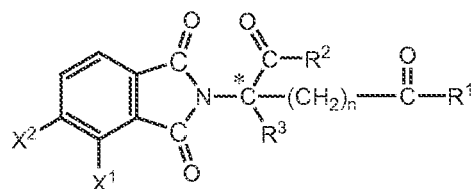


in which the carbon atom designated C* constitutes a center of chirality when n is not zero and R¹ is not R²; one of X¹ and X² is amino, nitro, alkyl of one to six carbons, or NH-Z, and the other of X¹ or X² is hydrogen; each of R¹ and R² independent of the other, is hydroxy or NH-Z; R³ is alkyl of one to six carbons, halo, or hydrogen; Z is hydrogen, aryl or an alkyl or acyl of one to six carbons; and n has a value of 0, 1, or 2.

[00200] Specific examples include, but are not limited to, 2-(4-amino-1-oxo-1,3-dihydro-isoindol-2-yl)-4-carbamoyl-butyric acid and 4-(4-amino-1-oxo-1,3-dihydro-isoindol-2-yl)-4-carbamoyl-butyric acid, which have the following structures, respectively, and pharmaceutically acceptable salts, solvates, prodrugs, and stereoisomers thereof:



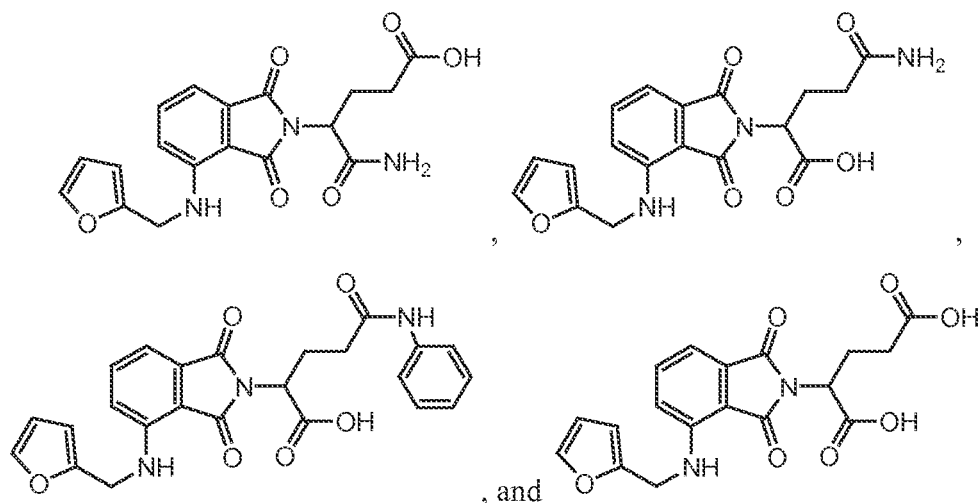
[00201] Other representative compounds are of formula:



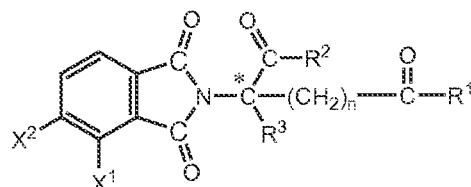
in which the carbon atom designated C* constitutes a center of chirality when n is not zero and R¹ is not R²; one of X¹ and X² is amino, nitro, alkyl of one to six carbons, or NH-Z, and the other of X¹ or X² is hydrogen; each of R¹ and R² independent of the other, is hydroxy or NH-Z; R³ is alkyl of one to six carbons, halo, or hydrogen; Z is hydrogen, aryl, or an alkyl or acyl of one to six carbons; and n has a value of 0, 1, or 2; and the salts thereof.

[00202] Specific examples include, but are not limited to, 4-carbamoyl-4-{4-[(furan-2-yl-methyl)-amino]-1,3-dioxo-1,3-dihydro-isoindol-2-yl}-butyric acid, 4-carbamoyl-2-{4-[(furan-2-yl-methyl)-amino]-1,3-dioxo-1,3-dihydro-isoindol-2-yl}-butyric acid, 2-{4-[(furan-2-yl-methyl)-amino]-1,3-dioxo-1,3-dihydro-isoindol-2-yl}-4-phenylcarbamoyl-butyric acid, and 2-{4-[(furan-2-yl-methyl)-amino]-1,3-dioxo-1,3-dihydro-isoindol-2-yl}-pentanedioic acid, which have the

following structures, respectively, and pharmaceutically acceptable salts, solvate, prodrugs, and stereoisomers thereof:



[00203] Other specific examples of the compounds are of formula:



wherein:

one of X^1 and X^2 is nitro, or NH-Z, and the other of X^1 or X^2 is hydrogen;

each of R^1 and R^2 , independent of the other, is hydroxy or NH-Z;

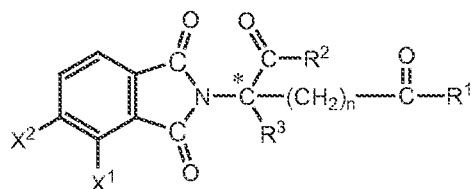
R^3 is alkyl of one to six carbons, halo, or hydrogen;

Z is hydrogen, phenyl, an acyl of one to six carbons, or an alkyl of one to six carbons; and

n has a value of 0, 1, or 2; and

if $-COR^2$ and $-(CH_2)_nCOR^1$ are different, the carbon atom designated C^* constitutes a center of chirality.

[00204] Other representative compounds are of formula:



wherein:

one of X^1 and X^2 is alkyl of one to six carbons;

each of R^1 and R^2 , independent of the other, is hydroxy or NH-Z;

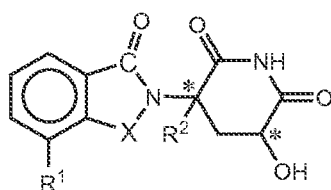
R^3 is alkyl of one to six carbons, halo, or hydrogen;

Z is hydrogen, phenyl, an acyl of one to six carbons, or an alkyl of one to six carbons; and

n has a value of 0, 1, or 2; and

if $-\text{COR}^2$ and $-(\text{CH}_2)_n\text{COR}^1$ are different, the carbon atom designated C^* constitutes a center of chirality.

[00205] Still other specific immunomodulatory compounds are isoindoline-1-one and isoindoline-1,3-dione substituted in the 2-position with 2,6-dioxo-3-hydroxypiperidin-5-yl described in U.S. patent no. 6,458,810, which is incorporated herein by reference. Representative compounds are of formula:



wherein:

the carbon atoms designated * constitute centers of chirality;

X is $-\text{C}(\text{O})-$ or $-\text{CH}_2-$;

R^1 is alkyl of 1 to 8 carbon atoms or $-\text{NHR}^3$;

R^2 is hydrogen, alkyl of 1 to 8 carbon atoms, or halogen; and

R^3 is hydrogen,

alkyl of 1 to 8 carbon atoms, unsubstituted or substituted with alkoxy of 1 to 8 carbon atoms, halo, amino, or alkylamino of 1 to 4 carbon atoms,

cycloalkyl of 3 to 18 carbon atoms,

phenyl, unsubstituted or substituted with alkyl of 1 to 8 carbon atoms, alkoxy of 1 to 8 carbon atoms, halo, amino, or alkylamino of 1 to 4 carbon atoms,

benzyl, unsubstituted or substituted with alkyl of 1 to 8 carbon atoms, alkoxy of 1 to 8 carbon atoms, halo, amino, or alkylamino of 1 to 4 carbon atoms, or $-\text{COR}^4$ in which

R^4 is hydrogen,

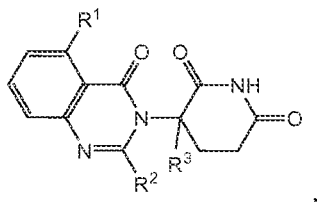
alkyl of 1 to 8 carbon atoms, unsubstituted or substituted with alkoxy of 1 to 8 carbon atoms, halo, amino, or alkylamino of 1 to 4 carbon atoms,

cycloalkyl of 3 to 18 carbon atoms,

phenyl, unsubstituted or substituted with alkyl of 1 to 8 carbon atoms, alkoxy of 1 to 8 carbon atoms, halo, amino, or alkylamino of 1 to 4 carbon atoms, or

benzyl, unsubstituted or substituted with alkyl of 1 to 8 carbon atoms, alkoxy of 1 to 8 carbon atoms, halo, amino, or alkylamino of 1 to 4 carbon atoms.

[00206] Other specific compounds provided herein are of formula:



and pharmaceutically acceptable salts, solvates, and stereoisomers thereof, wherein:

R^1 is: hydrogen; halo; $-(CH_2)_nOH$; (C_1-C_6) alkyl, optionally substituted with one or more halo; (C_1-C_6) alkoxy, optionally substituted with one or more halo; or $-(CH_2)_nNHR^a$, wherein R^a is:

hydrogen;

(C_1-C_6) alkyl, optionally substituted with one or more halo;

$-(CH_2)_n$ -(6 to 10 membered aryl);

$-C(O)-(CH_2)_n$ -(6 to 10 membered aryl) or $-C(O)-(CH_2)_n$ -(6 to 10 membered

heteroaryl), wherein the aryl or heteroaryl is optionally substituted with

one or more of: halo; $-SCF_3$; (C_1-C_6) alkyl, itself optionally substituted with one or more

halo; or (C_1-C_6) alkoxy, itself optionally substituted with one or more halo;

$-C(O)-(C_1-C_8)$ alkyl, wherein the alkyl is optionally substituted with one or more halo;

$-C(O)-(CH_2)_n$ -(C_3-C_{10} -cycloalkyl);

$-C(O)-(CH_2)_n-NR^bR^c$, wherein R^b and R^c are each independently:

hydrogen;

(C_1-C_6) alkyl, optionally substituted with one or more halo;

(C_1-C_6) alkoxy, optionally substituted with one or more halo; or

6 to 10 membered aryl, optionally substituted with one or more of:

halo; (C_1-C_6) alkyl, itself optionally substituted with one or more halo;

or (C_1-C_6) alkoxy, itself optionally substituted with one or more halo;

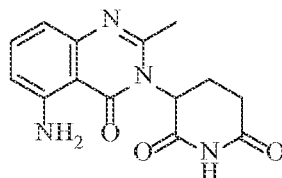
$-C(O)-(CH_2)_n-O-(C_1-C_6)$ alkyl; or

$-C(O)-(CH_2)_n-O-(CH_2)_n$ -(6 to 10 membered aryl);

R^2 is: hydrogen; $-(CH_2)_nOH$; phenyl; $-O-(C_1-C_6)$ alkyl; or (C_1-C_6) alkyl, optionally substituted with one or more halo;

R^3 is: hydrogen; or (C_1-C_6) alkyl, optionally substituted with one or more halo; and n is 0, 1, or 2.

[00207] Specific examples include, but are not limited to, 3-(5-amino-2-methyl-4-oxo-4*H*-quinazolin-3-yl)-piperidine-2,6-dione ("Compound A"), which has the following structure:

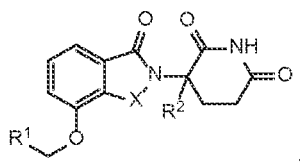


A

or an enantiomer or a mixture of enantiomers thereof; or a pharmaceutically acceptable salt, solvate, hydrate, co-crystal, clathrate, or polymorph thereof.

[00208] Compound A can be prepared according to the methods described in the Examples provided herein or as described in U.S. Pat. No. 7,635,700, the disclosure of which is incorporated herein by reference in its entirety. The compound can be also synthesized according to other methods apparent to those of skill in the art based upon the teaching herein. In certain embodiments, Compound A is in a crystalline form described in U.S. Provisional Pat. App. No. 61/451,806, filed March 11, 2011, which is incorporated herein by reference in its entirety. In some embodiments, the hydrochloride salt of Compound A is used in the methods provided herein. Methods of treating, preventing and/or managing cancers and other diseases using Compound A are described in U.S. Provisional Pat. App. No. 61/451,995, filed March 11, 2011, which is incorporated herein by reference in its entirety.

[00209] Other specific compounds provided herein are of formula:



or a pharmaceutically acceptable salt, solvate or stereoisomer thereof, wherein:

X is $C=O$ or CH_2 ;

R^1 is $-Y-R^3$;

R^2 is H or (C_1-C_6) alkyl;

Y is: 6 to 10 membered aryl, heteroaryl or heterocycle, each of which may be optionally substituted with one or more halogen; or a bond;

R^3 is: $-(CH_2)_n$ -aryl, $-O-(CH_2)_n$ -aryl or $-(CH_2)_n$ -O-aryl, wherein the aryl is optionally substituted with one or more: (C_1-C_6) alkyl, itself optionally substituted with one or more halogen; (C_1-C_6) alkoxy, itself substituted with one or more halogen; oxo; amino; carboxyl; cyano; hydroxyl; halogen; deuterium; 6 to 10 membered aryl or heteroaryl, optionally substituted with one or more (C_1-C_6) alkyl, (C_1-C_6) alkoxy or halogen; $-CONH_2$; or $-COO-(C_1-C_6)$ alkyl, wherein the alkyl may be optionally substituted with one or more halogen;

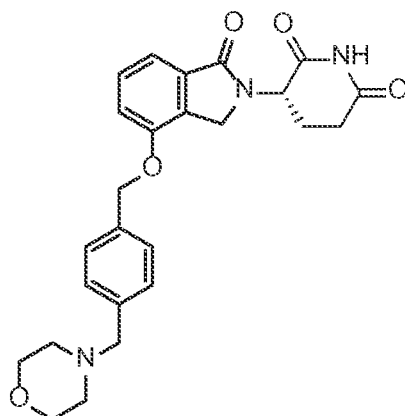
$-(CH_2)_n$ -heterocycle, $-O-(CH_2)_n$ -heterocycle or $-(CH_2)_n$ -O-heterocycle, wherein the heterocycle is optionally substituted with one or more: (C_1-C_6) alkyl, itself optionally substituted with one or more halogen; (C_1-C_6) alkoxy, itself substituted with one or more halogen; oxo; amino; carboxyl; cyano; hydroxyl; halogen; deuterium; 6 to 10 membered aryl or heteroaryl, optionally substituted with one or more (C_1-C_6) alkyl, (C_1-C_6) alkoxy or halogen; $-CONH_2$; or $-COO-(C_1-C_6)$ alkyl, wherein the alkyl may be optionally substituted with one or more halogen; or

$-(CH_2)_n$ -heteroaryl, $-O-(CH_2)_n$ -heteroaryl or $-(CH_2)_n$ -O-heteroaryl, wherein the heteroaryl is optionally substituted with one or more: (C_1-C_6) alkyl, itself optionally substituted with one or more halogen; (C_1-C_6) alkoxy, itself substituted with one or more halogen; oxo; amino; carboxyl; cyano; hydroxyl; halogen; deuterium; 6 to 10 membered aryl or heteroaryl, optionally substituted with one or more (C_1-C_6) alkyl, (C_1-C_6) alkoxy or halogen; $-CONH_2$; or $-COO-(C_1-C_6)$ alkyl, wherein the alkyl may be optionally substituted with one or more halogen; and

n is 0, 1, 2 or 3.

[00210] Specific examples include, but are not limited to, 3-(4-((4-(morpholinomethyl)benzyl)oxy)-1-oxoisindolin-2-yl)piperidine-2,6-dione. In one embodiment, provided herein is the (S) stereoisomer of 3-(4-((4-(morpholinomethyl)benzyl)oxy)-1-oxoisindolin-2-yl)piperidine-2,6-dione ("Compound B") *e.g.*, for use in the methods described herein. Racemic 3-(4-((4-(morpholinomethyl)benzyl)oxy)-1-oxoisindolin-2-yl)piperidine-2,6-dione and methods of preparing the same have been reported in U.S. Patent Publication No.

2011/0196150, which is incorporated herein by reference in its entirety. Compound B has the following structure:



B

[00211] All of the compounds described can either be commercially purchased or prepared according to the methods described in the patents or patent publications disclosed herein. Further, optically pure compounds can be asymmetrically synthesized or resolved using known resolving agents or chiral columns as well as other standard synthetic organic chemistry techniques. Additional information on immunomodulatory compounds, their preparation, and use can be found, for example, in U.S. Patent Application Publication Nos. US20060188475, US20060205787, and US20070049618, each of which is incorporated by reference herein in its entirety.

[00212] The immunomodulatory therapies may be small organic molecules having a molecular weight less than about 1,000 g/mol, and are not proteins, peptides, oligonucleotides, oligosaccharides or other macromolecules.

[00213] It should be noted that if there is a discrepancy between a depicted structure and a name given that structure, the depicted structure is to be accorded more weight. In addition, if the stereochemistry of a structure or a portion of a structure is not indicated with, for example, bold or dashed lines, the structure or portion of the structure is to be interpreted as encompassing all stereoisomers of it.

5.7 Combination Therapy

[00214] One or more additional therapies, such as additional active ingredients or agents, that can be used in combination with an immunomodulatory therapy, such as described in Section 5.6, *supra*. In a specific embodiment, one or more additional active ingredients or agents can be used in the methods and compositions provided herein with an immunomodulatory therapy. The one or

more additional therapies can be administered prior to, concurrently with, or subsequent to the administration of an immunomodulatory therapy. Administration of an immunomodulatory therapy and an additional active agent to a patient can occur simultaneously or sequentially by the same or different routes of administration. The suitability of a particular route of administration employed for a particular active agent will depend on the active agent itself (*e.g.*, whether it can be administered orally without decomposing prior to entering the blood stream) and the cancer being treated. Preferred routes of administration for the additional active agents or ingredients of the invention are known to those of ordinary skill in the art. *See, e.g., Physicians' Desk Reference.*

[00215] In certain embodiments, an immunomodulatory therapy and an additional active agent are cyclically administered to a patient with a hematological cancer (*e.g.*, DLBCL). Cycling therapy involves the administration of an active agent for a period of time, followed by a rest for a period of time, and repeating this sequential administration. Cycling therapy can reduce the development of resistance to one or more of the therapies, avoid or reduce the side effects of one of the therapies, and/or improves the efficacy of the treatment.

[00216] The additional active agents administered in combination with an immunomodulatory therapy can be large molecules (*e.g.*, proteins) or small molecules (*e.g.*, synthetic inorganic, organometallic, or organic molecules). In certain embodiments, the additional active agent is another immunomodulatory therapy. In other embodiments, the additional active agent is not an immunomodulatory therapy. Examples of large molecule active agents include, but are not limited to, hematopoietic growth factors, cytokines, and monoclonal and polyclonal antibodies. In certain embodiments, large molecule active agents are biological molecules, such as naturally occurring or artificially made proteins. Proteins that are useful include proteins that stimulate the survival and/or proliferation of hematopoietic precursor cells and immunologically active poietic cells *in vitro* or *in vivo*. Others stimulate the division and differentiation of committed erythroid progenitors in cells *in vitro* or *in vivo*. Particular proteins include, but are not limited to: interleukins, such as IL-2 (including recombinant IL-2 ("rIL2") and canarypox IL-2), IL-10, IL-12, and IL-18; interferons, such as interferon alfa-2a, interferon alfa-2b, interferon alfa-n1, interferon alfa-n3, interferon beta-I a, and interferon gamma-I b; GM-CSF and GM-CSF; and EPO.

[00217] Particular proteins that can be used in the methods and compositions of the disclosure include, but are not limited to: filgrastim, which is sold in the United States under the trade name NEUPOGEN.RTM. (Amgen, Thousand Oaks, Calif.); sargramostim, which is sold in the United States under the trade name LEUKINE.RTM. (Immunex, Seattle, Wash.); and recombinant EPO,

which is sold in the United States under the trade name EPGEN.RTM. (Amgen, Thousand Oaks, Calif.).

[00218] Inhibitors of ActRII receptors or activin-ActRII inhibitors may be used in the methods and compositions provided herein. ActRII receptors include ActRIIA inhibitors and ActRIIB inhibitors. Inhibitors of ActRII receptors can be polypeptides comprising activin-binding domains of ActRII. In certain embodiments, the activin-binding domain comprising polypeptides are linked to an Fc portion of an antibody (*i.e.*, a conjugate comprising an activin-binding domain comprising polypeptide of an ActRII receptor and an Fc portion of an antibody is generated). In certain embodiments, the activin-binding domain is linked to an Fc portion of an antibody via a linker, *e.g.*, a peptide linker. Examples of such non-antibody proteins selected for activin or ActRIIA binding and methods for design and selection of the same are found in WO/2002/088171, WO/2006/055689, WO/2002/032925, WO/2005/037989, US 2003/0133939, and US 2005/0238646, each of which is incorporated herein by reference in its entirety.

[00219] Recombinant and mutated forms of GM-CSF can be prepared as described in U.S. Pat. Nos. 5,391,485; 5,393,870; and 5,229,496; the disclosure of each of which is incorporated herein by reference in its entirety. Recombinant and mutated forms of G-CSF can be prepared as described in U.S. Pat. Nos. 4,810,643; 4,999,291; 5,528,823; and 5,580,755; the disclosure of each of which is incorporated herein by reference in its entirety.

[00220] This disclosure encompasses the use of native, naturally occurring, and recombinant proteins. The disclosure further encompasses mutants and derivatives (*e.g.*, modified forms) of naturally occurring proteins that exhibit, *in vivo*, at least some of the pharmacological activity of the proteins upon which they are based. Examples of mutants include, but are not limited to, proteins that have one or more amino acid residues that differ from the corresponding residues in the naturally occurring forms of the proteins. Also encompassed by the term “mutants” are proteins that lack carbohydrate moieties normally present in their naturally occurring forms (*e.g.*, nonglycosylated forms). Examples of derivatives include, but are not limited to, pegylated derivatives and fusion proteins, such as proteins formed by fusing IgG1 or IgG3 to the protein or active portion of the protein of interest. *See, e.g.*, Penichet, M. L. and Morrison, S. L., J. Immunol. Methods 248:91-101 (2001).

[00221] Antibodies that can be used in combination with an immunomodulatory therapy include monoclonal and polyclonal antibodies. Examples of antibodies include, but are not limited to, trastuzumab (HERCEPTIN®), rituximab (RITUXAN®), bevacizumab (AVASTIN®), pertuzumab

(OMNITARG™), tositumomab (BEXXAR®), edrecolomab (PANOREX®), panitumumab and G250. An immunomodulatory therapy provided herein can also be combined with or used in combination with anti-TNF-alpha antibodies.

[00222] Large molecule active agents may be administered in the form of anti-cancer vaccines. For example, vaccines that secrete, or cause the secretion of, cytokines such as IL-2, SCF, CXCL4 (platelet factor 4), G-CSF, and GM-CSF can be used in the methods, pharmaceutical compositions, and kits of the disclosure. *See, e.g.,* Emens, L. A., et al., *Curr. Opin. Mol. Ther.* 3(1):77-84 (2001).

[00223] Additional active agents that are small molecules can also be used to alleviate adverse effects associated with the administration of an immunomodulatory therapy. However, like some large molecules, many are believed to be capable of providing a synergistic effect when administered with (*e.g.,* before, after or simultaneously) the immunomodulatory therapy. Examples of small molecule additional active agents include, but are not limited to, anti-cancer agents, antibiotics, immunosuppressive agents, and steroids.

[00224] Examples of anti-cancer agents include, but are not limited to: abraxane; ace-11; acivicin; aclarubicin; acodazole hydrochloride; acronine; adozelesin; aldesleukin; altretamine; ambomycin; ametantrone acetate; amrubicin; amsacrine; anastrozole; anthramycin; asparaginase; asperlin; azacitidine; azetepa; azotomycin; batimastat; benzodepa; bicalutamide; bisantrene hydrochloride; bisnafide dimesylate; bizelesin; bleomycin sulfate; brequinar sodium; bropiramine; busulfan; cactinomycin; calusterone; caracemide; carbetimer; carboplatin; carmustine; carubicin hydrochloride; carzelesin; cedefingol; celecoxib (COX-2 inhibitor); chlorambucil; cirolemycin; cisplatin; cladribine; crisnatol mesylate; cyclophosphamide; cytarabine; dacarbazine; dactinomycin; daunorubicin hydrochloride; decitabine; dexormaplatin; dezaguanine; dezaguanine mesylate; diaziquone; docetaxel; doxorubicin; doxorubicin hydrochloride; droloxifene; droloxifene citrate; dromostanolone propionate; duazomycin; edatrexate; eflornithine hydrochloride; elsamitrucin; enloplatin; enpromate; epipropidine; epirubicin hydrochloride; erbulozole; esorubicin hydrochloride; estramustine; estramustine phosphate sodium; etanidazole; etoposide; etoposide phosphate; etoprine; fadrozole hydrochloride; fazarabine; fenretinide; floxuridine; fludarabine phosphate; fluorouracil; fluorocitabine; fosquidone; fostriecin sodium; gemcitabine; gemcitabine hydrochloride; herceptin; hydroxyurea; idarubicin hydrochloride; ifosfamide; ilmofofosine; iproplatin; irinotecan; irinotecan hydrochloride; lanreotide acetate; lapatinib; letrozole; leuprolide acetate; liarozole hydrochloride; lometrexol sodium; lomustine; losoxantrone hydrochloride; masoprocil;

maytansine; mechlorethamine hydrochloride; megestrol acetate; melengestrol acetate; melphalan; menogaril; mercaptopurine; methotrexate; methotrexate sodium; metoprine; meturedapa; mitindomide; mitocarcin; mitocromin; mitogillin; mitomalcin; mitomycin; mitosper; mitotane; mitoxantrone hydrochloride; mycophenolic acid; nocodazole; nogalamycin; ormaplatin; oxisuran; paclitaxel; pegaspargase; peliomycin; pentamustine; peplomycin sulfate; perfosfamide; pipobroman; piposulfan; piroxantrone hydrochloride; plicamycin; plomestane; porflmer sodium; porfiromycin; prednimustine; procarbazine hydrochloride; puromycin; puromycin hydrochloride; pyrazofurin; riboprime; romidepsin; safingol; safingol hydrochloride; semustine; simtrazene; sparfosate sodium; sparsomycin; spirogermanium hydrochloride; spiromustine; spiroplatin; stem cell treatments such as PDA-001; streptonigrin; streptozocin; sulofenur; talisomycin; tecogalan sodium; taxotere; tegafur; teloxantrone hydrochloride; temoporfin; teniposide; teroxirone; testolactone; thiamiprine; thioguanine; thiotepa; tiazofurin; tirapazamine; toremifene citrate; trestolone acetate; triciribine phosphate; trimetrexate; trimetrexate glucuronate; triptorelin; tubulazole hydrochloride; uracil mustard; uredepa; vapreotide; verteporfin; vinblastine sulfate; vincristine sulfate; vindesine; vindesine sulfate; vinepidine sulfate; vinglycinate sulfate; vinleurosine sulfate; vinorelbine tartrate; vinrosidine sulfate; vinzolidine sulfate; vorozole; zeniplatin; zinostatin; and zorubicin hydrochloride.

[00225] Other anti-cancer drugs include, but are not limited to: 20-epi-1,25 dihydroxyvitamin D3; 5-ethynyluracil; abiraterone; aclarubicin; acylfulvene; adecypenol; adozelesin; aldesleukin; ALL-TK antagonists; altretamine; ambamustine; amidox; amifostine; aminolevulinic acid; amrubicin; amsacrine; anagrelide; anastrozole; andrographolide; angiogenesis inhibitors; antagonist D; antagonist G; antarelix; anti-dorsalizing morphogenetic protein-1; antiandrogen, prostatic carcinoma; antiestrogen; antineoplaston; antisense oligonucleotides; aphidicolin glycinate; apoptosis gene modulators; apoptosis regulators; apurinic acid; ara-CDP-DL-PTBA; arginine deaminase; asulacrine; atamestane; atrimustine; axinastatin 1; axinastatin 2; axinastatin 3; azasetron; azatoxin; azatyrosine; baccatin III derivatives; balanol; batimastat; BCR/ABL antagonists; benzochlorins; benzoylstaurosporine; beta lactam derivatives; beta-alethine; betaclamycin B; betulinic acid; b-FGF inhibitor; bicalutamide; bisantrene; bisaziridinylspermine; bisnafide; bistratene A; bizelesin; breflate; broprimine; budotitane; buthionine sulfoximine; calcipotriol; calphostin C; camptothecin derivatives; capecitabine; carboxamide-amino-triazole; carboxyamidotriazole; CaRest M3; CARN 700; cartilage derived inhibitor; carzelesin; casein kinase inhibitors (ICOS); castanospermine; cecropin B; cetorelix; chlorins; chloroquinoxaline

sulfonamide; cicaprost; cis-porphyrin; cladribine; clomifene analogues; clotrimazole; collismycin A; collismycin B; combretastatin A4; combretastatin analogue; conagenin; crambescidin 816; crisnatol; cryptophycin 8; cryptophycin A derivatives; curacin A; cyclopentantraquinones; cycloplatam; cypemycin; cytarabine ocfosfate; cytolytic factor; cytostatin; dacliximab; decitabine; dehydrodidemnin B; deslorelin; dexamethasone; dexifosfamide; dexrazoxane; dexverapamil; diaziquone; didemnin B; didox; diethylnorspermine; dihydro-5-azacytidine; dihydrotaxol, 9-; dioxamycin; diphenyl spiromustine; docetaxel; docosanol; dolasetron; doxifluridine; doxorubicin; droloxifene; dronabinol; duocarmycin SA; ebselen; ecomustine; edelfosine; edrecolomab; eflornithine; elemene; emitefur; epirubicin; epristeride; estramustine analogue; estrogen agonists; estrogen antagonists; etanidazole; etoposide phosphate; exemestane; fadrozole; fazarabine; fenretinide; filgrastim; finasteride; flavopiridol; flezelastine; fluasterone; fludarabine; fluorodaunorubicin hydrochloride; forfenimex; formestane; fostriecin; fotemustine; gadolinium texaphyrin; gallium nitrate; galocitabine; ganirelix; gelatinase inhibitors; gemcitabine; glutathione inhibitors; hepsulfam; heregulin; hexamethylene bisacetamide; hypericin; ibandronic acid; idarubicin; idoxifene; idramantone; ilmofofosine; ilomastat; imatinib (*e.g.*, GLEEVEC®), imiquimod; immunostimulant peptides; insulin-like growth factor-1 receptor inhibitor; interferon agonists; interferons; interleukins; iobenguane; iododoxorubicin; ipomeanol, 4-; iroplact; irsogladine; isobengazole; isohomohalicondrin B; itasetron; jasplakinolide; kahalalide F; lamellarin-N triacetate; lanreotide; leinamycin; lenograstim; lentinan sulfate; leptolstatin; letrozole; leukemia inhibiting factor; leukocyte alpha interferon; leuprolide+estrogen+progesterone; leuprorelin; levamisole; liarozole; linear polyamine analogue; lipophilic disaccharide peptide; lipophilic platinum compounds; lissoclinamide 7; lobaplatin; lombricine; lometrexol; lonidamine; losoxantrone; loxoribine; lurtotecan; lutetium texaphyrin; lysofylline; lytic peptides; maitansine; mannostatin A; marimastat; masoprocil; maspin; matrilysin inhibitors; matrix metalloproteinase inhibitors; menogaril; merbarone; meterelin; methioninase; metoclopramide; MIF inhibitor; mifepristone; miltefosine; mirimostim; mitoguazone; mitolactol; mitomycin analogues; mitonafide; mitotoxin fibroblast growth factor-saporin; mitoxantrone; mofarotene; molgramostim; Erbitux, human chorionic gonadotrophin; monophosphoryl lipid A+myobacterium cell wall sk; mopidamol; mustard anticancer agent; mycaperoxide B; mycobacterial cell wall extract; myriaporone; N-acetyldinaline; N-substituted benzamides; nafarelin; nagrestip; naloxone+pentazocine; napavin; naphterpin; nartograstim; nedaplatin; nemorubicin; neridronic acid; nilutamide; nisamycin; nitric oxide modulators; nitroxide antioxidant; nitrullyn; oblimersen (GENASENSE®); O.sup.6-

benzylguanine; octreotide; okicenone; oligonucleotides; onapristone; ondansetron; ondansetron; oracin; oral cytokine inducer; ormaplatin; osaterone; oxaliplatin; oxaunomycin; paclitaxel; paclitaxel analogues; paclitaxel derivatives; palauamine; palmitoylrhizoxin; pamidronic acid; panaxytriol; panomifene; parabactin; pazelliptine; pegaspargase; peldesine; pentosan polysulfate sodium; pentostatin; pentrozole; perflubron; perfosfamide; perillyl alcohol; phenazinomycin; phenylacetate; phosphatase inhibitors; picibanil; pilocarpine hydrochloride; pirarubicin; piritrexim; placetin A; placetin B; plasminogen activator inhibitor; platinum complex; platinum compounds; platinum-triamine complex; porfimer sodium; porfiromycin; prednisone; propyl bis-acridone; prostaglandin J2; proteasome inhibitors; protein A-based immune modulator; protein kinase C inhibitor; protein kinase C inhibitors, microalgal; protein tyrosine phosphatase inhibitors; purine nucleoside phosphorylase inhibitors; purpurins; pyrazoloacridine; pyridoxylated hemoglobin polyoxyethylene conjugate; raf antagonists; raltitrexed; ramosetron; ras farnesyl protein transferase inhibitors; ras inhibitors; ras-GAP inhibitor; retelliptine demethylated; rhenium Re 186 etidronate; rhizoxin; ribozymes; RII retinamide; rohitukine; romurtide; roquinimex; rubiginone B1; ruboxyl; safingol; saintopin; SarCNU; sarcophytol A; sargramostim; Sdi 1 mimetics; semustine; senescence derived inhibitor 1; sense oligonucleotides; signal transduction inhibitors; sizofuran; sobuzoxane; sodium borocaptate; sodium phenylacetate; solverol; somatomedin binding protein; sonermin; sparfosic acid; spicamycin D; spiromustine; splenopentin; spongistatin 1; squalamine; stipiamide; stromelysin inhibitors; sulfinosine; superactive vasoactive intestinal peptide antagonist; suradista; suramin; swainsonine; tallimustine; tamoxifen methiodide; tauromustine; tazarotene; tecogalan sodium; tegafur; tellurapyrylium; telomerase inhibitors; temoporfin; teniposide; tetrachlorodecaoxide; tetrazomine; thaliblastine; thiocoraline; thrombopoietin; thrombopoietin mimetic; thymalfasin; thymopoietin receptor agonist; thymotrinan; thyroid stimulating hormone; tin ethyl etiopurpurin; tirapazamine; titanocene bichloride; topsentin; toremifene; translation inhibitors; tretinoin; triacetyluridine; tricyriline; trimetrexate; triptorelin; tropisetron; turosteride; tyrosine kinase inhibitors; tyrphostins; UBC inhibitors; ubenimex; urogenital sinus-derived growth inhibitory factor; urokinase receptor antagonists; vapreotide; variolin B; velaresol; veramine; verdins; verteporfin; vinorelbine; vinxaltine; vitaxin; vorozole; zanoterone; zeniplatin; zilascorb; and zinostatin stimalamer.

[00226] Specific additional active agents include, but are not limited to, oblimersen (GENASSENSE®), remicade, docetaxel, celecoxib, melphalan, dexamethasone (DECADRON®), steroids, gemcitabine, cisplatin, temozolomide, etoposide, cyclophosphamide, temodar,

carboplatin, procarbazine, gliadel, tamoxifen, topotecan, methotrexate, ARISA®, taxol, taxotere, fluorouracil, leucovorin, irinotecan, xeloda, CPT-11, interferon alpha, pegylated interferon alpha (*e.g.*, PEG INTRON-A), capecitabine, cisplatin, thiotepa, fludarabine, carboplatin, liposomal daunorubicin, cytarabine, doxorubicin, paclitaxel, vinblastine, IL-2, GM-CSF, dacarbazine, vinorelbine, zoledronic acid, palmitronate, biaxin, busulphan, prednisone, bisphosphonate, arsenic trioxide, vincristine, doxorubicin (DOXIL®), paclitaxel, ganciclovir, adriamycin, estramustine sodium phosphate) (EMCYT.degree.), sulindac, and etoposide.

5.8 Biological Samples

[00227] In certain embodiments, the various methods provided herein use samples (*e.g.*, biological samples) from subjects or individuals (*e.g.*, patients). In a specific embodiment, the subject is a patient with a hematological cancer, such as multiple myeloma, leukemia or a lymphoma. The subject can be a mammal, for example, a human. The subject can be male or female, and can be an adult, child or infant. Samples can be analyzed at a time during an active phase of a disease or disorder, or when a disease or disorder is inactive. In a specific embodiment, a sample is obtained from a subject prior, concurrently with and/or subsequent to administration of an immunomodulatory therapy. In certain embodiments, more than one sample from a subject can be obtained.

[00228] In certain embodiments, the sample used in the methods provided herein comprises body fluids from a subject. Non-limiting examples of body fluids include blood (*e.g.*, peripheral whole blood, peripheral blood), blood plasma, amniotic fluid, aqueous humor, bile, cerumen, cowper's fluid, pre-ejaculatory fluid, chyle, chyme, female ejaculate, interstitial fluid, lymph, menses, breast milk, mucus, pleural fluid, pus, saliva, sebum, semen, serum, sweat, tears, urine, vaginal lubrication, vomit, water, feces, internal body fluids, including cerebrospinal fluid surrounding the brain and the spinal cord, synovial fluid surrounding bone joints, intracellular fluid is the fluid inside cells, and vitreous humour the fluids in the eyeball. In some embodiments, the sample is a blood sample. The blood sample can be obtained using conventional techniques as described in, *e.g.* Innis *et al*, editors, PCR Protocols (Academic Press, 1990). White blood cells can be separated from blood samples using convention techniques or commercially available kits, *e.g.* RosetteSep™ kit (Stein Cell Technologies, Vancouver, Canada). Sub-populations of white blood cells, *e.g.* mononuclear cells, B cells, T cells, monocytes, granulocytes or lymphocytes, can be further isolated using conventional

techniques, *e.g.* magnetically activated cell sorting (MACS) (Miltenyi Biotec, Auburn, California) or fluorescently activated cell sorting (FACS) (Becton Dickinson, San Jose, California).

[00229] In one embodiment, the blood sample is from about 0.1 mL to about 10.0 mL, from about 0.2 mL to about 7 mL, from about 0.3 mL to about 5 mL, from about 0.4 mL to about 3.5 mL, or from about 0.5 mL to about 3 mL. In another embodiment, the blood sample is about 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 6.0, 7.0, 8.0, 9.0 or 10.0 mL.

[00230] In some embodiments, the sample used in the present methods comprises a biopsy (*e.g.*, a tumor biopsy). The biopsy can be from any organ or tissue, for example, skin, liver, lung, heart, colon, kidney, bone marrow, teeth, lymph node, hair, spleen, brain, breast, or other organs. Any biopsy technique known by those skilled in the art can be used for isolating a sample from a subject, for instance, open biopsy, close biopsy, core biopsy, incisional biopsy, excisional biopsy, or fine needle aspiration biopsy.

[00231] In one embodiment, the sample used in the methods provided herein is obtained from the subject prior to the subject receiving a treatment for the hematological cancer. In another embodiment, the sample is obtained from the subject during the subject receiving a treatment for the hematological cancer. In another embodiment, the sample is obtained from the subject after the subject receiving a treatment for the hematological cancer. In various embodiments, the treatment comprises administering an immunomodulatory therapy (*e.g.*, a compound provided in Section 5.6) to the subject.

[00232] In certain embodiments, the sample used in the methods provided herein comprises a plurality of cells. Such cells can include any type of cells, *e.g.*, stem cells, blood cells (*e.g.*, peripheral blood mononuclear cells), lymphocytes, B cells, T cells, monocytes, granulocytes, immune cells, or tumor or cancer cells. The tumor or cancer cells or a tumor tissue, such as a tumor biopsy or a tumor explants. T cells (T lymphocytes) include, for example, helper T cells (effector T cells or Th cells), cytotoxic T cells (CTLs), memory T cells, and regulatory T cells. In one embodiment, the cells used in the methods provided herein are CD3⁺ T cells, *e.g.*, as detected by flow cytometry. The number of T cells used in the methods can range from a single cell to about 10⁹ cells. B cells (B lymphocytes) include, for example, plasma B cells, dendritic cells, memory B cells, B1 cells, B2 cells, marginal-zone B cells, and follicular B cells. B cells can express immunoglobulins (antibodies, B cell receptor).

[00233] Specific cell populations can be obtained using a combination of commercially available antibodies (*e.g.*, Quest Diagnostic (San Juan Capistrano, Calif.); Dako (Denmark)).

[00234] In some embodiments, the cancer is a hematological cancer. In one embodiment, the blood cancer is multiple myeloma. In another embodiment, the blood cancer is chronic lymphocytic leukemia (CLL). In another embodiment, the blood cancer is DLBCL. In another embodiment, the blood cancer is myelodysplastic syndrome, an acute leukemia, *e.g.*, acute T cell leukemia, acute myelogenous leukemia (AML), acute promyelocytic leukemia, acute myeloblastic leukemia, acute megakaryoblastic leukemia, precursor B acute lymphoblastic leukemia, precursor T acute lymphoblastic leukemia, Burkitt's leukemia (Burkitt's lymphoma), or acute biphenotypic leukemia; a chronic leukemia, *e.g.*, chronic myeloid lymphoma, chronic myelogenous leukemia (CML), chronic monocytic leukemia, Small lymphocytic lymphoma, or B-cell prolymphocytic leukemia; hairy cell lymphoma; T-cell prolymphocytic leukemia; or a lymphoma, *e.g.*, histiocytic lymphoma, lymphoplasmacytic lymphoma (*e.g.*, Waldenström macroglobulinemia), splenic marginal zone lymphoma, plasma cell neoplasm (*e.g.*, plasma cell myeloma, plasmacytoma, a monoclonal immunoglobulin deposition disease, or a heavy chain disease), extranodal marginal zone B cell lymphoma (MALT lymphoma), nodal marginal zone B cell lymphoma (NMZL), follicular lymphoma, mantle cell lymphoma, diffuse large B cell lymphoma, mediastinal (thymic) large B cell lymphoma, intravascular large B cell lymphoma, primary effusion lymphoma, T cell large granular lymphocytic leukemia, aggressive NK cell leukemia, adult T cell leukemia/lymphoma, extranodal NK/T cell lymphoma, nasal type, enteropathy-type T cell lymphoma, hepatosplenic T cell lymphoma, blastic NK cell lymphoma, mycosis fungoides (Sezary syndrome), a primary cutaneous CD30-positive T cell lymphoproliferative disorder (*e.g.*, primary cutaneous anaplastic large cell lymphoma or lymphomatoid papulosis), angioimmunoblastic T cell lymphoma, peripheral T cell lymphoma, unspecified, anaplastic large cell lymphoma, a Hodgkin's lymphoma or a nodular lymphocyte-predominant Hodgkin's lymphoma.

[00235] In certain embodiments, the sample used in the methods provided herein is from a diseased tissue, *e.g.*, from an individual having a hematological cancer. In certain embodiments, the number of cells used in the methods provided herein can range from a single cell to about 10^9 cells. In some embodiments, the number of cells used in the methods provided herein is about 1×10^4 , 5×10^4 , 1×10^5 , 5×10^5 , 1×10^6 , 5×10^6 , 1×10^7 , 5×10^7 , 1×10^8 , or 5×10^8 .

[00236] The number and type of cells collected from a subject can be monitored, for example, by measuring changes in morphology and cell surface markers using standard cell detection techniques such as flow cytometry, cell sorting, immunocytochemistry (*e.g.*, staining with tissue specific or cell-marker specific antibodies) fluorescence activated cell sorting (FACS), magnetic activated cell

sorting (MACS), by examination of the morphology of cells using light or confocal microscopy, and/or by measuring changes in gene expression using techniques well known in the art, such as PCR and gene expression profiling. These techniques can be used, too, to identify cells that are positive for one or more particular markers. Fluorescence activated cell sorting (FACS) is a well-known method for separating particles, including cells, based on the fluorescent properties of the particles (Kamarch, 1987, *Methods Enzymol*, 151:150-165). Laser excitation of fluorescent moieties in the individual particles results in a small electrical charge allowing electromagnetic separation of positive and negative particles from a mixture. In one embodiment, cell surface marker-specific antibodies or ligands are labeled with distinct fluorescent labels. Cells are processed through the cell sorter, allowing separation of cells based on their ability to bind to the antibodies used. FACS sorted particles may be directly deposited into individual wells of 96-well or 384-well plates to facilitate separation and cloning.

[00237] In certain embodiments, subsets of cells are used in the methods provided herein. Methods to sort and isolate specific populations of cells are well-known in the art and can be based on cell size, morphology, or intracellular or extracellular markers. Such methods include, but are not limited to, flow cytometry, flow sorting, FACS, bead based separation such as magnetic cell sorting, size-based separation (*e.g.*, a sieve, an array of obstacles, or a filter), sorting in a microfluidics device, antibody-based separation, sedimentation, affinity adsorption, affinity extraction, density gradient centrifugation, laser capture microdissection, *etc.*

5.9 Methods for Detecting RNA Expression

[00238] Several methods of detecting or quantitating mRNA levels are known in the art. Exemplary methods include but are not limited to northern blots, ribonuclease protection assays, PCR-based methods, and the like. The mRNA sequence can be used to prepare a probe that is at least partially complementary. The probe can then be used to detect the mRNA sequence in a sample, using any suitable assay, such as PCR-based methods, Northern blotting, a dipstick assay, and the like.

[00239] In other embodiments, a nucleic acid assay for testing for immunomodulatory activity in a biological sample can be prepared. An assay typically contains a solid support and at least one nucleic acid contacting the support, where the nucleic acid corresponds to at least a portion of an mRNA encoded by a gene listed in Table 1, 2, 3 or 4. The assay can also have a means for detecting the altered expression of the mRNA in the sample.

[00240] The assay method can be varied depending on the type of mRNA information desired. Exemplary methods include but are not limited to Northern blots and PCR-based methods (*e.g.*, qRT-PCR). Methods such as qRT-PCR can also accurately quantitate the amount of the mRNA in a sample.

[00241] Any suitable assay platform can be used to determine the presence of the mRNA in a sample. For example, an assay may be in the form of a dipstick, a membrane, a chip, a disk, a test strip, a filter, a microsphere, a slide, a multiwell plate, or an optical fiber. An assay system may have a solid support on which a nucleic acid corresponding to the mRNA is attached. The solid support may comprise, for example, a plastic, silicon, a metal, a resin, glass, a membrane, a particle, a precipitate, a gel, a polymer, a sheet, a sphere, a polysaccharide, a capillary, a film a plate, or a slide. The assay components can be prepared and packaged together as a kit for detecting an mRNA.

[00242] The nucleic acid can be labeled, if desired, to make a population of labeled mRNAs. In general, a sample can be labeled using methods that are well known in the art (*e.g.*, using DNA ligase, terminal transferase, or by labeling the RNA backbone, *etc.*; *see, e.g.*, Ausubel, *et al.*, *Short Protocols in Molecular Biology*, 3rd ed., Wiley & Sons 1995 and Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Third Edition, 2001 Cold Spring Harbor, N.Y.). In some embodiments, the sample is labeled with fluorescent label. Exemplary fluorescent dyes include but are not limited to xanthene dyes, fluorescein dyes, rhodamine dyes, fluorescein isothiocyanate (FITC), 6 carboxyfluorescein (FAM), 6 carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 6 carboxy 4', 5' dichloro 2', 7' dimethoxyfluorescein (JOE or J), N,N,N',N' tetramethyl 6 carboxyrhodamine (TAMRA or T), 6 carboxy X rhodamine (ROX or R), 5 carboxyrhodamine 6G (R6G5 or G5), 6 carboxyrhodamine 6G (R6G6 or G6), and rhodamine 110; cyanine dyes, *e.g.* Cy3, Cy5 and Cy7 dyes; Alexa dyes, *e.g.* Alexa-fluor-555; coumarin, Diethylaminocoumarin, umbelliferone; benzimide dyes, *e.g.* Hoechst 33258; phenanthridine dyes, *e.g.* Texas Red; ethidium dyes; acridine dyes; carbazole dyes; phenoxazine dyes; porphyrin dyes; polymethine dyes, BODIPY dyes, quinoline dyes, Pyrene, Fluorescein Chlorotriazinyl, R110, Eosin, JOE, R6G, Tetramethylrhodamine, Lissamine, ROX, Naphthofluorescein, and the like.

[00243] In some embodiments, the mRNA sequences comprise at least one mRNA selected from the mRNAs encoded by the genes listed in Table 3, or a fragment thereof. The nucleic acids may be present in specific, addressable locations on a solid support; each corresponding to at least a portion

of mRNA sequences that are differentially expressed upon treatment of an immunomodulatory compound in a cell or a patient.

[00244] A typical mRNA assay method can contain the steps of 1) obtaining surface-bound subject probes; 2) hybridization of a population of mRNAs to the surface-bound probes under conditions sufficient to provide for specific binding (3) post-hybridization washes to remove nucleic acids not bound in the hybridization; and (4) detection of the hybridized mRNAs. The reagents used in each of these steps and their conditions for use may vary depending on the particular application.

[00245] Hybridization can be carried out under suitable hybridization conditions, which may vary in stringency as desired. Typical conditions are sufficient to produce probe/target complexes on a solid surface between complementary binding members, *i.e.*, between surface-bound subject probes and complementary mRNAs in a sample. In certain embodiments, stringent hybridization conditions may be employed.

[00246] Hybridization is typically performed under stringent hybridization conditions. Standard hybridization techniques (*e.g.* under conditions sufficient to provide for specific binding of target mRNAs in the sample to the probes) are described in Kallioniemi *et al.*, *Science* 258:818-821 (1992) and WO 93/18186. Several guides to general techniques are available, *e.g.*, Tijssen, *Hybridization with Nucleic Acid Probes*, Parts I and II (Elsevier, Amsterdam 1993). For descriptions of techniques suitable for *in situ* hybridizations, see Gall *et al. Meth. Enzymol.*, 21:470-480 (1981); and Angerer *et al.* in *Genetic Engineering: Principles and Methods* (Setlow and Hollaender, Eds.) Vol 7, pgs 43-65 (Plenum Press, New York 1985). Selection of appropriate conditions, including temperature, salt concentration, polynucleotide concentration, hybridization time, stringency of washing conditions, and the like will depend on experimental design, including source of sample, identity of capture agents, degree of complementarity expected, *etc.*, and may be determined as a matter of routine experimentation for those of ordinary skill in the art.

[00247] Those of ordinary skill will readily recognize that alternative but comparable hybridization and wash conditions can be utilized to provide conditions of similar stringency.

[00248] After the mRNA hybridization procedure, the surface bound polynucleotides are typically washed to remove unbound nucleic acids. Washing may be performed using any convenient washing protocol, where the washing conditions are typically stringent, as described above. The hybridization of the target mRNAs to the probes is then detected using standard techniques.

[00249] Other methods, such as PCR-based methods, can also be used to follow the expression of the genes in Table 1, 2, or 3. Examples of PCR methods can be found in the literature. Examples of PCR assays can be found in U.S. Patent No. 6,927,024, which is incorporated by reference herein in its entirety. Examples of RT-PCR methods can be found in U.S. Patent No. 7,122,799, which is incorporated by reference herein in its entirety. A method of fluorescent in situ PCR is described in U.S. Patent No. 7,186,507, which is incorporated by reference herein in its entirety.

[00250] In some embodiments, Real-Time Reverse Transcription-PCR (qRT-PCR) can be used for both the detection and quantification of RNA targets (Bustin, *et al.*, 2005, *Clin. Sci.*, 109:365-379). Quantitative results obtained by qRT-PCR are generally more informative than qualitative data. Thus, in some embodiments, qRT-PCR-based assays can be useful to measure mRNA levels during cell-based assays. The qRT-PCR method is also useful to monitor patient therapy. Examples of qRT-PCR-based methods can be found, for example, in U.S. Patent No. 7,101,663, which is incorporated by reference herein in its entirety.

[00251] In contrast to regular reverse transcriptase-PCR and analysis by agarose gels, real-time PCR gives quantitative results. An additional advantage of real-time PCR is the relative ease and convenience of use. Instruments for real-time PCR, such as the Applied Biosystems 7500, are available commercially, as are the reagents, such as TaqMan Sequence Detection chemistry. For example, TaqMan[®] Gene Expression Assays can be used, following the manufacturer's instructions. These kits are pre-formulated gene expression assays for rapid, reliable detection and quantification of human, mouse and rat mRNA transcripts. An exemplary PCR program, for example, is 50°C for 2 minutes, 95°C for 10 minutes, 40 cycles of 95°C for 15 seconds, then 60°C for 1 minute.

[00252] To determine the cycle number at which the fluorescence signal associated with a particular amplicon accumulation crosses the threshold (referred to as the CT), the data can be analyzed, for example, using a 7500 Real-Time PCR System Sequence Detection software v1.3 using the comparative CT relative quantification calculation method. Using this method, the output is expressed as a fold-change of expression levels. In some embodiments, the threshold level can be selected to be automatically determined by the software. In some embodiments, the threshold level is set to be above the baseline but sufficiently low to be within the exponential growth region of an amplification curve.

5.10 Methods for Detecting Protein Expression

[00253] Several protein detection and quantitation methods can be used to measure the level of proteins. Any suitable protein quantitation method can be used. In some embodiments, antibody-based methods are used. Exemplary methods that can be used include but are not limited to immunoblotting (western blot), enzyme-linked immunosorbent assay (ELISA), immunohistochemistry, flow cytometry, cytometric bead array, mass spectroscopy, and the like. Several types of ELISA are commonly used, including direct ELISA, indirect ELISA, and sandwich ELISA.

5.11 Kits

[00254] In one aspect, provided herein are pharmaceutical or assay kits comprising an immunomodulatory therapy or a pharmaceutical composition thereof, in one or more containers, and instructions for use. In certain embodiments, the kits useful for predicting the likelihood of an effective patient tumor response. In further embodiments, the immunomodulatory therapy, in a container, is accompanied by an apparatus or apparatus necessary for administering the compound or composition thereof to a subject.

[00255] In certain embodiments, a kit comprises an immunomodulatory therapy or pharmaceutical composition thereof, in a container, and a reagent or reagents necessary for carrying out an assay(s) described herein, in one or more other containers. In certain embodiments, the kit comprises a solid support, and a means for detecting the RNA or protein expression of at least one biomarker (e.g., a differentially expressed gene identified in Table 1, 2, 3, or 4) in a biological sample. Such a kit may employ, for example, a dipstick, a membrane, a chip, a disk, a test strip, a filter, a microsphere, a slide, a multiwell plate, or an optical fiber. The solid support of the kit can be, for example, a plastic, silicon, a metal, a resin, glass, a membrane, a particle, a precipitate, a gel, a polymer, a sheet, a sphere, a polysaccharide, a capillary, a film, a plate, or a slide.

[00256] In a specific embodiment, the pharmaceutical or assay kit comprises, in a container, an immunomodulatory therapy or a pharmaceutical composition thereof, and further comprises, in one or more containers, components for isolating RNA. In another specific embodiment, the pharmaceutical or assay kit comprises, in a container, an immunomodulatory therapy or a pharmaceutical composition, and further comprises, in one or more containers, components for conducting RT-PCR, RT-qPCR, deep sequencing or a microarray. In some embodiments, the kit comprises a solid support, nucleic acids contacting the support, where the nucleic acids are

complementary to at least 20, 50, 100, 200, 350, or more bases of mRNA, and a means for detecting the expression of the mRNA in a biological sample.

[00257] In another specific embodiment, the pharmaceutical or assay kit comprises, in a container, an immunomodulatory therapy or a pharmaceutical composition thereof, and further comprises, in one or more containers, components for isolating protein. In another specific embodiment, the pharmaceutical or assay kit comprises, in a container, an immunomodulatory therapy or a pharmaceutical composition, and further comprises, in one or more containers, components for conducting flow cytometry or an ELISA.

[00258] In another aspect, provided herein are kits for measuring biomarkers providing the materials necessary to measure the abundance of one or more of the gene products of the genes or a subset of genes (*e.g.*, one, two, three, four, five or more genes) in Table 1, 2, 3 or 4, or any combination thereof. Such kits may comprise materials and reagents required for measuring RNA or protein. In some embodiments, such kits include microarrays, wherein the microarray is comprised of oligonucleotides and/or DNA and/or RNA fragments which hybridize to one or more of the products of one or more of the genes or a subset of genes in Table 1, 2, 3 or 4, or any combination thereof. In some embodiments, such kits may include primers for PCR of either the RNA product or the cDNA copy of the RNA product of the genes or subset of genes, or both. In some embodiments, such kits may include primers for PCR as well as probes for Quantitative PCR. In some embodiments, such kits may include multiple primers and multiple probes wherein some of said probes have different fluorophores so as to permit multiplexing of multiple products of a gene product or multiple gene products. In some embodiments, such kits may further include materials and reagents for creating cDNA from RNA. In some embodiments, such kits may include antibodies specific for the protein products of a gene or subset of genes in Table 1, 2, 3, or 4, or any combination thereof. Such kits may additionally comprise materials and reagents for isolating RNA and/or proteins from a biological sample. In addition such kits may include materials and reagents for synthesizing cDNA from RNA isolated from a biological sample. In some embodiments, such kits may include, a computer program product embedded on computer readable media for predicting whether a patient is clinically sensitive to an immunomodulatory therapy. In some embodiments, the kits may include a computer program product embedded on a computer readable media along with instructions.

[00259] In some embodiments, kits for measuring the expression of one or more nucleic acid sequences of a gene or a subset of genes in Table 1, 2, 3 or 4 or a combination thereof. In a specific

embodiment, such kits measure the expression of one or more nucleic acid sequences associated with a gene or a subset of genes in Table 1, 2, 3 or 4, or a combination thereof. In accordance with this embodiment, the kits may comprise materials and reagents that are necessary for measuring the expression of particular nucleic acid sequence products of genes or a subset of genes in Table 1, 2, 3 or 4, or a combination thereof. For example, a microarray or RT-PCR kit may be produced for a specific condition and contain only those reagents and materials necessary for measuring the levels of specific RNA transcript products of the genes or a subset of genes in Table 1, 2, 3 or 4, or a combination thereof to predict whether a hematological cancer in a patient is clinically sensitive to an immunomodulatory therapy. Alternatively, in some embodiments, the kits can comprise materials and reagents that are not limited to those required to measure the expression of particular nucleic acid sequences of any particular gene in Table 1, 2, 3, or 4, or a combination thereof. For example, in certain embodiments, the kits comprise materials and reagents necessary for measuring the levels of expression of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more of the genes in Table 1, 2, 3 or 4, in addition to reagents and materials necessary for measuring the levels of the expression of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50 or more genes other than those in Table 1, 2, 3 or 4. In other embodiments, the kits contain reagents and materials necessary for measuring the levels of expression of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50 or more of the genes in Table 1, 2, 3 or 4, and 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300, 350, 400, 450, or more genes that are genes not in Table 1, 2, 3 or 4, or 1-10, 1-100, 1-150, 1-200, 1-300, 1-400, 1-500, 1-1000, 25-100, 25-200, 25-300, 25-400, 25-500, 25-1000, 100-150, 100-200, 100-300, 100-400, 100-500, 100-1000 or 500-1000 genes that are genes not in Table 1, 2, 3 or 4.

[00260] For nucleic acid microarray kits, the kits generally comprise probes attached to a solid support surface. In one such embodiment, probes can be either oligonucleotides or longer length probes including probes ranging from 150 nucleotides in length to 800 nucleotides in length. The probes may be labeled with a detectable label. In a specific embodiment, the probes are specific for one or more of the gene products in Table 1, 2, 3 or 4. The microarray kits may comprise instructions for performing the assay and methods for interpreting and analyzing the data resulting from the performance of the assay. In a specific embodiment, the kits comprise instructions for

predicting whether a hematological cancer in a patient is clinically sensitive to an immunomodulatory therapy. The kits may also comprise hybridization reagents and/or reagents necessary for detecting a signal produced when a probe hybridizes to a target nucleic acid sequence. Generally, the materials and reagents for the microarray kits are in one or more containers. Each component of the kit is generally in its own suitable container.

[00261] In certain embodiments, a nucleic acid microarray kit comprises materials and reagents necessary for measuring the levels of expression of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more of the genes identified in Table 1, 2, 3 or 4, or a combination thereof, in addition to reagents and materials necessary for measuring the levels of the expression of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50 or more genes other than those in Tables 1, 2, 3 or 4. In other embodiments, a nucleic acid microarray kit contains reagents and materials necessary for measuring the levels of expression of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50 or more of the genes in Table 1, 2, 3 or 4, or any combination thereof, and 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300, 350, 400, 450, or more genes that are not in Table 1, 2, 3 or 4, or 1-10, 1-100, 1-150, 1-200, 1-300, 1-400, 1-500, 1-1000, 25-100, 25-200, 25-300, 25-400, 25-500, 25-1000, 100-150, 100-200, 100-300, 100-400, 100-500, 100-1000 or 500-1000 genes that are not in Table 1, 2, 3 or 4.

[00262] For Quantitative PCR, the kits generally comprise pre-selected primers specific for particular nucleic acid sequences. The Quantitative PCR kits may also comprise enzymes suitable for amplifying nucleic acids (*e.g.*, polymerases such as Taq), and deoxynucleotides and buffers needed for the reaction mixture for amplification. The Quantitative PCR kits may also comprise probes specific for the nucleic acid sequences associated with or indicative of a condition. The probes may or may not be labeled with a fluorophore. The probes may or may not be labeled with a quencher molecule. In some embodiments the Quantitative PCR kits also comprise components suitable for reverse-transcribing RNA including enzymes (*e.g.*, reverse transcriptases such as AMV, MMLV and the like) and primers for reverse transcription along with deoxynucleotides and buffers needed for the reverse transcription reaction. Each component of the quantitative PCR kit is generally in its own suitable container. Thus, these kits generally comprise distinct containers suitable for each individual reagent, enzyme, primer and probe. Further, the quantitative PCR kits

may comprise instructions for performing the assay and methods for interpreting and analyzing the data resulting from the performance of the assay. In a specific embodiment, the kits contain instructions for predicting whether a hematological cancer in a patient is clinically sensitive to an immunomodulatory therapy.

[00263] For antibody based kits, the kit can comprise, for example: (1) a first antibody (which may or may not be attached to a solid support) which binds to a peptide, polypeptide or protein of interest; and, optionally, (2) a second, different antibody which binds to either the peptide, polypeptide or protein, or the first antibody and is conjugated to a detectable label (*e.g.*, a fluorescent label, radioactive isotope or enzyme). In a specific embodiment, the peptide, polypeptide or protein of interest is associated with or indicative of a condition (*e.g.*, a disease). The antibody-based kits may also comprise beads for conducting an immunoprecipitation. Each component of the antibody-based kits is generally in its own suitable container. Thus, these kits generally comprise distinct containers suitable for each antibody. Further, the antibody-based kits may comprise instructions for performing the assay and methods for interpreting and analyzing the data resulting from the performance of the assay. In a specific embodiment, the kits contain instructions for predicting whether a hematological cancer in a patient is clinically sensitive to an immunomodulatory therapy.

6. EXAMPLES

[00264] Certain embodiments of the invention are illustrated by the following non-limiting examples.

[00265] Gene expression differences between the baseline transcriptional profiles of refractory or relapsed diffuse large B-Cell lymphoma (DLBCL) patients who display response subsequent to lenalidomide treatment and those of patients who do not respond were investigated. A clinical trial was formed with four arms, each arm containing 25 patients. One arm contained patients classified as presenting germinal center B-cell-like DLBCL subtypes receiving lenalidomide, a second arm contained patients classified as presenting germinal center B-cell-like DLBCL subtypes receiving another therapy selected by the investigator, a third arm contained patients classified as presenting activated B-cell-like DLBCL subtypes receiving lenalidomide, and a fourth arm contained patients classified as presenting activated B-cell-like DLBCL subtypes receiving another therapy selected by the investigator. The patients in the four arms of the clinical trial received treatment until disease progression.

[00266] For purposes of this exploratory analysis, a subset of the clinical data associated to each patient comprised the therapy arm, Revlimid (REV) or control drug (CON), and their corresponding response to the drug in both categorical variable {complete response (CR), partial response (PR), establish disease (SD), progression disease (PD) and Death} and continuous variables as progression free survival (PFS) and overall (OS), unit weeks. It also includes the predicted DLBCL sub-type (ABC/GCB) and other demographic data.

[00267] Samples from patient biopsies taken prior to receiving therapy were hybridized to Affymetrix HG-U133 Plus 2.0 GeneChip™ microarrays (www.affymetrix.com/) at the Molecular Characterization & Clinical Assay Development Laboratory, SAIC Frederick National Laboratory for Cancer Research, SAIC-Frederick, Frederick, MD. Biopsy samples were flash-frozen at screen (FF), archived having been formalin-fixed and paraffin embedded (FFPE archive), or FFPE treated at screen. All patients are associated with at least one gene expression profile obtained from one of the three sample types, some are associated with more than one profile. The results described in this Section 6 were obtained from analysis of only those profiles relating to FF samples and which passed QC.

[00268] **Microarray Data QC**

[00269] Raw Affymetrix image (.cel) files were imported into the R statistical programming environment v3.0.0 (r-project.org) using functionality of the *Affy* package of the related Bioconductor suite of open-source bioinformatics software (bioconductor.org). Transcriptional profile QC was performed using the NUSE algorithm, implemented in the Bioconductor package *arrayQualityMetrics* (Kauffmann et al., 2009), applied to a log2 transformation of raw signal.

[00270] The RMA (Irizarry et al., 2003) algorithm was applied to background-correct, quantile normalize and summarize profiles that passed QC. Annotation of probe-sets to genes was performed using the R packages *annotate* (Gentleman, 2013) and *genefilter* (Gentleman et al., 2013) selecting only one probeset per gene (Entrez Gene ID) and choosing the most variable across profiles according to inter-quartile range in cases wherein multiple probe-sets map to a single gene.

[00271] **Clustering & Visualization**

[00272] Data visualization via clustering and heatmap graphics was implemented in the R statistical programming environment. Either Euclidean distance and correlation (1 – Pearson correlation) were used to represent inter-profile dissimilarity and (1-pearson correlation) to represent dissimilarity between genes across profiles. In both cases, hierarchical clustering using Ward's algorithm was applied. Comparative gene expression heatmaps were implemented using

gplots (Warnes et al., 2013) and heatmap.plus (Day, 2012) packages from the Bioconductor suite, with colours generated using palettes from the RColorBrewer™ package (Neuwirth, 2011). Prior to clustering and visualization, individual gene expression across profiles was standardized to have zero mean and unit variance.

[00273] Differential Expression

[00274] The SAM algorithm (Tusher et al., 2001), as implemented in the R/Bioconductor package *siggenes* (Schwender, 2012), was applied to assess statistical significance of differential gene expression across discrete profile groups. Significance values obtained from multiple hypothesis tests were corrected for false-discovery by permutation as implemented in the SAM algorithm.

[00275] The *Enrichr* (Chen et al., 2013) tool (available at amp.pharm.mssm.edu/Enrichr/) was used to assess statistical over-representation of gene categories among genes deemed differentially regulated. The tool combines 35 gene set libraries sorted by categories including transcription, pathways, ontologies, diseases, *etc.* and totaling 31,026 gene-sets.

[00276] Survival Analysis

[00277] The BioNet algorithm (Beisser et al., 2010), as implemented in the related Bioconductor package, was applied to the combined output of statistical tests for differential expression between refractory versus non-refractory best response groups and gene expression correlation with PFS and used the Human Interactome obtained from HINT (Das and Yu, 2012). Optimal response-related sub-networks were visualized via the Cytoscape platform (Saito et al., 2012; Shannon et al., 2003; Smoot et al., 2011).

[00278] The Reactome FI package (Wu and Stein, 2012) was implemented via Cytoscape and applied to Reactome annotation (Croft et al., 2011) imported with the software. The “microarray data analysis” option was applied, with database version 2012, absolute value for Pearson correlation, and an inflation parameter of 5.0 for the Markov Cluster Algorithm. After network generation, Biological Process and Pathway enrichment and survival analyses were generated using associated functionality of the package. Survival analyses were calculated per module upon import of corresponding PFS and censor information.

[00279] Cox regression models and Kaplan-Meier curves were performed using the R package *survival* (Terry M. Therneau, 2013; Terry M. Therneau and Patricia M. Grambsch, 2000).

[00280] Decomposition

[00281] Microarray gene expression profiles were decomposed using default functionality of the *CellMix* R/Bioconductor package (Gaujoux and Seoighe, 2013), which also provided collections of reference data used for decomposition. The decomposition method and reference collection of (Abbas et al., 2009) were applied to REV-DLC-001 profiles. Results were visualized and associated statistics calculated using native functionality of the R environment.

[00282] Results

[00283] Tables 3 and 4 provide lists of genes deemed significantly differentially regulated (empirical FDR 5%) pre-treatment, between patient groups determined as refractory and non-refractory further to Revlimid/lenalidomide therapy. Table 1 provides a list of genes deemed significantly upregulated (empirical FDR 5%) pre-treatment in patients non-refractory to further therapy relative to patients refractory to further Revlimid/lenalidomide therapy. Table 2 provides a list of genes deemed significantly downregulated (empirical FDR 5%) pre-treatment in patients non-refractory to further therapy relative to patients refractory to further Revlimid/lenalidomide therapy.

[00284] Analysis was performed on the FF sample profiles from the lenalidomide-arm and estimated relative proportions of the reference immune cell types were compared between profiles associated with binary lenalidomide response vs. non-response categories (see Figure 2). The distinction between lenalidomide response profiles and the non-responding profiles is characterized by lower estimated B-cell proportions and clear increases in estimated proportions of plasma cells, dendritic cells, and, in a smaller subset of responding patients, NK cells.

[00285] It is of note that estimated proportions of monocytes and cytotoxic T-cells do not correlate strongly with Revlimid response, despite interpretations of the preceding analyses having suggested their presence. Rather, the patterns displayed appear more related to an earlier 'host response' (Monti et al., 2005) or immune infiltrate in combination with a corresponding reduction in particular B-cell populations -- as in earlier interpretation of the combined THRLBCL (Van Loo et al., 2010) / host response (Monti et al., 2005) gene signatures.

[00286] Figure 4 displays estimated proportion of BCR-ligated B-cells (B aIgM) in baseline patient profiles plotted alongside corresponding progression free survival (PFS) further to lenalidomide treatment. The association between low estimated B aIgM proportion and relatively high PFS is striking, in particular in the knowledge that one patient with both low B aIgM proportion and low PFS (< 3 weeks) died shortly after starting treatment.

[00287] The estimated proportion of plasma cells displays the opposite tendency. This observation lends relevance to the decomposition data, as the two cell types are directly linked (Caven et al., 2007) and strong up-regulation of plasma cell marker differentiation marker PRDM1(BLIMP1) is observed in profiles associated with response to treatment. This pattern persists to the extent that the sign of a simple subtracted difference between estimated proportions of BCR-ligated B-cells and plasma cells across Revlimid arm profile decompositions (see Figure 5 (lenalidomide-arm)) provides a statistically significant difference in PFS between two patient groups thus defined (Wilcoxon rank sum, $p = 0.04$).

[00288] The response-related decomposition values for resting NK-cell proportions are interesting. Only four profiles are associated with non-zero estimated proportion of NK-cells, but these profiles are associated with PFS of 27, 31.9, 32.4 & 85.3 weeks. Clearly, were these estimations to bear out in practice (they include two very small estimated proportions, 0.114, 0.158, 0.004 & 0.002 respectively), the presence of NK cells in the tumor sample may provide a good indicator for Revlimid response enrichment.

[00289] Finally, relative estimated proportions of dendritic cells are higher and more stable than for NK cells, although they lack the binary 'on/off' nature of BCR-ligated B-cell and plasma cell proportions in relation to best response categories. Figure 3 displays the relationship between estimated DC proportion (resting + activated) and PFS. Taken together with the partially response-discriminant populations above, the results suggest potential for, for example, a focused flow cytometry screen for future patients more likely to respond to Revlimid treatment.

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- [00349] Table 1, Table, 2, Table 3 and Table 4 are provided below.

probeset	gene_symbol	ensembl_id	q.value	logFC	mean_nonRef	mean_Ref	Chromosome	chrom_band	gene_description
228754_at	SLC6A6	ENSG00000131389	0	0.9754805	8.981006	8.005526	3	p25.1	solute carrier family 6 (neurotransmitter transporter, taurine), member 6 [Source:HGNC Symbol;Acc:11052]
238327_at	ODF3B	ENSG00000177989	0.00273	1.0304117	8.897771	7.86736	22	q13.33	outer dense fiber of sperm tails 3B [Source:HGNC Symbol;Acc:34388]
208683_at	CAPN2	ENSG00000162909	0.00273	2.0591386	9.820198	7.761059	1	q41	calpain 2, (m/II) large subunit [Source:HGNC Symbol;Acc:1479]
218648_at	CRTC3	ENSG00000140577	0.00273	1.3932573	9.008044	7.614786	15	q26.1	CREB regulated transcription coactivator 3 [Source:HGNC Symbol;Acc:26148]
225146_at	FAM219A	ENSG00000164970	0.00273	0.7957467	8.091946	7.296199	9	p13.3	family with sequence similarity 219, member A [Source:HGNC Symbol;Acc:19920]
218589_at	IPAR6	ENSG00000139679	0.00273	2.4225735	9.179664	6.75709	13	q14.2	lysophosphatidic acid receptor 6 [Source:HGNC Symbol;Acc:15520]
217762_s_at	RAB31	ENSG00000168461	0.00273	1.7495761	10.13227	8.382693	18	p11.22	RAB31, member RAS oncogene family [Source:HGNC Symbol;Acc:9771]
201506_at	TGFBI	ENSG00000120708	0.00273	1.8055477	11.4844	9.678852	5	q31.1	transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:11771]
224862_at	GNAQ	ENSG00000156052	0.00273	2.0253634	6.97061	4.945246	9	q21.2	guanine nucleotide binding protein (G protein), q polypeptide [Source:HGNC Symbol;Acc:4390]
201425_at	ALDH2	ENSG00000111275	0.00273	1.9293787	10.60165	8.672267	12	q24.12	aldehyde dehydrogenase 2 family (mitochondrial) [Source:HGNC Symbol;Acc:404]
1555851_s_at	SEPW1	ENSG00000178980	0.00312	1.5331244	10.54942	9.016292	19	q13.33	selenoprotein W, 1 [Source:HGNC Symbol;Acc:10752]
205241_at	SCO2	ENSG00000130489	0.00312	0.8920118	9.145278	8.253267	22	q13.33	SCO2 cytochrome c oxidase assembly protein [Source:HGNC Symbol;Acc:10604]
218552_at	ECHDC2	ENSG00000121310	0.00312	1.3353136	9.234133	7.89882	1	p32.3	enoyl CoA hydratase domain containing 2 [Source:HGNC Symbol;Acc:23408]
55662_at	C10orf76	ENSG00000120029	0.00312	0.7212711	8.212153	7.490882	10	q24.32	chromosome 10 open reading frame 76 [Source:HGNC Symbol;Acc:25788]
204773_at	IL11RA	ENSG00000137070	0.004437	0.9173902	7.610983	6.693593	9	p13.3	interleukin 11 receptor, alpha [Source:HGNC Symbol;Acc:5967]
202600_s_at	NRIP1	ENSG00000180530	0.004437	1.662366	7.562455	5.900089	21	q21.1	nuclear receptor interacting protein 1 [Source:HGNC Symbol;Acc:8001]
221802_s_at	KIAA1598	ENSG00000187164	0.004818	1.8894563	8.343765	6.454309	10	q25.3	KIAA1598 [Source:HGNC Symbol;Acc:29319]
226000_at	CTTNBP2NL	ENSG00000143079	0.005157	1.4672863	7.674825	6.207539	1	p13.2	CTTNBP2 N-terminal like [Source:HGNC Symbol;Acc:25330]
222484_s_at	CXCL14	ENSG00000145824	0.005173	3.4617357	11.01983	7.558095	5	q31.1	chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;Acc:10640]
201012_at	ANXA1	ENSG00000135046	0.005188	1.8681422	10.78464	8.916494	9	q21.13	annexin A1 [Source:HGNC Symbol;Acc:533]
218854_at	DSE	ENSG00000111817	0.006453	1.6321343	9.397392	7.765258	6	q22.1	dermatan sulfate epimerase [Source:HGNC Symbol;Acc:21144]
214040_s_at	GSN	ENSG00000148180	0.006453	1.3451184	10.2628	8.917685	9	q33.2	gelsolin [Source:HGNC Symbol;Acc:4620]
201302_at	ANXA4	ENSG00000196975	0.006598	1.7017558	9.377174	7.675418	2	p13.3	annexin A4 [Source:HGNC Symbol;Acc:542]
208923_at	CYFIP1	ENSG00000068793	0.006598	1.4183371	9.308029	7.889692	15	q11.2	cytoplasmic FMR1 interacting protein 1 [Source:HGNC Symbol;Acc:13759]
224414_s_at	CARD6	ENSG00000132357	0.007208	1.298678	8.497051	7.198373	5	p13.1	caspase recruitment domain family, member 6 [Source:HGNC Symbol;Acc:16394]
205945_at	IL6R	ENSG00000160712	0.008097	1.7659924	8.874117	7.108125	1	q21.3	interleukin 6 receptor [Source:HGNC Symbol;Acc:6019]
200765_x_at	CTNNA1	ENSG00000044115	0.008097	1.1179416	9.63084	8.512898	5	q31.2	catenin (cadherin-associated protein), alpha 1, 102kDa [Source:HGNC Symbol;Acc:2509]
223228_at	LDOLC1L	ENSG00000188636	0.008097	1.239346	8.444984	7.205638	22	q13.31	leucine zipper, down-regulated in cancer 1-like [Source:HGNC Symbol;Acc:13343]
225842_at	PHLDA1	ENSG00000139289	0.008191	1.472676	8.29771	6.825034	12	q21.2	pleckstrin homology-like domain, family A, member 1 [Source:HGNC Symbol;Acc:8933]
201348_at	GPX3	ENSG00000211445	0.008351	2.1699179	11.32422	9.154304	5	q33.1	glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Acc:4555]
219885_at	SLFN12	ENSG00000172123	0.008351	1.2351533	6.097789	4.862636	17	q12	schlafen family member 12 [Source:HGNC Symbol;Acc:25500]
212830_at	MEGF9	ENSG00000106780	0.008351	1.2431752	6.734085	5.490909	9	q33.2	multiple EGF-like domains 9 [Source:HGNC Symbol;Acc:3234]
202687_s_at	TNFSF10	ENSG00000121858	0.008425	1.5293527	11.10527	9.57592	3	q26.31	tumor necrosis factor (ligand) superfamily, member 10 [Source:HGNC Symbol;Acc:11925]
217731_s_at	ITM2B	ENSG00000136156	0.009101	1.4493355	10.05153	8.602193	13	q14.2	integral membrane protein 2B [Source:HGNC Symbol;Acc:6174]
218694_at	ARMCX1	ENSG00000126947	0.009456	1.4991554	7.418732	5.919576	X	q22.1	armadillo repeat containing, X-linked 1 [Source:HGNC Symbol;Acc:18073]
202944_at	NAGA	ENSG00000198951	0.009456	0.9946444	8.604684	7.61004	22	q13.2	N-acetylgalactosaminidase, alpha- [Source:HGNC Symbol;Acc:7631]
212522_at	PDE8A	ENSG00000073417	0.009456	1.2124713	8.751053	7.538582	15	q25.3	phosphodiesterase 8A [Source:HGNC Symbol;Acc:8793]

226247_at	PLEKHA1	ENSG00000107679	0.009456	1.762189	8.231589	6.4694	10	q26.13	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1 [Source:HGNC Symbol;Acc:14335]
243423_at	TNIP1	ENSG00000145901	0.009621	1.0393627	6.139027	5.099664	5	q33.1	TNFAIP3 interacting protein 1 [Source:HGNC Symbol;Acc:16903]
229074_at	EHD4	ENSG00000103966	0.00995	1.116796	8.728409	7.611613	15	q15.1	EH-domain containing 4 [Source:HGNC Symbol;Acc:3245]
222154_s_at	SPATS2L	ENSG00000196141	0.00995	1.2398395	9.909155	8.669316	2	q33.1	spermatogenesis associated, serine-rich 2-like [Source:HGNC Symbol;Acc:24574]
200710_at	ACADVL	ENSG00000072778	0.011037	0.8720084	9.456312	8.584304	17	p13.1	acyl-CoA dehydrogenase, very long chain [Source:HGNC Symbol;Acc:92]
228791_at	LOC100129502	NA	0.011037	1.7938919	8.411267	6.617375	NA	NA	NA
208634_s_at	MACF1	ENSG00000127603	0.011768	1.2346253	10.26299	9.028368	1	p34.3	microtubule-actin crosslinking factor 1 [Source:HGNC Symbol;Acc:13664]
242487_at	CC2D1B	ENSG00000154222	0.011768	0.5238144	6.843606	6.319792	1	p32.3	coiled-coil and C2 domain containing 1B [Source:HGNC Symbol;Acc:29386]
218559_s_at	MAFB	ENSG00000204103	0.011768	1.8491222	11.31545	9.466329	20	q12	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B [Source:HGNC Symbol;Acc:6408]
201360_at	CST3	ENSG00000101439	0.011768	1.3533248	11.64386	10.29054	20	p11.21	cystatin C [Source:HGNC Symbol;Acc:2475]
206101_at	ECM2	ENSG00000106823	0.011768	1.7286086	7.156511	5.427902	9	q22.31	extracellular matrix protein 2, female organ and adipocyte specific [Source:HGNC Symbol;Acc:3154]
218004_at	BSDC1	ENSG00000160058	0.011768	0.5416922	8.948162	8.40647	1	p35.1	BSD domain containing 1 [Source:HGNC Symbol;Acc:25501]
36129_at	BGSM2	ENSG00000141258	0.011768	0.89385	9.48007	8.58622	17	p13.3	small G protein signaling modulator 2 [Source:HGNC Symbol;Acc:29026]
227889_at	LPCAT2	ENSG00000087253	0.011768	1.9822482	7.953706	5.971458	16	q12.2	lysophosphatidylcholine acyltransferase 2 [Source:HGNC Symbol;Acc:26032]
218043_s_at	AZI2	ENSG00000163512	0.011768	0.8638989	6.644285	5.780386	3	p24.1	5-azacytidine induced 2 [Source:HGNC Symbol;Acc:24002]
218066_at	SLC12A7	ENSG00000113504	0.011768	1.0053443	8.912722	7.907378	5	p15.33	solute carrier family 12 (potassium/chloride transporters), member 7 [Source:HGNC Symbol;Acc:10915]
58780_s_at	ARHGEF40	ENSG00000165801	0.011847	1.4859821	7.235422	5.74944	14	q11.2	Rho guanine nucleotide exchange factor (GEF) 40 [Source:HGNC Symbol;Acc:25516]
200660_at	S100A11	ENSG00000163191	0.01233	1.3882864	11.61066	10.22237	1	q21.3	S100 calcium binding protein A11 [Source:HGNC Symbol;Acc:10488]
212907_at	SLC30A1	ENSG00000170385	0.01233	1.1713121	9.350467	8.179154	1	q32.3	solute carrier family 30 (zinc transporter), member 1 [Source:HGNC Symbol;Acc:11012]
208999_at	SEPT8	ENSG00000164402	0.012828	1.1133968	8.412743	7.299346	5	q31.1	septin 8 [Source:HGNC Symbol;Acc:16511]
208949_s_at	LGALS3	ENSG00000131981	0.012937	1.4663704	11.76909	10.30272	14	q22.3	lectin, galactoside-binding, soluble, 3 [Source:HGNC Symbol;Acc:6563]
218311_at	MAP4K3	ENSG00000011566	0.012937	1.467988	7.560719	6.092731	2	p22.1	mitogen-activated protein kinase kinase kinase kinase 3 [Source:HGNC Symbol;Acc:6865]
203518_at	LYST	ENSG00000143669	0.013774	1.7813892	8.315307	6.533918	1	q42.3	lysosomal trafficking regulator [Source:HGNC Symbol;Acc:1968]
204137_at	GPR137B	ENSG00000077585	0.01568	2.0887506	9.969767	7.881016	1	q42.3	G protein-coupled receptor 137B [Source:HGNC Symbol;Acc:11862]
222217_s_at	SLC27A3	ENSG00000143554	0.01568	0.9016644	8.45229	7.550626	1	q21.3	solute carrier family 27 (fatty acid transporter), member 3 [Source:HGNC Symbol;Acc:10997]
201505_at	LAMB1	ENSG00000091136	0.015689	1.8347161	9.325408	7.490692	7	q31.1	laminin, beta 1 [Source:HGNC Symbol;Acc:6486]
217728_at	S100A6	ENSG00000197956	0.016157	0.9618026	11.17652	10.21472	1	q21.3	S100 calcium binding protein A6 [Source:HGNC Symbol;Acc:10496]
225483_at	VPS26B	ENSG00000151502	0.01616	0.7314643	8.008599	7.277135	11	q25	vacuolar protein sorting 26 homolog B (S. pombe) [Source:HGNC Symbol;Acc:28119]
202686_s_at	AXL	ENSG00000167601	0.016163	2.1648837	9.749176	7.584292	19	q13.2	AXL receptor tyrosine kinase [Source:HGNC Symbol;Acc:905]
227276_at	PLXDC2	ENSG00000120594	0.016167	1.9691918	9.857934	7.888742	10	p12.31	plexin domain containing 2 [Source:HGNC Symbol;Acc:21013]
228185_at	ZNF25	ENSG00000175395	0.016167	0.9293975	6.510839	5.581442	10	p11.1	zinc finger protein 25 [Source:HGNC Symbol;Acc:13043]
217892_s_at	LIMA1	ENSG00000050405	0.016167	1.8593217	9.968366	8.109044	12	q13.12	LIM domain and actin binding 1 [Source:HGNC Symbol;Acc:24636]
202727_s_at	IFNGR1	ENSG00000027697	0.016167	1.2033225	9.855228	8.651905	6	q23.3	interferon gamma receptor 1 [Source:HGNC Symbol;Acc:5439]
212112_s_at	STX12	ENSG00000117758	0.016167	0.8115894	8.768046	7.956457	1	p35.3	syntaxin 12 [Source:HGNC Symbol;Acc:11430]
203789_s_at	SEMA3C	ENSG00000075223	0.016167	1.8263518	6.851145	5.024793	7	q21.11	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C [Source:HGNC Symbol;Acc:10725]
200677_at	PTTG1IP	ENSG00000183255	0.016167	0.9443082	10.81552	9.871214	21	q22.3	pituitary tumor-transforming 1 interacting protein [Source:HGNC Symbol;Acc:13524]

222876_s_at	ADAP2	ENSG00000184060	0.016167	1.230284	9.947909	8.717625	17	q11.2	ArfGAP with dual PH domains 2 [Source:HGNC Symbol;Acc:16487]
210145_at	PLA2G4A	ENSG00000116711	0.016167	1.018587	5.59769	4.579103	1	q31.1	phospholipase A2, group IVA (cytosolic, calcium-dependent) [Source:HGNC Symbol;Acc:9035]
208109_s_at	LINC00597	NA	0.016167	1.2522138	6.056933	4.804719	NA	NA	NA
209651_at	TGFB1I1	ENSG00000140682	0.016167	1.6390689	8.383831	6.744762	16	p11.2	transforming growth factor beta 1 induced transcript 1 [Source:HGNC Symbol;Acc:11767]
212698_s_at	SEPT10	ENSG00000136522	0.016167	2.0293866	6.787502	4.758115	2	q13	septin 10 [Source:HGNC Symbol;Acc:14349]
212526_at	SPG20	ENSG00000133104	0.016167	1.308041	6.974473	5.666432	13	q13.3	spastic paraplegia 20 (Troyer syndrome) [Source:HGNC Symbol;Acc:18514]
209684_at	RIN2	ENSG00000132669	0.016167	1.9484987	9.25026	7.301761	20	p11.23	Ras and Rab interactor 2 [Source:HGNC Symbol;Acc:18750]
223204_at	FAM198B	ENSG00000164125	0.016167	1.5567047	7.718117	6.161412	4	q32.1	family with sequence similarity 198, member 8 [Source:HGNC Symbol;Acc:25312]
200673_at	LAPTM4A	ENSG00000068697	0.016167	1.052583	10.80128	9.748695	2	p24.1	lysosomal protein transmembrane 4 alpha [Source:HGNC Symbol;Acc:6924]
225384_at	DOCK7	ENSG00000116641	0.016167	0.820345	7.335351	6.515006	1	p31.3	dedicator of cytokinesis 7 [Source:HGNC Symbol;Acc:19190]
209210_s_at	FERMT2	ENSG00000073712	0.016167	1.600225	8.650583	7.050358	14	q22.1	fermitin family member 2 [Source:HGNC Symbol;Acc:15767]
201798_s_at	MYOF	ENSG00000138119	0.016167	1.9337214	9.90089	7.967169	10	q23.33	myoferlin [Source:HGNC Symbol;Acc:3656]
225949_at	NRBP2	ENSG00000185189	0.016167	1.1978158	8.229623	7.031807	8	q24.3	nuclear receptor binding protein 2 [Source:HGNC Symbol;Acc:19339]
208924_at	RNF11	ENSG00000123091	0.016167	1.3126563	7.905885	6.593229	1	p32.3	ring finger protein 11 [Source:HGNC Symbol;Acc:10056]
209004_s_at	FBXL5	ENSG00000118564	0.016167	1.0838058	10.00546	8.921656	4	p15.32	F-box and leucine-rich repeat protein 5 [Source:HGNC Symbol;Acc:13602]
226743_at	SLFN11	ENSG00000172716	0.016167	1.6530276	8.752878	7.099851	17	q12	schlafen family member 11 [Source:HGNC Symbol;Acc:26633]
228573_at	ANTXR2	ENSG00000163297	0.016167	1.2231191	6.502217	5.279098	4	q21.21	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
222065_s_at	FLII	ENSG00000177731	0.016167	0.7794236	9.687503	8.90808	17	p11.2	flightless I homolog (Drosophila) [Source:HGNC Symbol;Acc:3750]
212989_at	SGMS1	ENSG00000198964	0.016167	1.1804345	5.341958	4.161523	10	q11.23	sphingomyelin synthase 1 [Source:HGNC Symbol;Acc:29799]
202228_s_at	NPTN	ENSG00000156642	0.016167	1.1313461	9.703866	8.57252	15	q24.1	neuroplastin [Source:HGNC Symbol;Acc:17867]
227761_at	MYO5A	ENSG00000197535	0.016167	1.4777088	8.28231	6.804601	15	q21.2	myosin VA (heavy chain 12, myosin) [Source:HGNC Symbol;Acc:7602]
202133_at	WWTR1	ENSG0000018408	0.016167	1.9825407	8.759155	6.776615	3	q25.1	WW domain containing transcription regulator 1 [Source:HGNC Symbol;Acc:24042]
209960_at	HGF	ENSG0000019991	0.016167	1.2162213	4.738985	3.522763	7	q21.11	hepatocyte growth factor (hepatopoietin A; scatter factor) [Source:HGNC Symbol;Acc:4893]
212203_x_at	IFITM3	ENSG00000142089	0.016167	0.9994654	12.83133	11.83186	11	p15.5	interferon induced transmembrane protein 3 [Source:HGNC Symbol;Acc:5414]
212158_at	SDC2	ENSG00000169439	0.016167	1.6948793	8.399184	6.704305	8	q22.1	syndecan 2 [Source:HGNC Symbol;Acc:10659]
224797_at	ARRDC3	ENSG00000113369	0.016167	1.2808966	7.04992	5.769023	5	q14.3	arrestin domain containing 3 [Source:HGNC Symbol;Acc:29263]
203124_s_at	SLC11A2	ENSG00000110911	0.016167	1.3149816	8.210637	6.895655	12	q13.12	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 [Source:HGNC Symbol;Acc:10908]
1553034_at	SDCCAG8	ENSG00000054282	0.016167	0.6479854	7.598444	6.950458	1	q43	serologically defined colon cancer antigen 8 [Source:HGNC Symbol;Acc:10671]
226111_s_at	ZNF385A	ENSG00000161642	0.016167	1.0612964	9.529822	8.468525	12	q13.13	zinc finger protein 385A [Source:HGNC Symbol;Acc:17521]
231579_s_at	TIMP2	ENSG00000035862	0.016167	1.9509024	11.29034	9.339442	17	q25.3	TIMP metalloproteinase inhibitor 2 [Source:HGNC Symbol;Acc:11821]
202007_at	NID1	ENSG00000116962	0.016167	1.6171384	7.967908	6.350769	1	q42.3	nidogen 1 [Source:HGNC Symbol;Acc:7821]
201681_s_at	DLG5	ENSG00000151208	0.016382	1.584355	7.680377	6.096022	10	q22.3	discs, large homolog 5 (Drosophila) [Source:HGNC Symbol;Acc:2904]
212761_at	TCF7L2	ENSG00000148737	0.016678	1.5655854	7.595306	6.02972	10	q25.2	transcription factor 7-like 2 (T-cell specific, HMG-box) [Source:HGNC Symbol;Acc:11641]
224983_at	SCARB2	ENSG00000138760	0.016923	1.3192641	9.808333	8.489069	4	q21.1	scavenger receptor class B, member 2 [Source:HGNC Symbol;Acc:1665]
218706_s_at	GRAMD3	ENSG00000155324	0.016923	1.1289944	6.584781	5.455786	5	q23.2	GRAM domain containing 3 [Source:HGNC Symbol;Acc:24911]
203595_s_at	IFIT5	ENSG00000152778	0.017039	1.3141225	8.100951	6.786828	10	q23.31	interferon-induced protein with tetratricopeptide repeats 5 [Source:HGNC Symbol;Acc:13328]
225133_at	KLF3	ENSG00000109787	0.017271	1.8771599	7.744133	5.866973	4	p14	Kruppel-like factor 3 (basic) [Source:HGNC Symbol;Acc:16516]
204396_s_at	GRK5	ENSG00000198873	0.017458	0.9777677	8.134717	7.156949	10	q26.11	G protein-coupled receptor kinase 5 [Source:HGNC Symbol;Acc:4544]
210105_s_at	FYN	ENSG0000010810	0.017653	1.6156589	10.56934	8.953681	6	q21	FYN oncogene related to SRC, FGR, YES [Source:HGNC Symbol;Acc:4037]
201218_at	CTBP2	ENSG00000175029	0.017653	1.464242	7.445366	5.981124	10	q26.13	C-terminal binding protein 2 [Source:HGNC Symbol;Acc:2495]

203973_s_at	CEBPD	ENSG00000221869	0.017653	1.6141966	10.46813	8.85393	8	q11.21	CCAAT/enhancer binding protein (C/EBP), delta [Source:HGNC Symbol;Acc:1835]
243038_at	RBM43	ENSG00000184898	0.017653	0.9687316	7.01539	6.046658	2	q23.3	RNA binding motif protein 43 [Source:HGNC Symbol;Acc:24790]
212667_at	SPARC	ENSG00000113140	0.017653	2.0387778	9.760158	7.72138	5	q33.1	secreted protein, acidic, cysteine-rich (osteonectin) [Source:HGNC Symbol;Acc:11219]
209341_s_at	IKBKB	ENSG00000104365	0.017653	0.9809497	8.789651	7.808701	8	p11.21	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta [Source:HGNC Symbol;Acc:5960]
202336_s_at	PAM	ENSG00000145730	0.017653	1.3185154	9.289021	7.970505	5	q21.1	peptidylglycine alpha-amidating monooxygenase [Source:HGNC Symbol;Acc:8596]
212298_at	NRP1	ENSG00000099250	0.018067	1.7793457	9.257538	7.478193	10	p11.22	neuropilin 1 [Source:HGNC Symbol;Acc:8004]
221773_at	ELK3	ENSG00000111145	0.018896	1.6207184	8.175421	6.554703	12	q23.1	ELK3, ETS-domain protein (SRF accessory protein 2) [Source:HGNC Symbol;Acc:3325]
208316_x_at	ANXA2P2	ENSG00000231991	0.018902	0.8785493	10.01166	9.13311	9	p13.3	annexin A2 pseudogene 2 [Source:HGNC Symbol;Acc:539]
225188_at	RAPH1	ENSG00000173166	0.018902	2.0051889	7.673175	5.667987	2	q33.2	Ras association (RaGDS/AF-6) and pleckstrin homology domains 1 [Source:HGNC Symbol;Acc:14436]
212779_at	KIAA1109	ENSG00000138688	0.018902	0.9900719	8.187159	7.197087	4	q27	KIAA1109 [Source:HGNC Symbol;Acc:26953]
221748_s_at	TNS1	ENSG00000079308	0.018902	2.0203509	8.86943	6.84908	2	q35	tensin 1 [Source:HGNC Symbol;Acc:11973]
213379_at	COQ2	ENSG00000173085	0.018902	0.5237323	8.028911	7.505178	4	q21.23	coenzyme Q2 4-hydroxybenzoate polyprenyltransferase [Source:HGNC Symbol;Acc:25223]
211684_s_at	DYNC1I2	ENSG00000077380	0.018902	0.8229036	8.910623	8.08772	2	q31.1	dynein, cytoplasmic 1, intermediate chain 2 [Source:HGNC Symbol;Acc:2964]
201739_at	SGK1	ENSG00000118515	0.018902	1.4797614	10.75365	9.273888	6	q23.2	serum/glucocorticoid regulated kinase 1 [Source:HGNC Symbol;Acc:10810]
209090_s_at	SH3GLB1	ENSG00000097033	0.018902	0.9614008	9.962485	9.001085	1	p22.3	SH3-domain GRB2-like endophilin B1 [Source:HGNC Symbol;Acc:10833]
225171_at	ARHGAP18	ENSG00000146376	0.018902	1.5370749	8.677922	7.140848	6	q22.33	Rho GTPase activating protein 18 [Source:HGNC Symbol;Acc:21035]
204517_at	PPIC	ENSG00000168938	0.018902	1.4583399	7.874059	6.415719	5	q23.2	peptidylprolyl isomerase C (cyclophilin C) [Source:HGNC Symbol;Acc:9256]
213923_at	RAP2B	ENSG00000181467	0.018902	1.241375	10.18514	8.943765	3	q25.2	RAP2B, member of RAS oncogene family [Source:HGNC Symbol;Acc:9862]
201590_x_at	ANXA2	ENSG00000182718	0.018902	1.2223627	12.76742	11.54506	15	q22.2	annexin A2 [Source:HGNC Symbol;Acc:537]
202202_s_at	LAMA4	ENSG00000112769	0.018902	1.0953018	9.350315	8.255013	6	q21	laminin, alpha 4 [Source:HGNC Symbol;Acc:6484]
218718_at	PDGFC	ENSG00000145431	0.018921	2.1063846	7.633895	5.52751	4	q32.1	platelet derived growth factor C [Source:HGNC Symbol;Acc:8801]
206414_s_at	ASAP2	ENSG00000151693	0.018921	1.4747717	6.713855	5.239084	2	p25.1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2 [Source:HGNC Symbol;Acc:2721]
212169_at	FKBP9	ENSG00000122642	0.019065	1.1107524	8.896737	7.785985	7	p14.3	FK506 binding protein 9, 63 kDa [Source:HGNC Symbol;Acc:3725]
209348_s_at	MAF	ENSG00000178573	0.019065	2.155786	8.892164	6.736378	16	q23.2	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog [Source:HGNC Symbol;Acc:5776]
202011_at	TJP1	ENSG00000104067	0.019267	2.0936522	8.408239	6.314587	15	q13.1	tight junction protein 1 [Source:HGNC Symbol;Acc:11827]
226823_at	PHACTR4	ENSG00000204138	0.019506	0.7884982	7.613814	6.825316	1	p35.3	phosphatase and actin regulator 4 [Source:HGNC Symbol;Acc:25793]
201375_s_at	PPP2CB	ENSG00000104695	0.019506	0.8835548	10.00679	9.123237	8	p12	protein phosphatase 2, catalytic subunit, beta isozyme [Source:HGNC Symbol;Acc:9300]
202808_at	WBP1L	ENSG00000166272	0.019506	0.6672792	9.547031	8.879752	10	q24.32	WW domain binding protein 1-like [Source:HGNC Symbol;Acc:23510]
227911_at	ARHGAP28	ENSG00000088756	0.01988	1.6321361	5.975404	4.343267	18	p11.31	Rho GTPase activating protein 28 [Source:HGNC Symbol;Acc:25509]
206049_at	SELP	ENSG00000174175	0.01988	1.7100903	7.227627	5.517537	1	q24.2	selectin P (granule membrane protein 140kDa, antigen CD62) [Source:HGNC Symbol;Acc:10721]
202357_s_at	CFB	ENSG00000243649	0.01988	1.1573646	8.626327	7.468963	6	p21.33	complement factor B [Source:HGNC Symbol;Acc:1037]
217497_at	TYMP	ENSG00000025708	0.01988	0.8516144	8.694769	7.843155	22	q13.33	thymidine phosphorylase [Source:HGNC Symbol;Acc:3148]
204034_at	ETHE1	ENSG00000105755	0.01988	0.5289265	8.283721	7.754794	19	q13.31	ethylmalonic encephalopathy 1 [Source:HGNC Symbol;Acc:23287]
210139_s_at	PMP22	ENSG00000109099	0.01988	1.7494057	9.219437	7.470032	17	p12	peripheral myelin protein 22 [Source:HGNC Symbol;Acc:9118]
204114_at	NID2	ENSG00000087303	0.01988	1.6354339	7.748453	6.113019	14	q22.1	nidogen 2 (osteonidogen) [Source:HGNC Symbol;Acc:13389]
200878_at	EPAS1	ENSG00000116016	0.020134	1.6643506	10.74529	9.080936	2	p21	endothelial PAS domain protein 1 [Source:HGNC Symbol;Acc:3374]
202446_s_at	PLSCR1	ENSG00000188313	0.020139	1.410605	9.74777	8.337165	3	q24	phospholipid scramblase 1 [Source:HGNC Symbol;Acc:9092]
221139_s_at	CSAD	ENSG00000139631	0.020139	1.1033652	6.32666	5.223294	12	q13.13	cysteine sulfinic acid decarboxylase [Source:HGNC Symbol;Acc:18966]

221012_s_at	TRIM8	ENSG00000171206	0.020139	0.9021545	9.733515	8.831361	10	q24.32	tripartite motif containing 8 [Source:HGNC Symbol;Acc:15579]
1555832_s_at	KLF6	ENSG00000067082	0.020139	1.5050907	10.49276	8.987666	10	p15.1	Kruppel-like factor 6 [Source:HGNC Symbol;Acc:2235]
212859_x_at	MT1E	ENSG00000169715	0.020139	1.3116378	11.29222	9.98058	16	q12.2	metallothionein 1E [Source:HGNC Symbol;Acc:7397]
203729_at	EMP3	ENSG00000142227	0.020691	1.2426119	10.80078	9.558169	19	q13.33	epithelial membrane protein 3 [Source:HGNC Symbol;Acc:3335]
209238_at	STX3	ENSG00000166900	0.021317	1.0475218	7.816754	6.769232	11	q12.1	syntaxin 3 [Source:HGNC Symbol;Acc:11438]
228617_at	XAF1	ENSG00000132530	0.02132	1.8591633	9.784426	7.925263	17	p13.1	XIAP associated factor 1 [Source:HGNC Symbol;Acc:30932]
204436_at	PLEKHO2	ENSG00000241839	0.021661	0.8149093	9.412795	8.597885	15	q22.31	pleckstrin homology domain containing, family O member 2 [Source:HGNC Symbol;Acc:30026]
1555756_a_at	CLEC7A	ENSG00000172243	0.021739	1.9487017	9.541407	7.592705	12	p13.2	C-type lectin domain family 7, member A [Source:HGNC Symbol;Acc:14558]
202381_at	ADAM9	ENSG00000168615	0.022252	1.5225689	9.387992	7.865423	8	p11.22	ADAM metalloproteinase domain 9 [Source:HGNC Symbol;Acc:216]
202291_s_at	MGP	ENSG00000111341	0.022612	2.1289603	11.06084	8.931878	12	p12.3	matrix Gla protein [Source:HGNC Symbol;Acc:7060]
213056_at	FRMD4B	ENSG00000114541	0.022612	1.7413741	6.023278	4.281904	3	p14.1	FERM domain containing 4B [Source:HGNC Symbol;Acc:24886]
218162_at	OLFML3	ENSG00000116774	0.022612	1.5508457	8.32843	6.777584	1	p13.2	olfactomedin-like 3 [Source:HGNC Symbol;Acc:24956]
212845_at	SAMD4A	ENSG0000020577	0.022612	1.2467155	6.634447	5.387731	14	q22.2	sterile alpha motif domain containing 4A [Source:HGNC Symbol;Acc:23023]
218541_s_at	C8orf4	ENSG00000176907	0.022732	1.9762953	6.693744	4.717449	8	p11.21	chromosome 8 open reading frame 4 [Source:HGNC Symbol;Acc:1357]
1559005_s_at	CNTLN	ENSG00000044459	0.022732	1.3908169	6.512895	5.122078	9	p22.2	centlein, centrosomal protein [Source:HGNC Symbol;Acc:23432]
218909_at	RP56KC1	ENSG00000136643	0.022732	0.7521578	8.355674	7.603516	1	q32.3	ribosomal protein S6 kinase, 52kDa, polypeptide 1 [Source:HGNC Symbol;Acc:10439]
226384_at	PPAPDC1B	ENSG00000147535	0.022732	1.2111184	8.159726	6.948608	8	p11.23	phosphatidic acid phosphatase type 2 domain containing 1B [Source:HGNC Symbol;Acc:25026]
212509_s_at	MXRA7	ENSG00000182534	0.022732	1.4674759	9.764658	8.297182	17	q25.1	matrix-remodelling associated 7 [Source:HGNC Symbol;Acc:7541]
225975_at	PCDH18	ENSG00000189184	0.023159	1.7790238	7.236967	5.457943	4	q28.3	protocadherin 18 [Source:HGNC Symbol;Acc:14268]
201341_at	ENC1	ENSG00000171617	0.023416	1.4443337	8.066608	6.622274	5	q13.3	ectodermal-neural cortex 1 (with BTB domain) [Source:HGNC Symbol;Acc:3345]
203324_s_at	CAV2	ENSG00000105971	0.023506	1.952201	8.152024	6.199823	7	q31.2	caveolin 2 [Source:HGNC Symbol;Acc:1528]
212230_at	PPAP2B	ENSG00000162407	0.023506	1.8165102	9.071698	7.255187	1	p32.2	phosphatidic acid phosphatase type 2B [Source:HGNC Symbol;Acc:9229]
218632_at	HECTD3	ENSG00000126107	0.023506	0.7369004	9.627648	8.890747	1	p34.1	HECT domain containing E3 ubiquitin protein ligase 3 [Source:HGNC Symbol;Acc:26117]
212204_at	TMEM87A	ENSG00000103978	0.023515	0.8984928	9.007547	8.109054	15	q15.1	transmembrane protein 87A [Source:HGNC Symbol;Acc:24522]
226022_at	SASH1	ENSG00000111961	0.023515	2.0027112	7.610796	5.608085	6	q24.3	SAM and SH3 domain containing 1 [Source:HGNC Symbol;Acc:19182]
242800_at	NHS	ENSG00000188158	0.023677	1.1627115	6.713331	5.550619	X	p22.13	Nance-Horan syndrome (congenital cataracts and dental anomalies) [Source:HGNC Symbol;Acc:7820]
203477_at	COL15A1	ENSG00000204291	0.023677	1.6143067	8.436883	6.822576	9	q22.33	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
200857_s_at	NCOR1	ENSG00000141027	0.023677	0.7091943	8.662953	7.953759	17	p11.2	nuclear receptor corepressor 1 [Source:HGNC Symbol;Acc:7672]
224996_at	ASPH	ENSG00000198363	0.0237	1.5230174	7.874016	6.350998	8	q12.3	aspartate beta-hydroxylase [Source:HGNC Symbol;Acc:757]
223562_at	PARVG	ENSG00000138964	0.0237	1.5009148	9.669889	8.168975	22	q13.31	parvin, gamma [Source:HGNC Symbol;Acc:14654]
213353_at	ABCA5	ENSG00000154265	0.0237	0.9962432	8.332971	7.336728	17	q24.3	ATP-binding cassette, sub-family A (ABC1), member 5 [Source:HGNC Symbol;Acc:35]
209593_s_at	TOR1B	ENSG00000136816	0.0238	0.4661131	7.855148	7.389035	9	q34.11	torsin family 1, member B (torsin B) [Source:HGNC Symbol;Acc:11995]
35626_at	SGSH	ENSG00000181523	0.0238	0.7817095	9.79381	9.0121	17	q25.3	N-sulfoglucosamine sulfohydrolase [Source:HGNC Symbol;Acc:10818]
234994_at	TMEM200A	ENSG00000164484	0.0238	1.6120474	6.524548	4.9125	6	q23.1	transmembrane protein 200A [Source:HGNC Symbol;Acc:21075]
211456_x_at	MT1P2	NA	0.0238	1.0267142	11.33702	10.3103	NA	NA	NA
203501_at	CPQ	ENSG00000104324	0.024112	0.9862063	7.824448	6.838241	8	q22.1	carboxypeptidase Q [Source:HGNC Symbol;Acc:16910]
226155_at	FAM160B1	ENSG00000151553	0.024112	0.9499152	8.161808	7.211893	10	q25.3	family with sequence similarity 160, member B1 [Source:HGNC Symbol;Acc:29320]
1552258_at	LINC00152	ENSG00000222041	0.024124	1.1245258	8.139435	7.014909	2	p11.2	long intergenic non-protein coding RNA 152 [Source:HGNC Symbol;Acc:28717]
238025_at	MLKL	ENSG00000168404	0.024866	1.2159905	8.756993	7.541002	16	q23.1	mixed lineage kinase domain-like [Source:HGNC Symbol;Acc:26617]
219460_s_at	TMEM127	ENSG00000135956	0.024866	0.4546254	8.629221	8.174596	2	q11.2	transmembrane protein 127 [Source:HGNC Symbol;Acc:26038]
225522_at	AAK1	ENSG00000115977	0.024866	1.1728016	8.652908	7.480107	2	p13.3	AP2 associated kinase 1 [Source:HGNC Symbol;Acc:19679]

217757_at	A2M	ENSG00000175899	0.02498	1.5764623	12.02894	10.45248	12	p13.31	alpha-2-macroglobulin [Source:HGNC Symbol;Acc:7]
223168_at	RHO	ENSG00000116574	0.025427	1.5603849	7.215569	5.655184	1	q42.13	ras homolog family member U [Source:HGNC Symbol;Acc:17794]
1561615_s_at	SLC8A1	ENSG00000183023	0.025808	1.5650362	8.855137	7.290101	2	p22.1	solute carrier family 8 (sodium/calcium exchanger), member 1 [Source:HGNC Symbol;Acc:11068]
203758_at	CTSO	ENSG00000256043	0.026066	1.1560559	9.311624	8.155568	4	q32.1	cathepsin O [Source:HGNC Symbol;Acc:2542]
226552_at	IER5L	ENSG00000188483	0.026467	0.936727	7.611941	6.675214	9	q34.11	immediate early response 5-like [Source:HGNC Symbol;Acc:23679]
202766_s_at	FBN1	ENSG00000166147	0.027121	1.374538	7.745362	6.370824	15	q21.1	fibrillin 1 [Source:HGNC Symbol;Acc:3603]
225629_s_at	ZBTB4	ENSG00000174282	0.027121	1.019746	9.543581	8.523835	17	p13.1	zinc finger and BTB domain containing 4 [Source:HGNC Symbol;Acc:23847]
212136_at	ATP2B4	ENSG00000058668	0.027283	1.5266923	8.833219	7.306527	1	q32.1	ATPase, Ca ²⁺ transporting, plasma membrane 4 [Source:HGNC Symbol;Acc:817]
1555881_s_at	LZTS2	ENSG00000107816	0.027517	0.4402212	7.841075	7.400854	10	q24.31	leucine zipper, putative tumor suppressor 2 [Source:HGNC Symbol;Acc:29381]
57715_at	CALHM2	ENSG00000138172	0.027517	0.6960074	8.099815	7.403808	10	q24.33	calcium homeostasis modulator 2 [Source:HGNC Symbol;Acc:23493]
226601_at	SLC30A7	ENSG00000162695	0.027517	0.9372185	8.338968	7.401749	1	p21.2	solute carrier family 30 (zinc transporter), member 7 [Source:HGNC Symbol;Acc:19306]
217890_s_at	PARVA	ENSG00000197702	0.027517	1.5638318	9.160286	7.596454	11	p15.3	parvin, alpha [Source:HGNC Symbol;Acc:14652]
207624_s_at	RPGR	ENSG00000156313	0.027572	0.5262896	7.293504	6.767215	X	p11.4	retinitis pigmentosa GTPase regulator [Source:HGNC Symbol;Acc:10295]
212372_at	MYH10	ENSG00000133026	0.027572	1.0557138	8.323251	7.267537	17	p13.1	myosin, heavy chain 10, non-muscle [Source:HGNC Symbol;Acc:7568]
226820_at	ZNF362	ENSG00000160094	0.027572	0.8062413	8.807479	8.001238	1	p35.1	zinc finger protein 362 [Source:HGNC Symbol;Acc:18079]
202551_s_at	CRIM1	ENSG00000150938	0.027572	1.4256957	8.947674	7.521978	2	p22.3	cysteine rich transmembrane BMP regulator 1 (chordin-like) [Source:HGNC Symbol;Acc:2359]
208030_s_at	ADD1	ENSG00000087274	0.027643	0.584655	9.931156	9.346501	4	p16.3	adducin 1 (alpha) [Source:HGNC Symbol;Acc:243]
206618_at	IL18R1	ENSG00000115604	0.027643	1.4815374	7.518533	6.036996	2	q12.1	interleukin 18 receptor 1 [Source:HGNC Symbol;Acc:5988]
201212_at	LGMM	ENSG00000100600	0.027659	2.066812	10.16982	8.103011	14	q32.12	legumain [Source:HGNC Symbol;Acc:9472]
208782_at	FSTL1	ENSG00000163430	0.027737	1.3252445	10.08689	8.761649	3	q13.33	folliculin-like 1 [Source:HGNC Symbol;Acc:3972]
209191_at	TUBB6	ENSG00000176014	0.027737	1.6575274	9.832241	8.174714	18	p11.21	tubulin, beta class V [Source:HGNC Symbol;Acc:20776]
206875_s_at	SLK	ENSG00000065613	0.027737	1.0643734	8.057717	6.993344	10	q24.33	STE20-like kinase [Source:HGNC Symbol;Acc:11088]
212990_at	SYNJ1	ENSG00000159082	0.027737	1.0442604	7.114954	6.070594	21	q22.11	synaptojanin 1 [Source:HGNC Symbol;Acc:11503]
204193_at	CHKB	ENSG00000100288	0.027737	0.8998133	9.518634	8.618821	22	q13.33	choline kinase beta [Source:HGNC Symbol;Acc:1938]
203243_s_at	PDLIM5	ENSG00000163110	0.02803	1.1428446	7.842659	6.699815	4	q22.3	PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:17468]
227554_at	MAGI2-AS3	ENSG00000234456	0.02803	1.5835165	7.049678	5.466162	7	q21.11	MAGI2 antisense RNA 3 [Source:HGNC Symbol;Acc:40862]
224616_at	DYNC1L1	ENSG00000135720	0.02803	0.7957119	10.00718	9.211464	16	q22.1	dynein, cytoplasmic 1, light intermediate chain 2 [Source:HGNC Symbol;Acc:2966]
218901_at	PLSCR4	ENSG00000114698	0.028186	1.6412008	5.938607	4.297406	3	q24	phospholipid scramblase 4 [Source:HGNC Symbol;Acc:16497]
209050_s_at	RALGDS	ENSG00000160271	0.028199	0.8301435	9.509798	8.679655	9	q34.2	ral guanine nucleotide dissociation stimulator [Source:HGNC Symbol;Acc:9842]
209472_at	CCBL2	ENSG00000137944	0.028199	0.791466	9.348802	8.557336	1	p22.2	cysteine conjugate-beta lyase 2 [Source:HGNC Symbol;Acc:33238]
227542_at	SOCS6	ENSG00000170677	0.028199	1.310032	6.680389	5.370357	18	q22.2	suppressor of cytokine signaling 6 [Source:HGNC Symbol;Acc:16833]
204039_at	CEBPA	ENSG00000245848	0.028199	0.9298719	8.572793	7.642921	19	q13.11	CCAAT/enhancer binding protein (C/EBP), alpha [Source:HGNC Symbol;Acc:1833]
212586_at	CAST	ENSG00000153113	0.028199	0.7412945	9.204774	8.463479	5	q15	calpastatin [Source:HGNC Symbol;Acc:1515]
201280_s_at	DAB2	ENSG00000153071	0.028199	1.7797808	8.603167	6.823386	5	p13.1	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:2662]
201599_at	OAT	ENSG00000065154	0.028199	0.8899814	9.474237	8.584256	10	q26.13	ornithine aminotransferase [Source:HGNC Symbol;Acc:8091]
225334_at	C10orf32	ENSG00000166275	0.028199	0.7814388	8.253485	7.472047	10	q24.32	chromosome 10 open reading frame 32 [Source:HGNC Symbol;Acc:23516]
201334_s_at	ARHGEF12	ENSG00000196914	0.028227	1.1207523	9.211231	8.090479	11	q23.3	Rho guanine nucleotide exchange factor (GEF) 12 [Source:HGNC Symbol;Acc:14193]
229041_s_at	ITGB2-AS1	ENSG00000227039	0.02892	1.8343051	9.515398	7.681093	21	q22.3	ITGB2 antisense RNA 1 [Source:HGNC Symbol;Acc:44304]
212124_at	ZMI2	ENSG00000108175	0.02892	1.4720018	10.25153	8.779525	10	q22.3	zinc finger, MIZ-type containing 1 [Source:HGNC Symbol;Acc:16493]
204863_s_at	IL6ST	ENSG00000134352	0.02892	1.1450808	9.161299	8.016219	5	q11.2	interleukin 6 signal transducer (gp130, oncostatin M receptor) [Source:HGNC Symbol;Acc:6021]
215235_at	SPTAN1	ENSG00000197694	0.02892	0.6877124	10.61621	9.928495	9	q34.11	spectrin, alpha, non-erythrocytic 1 [Source:HGNC Symbol;Acc:11273]

212606_at	WDFY3	ENSG00000163625	0.02892	1.6875876	6.840272	5.152685	4	q21.23	WD repeat and FYVE domain containing 3 [Source:HGNC Symbol;Acc:20751]
212601_at	ZZEF1	ENSG00000074755	0.02892	0.4622513	8.027308	7.565057	17	p13.2	zinc finger, ZZ-type with EF-hand domain 1 [Source:HGNC Symbol;Acc:29027]
228577_x_at	ODF2L	ENSG00000122417	0.02892	0.9283355	7.13428	6.205945	1	p22.3	outer dense fiber of sperm tails 2-like [Source:HGNC Symbol;Acc:29225]
227776_at	ACER3	ENSG00000078124	0.02892	1.1794217	7.521437	6.342016	11	q13.5	alkaline ceramidase 3 [Source:HGNC Symbol;Acc:16066]
201146_at	NFE2L2	ENSG00000116044	0.02892	0.9705592	10.20237	9.231807	2	q31.2	nuclear factor (erythroid-derived 2)-like 2 [Source:HGNC Symbol;Acc:7782]
214807_at	LOC100509635	NA	0.02892	1.8398924	8.320893	6.481	NA	NA	NA
201185_at	HTRA1	ENSG00000166033	0.02892	1.815072	9.750466	7.935394	10	q26.13	HtrA serine peptidase 1 [Source:HGNC Symbol;Acc:9476]
209120_at	NR2F2	ENSG00000185551	0.029112	2.1914356	8.372705	6.181269	15	q26.2	nuclear receptor subfamily 2, group F, member 2 [Source:HGNC Symbol;Acc:7976]
226021_at	RDH10	ENSG00000121039	0.029112	1.1810757	6.837597	5.656521	8	q21.11	retinol dehydrogenase 10 (all-trans) [Source:HGNC Symbol;Acc:19975]
224480_s_at	AGPAT9	ENSG00000138678	0.029341	1.110871	4.910358	3.799487	4	q21.23	1-acylglycerol-3-phosphate O-acyltransferase 9 [Source:HGNC Symbol;Acc:28157]
212077_at	CALD1	ENSG00000122786	0.029341	1.7247901	10.1792	8.454405	7	q33	caldesmon 1 [Source:HGNC Symbol;Acc:1441]
204745_x_at	MT1G	ENSG00000125144	0.029341	1.0418968	10.90301	9.861108	16	q13	metallothionein 1G [Source:HGNC Symbol;Acc:7399]
227930_at	AGO4	ENSG00000134698	0.029586	1.1053521	6.925534	5.820182	1	p34.3	argonaute RISC catalytic component 4 [Source:HGNC Symbol;Acc:18424]
212636_at	QKI	ENSG00000112531	0.029711	1.3783407	8.509471	7.13113	6	q26	QKI, KH domain containing, RNA binding [Source:HGNC Symbol;Acc:21100]
202609_at	EP58	ENSG00000151491	0.029743	2.016396	8.302003	6.285607	12	p12.3	epidermal growth factor receptor pathway substrate 8 [Source:HGNC Symbol;Acc:3420]
207791_s_at	RAB1A	ENSG00000138069	0.029761	0.8342427	9.926541	9.092298	2	p14	RAB1A, member RAS oncogene family [Source:HGNC Symbol;Acc:9758]
226377_at	NFIC	ENSG00000141905	0.029761	1.124935	8.785641	7.660706	19	p13.3	nuclear factor I/C (CCAAT-binding transcription factor) [Source:HGNC Symbol;Acc:7786]
212607_at	AKT3	ENSG00000117020	0.029761	1.2861363	8.867901	7.581765	1	q44	v-akt murine thymoma viral oncogene homolog 3 [Source:HGNC Symbol;Acc:393]
220122_at	MCTP1	ENSG00000175471	0.029808	1.5794589	7.121595	5.542136	5	q15	multiple C2 domains, transmembrane 1 [Source:HGNC Symbol;Acc:26183]
225941_at	EIF4E3	ENSG00000163412	0.029808	1.3642413	7.790818	6.426577	3	p13	eukaryotic translation initiation factor 4E family member 3 [Source:HGNC Symbol;Acc:31837]
65635_at	ENGASE	ENSG00000167280	0.029836	0.5491265	9.240447	8.69132	17	q25.3	endo-beta-N-acetylglucosaminidase [Source:HGNC Symbol;Acc:24622]
202897_at	SIRPA	ENSG00000198053	0.029836	1.0792131	9.722842	8.643629	20	p13	signal-regulatory protein alpha [Source:HGNC Symbol;Acc:9662]
213817_at	IRAK3	ENSG00000090376	0.029836	1.4320001	6.594781	5.162781	12	q14.3	interleukin-1 receptor-associated kinase 3 [Source:HGNC Symbol;Acc:17020]
204703_at	IFT88	ENSG00000032742	0.029836	0.5556265	7.914095	7.358469	13	q12.11	intraflagellar transport 88 homolog (Chlamydomonas) [Source:HGNC Symbol;Acc:20606]
201029_s_at	CD99	ENSG00000002586	0.029836	1.1795508	11.79489	10.61534	X	p22.33	CD99 molecule [Source:HGNC Symbol;Acc:7082]
201105_at	LGALS1	ENSG00000100097	0.029836	1.0679695	12.55396	11.48599	22	q13.1	lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:6561]
228666_at	C15orf38	ENSG00000242498	0.029836	0.9655288	8.632863	7.667335	15	q26.1	chromosome 15 open reading frame 38 [Source:HGNC Symbol;Acc:28782]
213733_at	MYO1F	ENSG00000142347	0.029836	1.2120209	9.047983	7.835962	19	p13.2	myosin IF [Source:HGNC Symbol;Acc:7600]
225162_at	SH3D19	ENSG00000109686	0.029836	1.6977199	6.304496	4.606776	4	q31.3	SH3 domain containing 19 [Source:HGNC Symbol;Acc:30418]
221766_s_at	FAM46A	ENSG00000112773	0.030026	1.3074382	9.102394	7.794956	6	q14.1	family with sequence similarity 46, member A [Source:HGNC Symbol;Acc:18345]
235256_s_at	GALM	ENSG00000143891	0.030026	1.3208648	7.939207	6.618342	2	p22.1	galactose mutarotase (aldose 1-epimerase) [Source:HGNC Symbol;Acc:24063]
201417_at	SOX4	ENSG00000124766	0.030026	1.0943539	7.314555	6.220202	6	p22.3	SRY (sex determining region Y)-box 4 [Source:HGNC Symbol;Acc:11200]
201963_at	ACSL1	ENSG00000151726	0.030026	1.0262575	9.481285	8.455027	4	q35.1	acyl-CoA synthetase long-chain family member 1 [Source:HGNC Symbol;Acc:3569]
218983_at	C1RL	ENSG00000139178	0.030026	1.0535412	6.970689	5.917148	12	p13.31	complement component 1, r subcomponent-like [Source:HGNC Symbol;Acc:21265]
225442_at	DDR2	ENSG00000162733	0.030026	1.204158	8.120903	6.916745	1	q23.3	discoidin domain receptor tyrosine kinase 2 [Source:HGNC Symbol;Acc:2731]
225128_at	KDEL2	ENSG00000178202	0.030089	0.839869	7.886197	7.046328	11	q22.3	KDEL (Lys-Asp-Glu-Leu) containing 2 [Source:HGNC Symbol;Acc:28496]
225913_at	PEAK1	NA	0.030089	0.8774813	8.926048	8.048566	NA	NA	NA
238477_at	KIF1C	ENSG00000129250	0.030089	0.5143139	6.616652	6.102338	17	p13.2	kinesin family member 1C [Source:HGNC Symbol;Acc:6317]
1557236_at	APOL6	ENSG00000221963	0.030333	1.3530187	6.588335	5.235316	22	q12.3	apolipoprotein L, 6 [Source:HGNC Symbol;Acc:14870]
224764_at	ARHGAP21	ENSG00000107863	0.030504	0.7262548	8.341028	7.614773	10	p12.1	Rho GTPase activating protein 21 [Source:HGNC Symbol;Acc:23725]
204568_at	ATG14	ENSG00000126775	0.030504	0.6825568	7.833225	7.150668	14	q22.3	autophagy related 14 [Source:HGNC Symbol;Acc:19962]

202598_at	S100A13	ENSG00000189171	0.030504	0.9054696	10.25863	9.353158	1	q21.3	S100 calcium binding protein A13 [Source:HGNC Symbol;Acc:10490]
218815_s_at	TMEM51	ENSG00000171729	0.03053	0.8211201	9.101394	8.280274	1	p36.21	transmembrane protein 51 [Source:HGNC Symbol;Acc:25488]
204214_s_at	RAB32	ENSG00000118508	0.03053	0.9747791	8.206092	7.231313	6	q24.3	RAB32, member RAS oncogene family [Source:HGNC Symbol;Acc:9772]
226152_at	TTC7B	ENSG00000165914	0.030555	1.2258262	7.058997	5.833171	14	q32.11	tetratricopeptide repeat domain 7B [Source:HGNC Symbol;Acc:19858]
205590_at	RASGRP1	ENSG00000172575	0.030555	1.8115112	10.05801	8.2465	15	q14	RAS guanyl releasing protein 1 (calcium and DAG-regulated) [Source:HGNC Symbol;Acc:9878]
155579_s_at	PTPRM	ENSG00000173482	0.030555	1.1333216	7.834017	6.700695	18	p11.23	protein tyrosine phosphatase, receptor type, M [Source:HGNC Symbol;Acc:9675]
218486_at	KLF11	ENSG00000172059	0.030555	1.2762837	7.737116	6.460832	2	p25.1	Kruppel-like factor 11 [Source:HGNC Symbol;Acc:11811]
204451_at	FZD1	ENSG00000157240	0.030555	1.2800529	7.241574	5.961521	7	q21.13	frizzled family receptor 1 [Source:HGNC Symbol;Acc:4038]
226186_at	TMOD2	ENSG00000128872	0.030555	1.3625462	6.784226	5.42168	15	q21.2	tropomodulin 2 (neuronal) [Source:HGNC Symbol;Acc:11872]
225288_at	COL27A1	ENSG00000196739	0.030691	1.4054422	7.835002	6.429559	9	q32	collagen, type XXVII, alpha 1 [Source:HGNC Symbol;Acc:22986]
225163_at	FRMD4A	ENSG00000151474	0.030947	1.1375317	7.411625	6.274094	10	p13	FERM domain containing 4A [Source:HGNC Symbol;Acc:25491]
221541_at	CRISPLD2	ENSG00000103196	0.030947	1.7573923	8.718881	6.961489	16	q24.1	cysteine-rich secretory protein LCCL domain containing 2 [Source:HGNC Symbol;Acc:25248]
230480_at	PIWIL4	ENSG00000134627	0.030947	0.6575147	6.112214	5.4547	11	q21	piwi-like RNA-mediated gene silencing 4 [Source:HGNC Symbol;Acc:18444]
227444_at	ARMCX4	ENSG00000196440	0.030947	0.97698	6.028167	5.051187	X	q22.1	armadillo repeat containing, X-linked 4 [Source:HGNC Symbol;Acc:28615]
218285_s_at	BDH2	ENSG00000164039	0.030947	0.7247672	8.942667	8.2179	4	q24	3-hydroxybutyrate dehydrogenase, type 2 [Source:HGNC Symbol;Acc:32389]
209687_at	CXCL12	ENSG00000107562	0.030947	2.2250584	9.716134	7.491076	10	q11.21	chemokine (C-X-C motif) ligand 12 [Source:HGNC Symbol;Acc:10672]
203261_at	DCTN6	ENSG00000104671	0.030947	0.8065653	10.35688	9.550316	8	p12	dynactin 6 [Source:HGNC Symbol;Acc:16964]
227001_at	NIPAL2	ENSG00000104361	0.030947	1.3854199	8.211606	6.826186	8	q22.2	NIPA-like domain containing 2 [Source:HGNC Symbol;Acc:25854]
213119_at	SLC36A1	ENSG00000123643	0.030947	0.527649	8.18839	7.660741	5	q33.1	solute carrier family 36 (proton/amino acid symporter), member 1 [Source:HGNC Symbol;Acc:18761]
201089_at	ATP6V1B2	ENSG00000147416	0.030947	0.979669	10.05201	9.072342	8	p21.3	ATPase, H transporting, lysosomal 56/58kDa, V1 subunit B2 [Source:HGNC Symbol;Acc:854]
228937_at	LACC1	ENSG00000179630	0.030947	1.4347724	7.870869	6.436096	13	q14.11	laccase (multicopper oxidoreductase) domain containing 1 [Source:HGNC Symbol;Acc:26789]
219666_at	MS4A6A	ENSG00000110077	0.031011	2.1589072	10.17588	8.016976	11	q12.2	membrane-spanning 4-domains, subfamily A, member 6A [Source:HGNC Symbol;Acc:13375]
209160_at	AKR1C3	ENSG00000196139	0.031011	1.5583408	6.70255	5.144209	10	p15.1	aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:386]
203688_at	PKD2	ENSG00000118762	0.031011	1.224664	8.101781	6.877117	4	q22.1	polycystic kidney disease 2 (autosomal dominant) [Source:HGNC Symbol;Acc:9009]
209379_s_at	CCSER2	ENSG00000107771	0.031011	0.895303	6.749215	5.853912	10	q23.1	coiled-coil serine-rich protein 2 [Source:HGNC Symbol;Acc:29197]
202973_x_at	FAM13A	ENSG00000138640	0.031011	1.5090759	6.614676	5.1056	4	q22.1	family with sequence similarity 13, member A [Source:HGNC Symbol;Acc:19367]
222999_s_at	CCN12	ENSG00000221978	0.031011	0.5863072	9.418618	8.832311	1	p36.33	cyclin L2 [Source:HGNC Symbol;Acc:20570]
32811_at	MYO1C	ENSG00000197879	0.031088	0.6404769	9.336457	8.69598	17	p13.3	myosin IC [Source:HGNC Symbol;Acc:7597]
213737_x_at	GOLGA8I	ENSG00000153666	0.031114	1.2841014	9.220786	7.936684	15	q11.2	golgin A8 family, member I [Source:HGNC Symbol;Acc:26660]
202351_at	ITGAV	ENSG00000138448	0.031169	1.360409	9.310597	7.950188	2	q32.1	integrin, alpha V [Source:HGNC Symbol;Acc:6150]
226066_at	MITF	ENSG00000187098	0.031203	1.3946024	8.259922	6.86532	3	p14.1	microphthalmia-associated transcription factor [Source:HGNC Symbol;Acc:7105]
212453_at	KIAA1279	ENSG00000198954	0.031375	0.7010336	7.669603	6.96857	10	q22.1	KIAA1279 [Source:HGNC Symbol;Acc:23419]
223276_at	SMIM3	ENSG00000256235	0.031482	1.0571958	7.313512	6.256316	5	q33.1	small integral membrane protein 3 [Source:HGNC Symbol;Acc:30248]
63825_at	ABHD2	ENSG00000140526	0.031482	1.0510036	8.787775	7.736771	15	q26.1	abhydrolase domain containing 2 [Source:HGNC Symbol;Acc:18717]
203817_at	GUCY1B3	ENSG00000061918	0.031482	1.3742528	7.677666	6.303413	4	q32.1	guanylate cyclase 1, soluble, beta 3 [Source:HGNC Symbol;Acc:4687]
232090_at	DNM3OS	ENSG00000230630	0.031482	1.8766379	6.73819	4.861552	1	q24.3	DNM3 opposite strand/antisense RNA [Source:HGNC Symbol;Acc:41228]
218292_s_at	PRKAG2	ENSG00000106617	0.03163	0.7377637	7.332145	6.594381	7	q36.1	protein kinase, AMP-activated, gamma 2 non-catalytic subunit [Source:HGNC Symbol;Acc:9386]
1558173_a_at	LUZP1	ENSG00000169641	0.03163	0.7965467	9.005566	8.20902	1	p36.12	leucine zipper protein 1 [Source:HGNC Symbol;Acc:14985]
201438_at	COL6A3	ENSG00000163359	0.03163	1.6730976	11.52	9.846906	2	q37.3	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]

235458_at	HAVCR2	ENSG00000135077	0.03163	1.5671406	9.031225	7.464085	5	q33.3	hepatitis A virus cellular receptor 2 [Source:HGNC Symbol;Acc:18437]
223393_s_at	TSHZ3	ENSG00000121297	0.03163	1.3239929	7.607905	6.283912	19	q12	teashirt zinc finger homeobox 3 [Source:HGNC Symbol;Acc:30700]
215706_x_at	ZYX	ENSG00000159840	0.031657	0.8773626	10.71626	9.838895	7	q34	zyxin [Source:HGNC Symbol;Acc:13200]
219315_s_at	TMEM204	ENSG00000131634	0.0318	0.9451335	7.656937	6.711803	16	p13.3	transmembrane protein 204 [Source:HGNC Symbol;Acc:14158]
201296_s_at	WSB1	ENSG00000109046	0.0318	1.2622427	10.19944	8.937196	17	q11.1	WD repeat and SOCS box containing 1 [Source:HGNC Symbol;Acc:19221]
232231_at	RUNX2	ENSG00000124813	0.0318	2.284395	8.680094	6.395699	6	p21.1	runx-related transcription factor 2 [Source:HGNC Symbol;Acc:10472]
226225_at	MCC	ENSG00000171444	0.0318	1.7962144	5.490905	3.69469	5	q22.2	mutated in colorectal cancers [Source:HGNC Symbol;Acc:6935]
214660_at	ITGA1	ENSG00000213949	0.0318	0.9359119	4.662647	3.726735	5	q11.2	integrin, alpha 1 [Source:HGNC Symbol;Acc:6134]
216903_s_at	MICU1	ENSG00000107745	0.0318	0.5179458	8.825263	8.307317	10	q22.1	mitochondrial calcium uptake 1 [Source:HGNC Symbol;Acc:1530]
215111_s_at	TSC22D1	ENSG00000102804	0.0318	1.4896493	9.321974	7.832325	13	q14.11	TSC22 domain family, member 1 [Source:HGNC Symbol;Acc:16826]
200782_at	ANXA5	ENSG00000164111	0.0318	0.9613548	10.84305	9.881696	4	q27	annexin A5 [Source:HGNC Symbol;Acc:543]
226771_at	ATP8B2	ENSG00000143515	0.0318	1.0911816	8.208904	7.117722	1	q21.3	ATPase, aminophospholipid transporter, class I, type 8B, member 2 [Source:HGNC Symbol;Acc:13534]
212185_x_at	MT2A	ENSG00000125148	0.0318	1.0146409	12.36689	11.35225	16	q12.2	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
200986_at	SERPINC1	ENSG00000149131	0.031971	1.2398359	10.45704	9.217209	11	q12.1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 [Source:HGNC Symbol;Acc:1228]
221269_s_at	SH3BGL3	ENSG00000142669	0.031971	0.5644103	11.47106	10.90665	1	p36.11	SH3 domain binding glutamic acid-rich protein like 3 [Source:HGNC Symbol;Acc:15568]
202081_at	IER2	ENSG00000160888	0.031971	1.2239497	10.27327	9.049318	19	p13.2	immediate early response 2 [Source:HGNC Symbol;Acc:28871]
206995_x_at	SCARF1	ENSG00000074660	0.032439	0.7313947	6.493193	5.761798	17	p13.3	scavenger receptor class F, member 1 [Source:HGNC Symbol;Acc:16820]
204963_at	SSPN	ENSG00000123096	0.032493	1.9774021	7.971609	5.994207	12	p12.1	sarcospan [Source:HGNC Symbol;Acc:11322]
202192_s_at	GAS7	ENSG00000007237	0.032689	1.0554065	9.145391	8.089984	17	p13.1	growth arrest-specific 7 [Source:HGNC Symbol;Acc:4169]
224747_at	UBE2Q2	ENSG00000140367	0.032689	1.0044345	8.252427	7.247992	15	q24.2	ubiquitin-conjugating enzyme E2Q family member 2 [Source:HGNC Symbol;Acc:19248]
202136_at	ZMYND11	ENSG00000015171	0.032689	1.0017022	9.77863	8.776928	10	p15.3	zinc finger, MYND-type containing 11 [Source:HGNC Symbol;Acc:16966]
209970_x_at	CASP1	ENSG00000137752	0.03271	1.2604855	9.149475	7.888989	11	q22.3	caspase 1, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:1499]
234987_at	SAMHD1	ENSG00000101347	0.032727	1.4165041	9.200321	7.783817	20	q11.23	SAM domain and HD domain 1 [Source:HGNC Symbol;Acc:15925]
205173_x_at	CD58	ENSG00000116815	0.032727	1.6045445	9.9085	8.303956	1	p13.1	CD58 molecule [Source:HGNC Symbol;Acc:1688]
229732_at	ZNF823	ENSG00000197933	0.032727	0.5212517	4.981581	4.460329	19	p13.2	zinc finger protein 823 [Source:HGNC Symbol;Acc:30936]
37408_at	MRC2	ENSG0000011028	0.032727	0.9769173	9.11946	8.142542	17	q23.2	mannose receptor, C type 2 [Source:HGNC Symbol;Acc:16875]
208922_s_at	NXF1	ENSG00000162231	0.032727	0.7165582	10.10897	9.392408	11	q12.3	nuclear RNA export factor 1 [Source:HGNC Symbol;Acc:8071]
200766_at	CTSD	ENSG00000117984	0.032727	1.0316494	11.05559	10.02395	11	p15.5	cathepsin D [Source:HGNC Symbol;Acc:2529]
209129_at	TRIP6	ENSG00000087077	0.032727	0.6143954	8.270125	7.655729	7	q22.1	thyroid hormone receptor interactor 6 [Source:HGNC Symbol;Acc:12311]
228728_at	CPED1	ENSG00000106034	0.032727	1.3257067	6.216333	4.890626	7	q31.31	cadherin-like and PC-esterase domain containing 1 [Source:HGNC Symbol;Acc:26159]
223028_s_at	SNX9	ENSG00000130340	0.032727	1.5469591	9.600897	8.053938	6	q25.3	sorting nexin 9 [Source:HGNC Symbol;Acc:14973]
214464_at	CDC42BPA	ENSG00000143776	0.032727	1.5903569	8.711909	7.121553	1	q42.13	CDC42 binding protein kinase alpha (DMPK-like) [Source:HGNC Symbol;Acc:1737]
204059_s_at	ME1	ENSG00000065833	0.032727	2.1309538	7.883911	5.752957	6	q14.2	malic enzyme 1, NAD(P)-dependent, cytosolic [Source:HGNC Symbol;Acc:6983]
202481_at	DHRS3	ENSG00000162496	0.032727	1.3557175	9.3739	8.018183	1	p36.22	dehydrogenase/reductase (SDR family) member 3 [Source:HGNC Symbol;Acc:17693]
201426_s_at	VIM	ENSG00000026025	0.032727	0.86197	13.16644	12.30447	10	p13	vimentin [Source:HGNC Symbol;Acc:12692]
214177_s_at	PBXIP1	ENSG00000163346	0.032727	0.6439449	8.558974	7.915029	1	q21.3	pre-B-cell leukemia homeobox interacting protein 1 [Source:HGNC Symbol;Acc:21199]
218793_s_at	SCML1	ENSG00000047634	0.032727	1.7949304	7.348371	5.553441	X	p22.13	sex comb on midleg-like 1 (Drosophila) [Source:HGNC Symbol;Acc:10580]
201163_s_at	IGFBP7	ENSG00000163453	0.032727	1.2772891	11.02179	9.744497	4	q12	insulin-like growth factor binding protein 7 [Source:HGNC Symbol;Acc:5476]
225406_at	TWSG1	ENSG00000128791	0.032727	1.0154958	8.499218	7.483723	18	p11.22	twisted gastrulation homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:12429]
209071_s_at	RGS5	ENSG00000143248	0.032727	1.9992561	9.334306	7.33505	1	q23.3	regulator of G-protein signaling 5 [Source:HGNC Symbol;Acc:10001]

204206_at	MNT	ENSG00000070444	0.032727	0.4543166	8.03428	7.579963	17	p13.3	MNT, MAX dimerization protein [Source:HGNC Symbol;Acc:7188]
226026_at	DIRC2	ENSG00000138463	0.032727	1.2125934	8.349561	7.136968	3	q21.1	disrupted in renal carcinoma 2 [Source:HGNC Symbol;Acc:16628]
214683_s_at	CLK1	ENSG00000013441	0.032727	0.9215093	10.05348	9.131974	2	q33.1	CDC-like kinase 1 [Source:HGNC Symbol;Acc:2068]
218095_s_at	TMEM165	ENSG00000134851	0.032727	0.7881717	10.38715	9.598976	4	q12	transmembrane protein 165 [Source:HGNC Symbol;Acc:30760]
219316_s_at	FLVCR2	ENSG00000119686	0.032727	0.8558016	7.371184	6.515383	14	q24.3	feline leukemia virus subgroup C cellular receptor family, member 2 [Source:HGNC Symbol;Acc:20105]
226763_at	SESTD1	ENSG00000187231	0.032727	1.0596477	9.549725	8.490077	2	q31.2	SEC14 and spectrin domains 1 [Source:HGNC Symbol;Acc:18379]
227361_at	HS3ST3B1	ENSG00000125430	0.032727	1.5227184	7.752502	6.229784	17	p12	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 [Source:HGNC Symbol;Acc:5198]
205248_at	DOPEY2	ENSG00000142197	0.032727	0.619808	7.178375	6.558567	21	q22.12	dopey family member 2 [Source:HGNC Symbol;Acc:1291]
211026_s_at	MGLL	ENSG00000074416	0.032727	1.3462606	9.704251	8.35799	3	q21.3	monoglyceride lipase [Source:HGNC Symbol;Acc:17038]
212224_at	ALDH1A1	ENSG00000165092	0.032727	2.3279866	9.644018	7.316031	9	q21.13	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC Symbol;Acc:402]
201215_at	PLS3	ENSG00000102024	0.032727	1.846069	7.9037	6.057631	X	q23	plastin 3 [Source:HGNC Symbol;Acc:9091]
218432_at	FBXO3	ENSG00000110429	0.032727	0.9692028	6.759587	5.790384	11	p13	F-box protein 3 [Source:HGNC Symbol;Acc:13582]
212428_at	KIAA0368	ENSG00000136813	0.032727	0.5027122	8.88096	8.378248	9	q31.3	KIAA0368 [Source:HGNC Symbol;Acc:29020]
203394_s_at	HES1	ENSG00000114315	0.032727	1.1805255	9.074966	7.894441	3	q29	hairy and enhancer of split 1, (Drosophila) [Source:HGNC Symbol;Acc:5192]
235125_x_at	FAM73A	ENSG00000180488	0.032727	0.7890075	6.551391	5.762383	1	p31.1	family with sequence similarity 73, member A [Source:HGNC Symbol;Acc:24741]
224690_at	FAM210B	ENSG00000124098	0.032727	1.2185977	8.947456	7.728858	20	q13.2	family with sequence similarity 210, member B [Source:HGNC Symbol;Acc:16102]
219991_at	SLC2A9	ENSG00000109667	0.032727	0.7452065	7.42728	6.682073	4	p16.1	solute carrier family 2 (facilitated glucose transporter), member 9 [Source:HGNC Symbol;Acc:13446]
214560_at	FPR3	ENSG00000187474	0.032727	1.5525474	10.11159	8.55904	19	q13.41	formyl peptide receptor 3 [Source:HGNC Symbol;Acc:3828]
210946_at	PPAP2A	ENSG00000067113	0.032727	0.8694264	8.48212	7.612694	5	q11.2	phosphatidic acid phosphatase type 2A [Source:HGNC Symbol;Acc:9228]
210817_s_at	CALCOCO2	ENSG00000136436	0.032727	0.9010721	10.04862	9.147547	17	q21.32	calcium binding and coiled-coil domain 2 [Source:HGNC Symbol;Acc:29912]
208636_at	ACTN1	ENSG00000072110	0.032727	1.4921308	9.059967	7.567836	14	q24.1	actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
1561226_at	XCR1	ENSG00000173578	0.032727	0.9280383	4.980618	4.05258	3	p21.31	chemokine (C motif) receptor 1 [Source:HGNC Symbol;Acc:1625]
229256_at	PGM2L1	ENSG00000165434	0.032727	0.9502539	6.806744	5.85649	11	q13.4	phosphoglucomutase 2-like 1 [Source:HGNC Symbol;Acc:20898]
228131_at	ERCC1	ENSG00000012061	0.032727	0.6986806	8.644378	7.945697	19	q13.32	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence) [Source:HGNC Symbol;Acc:3433]
209310_s_at	CASP4	ENSG00000196954	0.032736	0.9103894	10.59028	9.679891	11	q22.3	caspase 4, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:1505]
218729_at	LXN	ENSG00000079257	0.032736	1.3734357	9.362978	7.989542	3	q25.32	latexin [Source:HGNC Symbol;Acc:13347]
227274_at	SYNJ2BP	ENSG00000213463	0.032835	0.9456553	8.969654	8.023999	14	q24.2	synaptojanin 2 binding protein [Source:HGNC Symbol;Acc:18955]
219147_s_at	NMRK1	ENSG00000106733	0.032835	1.031303	8.134786	7.103483	9	q21.13	nicotinamide riboside kinase 1 [Source:HGNC Symbol;Acc:26057]
205083_at	AOX1	ENSG00000138356	0.032835	1.3447575	6.346469	5.001711	2	q33.1	aldehyde oxidase 1 [Source:HGNC Symbol;Acc:553]
209109_s_at	TSPAN6	ENSG00000000003	0.03287	1.3163026	7.197532	5.88123	X	q22.1	tetraspanin 6 [Source:HGNC Symbol;Acc:11858]
225303_at	KIRREL	ENSG00000183853	0.03287	1.2844668	7.658036	6.373569	1	q23.1	kin of IRRE like (Drosophila) [Source:HGNC Symbol;Acc:15734]
225185_at	MRAS	ENSG00000158186	0.03287	1.0377007	7.834459	6.796758	3	q22.3	muscle RAS oncogene homolog [Source:HGNC Symbol;Acc:7227]
203716_s_at	DPP4	ENSG00000197635	0.03287	1.5099205	8.788772	7.278851	2	q24.2	dipeptidyl-peptidase 4 [Source:HGNC Symbol;Acc:3009]
204342_at	SLC25A24	ENSG00000085491	0.03287	0.9998009	8.623813	7.624012	1	p13.3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24 [Source:HGNC Symbol;Acc:20662]
202948_at	IL1R1	ENSG00000115594	0.033188	1.7497853	8.584053	6.834267	2	q11.2	interleukin 1 receptor, type I [Source:HGNC Symbol;Acc:5993]
212511_at	PICALM	ENSG00000073921	0.033188	0.7422533	6.915631	6.173378	11	q14.2	phosphatidylinositol binding clathrin assembly protein [Source:HGNC Symbol;Acc:15514]
214429_at	MTMR6	ENSG00000139505	0.033466	0.7697304	8.954555	8.184824	13	q12.13	myotubularin related protein 6 [Source:HGNC Symbol;Acc:7453]
214021_x_at	ITGB5	ENSG00000082781	0.033488	1.4359772	6.631669	5.195692	3	q21.2	integrin, beta 5 [Source:HGNC Symbol;Acc:6160]
227624_at	TET2	ENSG00000168769	0.033488	1.0769098	7.558846	6.481937	4	q24	tet methylcytosine dioxygenase 2 [Source:HGNC Symbol;Acc:25941]
225093_at	UTRN	ENSG00000152818	0.033488	1.5657154	10.04129	8.475572	6	q24.2	utrophin [Source:HGNC Symbol;Acc:12635]

227379_at	MBOAT1	ENSG00000172197	0.033637	1.2267144	7.197727	5.971012	6	p22.3	membrane bound O-acyltransferase domain containing 1 [Source:HGNC Symbol;Acc:21579]
213139_at	SNAI2	ENSG00000019549	0.033801	1.5495817	6.95332	5.403738	8	q11.21	snail family zinc finger 2 [Source:HGNC Symbol;Acc:11094]
212099_at	RHOB	ENSG00000143878	0.033801	1.5631977	9.851473	8.288275	2	p24.1	ras homolog family member B [Source:HGNC Symbol;Acc:668]
204894_s_at	AOC3	ENSG00000131471	0.033801	1.4887152	6.950874	5.462159	17	q21.31	amine oxidase, copper containing 3 [Source:HGNC Symbol;Acc:550]
219432_at	EVC	ENSG00000072840	0.033801	0.9734954	7.657381	6.683885	4	p16.2	Ellis van Creveld syndrome [Source:HGNC Symbol;Acc:3497]
55065_at	MARK4	ENSG00000007047	0.033801	0.4501318	7.655069	7.204937	19	q13.32	MAP/microtubule affinity-regulating kinase 4 [Source:HGNC Symbol;Acc:13538]
226353_at	SPPL2A	ENSG00000138600	0.034001	1.0860363	9.824238	8.738201	15	q21.2	signal peptide peptidase like 2A [Source:HGNC Symbol;Acc:30227]
216598_s_at	CCL2	ENSG00000108691	0.034001	1.5741003	11.80437	10.23027	17	q12	chemokine (C-C motif) ligand 2 [Source:HGNC Symbol;Acc:10618]
226568_at	FAM102B	ENSG00000162636	0.034001	1.1949347	7.320321	6.125386	1	p13.3	family with sequence similarity 102, member B [Source:HGNC Symbol;Acc:27637]
218764_at	PRKCH	ENSG00000027075	0.034091	1.3242248	8.842467	7.518243	14	q23.1	protein kinase C, eta [Source:HGNC Symbol;Acc:9403]
225984_at	PRKAA1	ENSG00000132356	0.034118	0.7616255	6.863442	6.101816	5	p13.1	protein kinase, AMP-activated, alpha 1 catalytic subunit [Source:HGNC Symbol;Acc:9376]
201542_at	SAR1A	ENSG00000079332	0.034118	0.7356457	9.772431	9.036785	10	q22.1	SAR1 homolog A (S. cerevisiae) [Source:HGNC Symbol;Acc:10534]
203455_s_at	SAT1	ENSG00000130066	0.034118	1.31652	11.13299	9.816473	X	p22.11	spermidine/spermine N1-acetyltransferase 1 [Source:HGNC Symbol;Acc:10540]
225922_at	FNIP2	ENSG00000052795	0.034118	1.5195275	8.166224	6.646697	4	q32.1	folliculin interacting protein 2 [Source:HGNC Symbol;Acc:29280]
218665_at	FZD4	ENSG00000174804	0.034118	1.0211632	7.416231	6.395068	11	q14.2	frizzled family receptor 4 [Source:HGNC Symbol;Acc:4042]
221666_s_at	PYCARD	ENSG00000103490	0.034191	0.6061082	9.397236	8.791128	16	p11.2	PYD and CARD domain containing [Source:HGNC Symbol;Acc:16608]
201058_s_at	MYL9	ENSG00000101335	0.034191	1.2676991	10.37627	9.108573	20	q11.23	myosin, light chain 9, regulatory [Source:HGNC Symbol;Acc:15754]
203397_s_at	GALNT3	ENSG00000115339	0.034191	1.3066403	5.451049	4.144409	2	q24.3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 3 (GalNAc-T3) [Source:HGNC Symbol;Acc:4125]
222453_at	CYBRD1	ENSG00000071967	0.034191	1.3157278	9.001392	7.685664	2	q31.1	cytochrome b reductase 1 [Source:HGNC Symbol;Acc:20797]
208146_s_at	CPVL	ENSG00000106066	0.034191	1.9432647	9.534937	7.591672	7	p14.3	carboxypeptidase, vitellogenic-like [Source:HGNC Symbol;Acc:14399]
227334_at	USP54	ENSG00000166348	0.034191	0.5950048	7.632457	7.037452	10	q22.2	ubiquitin specific peptidase 54 [Source:HGNC Symbol;Acc:23513]
226534_at	KITLG	ENSG00000049130	0.034191	1.6871203	6.504808	4.817688	12	q21.32	KIT ligand [Source:HGNC Symbol;Acc:6343]
229120_s_at	CDC42SE1	ENSG00000197622	0.034191	1.0261208	9.039742	8.013621	1	q21.3	CDC42 small effector 1 [Source:HGNC Symbol;Acc:17719]
225066_at	PPP2R2D	ENSG00000175470	0.034191	0.4100232	6.515125	6.105102	10	q26.3	protein phosphatase 2, regulatory subunit B, delta [Source:HGNC Symbol;Acc:23732]
211977_at	GPR107	ENSG00000148358	0.034191	0.4150635	7.32333	6.908267	9	q34.11	G protein-coupled receptor 107 [Source:HGNC Symbol;Acc:17830]
217967_s_at	FAM129A	ENSG00000135842	0.034191	1.6316176	9.361852	7.730234	1	q25.3	family with sequence similarity 129, member A [Source:HGNC Symbol;Acc:16784]
207705_s_at	NINL	ENSG00000101004	0.034191	0.4580325	7.469272	7.011239	20	p11.21	ninein-like [Source:HGNC Symbol;Acc:29163]
230029_x_at	UBR3	ENSG00000144357	0.034212	0.7132327	7.406814	6.693581	2	q31.1	ubiquitin protein ligase E3 component n-recognin 3 (putative) [Source:HGNC Symbol;Acc:30467]
227236_at	TSPAN2	ENSG00000134198	0.03424	1.1605259	6.827258	5.666732	1	p13.2	tetraspanin 2 [Source:HGNC Symbol;Acc:20659]
202510_s_at	TNFAIP2	ENSG00000185215	0.03424	1.6113115	10.98695	9.375641	14	q32.32	tumor necrosis factor, alpha-induced protein 2 [Source:HGNC Symbol;Acc:11895]
202450_s_at	CTSK	ENSG00000143387	0.034334	2.0587683	10.3433	8.284534	1	q21.3	cathepsin K [Source:HGNC Symbol;Acc:2536]
226395_at	HOOK3	ENSG00000168172	0.034361	0.9073842	9.099733	8.192349	8	p11.21	hook homolog 3 (Drosophila) [Source:HGNC Symbol;Acc:23576]
219403_s_at	HPSE	ENSG00000173083	0.034374	1.2733775	7.073411	5.800034	4	q21.23	heparanase [Source:HGNC Symbol;Acc:5164]
227623_at	CACNA2D1	ENSG00000153956	0.034401	1.5093742	5.523191	4.013817	7	q21.11	calcium channel, voltage-dependent, alpha 2/delta subunit 1 [Source:HGNC Symbol;Acc:1399]
202239_at	PARP4	ENSG00000102699	0.034401	0.9202135	9.568361	8.648148	13	q12.12	poly (ADP-ribose) polymerase family, member 4 [Source:HGNC Symbol;Acc:271]
204646_at	DPYD	ENSG00000188641	0.034481	1.7165381	8.184742	6.468204	1	p21.3	dihydropyrimidine dehydrogenase [Source:HGNC Symbol;Acc:3012]
209335_at	DCN	ENSG00000011465	0.034607	2.0562205	8.106748	6.050528	12	q21.33	decorin [Source:HGNC Symbol;Acc:2705]
202341_s_at	TRIM2	ENSG00000109654	0.034607	1.1549983	7.682678	6.52768	4	q31.3	tripartite motif containing 2 [Source:HGNC Symbol;Acc:15974]
203386_at	TBC1D4	ENSG00000136111	0.034612	1.5986356	9.927925	8.329289	13	q22.2	TBC1 domain family, member 4 [Source:HGNC Symbol;Acc:19165]
202465_at	PCOLCE	ENSG00000106333	0.034687	1.1107939	9.858341	8.747547	7	q22.1	procollagen C-endopeptidase enhancer [Source:HGNC Symbol;Acc:8738]
218501_at	ARHGEF3	ENSG00000163947	0.03471	1.211901	9.645779	8.433878	3	p14.3	Rho guanine nucleotide exchange factor (GEF) 3 [Source:HGNC Symbol;Acc:683]

203935_at	ACVR1	ENSG00000115170	0.03471	0.9297485	7.59294	6.663191	2	q24.1	activin A receptor, type I [Source:HGNC Symbol;Acc:171]
227726_at	RNF166	ENSG00000158717	0.034778	0.7652554	6.490242	5.724987	16	q24.3	ring finger protein 166 [Source:HGNC Symbol;Acc:28856]
225351_at	FAM45A	ENSG00000119979	0.034778	0.712687	7.985558	7.272871	10	q26.11	family with sequence similarity 45, member A [Source:HGNC Symbol;Acc:31793]
209967_s_at	CREM	ENSG00000095794	0.034778	1.4987082	8.008163	6.509455	10	p11.21	cAMP responsive element modulator [Source:HGNC Symbol;Acc:2352]
217767_at	C3	ENSG00000125730	0.034902	1.610303	11.06256	9.452253	19	p13.3	complement component 3 [Source:HGNC Symbol;Acc:1318]
202377_at	LEPROT	ENSG00000213625	0.034902	0.9587583	8.927718	7.96896	1	p31.3	leptin receptor overlapping transcript [Source:HGNC Symbol;Acc:29477]
212067_s_at	C1R	ENSG00000159403	0.034902	1.0958838	10.9773	9.881414	12	p13.31	complement component 1, r subcomponent [Source:HGNC Symbol;Acc:1246]
206461_x_at	MT1H	ENSG00000205358	0.034907	0.9374798	10.9411	10.00362	16	q13	metallothionein 1H [Source:HGNC Symbol;Acc:7400]
212651_at	RHOBTB1	ENSG00000072422	0.03492	1.2780518	5.303259	4.025208	10	q21.2	Rho-related BTB domain containing 1 [Source:HGNC Symbol;Acc:18738]
213077_at	YTHDC2	ENSG00000047188	0.03492	1.0822747	7.160913	6.078638	5	q22.2	YTH domain containing 2 [Source:HGNC Symbol;Acc:24721]
238617_at	KIF26B	ENSG00000162849	0.03492	1.8167267	7.548087	5.73136	1	q44	kinesin family member 26B [Source:HGNC Symbol;Acc:25484]
201540_at	FHL1	ENSG00000022267	0.03492	2.0909145	8.481468	6.390554	X	q26.3	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:3702]
227325_at	PRR24	ENSG00000257704	0.03492	0.5900983	7.823938	7.23384	19	q13.32	proline rich 24 [Source:HGNC Symbol;Acc:27406]
208093_s_at	NDEL1	ENSG00000166579	0.034947	0.7410348	8.576081	7.835046	17	p13.1	nudE nuclear distribution E homolog (A. nidulans)-like 1 [Source:HGNC Symbol;Acc:17620]
202006_at	PTPN12	ENSG00000127947	0.035089	1.0182628	9.540274	8.522011	7	q11.23	protein tyrosine phosphatase, non-receptor type 12 [Source:HGNC Symbol;Acc:9645]
209216_at	WDR45	ENSG00000196998	0.035089	0.696795	8.826888	8.130093	X	p11.23	WD repeat domain 45 [Source:HGNC Symbol;Acc:28912]
225782_at	MSR83	ENSG00000174099	0.035089	1.4443755	6.514716	5.07034	12	q14.3	methionine sulfoxide reductase B3 [Source:HGNC Symbol;Acc:27375]
200602_at	APP	ENSG00000142192	0.035089	1.32593	9.055535	7.729605	21	q21.3	amyloid beta (A4) precursor protein [Source:HGNC Symbol;Acc:620]
226939_at	CPEB2	ENSG00000137449	0.035264	1.2264987	7.611624	6.385126	4	p15.33	cytoplasmic polyadenylation element binding protein 2 [Source:HGNC Symbol;Acc:21745]
218986_s_at	DDX60	ENSG00000137628	0.035316	1.4860214	8.318531	6.83251	4	q32.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 [Source:HGNC Symbol;Acc:25942]
203139_at	DAPK1	ENSG00000196730	0.035316	1.7079489	8.912548	7.204599	9	q21.33	death-associated protein kinase 1 [Source:HGNC Symbol;Acc:2674]
213764_s_at	MFAP5	ENSG00000197614	0.035435	1.2979822	5.790529	4.492547	12	p13.31	microfibrillar associated protein 5 [Source:HGNC Symbol;Acc:29673]
202565_s_at	SVIL	ENSG00000197321	0.035639	1.3890512	8.635445	7.246394	10	p11.23	supervillin [Source:HGNC Symbol;Acc:11480]
210968_s_at	RTN4	ENSG00000115310	0.03577	0.8295931	10.69653	9.866939	2	p16.1	reticulon 4 [Source:HGNC Symbol;Acc:14085]
225562_at	RASA3	ENSG00000185989	0.03578	0.9721275	9.062085	8.089957	13	q34	RAS p21 protein activator 3 [Source:HGNC Symbol;Acc:20331]
218454_at	PLBD1	ENSG00000121316	0.035786	1.4419824	10.25392	8.811935	12	p13.1	phospholipase B domain containing 1 [Source:HGNC Symbol;Acc:26215]
209467_s_at	MKNK1	ENSG00000079277	0.035868	0.7832944	8.294847	7.511553	1	p33	MAP kinase interacting serine/threonine kinase 1 [Source:HGNC Symbol;Acc:7110]
226869_at	MEGF6	ENSG00000162591	0.03595	1.2650434	7.859101	6.594058	1	p36.32	multiple EGF-like-domains 6 [Source:HGNC Symbol;Acc:3232]
221569_at	AHL1	ENSG00000135541	0.03595	1.0761406	7.793652	6.717512	6	q23.3	Abelson helper integration site 1 [Source:HGNC Symbol;Acc:21575]
1569157_s_at	ZNF846	ENSG00000196605	0.03595	0.7746233	6.057018	5.282395	19	p13.2	zinc finger protein 846 [Source:HGNC Symbol;Acc:27260]
218132_s_at	TSEN34	ENSG00000170892	0.03595	0.4388666	8.237399	7.798532	19	q13.42	tRNA splicing endonuclease 34 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:15506]
201591_s_at	NISCH	ENSG0000010322	0.036284	0.4056482	8.996513	8.590865	3	p21.1	nischarin [Source:HGNC Symbol;Acc:18006]
227098_at	DUSP18	ENSG00000167065	0.036417	0.4821636	7.203923	6.721759	22	q12.2	dual specificity phosphatase 18 [Source:HGNC Symbol;Acc:18484]
203910_at	ARHGAP29	ENSG00000137962	0.036417	1.5131699	7.336341	5.823171	1	p21.3	Rho GTPase activating protein 29 [Source:HGNC Symbol;Acc:30207]
1555847_a_at	LOC284454	NA	0.036417	0.9290134	9.021958	8.092945	NA	NA	NA
241353_s_at	LOC100507507	NA	0.036417	0.563124	6.938192	6.375068	NA	NA	NA
202225_at	CRK	ENSG00000167193	0.036417	0.7660484	9.380488	8.614439	17	p13.3	v-crk avian sarcoma virus CT10 oncogene homolog [Source:HGNC Symbol;Acc:2362]
212915_at	PDZRN3	ENSG00000121440	0.036491	1.3125793	6.719045	5.406466	3	p13	PDZ domain containing ring finger 3 [Source:HGNC Symbol;Acc:17704]
202920_at	ANK2	ENSG00000145362	0.036491	1.4633941	8.124628	6.661234	4	q25	ankyrin 2, neuronal [Source:HGNC Symbol;Acc:493]
235391_at	FAM92A1	ENSG00000188343	0.036548	0.6211362	7.223439	6.602303	8	q22.1	family with sequence similarity 92, member A1 [Source:HGNC Symbol;Acc:30452]
224906_at	ANO6	ENSG00000177119	0.036675	0.8771124	8.664683	7.787571	12	q12	anoctamin 6 [Source:HGNC Symbol;Acc:25240]

227087_at	INPP4A	ENSG00000040933	0.036675	1.0267894	8.031874	7.005085	2	q11.2	inositol polyphosphate-4-phosphatase, type I, 107kDa [Source:HGNC Symbol;Acc:6074]
225931_s_at	RNF213	ENSG00000173821	0.036802	1.1072523	9.749178	8.641926	17	q25.3	ring finger protein 213 [Source:HGNC Symbol;Acc:14539]
212690_at	DDHD2	ENSG00000085788	0.036831	0.8783562	9.176867	8.298511	8	p11.23	DDHD domain containing 2 [Source:HGNC Symbol;Acc:29106]
209003_at	SLC25A11	ENSG00000108528	0.036891	0.4377232	7.954667	7.516944	17	p13.2	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 [Source:HGNC Symbol;Acc:10981]
202206_at	ARL4C	ENSG00000138042	0.036891	1.3898051	9.321387	7.931582	2	q37.1	ADP-ribosylation factor-like 4C [Source:HGNC Symbol;Acc:698]
232000_at	TTC39B	ENSG00000155158	0.037068	1.3565126	4.978733	3.62222	9	p22.3	tetratricopeptide repeat domain 39B [Source:HGNC Symbol;Acc:23704]
225386_s_at	HNRPLL	NA	0.037068	1.4593954	9.121602	7.662206	NA	NA	NA
226409_at	TBC1D20	ENSG00000125875	0.037068	0.5055858	8.965324	8.459738	20	p13	TBC1 domain family, member 20 [Source:HGNC Symbol;Acc:16133]
204066_s_at	AGAP1	ENSG00000157985	0.037088	1.0789416	6.07508	4.996139	2	q37.2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 [Source:HGNC Symbol;Acc:16922]
212441_at	KIAA0232	ENSG00000170871	0.037088	0.5902105	8.606786	8.016575	4	p16.1	KIAA0232 [Source:HGNC Symbol;Acc:28992]
225726_s_at	PLEKHH1	ENSG00000054690	0.037088	0.9526951	5.964958	5.012263	14	q24.1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 [Source:HGNC Symbol;Acc:17733]
232094_at	KATNBL1	ENSG00000134152	0.037088	0.5971703	7.264443	6.667273	15	q14	katanin p80 subunit B-like 1 [Source:HGNC Symbol;Acc:26199]
225604_s_at	GLIPR2	ENSG00000122694	0.037324	0.8539107	7.844159	6.990248	9	p13.3	GLI pathogenesis-related 2 [Source:HGNC Symbol;Acc:18007]
205225_at	ESR1	ENSG00000091831	0.037324	1.3824683	6.467921	5.085453	6	q25.1	estrogen receptor 1 [Source:HGNC Symbol;Acc:3467]
218838_s_at	TTC31	ENSG00000115282	0.037324	0.6726502	8.524158	7.851508	2	p13.1	tetratricopeptide repeat domain 31 [Source:HGNC Symbol;Acc:25759]
227961_at	CTSB	ENSG00000164733	0.037324	1.3381396	10.24117	8.903035	8	p23.1	cathepsin B [Source:HGNC Symbol;Acc:2527]
1558041_a_at	KIAA0895L	ENSG00000196123	0.037413	0.8767425	7.925107	7.048364	16	q22.1	KIAA0895-like [Source:HGNC Symbol;Acc:34408]
209540_at	IGF1	ENSG00000017427	0.037413	1.5225095	8.256633	6.734124	12	q23.2	insulin-like growth factor 1 (somatomedin C) [Source:HGNC Symbol;Acc:5464]
203651_at	ZFYVE16	ENSG00000039319	0.037413	1.0251416	8.527484	7.502343	5	q14.1	zinc finger, FYVE domain containing 16 [Source:HGNC Symbol;Acc:20756]
224900_at	ANKFY1	ENSG00000185722	0.037546	0.532953	8.58147	8.048518	17	p13.2	ankyrin repeat and FYVE domain containing 1 [Source:HGNC Symbol;Acc:20763]
223441_at	SLC17A5	ENSG00000119899	0.037627	0.645006	6.824616	6.17961	6	q13	solute carrier family 17 (anion/sugar transporter), member 5 [Source:HGNC Symbol;Acc:10933]
204294_at	AMT	ENSG00000145020	0.037627	0.3994342	8.335214	7.935779	3	p21.31	aminomethyltransferase [Source:HGNC Symbol;Acc:473]
204040_at	RNF144A	ENSG00000151692	0.037682	1.4813478	6.933004	5.451656	2	p25.2	ring finger protein 144A [Source:HGNC Symbol;Acc:20457]
225272_at	SAT2	ENSG00000141504	0.037706	0.6186121	9.078151	8.459538	17	p13.1	spermidine/spermine N1-acetyltransferase family member 2 [Source:HGNC Symbol;Acc:23160]
204464_s_at	EDNRA	ENSG00000151617	0.037706	1.4248341	7.17677	5.751936	4	q31.22	endothelin receptor type A [Source:HGNC Symbol;Acc:3179]
205011_at	VWA5A	ENSG00000110002	0.037706	1.5010688	8.178127	6.677058	11	q24.2	von Willebrand factor A domain containing 5A [Source:HGNC Symbol;Acc:6658]
212765_at	CAMSAP2	ENSG00000118200	0.037714	1.0702776	7.585165	6.514887	1	q32.1	calmodulin regulated spectrin-associated protein family, member 2 [Source:HGNC Symbol;Acc:29188]
212624_s_at	CHN1	ENSG00000128656	0.037755	1.1993666	8.33942	7.140053	2	q31.1	chimerin 1 [Source:HGNC Symbol;Acc:1943]
209213_at	CBR1	ENSG00000159228	0.037828	0.71634	9.378176	8.661836	21	q22.12	carbonyl reductase 1 [Source:HGNC Symbol;Acc:1548]
207738_s_at	NCKAP1	ENSG00000061676	0.037828	1.7420168	5.909032	4.167015	2	q32.1	NCK-associated protein 1 [Source:HGNC Symbol;Acc:7666]
206856_at	LILRB5	ENSG00000105609	0.03795	1.5873193	8.757092	7.169773	19	q13.42	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 [Source:HGNC Symbol;Acc:6609]
200697_at	HK1	ENSG00000156515	0.037989	0.4970804	10.98017	10.48308	10	q22.1	hexokinase 1 [Source:HGNC Symbol;Acc:4922]
219134_at	ELTD1	ENSG00000162618	0.03804	1.633117	7.997273	6.364156	1	p31.1	EGF, latrophilin and seven transmembrane domain containing 1 [Source:HGNC Symbol;Acc:20822]
222294_s_at	RAB27A	ENSG00000069974	0.038154	1.5128756	7.227373	5.714497	15	q21.3	RAB27A, member RAS oncogene family [Source:HGNC Symbol;Acc:9766]
201057_s_at	GOLGB1	ENSG00000173230	0.03845	0.6396181	9.220834	8.581216	3	q13.33	golgin B1 [Source:HGNC Symbol;Acc:4429]
218017_s_at	HGSNAT	ENSG00000165102	0.038567	1.101893	8.583363	7.48147	8	p11.21	heparan-alpha-glucosaminide N-acetyltransferase [Source:HGNC Symbol;Acc:26527]
226905_at	FAM101B	ENSG00000183688	0.03866	1.3556387	8.832382	7.476743	17	p13.3	family with sequence similarity 101, member B [Source:HGNC Symbol;Acc:28705]

226616_s_at	NDUFV3	ENSG00000160194	0.038672	0.6620698	10.466	9.803934	21	q22.3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa [Source:HGNC Symbol;Acc:7719]
215127_s_at	RBMS1	ENSG00000153250	0.038708	0.9857614	9.060146	8.074385	2	q24.2	RNA binding motif, single stranded interacting protein 1 [Source:HGNC Symbol;Acc:9907]
212373_at	FEM1B	ENSG00000169018	0.038897	0.9618687	8.428165	7.466297	15	q23	fem-1 homolog b (C. elegans) [Source:HGNC Symbol;Acc:3649]
222750_s_at	SRD5A3	ENSG00000128039	0.038897	0.7626054	8.251817	7.489212	4	q12	steroid 5 alpha-reductase 3 [Source:HGNC Symbol;Acc:25812]
236006_s_at	AKAP10	ENSG00000108599	0.039007	0.6550377	7.828287	7.173249	17	p11.2	A kinase (PRKA) anchor protein 10 [Source:HGNC Symbol;Acc:368]
224733_at	CMTM3	ENSG00000140931	0.039182	0.6902697	9.982739	9.292469	16	q21	CKLF-like MARVEL transmembrane domain containing 3 [Source:HGNC Symbol;Acc:19174]
204981_at	SLC22A18	ENSG00000110628	0.039182	0.5611839	7.58994	7.028756	11	p15.4	solute carrier family 22, member 18 [Source:HGNC Symbol;Acc:10964]
223077_at	TMOD3	ENSG00000138594	0.03924	1.0922066	7.964721	6.872514	15	q21.2	tropomodulin 3 (ubiquitous) [Source:HGNC Symbol;Acc:11873]
209686_at	S100B	ENSG00000160307	0.039241	0.9012906	6.761868	5.860578	21	q22.3	S100 calcium binding protein B [Source:HGNC Symbol;Acc:10500]
225325_at	MFSDB	ENSG00000151690	0.039241	0.8394079	8.69193	7.852522	2	q32.2	major facilitator superfamily domain containing 6 [Source:HGNC Symbol;Acc:24711]
205236_x_at	SOD3	ENSG00000109610	0.03958	0.8919006	8.451633	7.559732	4	p15.2	superoxide dismutase 3, extracellular [Source:HGNC Symbol;Acc:11181]
228220_at	FCHO2	ENSG00000157107	0.03958	1.5637625	8.795856	7.232094	5	q13.2	FCH domain only 2 [Source:HGNC Symbol;Acc:25180]
205904_at	MICA	ENSG00000204520	0.03958	0.4272285	7.684754	7.257525	6	p21.33	MHC class I polypeptide-related sequence A [Source:HGNC Symbol;Acc:7090]
226777_at	ADAM12	ENSG00000148848	0.03958	1.9432471	7.771445	5.828198	10	q26.2	ADAM metalloproteinase domain 12 [Source:HGNC Symbol;Acc:190]
213618_at	ARAP2	ENSG00000047365	0.03958	1.0280821	7.620559	6.592477	4	p14	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2 [Source:HGNC Symbol;Acc:16924]
205624_at	CPA3	ENSG00000163751	0.03958	2.1511989	6.492962	4.341763	3	q24	carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:2298]
215268_at	KIAA0754	ENSG00000255103	0.03958	0.8091048	6.285141	5.476036	1	p34.3	KIAA0754 [Source:HGNC Symbol;Acc:29111]
203672_x_at	TPMT	ENSG00000137364	0.03958	0.5543757	9.62339	9.069015	6	p22.3	thiopurine S-methyltransferase [Source:HGNC Symbol;Acc:12014]
1555229_a_at	C1S	ENSG00000182326	0.03958	1.5628333	10.46271	8.899877	12	p13.31	complement component 1, s subcomponent [Source:HGNC Symbol;Acc:1247]
203855_at	WDR47	ENSG00000085433	0.03958	0.7150022	7.128001	6.412998	1	p13.3	WD repeat domain 47 [Source:HGNC Symbol;Acc:29141]
207072_at	IL18RAP	ENSG00000115607	0.03958	0.9816906	7.548943	6.567253	2	q12.1	interleukin 18 receptor accessory protein [Source:HGNC Symbol;Acc:5989]
221935_s_at	EOGT	ENSG00000163378	0.039608	0.8358766	7.127104	6.291227	3	p14.1	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase [Source:HGNC Symbol;Acc:28526]
203232_s_at	ATXN1	ENSG00000124788	0.039608	1.4864727	8.293823	6.80735	6	p22.3	ataxin 1 [Source:HGNC Symbol;Acc:10548]
202096_s_at	TSPO	ENSG00000100300	0.03977	0.6186136	9.561586	8.942973	22	q13.2	translocator protein (18kDa) 2 [Source:HGNC Symbol;Acc:1158]
224813_at	WASL	ENSG00000106299	0.03977	0.8102345	8.822272	8.012038	7	q31.32	Wiskott-Aldrich syndrome-like [Source:HGNC Symbol;Acc:12735]
213455_at	FAM114A1	ENSG00000197712	0.039797	0.841638	7.947072	7.105434	4	p14	family with sequence similarity 114, member A1 [Source:HGNC Symbol;Acc:25087]
226873_at	FAM63B	ENSG00000128923	0.039878	0.7816817	7.054056	6.272374	15	q21.3	family with sequence similarity 63, member B [Source:HGNC Symbol;Acc:26954]
1554503_a_at	OSCAR	ENSG00000170909	0.040083	0.4815944	6.652983	6.171388	19	q13.42	osteoclast associated, immunoglobulin-like receptor [Source:HGNC Symbol;Acc:29960]
206118_at	STAT4	ENSG00000138378	0.040381	1.6428433	7.763744	6.120901	2	q32.3	signal transducer and activator of transcription 4 [Source:HGNC Symbol;Acc:11365]
210970_s_at	IBTK	ENSG00000005700	0.040543	0.7538865	8.260872	7.506986	6	q14.1	inhibitor of Bruton agammaglobulinemia tyrosine kinase [Source:HGNC Symbol;Acc:17853]
227113_at	ADHFE1	ENSG00000147576	0.040543	0.7061362	8.382822	7.676686	8	q13.1	alcohol dehydrogenase, iron containing, 1 [Source:HGNC Symbol;Acc:16354]
202949_s_at	FHL2	ENSG00000115641	0.040594	1.4031826	7.613598	6.210416	2	q12.2	four and a half LIM domains 2 [Source:HGNC Symbol;Acc:3703]
225579_at	PQLC3	ENSG00000162976	0.040597	1.1136678	9.537873	8.424205	2	p25.1	PQ loop repeat containing 3 [Source:HGNC Symbol;Acc:28503]
235291_s_at	FLJ32255	NA	0.040716	1.1196959	7.867314	6.747618	NA	NA	NA
203939_at	NTSE	ENSG00000135318	0.040733	0.8061792	7.425231	6.619052	6	q14.3	5'-nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:8021]
214274_s_at	ACAA1	ENSG00000060971	0.040794	0.5024191	9.465452	8.963033	3	p22.2	acetyl-CoA acyltransferase 1 [Source:HGNC Symbol;Acc:82]
204046_at	PLCB2	ENSG00000137841	0.040802	0.5337836	8.533797	8.000014	15	q15.1	phospholipase C, beta 2 [Source:HGNC Symbol;Acc:9055]
202392_s_at	PISD	ENSG00000241878	0.041073	0.3563642	8.566583	8.210719	22	q12.2	phosphatidylserine decarboxylase [Source:HGNC Symbol;Acc:8999]

218326_s_at	LGR4	ENSG00000205213	0.041073	1.2551214	5.02211	3.766988	11	p14.1	leucine-rich repeat containing G protein-coupled receptor 4 [Source:HGNC Symbol;Acc:13299]
229119_s_at	ZSWIM7	ENSG00000214941	0.041073	1.0247863	7.91053	6.885744	17	p12	zinc finger, SWIM-type containing 7 [Source:HGNC Symbol;Acc:26993]
206491_s_at	NAPA	ENSG00000105402	0.041415	0.4954364	9.333764	8.838328	19	q13.33	N-ethylmaleimide-sensitive factor attachment protein, alpha [Source:HGNC Symbol;Acc:7641]
227450_at	ERP27	ENSG00000139055	0.041415	0.9661967	6.328914	5.362718	12	p12.3	endoplasmic reticulum protein 27 [Source:HGNC Symbol;Acc:26495]
200866_s_at	PSAP	ENSG00000197746	0.041415	1.0853598	11.69849	10.61313	10	q22.1	prosaposin [Source:HGNC Symbol;Acc:9498]
200720_s_at	ACTR1A	ENSG00000138107	0.041415	0.4967534	8.824862	8.328108	10	q24.32	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast) [Source:HGNC Symbol;Acc:167]
232064_at	FER	ENSG00000151422	0.041415	0.6560546	7.136386	6.480331	5	q21.3	fer (fps/fes related) tyrosine kinase [Source:HGNC Symbol;Acc:3655]
217922_at	MAN1A2	ENSG00000198162	0.041445	0.6973684	8.202283	7.504915	1	p12	mannosidase, alpha, class 1A, member 2 [Source:HGNC Symbol;Acc:6822]
201944_at	HEXB	ENSG00000049860	0.04157	1.0109447	11.5932	10.58226	5	q13.3	hexosaminidase B (beta polypeptide) [Source:HGNC Symbol;Acc:4879]
210986_s_at	TPM1	ENSG00000140416	0.04157	1.6503375	9.944608	8.294271	15	q22.2	tropomyosin 1 (alpha) [Source:HGNC Symbol;Acc:12010]
227568_at	HECTD2	ENSG00000165338	0.04157	1.1199318	6.685061	5.565129	10	q23.32	HECT domain containing E3 ubiquitin protein ligase 2 [Source:HGNC Symbol;Acc:26736]
200645_at	GABARAP	ENSG00000170296	0.04157	0.6317473	11.38104	10.7493	17	p13.1	GABA(A) receptor-associated protein [Source:HGNC Symbol;Acc:4067]
219892_at	TM6SF1	ENSG00000136404	0.04157	1.5187197	7.818959	6.300239	15	q25.2	transmembrane 6 superfamily member 1 [Source:HGNC Symbol;Acc:11860]
222431_at	SPIN1	ENSG00000106723	0.04157	0.7028249	9.18628	8.483455	9	q22.1	spindlin 1 [Source:HGNC Symbol;Acc:11243]
203665_at	HMOX1	ENSG00000100292	0.04157	1.0199085	9.506814	8.486905	22	q12.3	heme oxygenase (decycling) 1 [Source:HGNC Symbol;Acc:5013]
202506_at	SSFA2	ENSG00000138434	0.04157	0.9475539	8.018471	7.070918	2	q31.3	sperm specific antigen 2 [Source:HGNC Symbol;Acc:11319]
221899_at	N4BP2L2	ENSG00000244754	0.04157	0.8653353	9.046774	8.181439	13	q13.1	NEDD4 binding protein 2-like 2 [Source:HGNC Symbol;Acc:26916]
203668_at	MAN2C1	ENSG00000140400	0.04169	0.6339166	8.66367	8.029753	15	q24.2	mannosidase, alpha, class 2C, member 1 [Source:HGNC Symbol;Acc:6827]
206295_at	IL18	ENSG00000150782	0.041917	1.2921744	9.298736	8.006561	11	q23.1	interleukin 18 (interferon-gamma-inducing factor) [Source:HGNC Symbol;Acc:5986]
228152_s_at	DDX60L	ENSG00000181381	0.041917	1.4213436	7.853792	6.432448	4	q32.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like [Source:HGNC Symbol;Acc:26429]
228341_at	NUDT16	ENSG00000198585	0.041917	0.8132856	6.707602	5.894316	3	q22.1	nudix (nucleoside diphosphate linked moiety X)-type motif 16 [Source:HGNC Symbol;Acc:26442]
218164_at	SPATA20	ENSG00000006282	0.041917	0.5879296	9.023334	8.435404	17	q21.33	spermatogenesis associated 20 [Source:HGNC Symbol;Acc:26125]
227070_at	GLT8D2	ENSG00000120820	0.041917	1.7573511	5.840318	4.082966	12	q23.3	glycosyltransferase 8 domain containing 2 [Source:HGNC Symbol;Acc:24890]
213083_at	SLC35D2	ENSG00000130958	0.041917	0.8293654	7.315854	6.486489	9	q22.32	solute carrier family 35 (UDP-GlcNAc/UDP-glucose transporter), member D2 [Source:HGNC Symbol;Acc:20799]
224772_at	NAV1	ENSG00000134369	0.041917	1.0514789	7.602146	6.550667	1	q32.1	neuron navigator 1 [Source:HGNC Symbol;Acc:15989]
229287_at	PCNX	ENSG00000100731	0.041917	0.9439305	7.566202	6.622271	14	q24.2	pecanex homolog (Drosophila) [Source:HGNC Symbol;Acc:19740]
201200_at	CREG1	ENSG00000143162	0.041917	1.0581554	11.10069	10.04253	1	q24.2	cellular repressor of E1A-stimulated genes 1 [Source:HGNC Symbol;Acc:2351]
229450_at	IFIT3	ENSG00000119917	0.041917	1.6631975	9.084235	7.421037	10	q23.31	interferon-induced protein with tetratricopeptide repeats 3 [Source:HGNC Symbol;Acc:5411]
228249_at	C11orf74	ENSG00000166352	0.041917	0.8487982	5.174339	4.325541	11	p12	chromosome 11 open reading frame 74 [Source:HGNC Symbol;Acc:25142]
38487_at	STAB1	ENSG00000010327	0.042059	1.0905804	9.31099	8.22041	3	p21.1	stabilin 1 [Source:HGNC Symbol;Acc:18628]
202974_at	MPP1	ENSG00000130830	0.042059	1.0629761	9.61456	8.551584	X	q28	membrane protein, palmitoylated 1, 55kDa [Source:HGNC Symbol;Acc:7219]
226510_at	HEATR5A	ENSG00000129493	0.042059	0.7510398	7.259761	6.508721	14	q12	HEAT repeat containing 5A [Source:HGNC Symbol;Acc:20276]
228282_at	MFS8	ENSG00000164073	0.042059	0.8192732	7.582661	6.763388	4	q28.2	major facilitator superfamily domain containing 8 [Source:HGNC Symbol;Acc:28486]
203675_at	NUCB2	ENSG00000070081	0.042059	0.9057747	9.751698	8.845924	11	p15.1	nucleobindin 2 [Source:HGNC Symbol;Acc:8044]
228384_s_at	PYROXD2	ENSG00000119943	0.042059	0.3040111	6.385891	6.08188	10	q24.2	pyridine nucleotide-disulphide oxidoreductase domain 2 [Source:HGNC Symbol;Acc:23517]
229367_s_at	GIMAP6	ENSG00000133561	0.042059	1.4090136	8.888668	7.479654	7	q36.1	GTPase, IMAP family member 6 [Source:HGNC Symbol;Acc:21918]
218309_at	CAMK2N1	ENSG00000162545	0.042059	1.2605333	7.868837	6.608303	1	p36.12	calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC

									Symbol;Acc:24190]
34726_at	CACNB3	ENSG00000167535	0.042059	0.4136308	6.934617	6.520986	12	q13.12	calcium channel, voltage-dependent, beta 3 subunit [Source:HGNC Symbol;Acc:1403]
212670_at	ELN	ENSG00000049540	0.042059	1.2311529	8.8137	7.582547	7	q11.23	elastin [Source:HGNC Symbol;Acc:3327]
229800_at	DCLK1	ENSG00000133083	0.042059	1.4985924	6.412071	4.913479	13	q13.3	doublecortin-like kinase 1 [Source:HGNC Symbol;Acc:2700]
201975_at	CLIP1	ENSG00000130779	0.042246	1.0285112	8.482483	7.453972	12	q24.31	CAP-GLY domain containing linker protein 1 [Source:HGNC Symbol;Acc:10461]
224413_s_at	TM2D2	ENSG00000169490	0.042248	0.6130057	9.024042	8.411037	8	p11.22	TM2 domain containing 2 [Source:HGNC Symbol;Acc:24127]
204011_at	SPRY2	ENSG00000136158	0.042332	1.3188526	7.198128	5.879276	13	q31.1	sprouty homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:11270]
235033_at	NPEPL1	ENSG00000215440	0.042332	0.7632057	5.890585	5.12738	20	q13.32	aminopeptidase-like 1 [Source:HGNC Symbol;Acc:16244]
228348_at	LINS	ENSG00000140471	0.042351	0.8898302	8.824668	7.934838	15	q26.3	lines homolog (Drosophila) [Source:HGNC Symbol;Acc:30922]
227628_at	GPX8	ENSG00000164294	0.042351	1.180448	6.970795	5.790347	5	q11.2	glutathione peroxidase 8 (putative) [Source:HGNC Symbol;Acc:33100]
1557112_a_at	VP53	ENSG00000141252	0.042351	0.5180325	7.975808	7.457775	17	p13.3	vacuolar protein sorting 53 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:25608]
228071_at	GIMAP7	ENSG00000179144	0.042351	1.647364	8.992109	7.344745	7	q36.1	GTPase, IMAP family member 7 [Source:HGNC Symbol;Acc:22404]
209264_s_at	TSPAN4	ENSG00000214063	0.042351	0.6817548	9.0067	8.324945	11	p15.5	tetraspanin 4 [Source:HGNC Symbol;Acc:11859]
208892_s_at	DUSP6	ENSG00000139318	0.042351	1.2289738	7.99204	6.763066	12	q21.33	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:3072]
201315_x_at	IFITM2	ENSG00000185201	0.042351	0.7393922	11.67358	10.93419	11	p15.5	interferon induced transmembrane protein 2 [Source:HGNC Symbol;Acc:5413]
222802_at	EDN1	ENSG00000078401	0.042351	1.4605418	6.322746	4.862204	6	p24.1	endothelin 1 [Source:HGNC Symbol;Acc:3176]
1553395_a_at	CD200R1	ENSG00000163606	0.042351	1.2569103	6.464779	5.207868	3	q13.2	CD200 receptor 1 [Source:HGNC Symbol;Acc:24235]
226399_at	DNAJB14	ENSG00000164031	0.042351	0.8499477	8.162884	7.312937	4	q23	Dnaj (Hsp40) homolog, subfamily B, member 14 [Source:HGNC Symbol;Acc:25881]
226490_at	NHSL1	ENSG00000135540	0.042351	1.1946659	7.117631	5.922965	6	q24.1	NHS-like 1 [Source:HGNC Symbol;Acc:21021]
222513_s_at	SORBS1	ENSG00000095637	0.042351	1.325461	8.112293	6.786832	10	q24.1	sorbin and SH3 domain containing 1 [Source:HGNC Symbol;Acc:14565]
218705_s_at	SNX24	ENSG00000064652	0.042351	0.9094316	7.531422	6.62199	5	q23.2	sorting nexin 24 [Source:HGNC Symbol;Acc:21533]
226837_at	SPRED1	ENSG00000166068	0.042351	1.2128712	7.561562	6.34869	15	q14	sprouty-related, EVH1 domain containing 1 [Source:HGNC Symbol;Acc:20249]
225338_at	ZYG11B	ENSG00000162378	0.042351	0.6244781	7.31379	6.689312	1	p32.3	zyg-11 family member B, cell cycle regulator [Source:HGNC Symbol;Acc:25820]
204955_at	SRPX	ENSG00000101955	0.042351	1.7691767	7.330012	5.560835	X	p11.4	sushi-repeat containing protein, X-linked [Source:HGNC Symbol;Acc:11309]
210840_s_at	IQGAP1	ENSG00000140575	0.042351	0.8156678	10.60381	9.788142	15	q26.1	IQ motif containing GTPase activating protein 1 [Source:HGNC Symbol;Acc:6110]
201494_at	PRCP	ENSG00000137509	0.042351	0.8806117	10.84225	9.961639	11	q14.1	prolylcarboxypeptidase (angiotensinase C) [Source:HGNC Symbol;Acc:9344]
204415_at	IFI6	ENSG00000126709	0.042351	1.1130836	9.366478	8.253394	1	p36.11	interferon, alpha-inducible protein 6 [Source:HGNC Symbol;Acc:4054]
209290_s_at	NFIB	ENSG00000147862	0.042351	1.6557745	8.409196	6.753422	9	p22.3	nuclear factor I/B [Source:HGNC Symbol;Acc:7785]
221474_at	MYL12B	ENSG00000118680	0.04242	0.5861311	10.97279	10.38666	18	p11.31	myosin, light chain 12B, regulatory [Source:HGNC Symbol;Acc:29827]
235747_at	SLC25A16	ENSG00000122912	0.04242	0.5460494	7.042745	6.496696	10	q21.3	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16 [Source:HGNC Symbol;Acc:10986]
201924_at	AFF1	ENSG00000172493	0.04242	0.9520638	10.24162	9.289557	4	q21.3	AF4/FMR2 family, member 1 [Source:HGNC Symbol;Acc:7135]
218045_x_at	PTMS	ENSG00000159335	0.042596	0.6071624	9.924388	9.317226	12	p13.31	parathyromosin [Source:HGNC Symbol;Acc:9629]
213943_at	TWIST1	ENSG00000122691	0.042596	1.1687342	7.271938	6.103204	7	p21.1	twist basic helix-loop-helix transcription factor 1 [Source:HGNC Symbol;Acc:12428]
226752_at	FAM174A	ENSG00000174132	0.042596	0.9287163	5.776449	4.847732	5	q21.1	family with sequence similarity 174, member A [Source:HGNC Symbol;Acc:24943]
201876_at	PON2	ENSG00000105854	0.04272	1.1875711	9.054738	7.867167	7	q21.3	paraoxonase 2 [Source:HGNC Symbol;Acc:9205]
1554240_a_at	ITGAL	ENSG00000005844	0.042882	1.3025054	9.317163	8.014657	16	p11.2	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) [Source:HGNC Symbol;Acc:6148]
203989_x_at	F2R	ENSG00000181104	0.042891	1.2465199	7.440039	6.193519	5	q13.3	coagulation factor II (thrombin) receptor [Source:HGNC Symbol;Acc:3537]
226425_at	CLIP4	ENSG00000115295	0.042891	1.4998601	7.783328	6.283468	2	p23.2	CAP-GLY domain containing linker protein family, member 4 [Source:HGNC Symbol;Acc:26108]
200762_at	DPYSL2	ENSG00000092964	0.042891	1.1591718	9.328124	8.168952	8	p21.2	dihydropyrimidinase-like 2 [Source:HGNC Symbol;Acc:3014]
223681_s_at	INADL	ENSG00000132849	0.042891	1.2509988	6.181877	4.930878	1	p31.3	InaD-like (Drosophila) [Source:HGNC Symbol;Acc:28881]
211986_at	AHNAK	ENSG00000124942	0.042891	1.3341466	11.47856	10.14441	11	q12.3	AHNAK nucleoprotein [Source:HGNC Symbol;Acc:347]
204112_s_at	HNMT	ENSG00000150540	0.042891	1.303475	8.681933	7.378458	2	q22.1	histamine N-methyltransferase [Source:HGNC Symbol;Acc:5028]

235360_at	PLEKHM3	ENSG00000178385	0.042891	0.4363264	7.481078	7.044751	2	q33.3	pleckstrin homology domain containing, family M, member 3 [Source:HGNC Symbol;Acc:34006]
209276_s_at	GLRX	ENSG00000173221	0.04294	1.1533528	10.46513	9.31178	5	q15	glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:4330]
226113_at	ZNF436	ENSG00000125945	0.042951	0.9676351	7.934453	6.966818	1	p36.12	zinc finger protein 436 [Source:HGNC Symbol;Acc:20814]
201694_s_at	EGR1	ENSG00000120738	0.043033	2.3562082	9.680723	7.324515	5	q31.2	early growth response 1 [Source:HGNC Symbol;Acc:3238]
204417_at	GALC	ENSG00000054983	0.043091	1.1819717	9.186049	8.004078	14	q31.3	galactosylceramidase [Source:HGNC Symbol;Acc:4115]
211178_s_at	PSTPIP1	ENSG00000140368	0.043103	0.5580401	8.764375	8.206335	15	q24.3	proline-serine-threonine phosphatase interacting protein 1 [Source:HGNC Symbol;Acc:9580]
203088_at	FBLN5	ENSG00000140092	0.043103	1.5746104	8.128332	6.553721	14	q32.12	fibulin 5 [Source:HGNC Symbol;Acc:3602]
218450_at	HEBP1	ENSG00000013583	0.043103	0.7563211	8.459513	7.703192	12	p13.1	heme binding protein 1 [Source:HGNC Symbol;Acc:17176]
210113_s_at	NLRP1	ENSG00000091592	0.043128	0.6544652	7.398937	6.744472	17	p13.2	NLR family, pyrin domain containing 1 [Source:HGNC Symbol;Acc:14374]
225673_at	MYADM	ENSG00000179820	0.043128	1.1859735	9.460657	8.274684	19	q13.42	myeloid-associated differentiation marker [Source:HGNC Symbol;Acc:7544]
31874_at	GAS2L1	ENSG00000185340	0.043128	0.9591258	7.063628	6.104502	22	q12.2	growth arrest-specific 2 like 1 [Source:HGNC Symbol;Acc:16955]
222597_at	SNAP29	ENSG00000099940	0.043128	0.523138	8.682269	8.159131	22	q11.21	synaptosomal-associated protein, 29kDa [Source:HGNC Symbol;Acc:11133]
226279_at	PRSS23	ENSG00000150687	0.043153	1.3604367	7.675135	6.314698	11	q14.2	protease, serine, 23 [Source:HGNC Symbol;Acc:14370]
235570_at	RBMS3	ENSG00000144642	0.043153	1.7823279	7.335633	5.553305	3	p24.1	RNA binding motif, single stranded interacting protein 3 [Source:HGNC Symbol;Acc:13427]
214830_at	SLC38A6	ENSG00000139974	0.04325	1.2769308	7.341343	6.064412	14	q23.1	solute carrier family 38, member 6 [Source:HGNC Symbol;Acc:19863]
201366_at	ANXA7	ENSG00000138279	0.04326	0.7630117	8.850377	8.087365	10	q22.2	annexin A7 [Source:HGNC Symbol;Acc:545]
203179_at	GALT	ENSG00000213930	0.043316	0.4101715	8.833284	8.423113	9	p13.3	galactose-1-phosphate uridylyltransferase [Source:HGNC Symbol;Acc:4135]
225919_s_at	C9orf72	ENSG00000147894	0.043475	0.8552519	8.18141	7.326158	9	p21.2	chromosome 9 open reading frame 72 [Source:HGNC Symbol;Acc:28337]
36711_at	MAFF	ENSG00000185022	0.043475	1.042386	5.605979	4.563593	22	q13.1	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F [Source:HGNC Symbol;Acc:6780]
205174_s_at	QPCT	ENSG00000115828	0.043531	1.2617245	8.418599	7.156874	2	p22.2	glutamyl-peptide cyclotransferase [Source:HGNC Symbol;Acc:9753]
225032_at	FNDCC3B	ENSG00000075420	0.043657	1.1481117	9.690617	8.542506	3	q26.31	fibronectin type III domain containing 3B [Source:HGNC Symbol;Acc:24670]
225283_at	ARRDC4	ENSG00000140450	0.043675	1.2632774	6.919418	5.656141	15	q26.2	arrestin domain containing 4 [Source:HGNC Symbol;Acc:28087]
212820_at	DMXL2	ENSG00000104093	0.043693	1.7237553	9.098754	7.374999	15	q21.2	Dmx-like 2 [Source:HGNC Symbol;Acc:2938]
202411_at	IFI27	ENSG00000165949	0.043693	1.4199045	10.65301	9.233109	14	q32.12	interferon, alpha-inducible protein 27 [Source:HGNC Symbol;Acc:5397]
201444_s_at	ATP6AP2	ENSG00000182220	0.043693	0.8481282	9.927791	9.079663	X	p11.4	ATPase, H transporting, lysosomal accessory protein 2 [Source:HGNC Symbol;Acc:18305]
212209_at	MED13L	ENSG00000123066	0.043693	0.718689	7.683203	6.964514	12	q24.21	mediator complex subunit 13-like [Source:HGNC Symbol;Acc:22962]
228082_at	CLMP	ENSG00000166250	0.043693	0.811086	8.019361	7.208275	11	q24.1	CXADR-like membrane protein [Source:HGNC Symbol;Acc:24039]
201579_at	FAT1	ENSG00000083857	0.043693	1.1996966	6.984438	5.784741	4	q35.2	FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
201050_at	PLD3	ENSG00000105223	0.043739	0.872713	11.22151	10.34879	19	q13.2	phospholipase D family, member 3 [Source:HGNC Symbol;Acc:17158]
205726_at	DIAPH2	ENSG00000147202	0.043865	0.8243238	7.524442	6.700118	X	q21.33	diaphanous-related formin 2 [Source:HGNC Symbol;Acc:2877]
212717_at	PLEKHM1	ENSG00000225190	0.043869	0.3500827	8.468551	8.118469	17	q21.31	pleckstrin homology domain containing, family M (with RUN domain) member 1 [Source:HGNC Symbol;Acc:29017]
202827_s_at	MMP14	ENSG00000157227	0.04395	1.0934303	9.702738	8.609308	14	q11.2	matrix metalloproteinase 14 (membrane-inserted) [Source:HGNC Symbol;Acc:7160]
201594_s_at	PPP4R1	ENSG00000154845	0.04395	0.8180394	9.274119	8.456079	18	p11.22	protein phosphatase 4, regulatory subunit 1 [Source:HGNC Symbol;Acc:9320]
203460_s_at	PSEN1	ENSG00000080815	0.04395	0.8139024	8.845797	8.031895	14	q24.2	presenilin 1 [Source:HGNC Symbol;Acc:9508]
221840_at	PTPRE	ENSG00000132334	0.044017	1.2948506	8.885638	7.590787	10	q26.2	protein tyrosine phosphatase, receptor type, E [Source:HGNC Symbol;Acc:9669]
203410_at	AP3M2	ENSG00000070718	0.044043	0.7683391	7.036583	6.268244	8	p11.21	adaptor-related protein complex 3, mu 2 subunit [Source:HGNC Symbol;Acc:570]
226582_at	LOC400043	NA	0.044043	0.8694792	6.734431	5.864952	NA	NA	NA
209600_s_at	ACOX1	ENSG00000161533	0.044043	0.6483325	8.512058	7.863726	17	q25.1	acyl-CoA oxidase 1, palmitoyl [Source:HGNC Symbol;Acc:119]
221814_at	GPR124	ENSG00000020181	0.044043	1.0958806	8.488648	7.392767	8	p11.23	G protein-coupled receptor 124 [Source:HGNC Symbol;Acc:17849]
230836_at	ST8SIA4	ENSG00000113532	0.044043	1.0174978	7.57919	6.561693	5	q21.1	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 4 [Source:HGNC

										Symbol;Acc:10871]
204270_at	SKI	ENSG00000157933	0.044043	0.8960351	9.220481	8.324446	1	p36.33	v-ski avian sarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:10896]	
200872_at	S100A10	ENSG00000197747	0.044043	0.8622314	12.14558	11.28335	1	q21.3	S100 calcium binding protein A10 [Source:HGNC Symbol;Acc:10487]	
219761_at	CLEC1A	ENSG00000150048	0.044043	1.2912893	6.704346	5.413057	12	p13.2	C-type lectin domain family 1, member A [Source:HGNC Symbol;Acc:24355]	
212708_at	MSL1	ENSG00000188895	0.044043	0.8560698	9.529726	8.673656	17	q21.1	male-specific lethal 1 homolog (Drosophila) [Source:HGNC Symbol;Acc:27905]	
204326_x_at	MT1X	ENSG00000187193	0.04407	1.0017293	10.86485	9.863125	16	q13	metallothionein 1X [Source:HGNC Symbol;Acc:7405]	
241392_at	TMEM39A	ENSG00000176142	0.04407	0.341471	6.928602	6.587131	3	q13.33	transmembrane protein 39A [Source:HGNC Symbol;Acc:25600]	
205771_s_at	AKAP7	ENSG00000118507	0.04407	0.7319958	6.526725	5.794729	6	q23.2	A kinase (PRKA) anchor protein 7 [Source:HGNC Symbol;Acc:377]	
206227_at	CHLP	ENSG00000138615	0.04407	2.2575028	8.735998	6.478495	15	q22.31	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase [Source:HGNC Symbol;Acc:1980]	
204158_s_at	TCIRG1	ENSG00000110719	0.04407	0.5930798	9.597157	9.004077	11	q13.2	T-cell, immune regulator 1, ATPase, H transporting, lysosomal V0 subunit A3 [Source:HGNC Symbol;Acc:11647]	
212948_at	CAMTA2	ENSG00000108509	0.04407	0.5383882	9.486336	8.947948	17	p13.2	calmodulin binding transcription activator 2 [Source:HGNC Symbol;Acc:18807]	
218241_at	GOLGA5	ENSG00000066455	0.044078	0.5034783	7.912464	7.408985	14	q32.12	golgin A5 [Source:HGNC Symbol;Acc:4428]	
203042_at	LAMP2	ENSG00000005893	0.044078	1.3866138	9.189891	7.803278	X	q24	lysosomal-associated membrane protein 2 [Source:HGNC Symbol;Acc:6501]	
223264_at	MESDC1	ENSG00000140406	0.044215	0.6585783	8.668695	8.010116	15	q25.1	mesoderm development candidate 1 [Source:HGNC Symbol;Acc:13519]	
243141_at	SGMS2	ENSG00000164023	0.044313	1.0856346	5.816519	4.730885	4	q25	sphingomyelin synthase 2 [Source:HGNC Symbol;Acc:28395]	
212513_s_at	USP33	ENSG00000077254	0.044313	0.8692058	8.910601	8.041395	1	p31.1	ubiquitin specific peptidase 33 [Source:HGNC Symbol;Acc:20059]	
44111_at	VPS33B	ENSG00000184056	0.044313	0.7185294	7.769682	7.051153	15	q26.1	vacuolar protein sorting 33 homolog B (yeast) [Source:HGNC Symbol;Acc:12712]	
203044_at	CHSY1	ENSG00000131873	0.044778	0.8603129	9.374891	8.514578	15	q26.3	chondroitin sulfate synthase 1 [Source:HGNC Symbol;Acc:17198]	
201133_s_at	PJA2	ENSG00000198961	0.045063	0.9288514	8.789327	7.860476	5	q21.3	praja ring finger 2, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:17481]	
238478_at	BNC2	ENSG00000173068	0.045109	1.5819289	6.500666	4.918737	9	p22.2	basonuclin 2 [Source:HGNC Symbol;Acc:30988]	
207121_s_at	MAPK6	ENSG00000069956	0.045217	0.9719614	9.250325	8.278364	15	q21.2	mitogen-activated protein kinase 6 [Source:HGNC Symbol;Acc:6879]	
226757_at	IFIT2	ENSG00000119922	0.045217	1.2581633	7.398381	6.140218	10	q23.31	interferon-induced protein with tetratricopeptide repeats 2 [Source:HGNC Symbol;Acc:5409]	
224929_at	TMEM173	ENSG00000184584	0.045217	0.9769018	8.795662	7.81876	5	q31.2	transmembrane protein 173 [Source:HGNC Symbol;Acc:27962]	
219013_at	GALNT11	ENSG00000178234	0.045217	0.6247652	8.111616	7.486851	7	q36.1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 11 (GalNAc-T11) [Source:HGNC Symbol;Acc:19875]	
203732_at	TRIP4	ENSG00000103671	0.045217	0.5349917	8.282764	7.747772	15	q22.31	thyroid hormone receptor interactor 4 [Source:HGNC Symbol;Acc:12310]	
206991_s_at	CCR5	ENSG00000160791	0.045321	1.4988998	8.807196	7.308296	3	p21.31	chemokine (C-C motif) receptor 5 (gene/pseudogene) [Source:HGNC Symbol;Acc:1606]	
212192_at	KCTD12	ENSG00000178695	0.045321	1.241112	11.04262	9.801504	13	q22.3	potassium channel tetramerization domain containing 12 [Source:HGNC Symbol;Acc:14678]	
212071_s_at	SPTBN1	ENSG00000115306	0.045389	1.1482987	10.50839	9.360088	2	p16.2	spectrin, beta, non-erythrocytic 1 [Source:HGNC Symbol;Acc:11275]	
204194_at	BACH1	ENSG00000156273	0.045389	0.6844954	7.33134	6.646844	21	q21.3	BTB and CNC homology 1, basic leucine zipper transcription factor 1 [Source:HGNC Symbol;Acc:935]	
213469_at	PGAP1	ENSG00000197121	0.045389	0.8013879	4.677932	3.876544	2	q33.1	post-GPI attachment to proteins 1 [Source:HGNC Symbol;Acc:25712]	
207173_x_at	CDH11	ENSG00000140937	0.045389	1.855492	9.112093	7.256601	16	q21	cadherin 11, type 2, OB-cadherin (osteoblast) [Source:HGNC Symbol;Acc:1750]	
202020_s_at	LANCL1	ENSG00000115365	0.045389	0.7225894	9.184946	8.462357	2	q34	LanC lantibiotic synthetase component C-like 1 (bacterial) [Source:HGNC Symbol;Acc:6508]	
201384_s_at	NBR1	ENSG00000188554	0.045622	0.6971938	9.452834	8.75564	17	q21.31	neighbor of BRCA1 gene 1 [Source:HGNC Symbol;Acc:6746]	
213004_at	ANGPTL2	ENSG00000136859	0.04565	1.4882714	9.435206	7.946935	9	q33.3	angiopoietin-like 2 [Source:HGNC Symbol;Acc:490]	
203310_at	STXBP3	ENSG00000116266	0.045775	0.7707987	7.721639	6.950841	1	p13.3	syntaphin binding protein 3 [Source:HGNC Symbol;Acc:11446]	
212239_at	PIK3R1	ENSG00000145675	0.045775	0.7377508	9.025386	8.287636	5	q13.1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) [Source:HGNC Symbol;Acc:8979]	
225864_at	FAM84B	ENSG00000168672	0.045775	1.6779147	6.194231	4.516317	8	q24.21	family with sequence similarity 84, member B [Source:HGNC Symbol;Acc:24166]	

218679_s_at	VPS28	ENSG00000160948	0.04581	0.3909079	9.69126	9.300352	8	q24.3	vacuolar protein sorting 28 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:18178]
211964_at	COL4A2	ENSG00000134871	0.045857	1.2328119	10.70556	9.472749	13	q34	collagen, type IV, alpha 2 [Source:HGNC Symbol;Acc:2203]
212501_at	CEBPB	ENSG00000172216	0.045857	0.7382385	10.55473	9.816494	20	q13.13	CCAAT/enhancer binding protein (C/EBP), beta [Source:HGNC Symbol;Acc:1834]
215596_s_at	LTN1	ENSG00000198862	0.045857	0.6006951	9.123146	8.522451	21	q21.3	listerin E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc:13082]
235306_at	GIMAP8	ENSG00000171115	0.045949	1.1415232	7.866982	6.725458	7	q36.1	GTPase, IMAP family member 8 [Source:HGNC Symbol;Acc:21792]
213746_s_at	FLNA	ENSG00000196924	0.045983	0.6709764	10.55453	9.883554	X	q28	filamin A, alpha [Source:HGNC Symbol;Acc:3754]
200982_s_at	ANXA6	ENSG00000197043	0.045983	0.9677565	9.852305	8.884549	5	q33.1	annexin A6 [Source:HGNC Symbol;Acc:544]
227029_at	FAM177A1	ENSG00000151327	0.046043	0.8330088	6.455042	5.622033	14	q13.2	family with sequence similarity 177, member A1 [Source:HGNC Symbol;Acc:19829]
225695_at	SLC35F6	ENSG00000213699	0.046225	0.7246104	9.024413	8.299803	2	p23.3	solute carrier family 35, member F6 [Source:HGNC Symbol;Acc:26055]
230263_s_at	DOCK5	ENSG00000147459	0.046636	0.9841685	5.975225	4.991057	8	p21.2	dedicator of cytokinesis 5 [Source:HGNC Symbol;Acc:23476]
219860_at	LY6G5C	ENSG00000204428	0.04666	0.4988369	6.319773	5.820936	6	p21.33	lymphocyte antigen 6 complex, locus G5C [Source:HGNC Symbol;Acc:13932]
216620_s_at	ARHGEF10	ENSG00000104728	0.04666	1.0059164	8.015577	7.009661	8	p23.3	Rho guanine nucleotide exchange factor (GEF) 10 [Source:HGNC Symbol;Acc:14103]
209298_s_at	ITSN1	ENSG00000205726	0.046712	1.2772025	5.880818	4.603616	21	q22.11	intersectin 1 (SH3 domain protein) [Source:HGNC Symbol;Acc:6183]
219383_at	PRR5L	ENSG00000135362	0.046712	0.8741436	4.47531	3.601166	11	p13	proline rich 5 like [Source:HGNC Symbol;Acc:25878]
218204_s_at	FYCO1	ENSG00000163820	0.046712	0.4753249	7.84106	7.365735	3	p21.31	FYVE and coiled-coil domain containing 1 [Source:HGNC Symbol;Acc:14673]
212637_s_at	WWP1	ENSG00000123124	0.046712	0.9223494	7.411309	6.48896	8	q21.3	WW domain containing E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc:17004]
200784_s_at	LRP1	ENSG00000123384	0.046712	0.8354694	10.71172	9.876255	12	q13.3	low density lipoprotein receptor-related protein 1 [Source:HGNC Symbol;Acc:6692]
202668_at	EFNB2	ENSG00000125266	0.046712	1.3006186	7.729295	6.428677	13	q33.3	ephrin-B2 [Source:HGNC Symbol;Acc:3227]
211926_s_at	MYH9	ENSG00000100345	0.046851	0.5140278	10.37284	9.858809	22	q12.3	myosin, heavy chain 9, non-muscle [Source:HGNC Symbol;Acc:7579]
207181_s_at	CASP7	ENSG00000165806	0.046856	0.8773186	8.172928	7.295609	10	q25.3	caspase 7, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:1508]
203940_s_at	VASH1	ENSG00000071246	0.046904	0.759053	8.993567	8.234514	14	q24.3	vasohibin 1 [Source:HGNC Symbol;Acc:19964]
225046_at	LOC389831	NA	0.046904	1.209299	9.502744	8.293445	NA	NA	NA
229699_at	LOC100129550	NA	0.046904	0.7875228	7.252125	6.464602	NA	NA	NA
1555997_s_at	IGFBP5	ENSG00000115461	0.046904	2.0893027	9.039541	6.950238	2	q35	insulin-like growth factor binding protein 5 [Source:HGNC Symbol;Acc:5474]
221858_at	TBC1D12	ENSG00000108239	0.046904	0.9754493	6.730089	5.75464	10	q23.33	TBC1 domain family, member 12 [Source:HGNC Symbol;Acc:29082]
202123_s_at	ABL1	ENSG00000097007	0.046904	0.5359328	8.956464	8.420531	9	q34.12	c-abl oncogene 1, non-receptor tyrosine kinase [Source:HGNC Symbol;Acc:76]
209189_at	FOS	ENSG00000170345	0.046904	2.3113953	8.928569	6.617174	14	q24.3	FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:3796]
231697_s_at	VMP1	ENSG00000062716	0.046904	1.3376767	9.338249	8.000572	17	q23.1	vacuole membrane protein 1 [Source:HGNC Symbol;Acc:29559]
231823_s_at	SH3PXD2B	ENSG00000174705	0.046907	1.3421906	8.749657	7.407467	5	q35.1	SH3 and PX domains 2B [Source:HGNC Symbol;Acc:29242]
226917_s_at	ANAPC4	ENSG00000053900	0.046907	0.7157989	9.420943	8.705144	4	p15.2	anaphase promoting complex subunit 4 [Source:HGNC Symbol;Acc:19990]
213135_at	TIAM1	ENSG00000156299	0.04696	1.432496	8.128731	6.696235	21	q22.11	T-cell lymphoma invasion and metastasis 1 [Source:HGNC Symbol;Acc:11805]
222793_at	DDX58	ENSG00000107201	0.046977	0.7930309	6.897065	6.104034	9	p21.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 [Source:HGNC Symbol;Acc:19102]
235059_at	RAB12	ENSG00000206418	0.047161	0.7361697	8.288455	7.552285	18	p11.22	RAB12, member RAS oncogene family [Source:HGNC Symbol;Acc:31332]
213364_s_at	SNX1	ENSG00000028528	0.047358	0.9413216	7.632326	6.691004	15	q22.31	sorting nexin 1 [Source:HGNC Symbol;Acc:11172]
213194_at	ROBO1	ENSG00000169855	0.047358	1.2023648	8.299204	7.09684	3	p12.2	roundabout, axon guidance receptor, homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:10249]
223434_at	GBP3	ENSG00000117226	0.047368	1.7670063	8.155929	6.388923	1	p22.2	guanylate binding protein 3 [Source:HGNC Symbol;Acc:4184]
201464_x_at	JUN	ENSG00000177606	0.047577	1.4116477	9.379206	7.967558	1	p32.1	jun proto-oncogene [Source:HGNC Symbol;Acc:6204]
228325_at	KIAA0146	NA	0.047577	1.6371158	6.878768	5.241652	NA	NA	NA
226639_at	SFT2D3	ENSG00000173349	0.04777	0.4029701	7.472242	7.069272	2	q14.3	SFT2 domain containing 3 [Source:HGNC Symbol;Acc:28767]
204204_at	SLC31A2	ENSG00000136867	0.047785	1.078147	7.858562	6.780415	9	q32	solute carrier family 31 (copper transporter), member 2 [Source:HGNC

									Symbol;Acc:11017]
213659_at	ZNF75D	ENSG00000186376	0.047785	0.6654956	7.859604	7.194108	X	q26.3	zinc finger protein 75D [Source:HGNC Symbol;Acc:13145]
219165_at	PDLIM2	ENSG00000120913	0.047788	0.5378302	8.659829	8.121999	8	p21.3	PDZ and LIM domain 2 (mystique) [Source:HGNC Symbol;Acc:13992]
202704_at	TOB1	ENSG00000141232	0.047841	1.1577332	7.864873	5.707139	17	q21.33	transducer of ERBB2, 1 [Source:HGNC Symbol;Acc:11979]
201059_at	CTTN	ENSG00000085733	0.047841	1.13298	8.126829	6.993849	11	q13.3	cortactin [Source:HGNC Symbol;Acc:3338]
208626_s_at	VAT1	ENSG00000108828	0.047843	0.9455257	10.23981	9.294287	17	q21.31	vesicle amine transport protein 1 homolog (T. californica) [Source:HGNC Symbol;Acc:16919]
224285_at	GPR174	ENSG00000147138	0.047886	1.197457	7.961716	6.764259	X	q21.1	G protein-coupled receptor 174 [Source:HGNC Symbol;Acc:30245]
202746_at	ITM2A	ENSG00000078596	0.047974	1.7562969	8.555659	6.799362	X	q21.1	integral membrane protein 2A [Source:HGNC Symbol;Acc:6173]
1557749_at	EHBP1L1	ENSG00000173442	0.047976	1.3008188	7.376098	6.075279	11	q13.1	EH domain binding protein 1-like 1 [Source:HGNC Symbol;Acc:30682]
208671_at	SERINC1	ENSG00000111897	0.047976	0.9726095	8.57887	7.606261	6	q22.31	serine incorporator 1 [Source:HGNC Symbol;Acc:13464]
235199_at	RNF125	ENSG00000101695	0.048039	1.0642075	7.065692	6.001485	18	q12.1	ring finger protein 125, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:21150]
236565_s_at	LARP6	ENSG00000166173	0.048103	0.6843004	5.230392	4.546092	15	q23	La ribonucleoprotein domain family, member 6 [Source:HGNC Symbol;Acc:24012]
204575_s_at	MMP19	ENSG00000123342	0.048165	0.946556	7.578627	6.632071	12	q13.2	matrix metalloproteinase 19 [Source:HGNC Symbol;Acc:7165]
221653_x_at	APOL2	ENSG00000128335	0.048165	0.5885832	10.11617	9.527585	22	q12.3	apolipoprotein L 2 [Source:HGNC Symbol;Acc:619]
224804_s_at	FAM219B	ENSG00000178761	0.048165	0.6515628	8.895176	8.243613	15	q24.1	family with sequence similarity 219, member B [Source:HGNC Symbol;Acc:24695]
202820_at	AHR	ENSG00000106546	0.048165	1.1914252	8.43326	7.241835	7	p21.1	aryl hydrocarbon receptor [Source:HGNC Symbol;Acc:348]
204082_at	PBX3	ENSG00000167081	0.048165	0.6358091	8.576776	7.940967	9	q33.3	pre-B-cell leukemia homeobox 3 [Source:HGNC Symbol;Acc:8634]
218109_s_at	MFSD1	ENSG00000118855	0.048305	1.1396733	10.13941	8.999736	3	q25.32	major facilitator superfamily domain containing 1 [Source:HGNC Symbol;Acc:25874]
231897_at	PTGR1	ENSG00000106853	0.048305	1.1548912	7.789451	6.63456	9	q31.3	prostaglandin reductase 1 [Source:HGNC Symbol;Acc:18429]
205786_s_at	ITGAM	ENSG00000169896	0.048306	1.1378078	8.121972	6.984164	16	p11.2	integrin, alpha M (complement component 3 receptor 3 subunit) [Source:HGNC Symbol;Acc:6149]
203510_at	MET	ENSG00000105976	0.048306	1.6502092	7.842579	6.19237	7	q31.2	met proto-oncogene [Source:HGNC Symbol;Acc:7029]
224896_s_at	TTL	ENSG00000114999	0.048306	0.5603672	8.810442	8.250075	2	q13	tubulin tyrosine ligase [Source:HGNC Symbol;Acc:21586]
232645_at	LOC153684	NA	0.048306	0.888957	7.159878	6.270921	NA	NA	NA
226576_at	ARHGAP26	ENSG00000145819	0.048306	0.8225882	6.112706	5.290117	5	q31.3	Rho GTPase activating protein 26 [Source:HGNC Symbol;Acc:17073]
219191_s_at	BIN2	ENSG00000110934	0.048306	1.0978185	9.340657	8.242838	12	q13.13	bridging integrator 2 [Source:HGNC Symbol;Acc:1053]
214853_s_at	SHC1	ENSG00000160691	0.048306	0.5806619	10.02587	9.445211	1	q21.3	SHC (Src homology 2 domain containing) transforming protein 1 [Source:HGNC Symbol;Acc:10840]
224358_s_at	MS4A7	ENSG00000166927	0.048314	2.066881	8.506524	6.439643	11	q12.2	membrane-spanning 4-domains, subfamily A, member 7 [Source:HGNC Symbol;Acc:13378]
209164_s_at	CYB561	ENSG00000008283	0.04856	0.8626733	8.334774	7.472101	17	q23.3	cytochrome b561 [Source:HGNC Symbol;Acc:2571]
222175_s_at	MED15	ENSG00000099917	0.04856	0.4451901	9.6034	9.15821	22	q11.21	mediator complex subunit 15 [Source:HGNC Symbol;Acc:14248]
219469_at	DYNC2H1	ENSG00000187240	0.04857	0.6595986	6.55585	5.896251	11	q22.3	dynein, cytoplasmic 2, heavy chain 1 [Source:HGNC Symbol;Acc:2962]
226143_at	RAI1	ENSG00000108557	0.04857	1.2083934	8.541448	7.333054	17	p11.2	retinoic acid induced 1 [Source:HGNC Symbol;Acc:9834]
212681_at	EPB41L3	ENSG00000082397	0.048619	1.3472919	8.071549	6.724257	18	p11.31	erythrocyte membrane protein band 4.1-like 3 [Source:HGNC Symbol;Acc:3380]
215784_at	CD1E	ENSG00000158488	0.04871	1.1453683	5.448261	4.302893	1	q23.1	CD1e molecule [Source:HGNC Symbol;Acc:1638]
211161_s_at	COL3A1	ENSG00000168542	0.04871	2.0294663	11.58326	9.553789	2	q32.2	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
209906_at	C3AR1	ENSG00000171860	0.04881	1.1815832	9.984971	8.803387	12	p13.31	complement component 3a receptor 1 [Source:HGNC Symbol;Acc:1319]
200625_s_at	CAP1	ENSG00000131236	0.048952	0.8385932	11.78723	10.94863	1	p34.2	CAP, adenylate cyclase-associated protein 1 (yeast) [Source:HGNC Symbol;Acc:20040]
209550_at	NDN	ENSG00000182636	0.048952	0.8892051	8.585921	7.696716	15	q11.2	neccdin, melanoma antigen (MAGE) family member [Source:HGNC Symbol;Acc:7675]
214039_s_at	LAPTM4B	ENSG00000104341	0.048974	1.6628259	7.882224	6.219398	8	q22.1	lysosomal protein transmembrane 4 beta [Source:HGNC Symbol;Acc:13646]
209356_x_at	EFEMP2	ENSG00000172638	0.049064	0.7587052	8.007888	7.249183	11	q13.1	EGF containing fibulin-like extracellular matrix protein 2 [Source:HGNC

									Symbol;Acc:3219]
207276_at	CDR1	ENSG00000184258	0.049178	1.8925946	9.606612	7.714017	X	q27.1	cerebellar degeneration-related protein 1, 34kDa [Source:HGNC Symbol;Acc:1798]
209955_s_at	FAP	ENSG00000078098	0.049178	1.4777063	8.251596	6.77389	2	q24.2	fibroblast activation protein, alpha [Source:HGNC Symbol;Acc:3590]
226844_at	MOB3B	ENSG00000120162	0.049203	1.1637648	6.92211	5.758345	9	p21.2	MOB kinase activator 3B [Source:HGNC Symbol;Acc:23825]
222468_at	KIAA0319L	ENSG00000142687	0.049203	0.3011724	8.203036	7.901864	1	p34.3	KIAA0319-like [Source:HGNC Symbol;Acc:30071]
226056_at	ARHGAP31	ENSG00000031081	0.049247	0.7875162	8.433132	7.645616	3	q13.33	Rho GTPase activating protein 31 [Source:HGNC Symbol;Acc:29216]
226695_at	PRRX1	ENSG00000116132	0.049316	1.7627347	9.80378	8.041045	1	q24.2	paired related homeobox 1 [Source:HGNC Symbol;Acc:9142]
204844_at	ENPEP	ENSG00000138792	0.049442	0.6595157	4.491515	3.831999	4	q25	glutamyl aminopeptidase (aminopeptidase A) [Source:HGNC Symbol;Acc:3355]
200612_s_at	AP2B1	ENSG00000006125	0.049442	0.5957471	8.555796	7.960049	17	q12	adaptor-related protein complex 2, beta 1 subunit [Source:HGNC Symbol;Acc:563]
200923_at	LGALS3BP	ENSG00000108679	0.049442	0.9211334	10.07362	9.152489	17	q25.3	lectin, galactoside-binding, soluble, 3 binding protein [Source:HGNC Symbol;Acc:6564]
208074_s_at	AP2S1	ENSG00000042753	0.049593	0.5957933	10.51239	9.916594	19	q13.32	adaptor-related protein complex 2, sigma 1 subunit [Source:HGNC Symbol;Acc:565]
200897_s_at	PALLD	ENSG00000129116	0.049599	1.6018945	9.526129	7.924234	4	q32.3	palladin, cytoskeletal associated protein [Source:HGNC Symbol;Acc:17068]
209667_at	CE52	ENSG00000172831	0.049599	0.5127909	8.055154	7.542363	16	q22.1	carboxylesterase 2 [Source:HGNC Symbol;Acc:1864]
225785_at	REEP3	ENSG00000165476	0.049649	1.1129933	7.249649	6.136656	10	q21.3	receptor accessory protein 3 [Source:HGNC Symbol;Acc:23711]
227265_at	FGL2	ENSG00000127951	0.049649	1.7680217	9.464203	7.696181	7	q11.23	fibrinogen-like 2 [Source:HGNC Symbol;Acc:3696]
226679_at	SLC26A11	ENSG00000181045	0.049649	1.3774827	8.62206	7.244577	17	q25.3	solute carrier family 26, member 11 [Source:HGNC Symbol;Acc:14471]
202441_at	ERLIN1	ENSG00000107566	0.049691	0.5854142	8.619248	8.033834	10	q24.31	ER lipid raft associated 1 [Source:HGNC Symbol;Acc:16947]
227758_at	RRG	ENSG00000134533	0.049698	1.1309377	5.789853	4.658915	12	p12.3	RAS-like, estrogen-regulated, growth inhibitor [Source:HGNC Symbol;Acc:15980]
204036_at	LPAR1	ENSG00000198121	0.049814	1.4440394	6.674595	5.230556	9	q31.3	lysophosphatidic acid receptor 1 [Source:HGNC Symbol;Acc:3166]
225755_at	KLHDC8B	ENSG00000185909	0.049849	0.8512009	8.005692	7.154491	3	p21.31	kelch domain containing 8B [Source:HGNC Symbol;Acc:28557]
209571_at	CIR1	ENSG00000138433	0.049849	0.3762687	8.299113	7.922845	2	q31.1	corepressor interacting with RBP1, 1 [Source:HGNC Symbol;Acc:24217]
210184_at	ITGAX	ENSG00000140678	0.049853	1.1127795	8.872884	7.760104	16	p11.2	integrin, alpha X (complement component 3 receptor 4 subunit) [Source:HGNC Symbol;Acc:6152]
217940_s_at	CARKD	ENSG00000213995	0.049853	0.4806867	8.908728	8.428041	13	q34	carbohydrate kinase domain containing [Source:HGNC Symbol;Acc:25576]
212993_at	NACC2	ENSG00000148411	0.050115	1.1149639	7.888032	6.773068	9	q34.3	NACC family member 2, BEN and BTB (POZ) domain containing [Source:HGNC Symbol;Acc:23846]
1562876_s_at	LOC541471	NA	0.050218	0.6825624	3.603678	2.921115	NA	NA	NA
242268_at	CELF2	ENSG00000048740	0.050218	1.5536681	7.210053	5.656385	10	p14	CUGBP, Elav-like family member 2 [Source:HGNC Symbol;Acc:2550]
213125_at	OLFML2B	ENSG00000162745	0.050218	0.7874654	8.741576	7.95411	1	q23.3	olfactomedin-like 2B [Source:HGNC Symbol;Acc:24558]
221257_x_at	FBXO38	ENSG00000145868	0.050301	0.5976252	7.698195	7.10057	5	q32	F-box protein 38 [Source:HGNC Symbol;Acc:28844]
236782_at	SAMD3	ENSG00000164483	0.0504	1.0727407	7.59099	6.51825	6	q23.1	sterile alpha motif domain containing 3 [Source:HGNC Symbol;Acc:21574]
1554690_a_at	TACC1	ENSG00000147526	0.050506	1.079368	9.700335	8.620967	8	p11.22	transforming, acidic coiled-coil containing protein 1 [Source:HGNC Symbol;Acc:11522]
203431_s_at	ARHGAP32	ENSG00000134909	0.050519	1.2383399	6.793821	5.555481	11	q24.3	Rho GTPase activating protein 32 [Source:HGNC Symbol;Acc:17399]
226711_at	FOXN2	ENSG00000170802	0.050636	0.9371015	9.838676	8.901574	2	p16.3	forkhead box N2 [Source:HGNC Symbol;Acc:5281]
203562_at	FEZ1	ENSG00000149557	0.050636	1.4246364	7.169091	5.744454	11	q24.2	fasciculation and elongation protein zeta 1 (zyglin I) [Source:HGNC Symbol;Acc:3659]
201508_at	IGFBP4	ENSG00000141753	0.050636	1.2181533	10.95048	9.732328	17	q21.2	insulin-like growth factor binding protein 4 [Source:HGNC Symbol;Acc:5473]
209933_s_at	CD300A	ENSG00000167851	0.050888	1.0639508	8.6536	7.589649	17	q25.1	CD300a molecule [Source:HGNC Symbol;Acc:19319]
226751_at	CNRIP1	ENSG00000119865	0.050983	1.0463666	7.446207	6.39984	2	p14	cannabinoid receptor interacting protein 1 [Source:HGNC Symbol;Acc:24546]
203303_at	DYNLT3	ENSG00000165169	0.050983	0.8389781	9.479702	8.640724	X	p11.4	dynein, light chain, Tctex-type 3 [Source:HGNC Symbol;Acc:11694]
1556698_a_at	GPRIN3	ENSG00000185477	0.050983	1.2153376	6.331782	5.116444	4	q22.1	GPRIN family member 3 [Source:HGNC Symbol;Acc:27733]
223454_at	CXCL16	ENSG00000161921	0.050983	0.9870947	9.755065	8.76797	17	p13.2	chemokine (C-X-C motif) ligand 16 [Source:HGNC Symbol;Acc:16642]
202032_s_at	MAN2A2	ENSG00000196547	0.050983	0.8858919	9.564687	8.678795	15	q26.1	mannosidase, alpha, class 2A, member 2 [Source:HGNC Symbol;Acc:6825]
205779_at	RAMP2	ENSG00000131477	0.051156	0.9338225	8.483655	7.549832	17	q21.31	receptor (G protein-coupled) activity modifying protein 2 [Source:HGNC

									Symbol;Acc:9844]
209110_s_at	RGL2	ENSG00000237441	0.051156	0.6625429	8.743822	8.081279	6	p21.32	ral guanine nucleotide dissociation stimulator-like 2 [Source:HGNC Symbol;Acc:9769]
209935_at	ATP2C1	ENSG0000017260	0.051156	0.6570157	6.368275	5.71126	3	q22.1	ATPase, Ca ²⁺ transporting, type 2C, member 1 [Source:HGNC Symbol;Acc:13211]
214453_s_at	IFI44	ENSG00000137965	0.051156	1.6331853	9.486684	7.853498	1	p31.1	interferon-induced protein 44 [Source:HGNC Symbol;Acc:16938]
201063_at	RCN1	ENSG00000049449	0.051233	0.7028097	9.216223	8.513413	11	p13	reticulocalbin 1, EF-hand calcium binding domain [Source:HGNC Symbol;Acc:9934]
213222_at	PLCB1	ENSG00000182621	0.051361	0.7004754	4.53598	3.835504	20	p12.3	phospholipase C, beta 1 (phosphoinositide-specific) [Source:HGNC Symbol;Acc:15917]
201069_at	MMP2	ENSG00000087245	0.051361	1.6913538	10.01928	8.32793	16	q12.2	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) [Source:HGNC Symbol;Acc:7166]
200661_at	CTSA	ENSG00000064601	0.051361	0.720607	10.64337	9.922764	20	q13.12	cathepsin A [Source:HGNC Symbol;Acc:9251]
213258_at	TFPI	ENSG00000003436	0.051379	1.4194378	8.02985	6.610412	2	q32.1	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) [Source:HGNC Symbol;Acc:11760]
225414_at	RNF149	ENSG00000163162	0.051422	0.8046724	9.11227	8.307597	2	q11.2	ring finger protein 149 [Source:HGNC Symbol;Acc:23137]
219397_at	COQ10B	ENSG00000115520	0.051422	0.6544798	7.359952	6.705472	2	q33.1	coenzyme Q10 homolog B (S. cerevisiae) [Source:HGNC Symbol;Acc:25819]
222127_s_at	EXOC1	ENSG00000090989	0.051603	0.7543635	9.746304	8.99194	4	q12	exocyst complex component 1 [Source:HGNC Symbol;Acc:30380]
223220_s_at	PARP9	ENSG00000138496	0.051603	0.9799493	9.260982	8.281032	3	q21.1	poly (ADP-ribose) polymerase family, member 9 [Source:HGNC Symbol;Acc:24118]
213422_s_at	MXRA8	ENSG00000162576	0.051603	1.2422437	8.999253	7.75701	1	p36.33	matrix-remodelling associated 8 [Source:HGNC Symbol;Acc:7542]
203153_at	IFIT1	ENSG00000185745	0.051753	1.5289266	7.719972	6.191046	10	q23.31	interferon-induced protein with tetratricopeptide repeats 1 [Source:HGNC Symbol;Acc:5407]
202100_at	RAIB	ENSG00000144118	0.051843	0.6714025	8.880756	8.209353	2	q14.2	v-rat simian leukemia viral oncogene homolog B [Source:HGNC Symbol;Acc:9840]
224895_at	YAP1	ENSG00000137693	0.051946	1.4909459	7.474063	5.983117	11	q22.1	Yes-associated protein 1 [Source:HGNC Symbol;Acc:16262]
201368_at	ZFP36L2	ENSG00000152518	0.052319	0.9647118	10.56869	9.603976	2	p21	ZFP36 ring finger protein-like 2 [Source:HGNC Symbol;Acc:1108]
212027_at	RBM25	ENSG00000119707	0.052384	0.6781906	9.494824	8.816633	14	q24.2	RNA binding motif protein 25 [Source:HGNC Symbol;Acc:23244]
221942_s_at	GUCY1A3	ENSG00000164116	0.05244	1.3677707	7.987539	6.619768	4	q32.1	guanylate cyclase 1, soluble, alpha 3 [Source:HGNC Symbol;Acc:4685]
213800_at	CFH	ENSG00000000971	0.05244	1.2322861	7.757237	6.524951	1	q31.3	complement factor H [Source:HGNC Symbol;Acc:4883]
1554999_at	RASGEF1B	ENSG00000138670	0.052614	1.4173975	6.341497	4.9241	4	q21.22	RasGEF domain family, member 1B [Source:HGNC Symbol;Acc:24881]
218606_at	ZDHHC7	ENSG00000153786	0.052737	0.3905379	8.928964	8.538426	16	q24.1	zinc finger, DHHC-type containing 7 [Source:HGNC Symbol;Acc:18459]
204083_s_at	TPM2	ENSG00000198467	0.052794	1.005641	10.06504	9.059402	9	p13.3	tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:12011]
1553955_at	PPP1R21	ENSG00000162869	0.052933	0.8388302	8.37991	7.54108	2	p16.3	protein phosphatase 1, regulatory subunit 21 [Source:HGNC Symbol;Acc:30595]
228083_at	CACNA2D4	ENSG00000151062	0.052933	0.833099	7.252949	6.41985	12	p13.33	calcium channel, voltage-dependent, alpha 2/delta subunit 4 [Source:HGNC Symbol;Acc:20202]
227304_at	SMCR8	ENSG00000176994	0.052933	0.7999914	8.377827	7.577836	17	p11.2	Smith-Magenis syndrome chromosome region, candidate 8 [Source:HGNC Symbol;Acc:17921]
225710_at	GNB4	ENSG00000114450	0.052933	1.0875404	8.393035	7.305494	3	q26.33	guanine nucleotide binding protein (G protein), beta polypeptide 4 [Source:HGNC Symbol;Acc:20731]
204154_at	CDO1	ENSG00000129596	0.052989	1.1929186	5.120926	3.928008	5	q22.3	cysteine dioxygenase type 1 [Source:HGNC Symbol;Acc:1795]
228318_s_at	CRIPAK	ENSG00000179979	0.053008	0.5311063	6.682491	6.151384	4	p16.3	cysteine-rich PAK1 inhibitor [Source:HGNC Symbol;Acc:26619]
227013_at	LATS2	ENSG00000150457	0.053008	1.1010683	7.793207	6.692139	13	q12.11	large tumor suppressor kinase 2 [Source:HGNC Symbol;Acc:6515]
1558692_at	C1orf85	ENSG00000198715	0.05311	0.572439	5.400512	4.828073	1	q22	chromosome 1 open reading frame 85 [Source:HGNC Symbol;Acc:29436]
213238_at	ATP10D	ENSG00000145246	0.05311	1.0510381	8.61573	7.564692	4	p12	ATPase, class V, type 10D [Source:HGNC Symbol;Acc:13549]
201850_at	CAPG	ENSG00000042493	0.053135	0.8093839	10.7541	9.944719	2	p11.2	capping protein (actin filament), gelsolin-like [Source:HGNC Symbol;Acc:1474]
209717_at	EVI5	ENSG00000067208	0.05314	0.7114496	7.081763	6.370314	1	p22.1	ecotropic viral integration site 5 [Source:HGNC Symbol;Acc:3501]
227388_at	TUSC1	ENSG00000198680	0.053261	1.5643673	8.139273	6.574905	9	p21.2	tumor suppressor candidate 1 [Source:HGNC Symbol;Acc:31010]
200771_at	LAMC1	ENSG00000135862	0.053546	0.8858041	8.418292	7.532487	1	q25.3	laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;Acc:6492]
229055_at	GPR68	ENSG00000119714	0.053546	0.8377005	9.226091	8.38839	14	q32.11	G protein-coupled receptor 68 [Source:HGNC Symbol;Acc:4519]
200927_s_at	RAB14	ENSG00000119396	0.053624	0.5226401	8.220466	7.697826	9	q33.2	RAB14, member RAS oncogene family [Source:HGNC Symbol;Acc:16524]

225447_at	GPD2	ENSG00000115159	0.053624	0.9677597	8.485215	7.517456	2	q24.1	glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Source:HGNC Symbol;Acc:4456]
225525_at	KIAA1671	ENSG00000197077	0.0538	1.4467482	7.312948	5.866199	22	q11.23	KIAA1671 [Source:HGNC Symbol;Acc:29345]
209649_at	STAM2	ENSG00000115145	0.053804	0.7574983	7.629712	6.872214	2	q23.3	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2 [Source:HGNC Symbol;Acc:11358]
219492_at	CHIC2	ENSG00000109220	0.054092	0.6729025	8.386462	7.713559	4	q12	cysteine-rich hydrophobic domain 2 [Source:HGNC Symbol;Acc:1935]
1560060_s_at	VPS37C	ENSG00000167987	0.054133	0.5575703	8.463034	7.905464	11	q12.2	vacuolar protein sorting 37 homolog C (S. cerevisiae) [Source:HGNC Symbol;Acc:26097]
217947_at	CMTM6	ENSG00000091317	0.054172	0.7023048	10.47748	9.775178	3	p22.3	CKLF-like MARVEL transmembrane domain containing 6 [Source:HGNC Symbol;Acc:19177]
219078_at	GPATCH2	ENSG00000092978	0.054197	0.9518562	7.045736	6.09388	1	q41	G patch domain containing 2 [Source:HGNC Symbol;Acc:25499]
203854_at	CFI	ENSG00000205403	0.054292	1.2057395	6.704059	5.49832	4	q25	complement factor I [Source:HGNC Symbol;Acc:5394]
209637_s_at	RG512	ENSG00000159788	0.054328	0.5021003	7.515978	7.013877	4	p16.3	regulator of G-protein signaling 12 [Source:HGNC Symbol;Acc:9994]
202252_at	RAB13	ENSG00000143545	0.05435	0.9137575	9.579586	8.665828	1	q21.3	RAB13, member RAS oncogene family [Source:HGNC Symbol;Acc:9762]
227373_at	ATXN1L	ENSG00000224470	0.05435	0.7597165	8.404084	7.644368	16	q22.2	ataxin 1-like [Source:HGNC Symbol;Acc:33279]
207469_s_at	PIR	ENSG00000087842	0.05446	0.663779	6.265059	5.60128	X	p22.2	pirin (iron-binding nuclear protein) [Source:HGNC Symbol;Acc:30048]
212543_at	AIM1	ENSG00000112297	0.054464	0.7881191	9.68228	8.894161	6	q21	absent in melanoma 1 [Source:HGNC Symbol;Acc:356]
208983_s_at	PECAM1	NA	0.054524	1.305077	10.69254	9.387459	NA	NA	NA
226438_at	SNTB1	ENSG00000172164	0.054649	0.8096096	6.953942	6.144333	8	q24.12	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) [Source:HGNC Symbol;Acc:11168]
201567_s_at	GOLGA4	ENSG00000144674	0.054737	0.5440613	8.834092	8.29003	3	p22.2	golgin A4 [Source:HGNC Symbol;Acc:4427]
204520_x_at	BRD1	ENSG00000100425	0.054846	0.4383699	9.00874	8.57037	22	q13.33	bromodomain containing 1 [Source:HGNC Symbol;Acc:1102]
217828_at	SLTM	ENSG00000137776	0.054846	0.8307026	8.864809	8.034107	15	q22.1	SAFB-like, transcription modulator [Source:HGNC Symbol;Acc:20709]
224689_at	MANBAL	ENSG00000101363	0.054846	0.3402156	9.457076	9.11686	20	q11.23	mannosidase, beta A, lysosomal-like [Source:HGNC Symbol;Acc:15799]
219157_at	KLHL2	ENSG00000109466	0.054893	0.6367528	8.271661	7.634908	4	q32.3	kelch-like family member 2 [Source:HGNC Symbol;Acc:6353]
232024_at	GIMAP2	ENSG00000106560	0.05502	1.1621322	7.593743	6.431611	7	q36.1	GTPase, IMAP family member 2 [Source:HGNC Symbol;Acc:21789]
219087_at	ASPN	ENSG00000106819	0.055081	1.8444311	7.912112	6.067681	9	q22.31	asporin [Source:HGNC Symbol;Acc:14872]
213010_at	PRKCDBP	ENSG00000170955	0.055081	0.6667374	7.157466	6.490729	11	p15.4	protein kinase C, delta binding protein [Source:HGNC Symbol;Acc:9400]
219570_at	KIF16B	ENSG00000089177	0.055081	0.9395247	6.792996	5.853471	20	p12.1	kinesin family member 16B [Source:HGNC Symbol;Acc:15869]
214066_x_at	NPR2	ENSG00000159899	0.055081	0.4995605	7.871515	7.371954	9	p13.3	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B) [Source:HGNC Symbol;Acc:7944]
228372_at	C10orf128	ENSG00000204161	0.055081	1.2282534	8.331788	7.103535	10	q11.23	chromosome 10 open reading frame 128 [Source:HGNC Symbol;Acc:27274]
230276_at	FAM49A	ENSG00000197872	0.055081	1.2864889	6.31294	5.026451	2	p24.2	family with sequence similarity 49, member A [Source:HGNC Symbol;Acc:25373]
203002_at	AMOTL2	ENSG00000114019	0.055081	1.3811705	7.607053	6.225883	3	q22.2	angiomotin like 2 [Source:HGNC Symbol;Acc:17812]
225688_s_at	PHLDB2	ENSG00000144824	0.055081	1.6421107	7.415402	5.773291	3	q13.2	pleckstrin homology-like domain, family B, member 2 [Source:HGNC Symbol;Acc:29573]
1553678_a_at	ITGB1	ENSG00000150093	0.055081	0.7623281	9.604847	8.842519	10	p11.22	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) [Source:HGNC Symbol;Acc:6153]
203476_at	TPBG	ENSG00000146242	0.055081	1.4028702	8.397859	6.994989	6	q14.1	trophoblast glycoprotein [Source:HGNC Symbol;Acc:12004]
201180_s_at	GNAI3	ENSG00000065135	0.055081	0.7164849	9.753543	9.037058	1	p13.3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 [Source:HGNC Symbol;Acc:4387]
220141_at	C11orf63	ENSG00000109944	0.055081	0.5302891	5.631726	5.101437	11	q24.1	chromosome 11 open reading frame 63 [Source:HGNC Symbol;Acc:26288]
227923_at	SHANK3	ENSG00000251322	0.055081	1.1756261	7.738818	6.563191	22	q13.33	SH3 and multiple ankyrin repeat domains 3 [Source:HGNC Symbol;Acc:14294]
235334_at	ST6GALNAC3	ENSG00000184005	0.055081	0.8325709	5.744061	4.91149	1	p31.1	ST6 (alpha-N-acetyl-neuraminy)-2,3-beta-galactosyl-1,3)-N-acetylglactosaminide alpha-2,6-sialyltransferase 3 [Source:HGNC Symbol;Acc:19343]
235411_at	PGBD1	ENSG00000137338	0.055081	0.4549063	5.741778	5.286872	6	p22.1	piggyBac transposable element derived 1 [Source:HGNC Symbol;Acc:19398]
216689_x_at	ARHGAP1	ENSG00000175220	0.055086	0.5210108	9.747526	9.226515	11	p11.2	Rho GTPase activating protein 1 [Source:HGNC Symbol;Acc:673]

202932_at	YES1	ENSG00000176105	0.055086	1.2124045	6.25973	5.047325	18	p11.32	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 [Source:HGNC Symbol;Acc:12841]
212293_at	HIPK1	ENSG00000163349	0.055095	0.6908166	7.914422	7.223606	1	p13.2	homeodomain interacting protein kinase 1 [Source:HGNC Symbol;Acc:19006]
225618_at	ARHGAP27	ENSG00000159314	0.055334	0.4730209	7.935837	7.462816	17	q21.31	Rho GTPase activating protein 27 [Source:HGNC Symbol;Acc:31813]
201242_s_at	ATP1B1	ENSG00000143153	0.055334	1.2831495	7.126474	5.843325	1	q24.2	ATPase, sodium-transporting, beta 1 polypeptide [Source:HGNC Symbol;Acc:804]
203583_at	UNC50	ENSG00000115446	0.055334	0.4527831	8.989706	8.536923	2	q11.2	unc-50 homolog (C. elegans) [Source:HGNC Symbol;Acc:16046]
1557938_s_at	PTRF	ENSG00000177469	0.055334	0.8943521	8.2614	7.367048	17	q21.2	polymerase I and transcript release factor [Source:HGNC Symbol;Acc:9688]
242321_at	PTPN14	ENSG00000152104	0.055342	1.3269817	5.787995	4.461014	1	q41	protein tyrosine phosphatase, non-receptor type 14 [Source:HGNC Symbol;Acc:9647]
212950_at	GPR116	ENSG00000069122	0.055342	1.4662875	6.762014	5.295727	6	p12.3	G protein-coupled receptor 116 [Source:HGNC Symbol;Acc:19030]
205639_at	AOAH	ENSG00000136250	0.055342	0.6545201	9.612123	8.957603	7	p14.2	acyloxyacyl hydrolase (neutrophil) [Source:HGNC Symbol;Acc:548]
223209_s_at	VIMP	ENSG00000131871	0.055342	0.8381324	9.523564	8.685432	15	q26.3	VCP-interacting membrane protein [Source:HGNC Symbol;Acc:30396]
208131_s_at	PTGIS	ENSG00000124212	0.055389	1.3212	7.49094	6.16974	20	q13.13	prostaglandin I2 (prostacyclin) synthase [Source:HGNC Symbol;Acc:9603]
227833_s_at	MBD6	ENSG00000166987	0.055397	0.7519226	10.5182	9.766277	12	q13.3	methyl-CpG binding domain protein 6 [Source:HGNC Symbol;Acc:20445]
208991_at	STAT3	ENSG00000168610	0.055397	0.946587	9.530425	8.583838	17	q21.2	signal transducer and activator of transcription 3 (acute-phase response factor) [Source:HGNC Symbol;Acc:11364]
216361_s_at	KAT6A	ENSG00000083168	0.055397	0.6517457	7.927872	7.276126	8	p11.21	K(lysine) acetyltransferase 6A [Source:HGNC Symbol;Acc:13013]
1554106_at	NBEAL1	ENSG00000144426	0.055397	0.6619161	7.462248	6.800332	2	q33.2	neurobeachin-like 1 [Source:HGNC Symbol;Acc:20681]
209357_at	CITED2	ENSG00000164442	0.055397	1.2323825	9.303495	8.071112	6	q24.1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 [Source:HGNC Symbol;Acc:1987]
53720_at	C19orf66	ENSG00000130813	0.055432	0.9673751	9.679982	8.712607	19	p13.2	chromosome 19 open reading frame 66 [Source:HGNC Symbol;Acc:25649]
228964_at	PRDM1	ENSG00000057657	0.055432	1.9550529	9.250668	7.295615	6	q21	PR domain containing 1, with ZNF domain [Source:HGNC Symbol;Acc:9346]
228624_at	TMEM144	ENSG00000164124	0.055512	0.8881157	6.820513	5.932397	4	q32.1	transmembrane protein 144 [Source:HGNC Symbol;Acc:25633]
225626_at	PAG1	ENSG00000076641	0.055625	1.6483207	9.726492	8.078172	8	q21.13	phosphoprotein associated with glycosphingolipid microdomains 1 [Source:HGNC Symbol;Acc:30043]
225885_at	EEA1	ENSG00000102189	0.055625	0.7278215	7.739963	7.012141	12	q22	early endosome antigen 1 [Source:HGNC Symbol;Acc:3185]
236172_at	LTB4R	ENSG00000213903	0.055654	1.0840457	7.387481	6.303435	14	q12	leukotriene B4 receptor [Source:HGNC Symbol;Acc:6713]
201953_at	CIB1	ENSG00000185043	0.055677	0.7092542	9.414667	8.705413	15	q26.1	calcium and integrin binding 1 (calmyrin) [Source:HGNC Symbol;Acc:16920]
213069_at	HEG1	ENSG00000173706	0.055677	1.0582971	9.011754	7.953457	3	q21.2	heart development protein with EGF-like domains 1 [Source:HGNC Symbol;Acc:29227]
226885_at	RNF217	ENSG00000146373	0.055688	1.5079517	5.917911	4.409959	6	q22.31	ring finger protein 217 [Source:HGNC Symbol;Acc:21487]
203038_at	PTPRK	ENSG00000152894	0.055688	1.5495332	8.029703	6.48017	6	q22.33	protein tyrosine phosphatase, receptor type, K [Source:HGNC Symbol;Acc:9674]
240703_s_at	HERC1	ENSG00000103657	0.0557	0.9617872	6.445278	5.483491	15	q22.31	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1 [Source:HGNC Symbol;Acc:4867]
221641_s_at	ACOT9	ENSG00000123130	0.055792	0.5924097	9.037041	8.444631	X	p22.11	acyl-CoA thioesterase 9 [Source:HGNC Symbol;Acc:17152]
210845_s_at	PLAUR	ENSG0000011422	0.055813	0.9963797	8.866071	7.869692	19	q13.31	plasminogen activator, urokinase receptor [Source:HGNC Symbol;Acc:9053]
212097_at	CAV1	ENSG00000105974	0.055813	1.7271465	8.888796	7.16165	7	q31.2	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;Acc:1527]
243198_at	TEX9	ENSG00000151575	0.055813	1.5584665	6.115528	4.557062	15	q21.3	testis expressed 9 [Source:HGNC Symbol;Acc:29585]
204122_at	TYROBP	ENSG00000011600	0.055813	1.1533455	11.48996	10.33661	19	q13.12	TYRO protein tyrosine kinase binding protein [Source:HGNC Symbol;Acc:12449]
226343_at	DPP8	ENSG00000074603	0.055813	0.6675677	8.292782	7.625214	15	q22.31	dipeptidyl-peptidase 8 [Source:HGNC Symbol;Acc:16490]
205715_at	BST1	ENSG00000109743	0.056096	0.3449558	7.186266	6.84131	4	p15.32	bone marrow stromal cell antigen 1 [Source:HGNC Symbol;Acc:1118]
211980_at	COL4A1	ENSG00000187498	0.056096	1.2236466	10.90018	9.676529	13	q34	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
213572_s_at	SERPINB1	ENSG00000021355	0.056096	0.8525835	9.44718	8.594597	6	p25.2	serpin peptidase inhibitor, clade B (ovalbumin), member 1 [Source:HGNC Symbol;Acc:3311]
209047_at	AQP1	ENSG00000240583	0.056096	1.7116894	8.767181	7.055491	7	p14.3	aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc:633]
214077_x_at	MEIS3P1	ENSG00000179277	0.056096	0.9245864	8.655448	7.730862	17	p12	Meis homeobox 3 pseudogene 1 [Source:HGNC Symbol;Acc:7002]
202946_s_at	BTBD3	ENSG00000132640	0.056282	1.0081645	5.025902	4.017738	20	p12.2	BTB (POZ) domain containing 3 [Source:HGNC Symbol;Acc:15854]

242953_at	ZNF234	ENSG00000263002	0.056316	0.8636423	6.410969	5.547327	19	q13.31	zinc finger protein 234 [Source:HGNC Symbol;Acc:13027]
218380_at	LOC728392	NA	0.056643	0.6598628	8.050296	7.390433	NA	NA	NA
215000_s_at	FEZ2	ENSG00000171055	0.056643	0.8955219	9.749837	8.854315	2	p22.2	fasciculation and elongation protein zeta 2 (zyglin II) [Source:HGNC Symbol;Acc:3660]
229238_at	C17orf97	ENSG00000187624	0.056643	0.7936262	7.026858	6.233231	17	p13.3	chromosome 17 open reading frame 97 [Source:HGNC Symbol;Acc:33800]
219700_at	PLXDC1	ENSG00000161381	0.056643	1.3037293	7.282377	5.978648	17	q12	plexin domain containing 1 [Source:HGNC Symbol;Acc:20945]
202432_at	PPP3CB	ENSG00000107758	0.056855	0.5946658	8.65429	8.059624	10	q22.2	protein phosphatase 3, catalytic subunit, beta isoform [Source:HGNC Symbol;Acc:9315]
1558711_at	FAM13A-AS1	ENSG00000248019	0.056858	0.6634859	6.443456	5.77997	4	q22.1	FAM13A antisense RNA 1 [Source:HGNC Symbol;Acc:19370]
202304_at	FNDC3A	ENSG00000102531	0.056858	0.9582776	8.951197	7.992919	13	q14.2	fibronectin type III domain containing 3A [Source:HGNC Symbol;Acc:20296]
213429_at	BICC1	ENSG00000122870	0.056858	1.4554356	5.911437	4.456001	10	q21.1	bicaudal C homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:19351]
203388_at	ARRB2	ENSG00000141480	0.056858	0.7900371	8.830551	8.040514	17	p13.2	arrestin, beta 2 [Source:HGNC Symbol;Acc:712]
205140_at	FPGT	ENSG00000254685	0.056863	0.7461301	7.424392	6.678262	1	p31.1	fucose-1-phosphate guanylyltransferase [Source:HGNC Symbol;Acc:3825]
226594_at	ENTPD5	ENSG00000187097	0.056942	0.5571412	7.324717	6.767575	14	q24.3	ectonucleoside triphosphate diphosphohydrolase 5 [Source:HGNC Symbol;Acc:3367]
219506_at	C1orf54	ENSG00000118292	0.056942	1.1443229	10.50282	9.358498	1	q21.2	chromosome 1 open reading frame 54 [Source:HGNC Symbol;Acc:26258]
209230_s_at	NUPR1	ENSG00000176046	0.056997	1.1081006	11.12844	10.02034	16	p11.2	nuclear protein, transcriptional regulator, 1 [Source:HGNC Symbol;Acc:29990]
205498_at	GHR	ENSG00000112964	0.057095	1.3991555	5.181886	3.782731	5	p13.1	growth hormone receptor [Source:HGNC Symbol;Acc:4263]

[00351]

TABLE 2

probeset	gene_symbol	ensembl_id	q.value	logFC	mean_nonRef	mean_Ref	Chromosome	chrom_band	gene_description
230325_at	LOC100133985	NA	0.00809665	-0.911640912	5.838505821	6.750146733	NA	NA	NA
231463_at	CNTD1	ENSG00000176563	0.008351401	-0.538973445	3.84343028	4.382403725	17	q21.31	cyclin N-terminal domain containing 1 [Source:HGNC Symbol;Acc:26847]
1558844_at	LOC100506127	NA	0.009456042	-0.617533967	6.109066414	6.726600381	NA	NA	NA
1559507_at	LOC100130357	NA	0.009950302	-0.519619931	5.450658035	5.970277966	NA	NA	NA
229378_at	STOX1	ENSG00000165730	0.011768387	-0.593708902	3.913537756	4.507246657	10	q21.3	storkhead box 1 [Source:HGNC Symbol;Acc:23508]
207965_at	NEUROG3	ENSG00000122859	0.012330232	-0.438710752	7.869470101	8.308180853	10	q22.1	neurogenin 3 [Source:HGNC Symbol;Acc:13806]
1552349_a_at	PRSS33	ENSG00000103355	0.013773579	-0.538188858	5.578662199	6.116851057	16	p13.3	protease, serine, 33 [Source:HGNC Symbol;Acc:30405]
1566134_at	CARHSP1	ENSG00000153048	0.014454348	-0.556432401	6.9668382	7.523270601	16	p13.2	calcium regulated heat stable protein 1, 24kDa [Source:HGNC Symbol;Acc:17150]
206602_s_at	HOXD3	ENSG00000128652	0.016154072	-0.644932774	6.906842818	7.551775592	2	q31.1	homeobox D3 [Source:HGNC Symbol;Acc:5137]
236374_at	CTXN3	ENSG00000205279	0.016166047	-0.525752287	4.906041398	5.431793686	5	q23.2	cortexin 3 [Source:HGNC Symbol;Acc:31110]
1560963_a_at	LOC100506379	NA	0.016166613	-0.647132124	5.446495421	6.093627545	NA	NA	NA
1553837_at	PGAM5	ENSG00000247077	0.016166613	-0.466015193	6.896008593	7.362023785	12	q24.33	phosphoglycerate mutase family member 5 [Source:HGNC Symbol;Acc:28763]
1554763_at	UBE2DNL	ENSG00000229547	0.016166613	-0.423010772	5.56336289	5.986373662	X	q21.1	ubiquitin-conjugating enzyme E2D N-terminal like (pseudogene) [Source:HGNC Symbol;Acc:28656]
219840_s_at	TCL6	ENSG00000187621	0.016166613	-1.34245305	4.185464373	5.527917423	14	q32.13	T-cell leukemia/lymphoma 6 (non-protein coding) [Source:HGNC Symbol;Acc:13463]
222896_at	TMEM38A	ENSG00000072954	0.016166613	-0.778177457	6.257085542	7.035262999	19	p13.11	transmembrane protein 38A [Source:HGNC Symbol;Acc:28462]
205688_at	TFAP4	ENSG00000090447	0.016166613	-0.616680115	7.99573016	8.612410275	16	p13.3	transcription factor AP-4 (activating enhancer binding protein 4) [Source:HGNC Symbol;Acc:11745]
1557021_s_at	LOC100507250	NA	0.016166613	-0.767424763	6.40032636	7.167751123	NA	NA	NA
237880_at	LOC100506457	NA	0.016166613	-0.776375557	6.296009341	7.072384898	NA	NA	NA
210450_at	IGHV5-78	ENSG00000211978	0.016166613	-0.929279909	5.444682435	6.373962344	14	q32.33	immunoglobulin heavy variable 5-78 (pseudogene) [Source:HGNC Symbol;Acc:5660]
1570336_at	BDH1	ENSG00000161267	0.016166613	-0.600927396	5.439307091	6.040234486	3	q29	3-hydroxybutyrate dehydrogenase, type 1 [Source:HGNC Symbol;Acc:1027]
219076_s_at	PXMP2	ENSG00000176894	0.016166613	-0.603766933	7.746523407	8.35029034	12	q24.33	peroxisomal membrane protein 2, 22kDa [Source:HGNC Symbol;Acc:9716]
230467_at	TMEM52	ENSG00000178821	0.016166613	-0.547705024	5.782176283	6.329881307	1	p36.33	transmembrane protein 52 [Source:HGNC Symbol;Acc:27916]
207689_at	TBX10	ENSG00000167800	0.016166613	-0.58354262	5.120413125	5.703955745	11	q13.2	T-box 10 [Source:HGNC Symbol;Acc:11593]
210165_at	DNASE1	ENSG00000213918	0.0170385	-0.638225732	6.797117147	7.435342879	16	p13.3	deoxyribonuclease I [Source:HGNC Symbol;Acc:2956]
1558431_at	NHLRC4	ENSG00000257108	0.017271459	-0.440024521	7.110293049	7.55031757	16	p13.3	NHL repeat containing 4 [Source:HGNC Symbol;Acc:26700]
210122_at	PRM2	ENSG00000122304	0.017305066	-0.594945443	6.297604855	6.892550298	16	p13.13	protamine 2 [Source:HGNC Symbol;Acc:9448]
1569270_at	LOC100134368	NA	0.017653225	-0.524095679	4.998433733	5.522529412	NA	NA	NA
232781_at	LHX4	ENSG00000121454	0.017653225	-0.471163014	6.387893416	6.859056431	1	q25.2	LIM homeobox 4 [Source:HGNC Symbol;Acc:21734]
206151_x_at	CELA3B	ENSG00000219073	0.0179046	-0.389566615	6.698451608	7.088018223	1	p36.12	chymotrypsin-like elastase family, member 3B [Source:HGNC Symbol;Acc:15945]
1553780_at	LINC00638	ENSG00000258701	0.0179681	-0.442959091	5.985279128	6.428238219	14	q32.33	long intergenic non-protein coding RNA 638 [Source:HGNC Symbol;Acc:28325]
1564386_at	TXNDC8	ENSG00000204193	0.018383789	-0.402808114	4.569887895	4.972696009	9	q31.3	thioredoxin domain containing 8 (spermatozoa) [Source:HGNC Symbol;Acc:31454]
207116_s_at	GAPDH5	ENSG00000105679	0.018896313	-0.439395893	6.265814968	6.705210861	19	q13.12	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic

									[Source:HGNC Symbol;Acc:24864]
1552564_at	NUDT9P1	NA	0.018901839	-0.627097479	5.209804097	5.836901576	NA	NA	NA
1552811_at	WFIKN1	ENSG00000127578	0.018901839	-0.407943586	7.383936771	7.791880357	16	p13.3	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 1 [Source:HGNC Symbol;Acc:30912]
244543_s_at	BCDIN3D-AS1	ENSG00000258057	0.018901839	-0.517606933	6.104813842	6.622420775	12	q13.12	BCDIN3D antisense RNA 1 [Source:HGNC Symbol;Acc:44113]
1555124_at	LOC100129726	NA	0.018901839	-0.737667282	6.31928006	7.056947342	NA	NA	NA
1553541_at	LMX1A	ENSG00000162761	0.018921376	-0.477745764	4.729705201	5.207450965	1	q23.3	LIM homeobox transcription factor 1, alpha [Source:HGNC Symbol;Acc:6653]
1553178_a_at	SSTR3	ENSG00000183473	0.019065055	-0.49695403	6.605956381	7.10291041	22	q13.1	somatostatin receptor 3 [Source:HGNC Symbol;Acc:11332]
1558289_at	RFT1	ENSG00000163933	0.019506232	-0.356946278	6.437355142	6.794301421	3	p21.1	RFT1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:30220]
208034_s_at	PROZ	ENSG00000126231	0.019879747	-0.413177596	7.086538428	7.499716024	13	q34	protein Z, vitamin K-dependent plasma glycoprotein [Source:HGNC Symbol;Acc:9460]
1553444_a_at	C1orf127	ENSG00000175262	0.019879747	-0.456161699	7.310783447	7.766945146	1	p36.22	chromosome 1 open reading frame 127 [Source:HGNC Symbol;Acc:26730]
220077_at	CCDC134	ENSG00000100147	0.019879747	-0.431568198	7.194190518	7.625758716	22	q13.2	coiled-coil domain containing 134 [Source:HGNC Symbol;Acc:26185]
215756_at	LOC730227	NA	0.019879747	-0.466760373	5.640296789	6.107057162	NA	NA	NA
242226_at	LOC100288079	NA	0.019879747	-0.466011928	4.501905981	4.967917909	NA	NA	NA
207159_x_at	CRTC1	ENSG00000105662	0.019974794	-0.342848645	8.582700549	8.925549194	19	p13.11	CREB regulated transcription coactivator 1 [Source:HGNC Symbol;Acc:16062]
1564072_at	MYH16	ENSG00000002079	0.020133959	-0.513849511	5.117985644	5.631835155	7	q22.1	myosin, heavy chain 16 pseudogene [Source:HGNC Symbol;Acc:31038]
206112_at	ANKRD7	ENSG00000106013	0.020139089	-0.584007767	3.631160633	4.2151684	7	q31.31	ankyrin repeat domain 7 [Source:HGNC Symbol;Acc:18588]
244488_at	LSM14B	ENSG00000149657	0.020139089	-0.471204404	5.404535566	5.87573997	20	q13.33	LSM14B, SCD6 homolog B (S. cerevisiae) [Source:HGNC Symbol;Acc:15887]
243022_at	LOC100506631	NA	0.020691131	-0.472548595	6.586231468	7.058780063	NA	NA	NA
223630_at	C7orf13	ENSG00000244291	0.021317074	-0.621418392	6.683076994	7.304495386	7	q36.3	chromosome 7 open reading frame 13 [Source:HGNC Symbol;Acc:17126]
207366_at	KCNS1	ENSG00000124134	0.021317074	-0.522556921	5.734453296	6.257010217	20	q13.12	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 1 [Source:HGNC Symbol;Acc:6300]
1569532_a_at	LCN15	ENSG00000177984	0.021317074	-0.463360876	6.730953106	7.194313982	9	q34.3	lipocalin 15 [Source:HGNC Symbol;Acc:33777]
208291_s_at	TH	ENSG00000180176	0.02166097	-0.435400549	5.849357981	6.284758531	11	p15.5	tyrosine hydroxylase [Source:HGNC Symbol;Acc:11782]
239119_at	DNAJC3-AS1	ENSG00000247400	0.022611564	-0.889794242	6.485868079	7.375662321	13	q32.1	DNAJC3 antisense RNA 1 (head to head) [Source:HGNC Symbol;Acc:39808]
240185_at	LOC100147773	NA	0.022611564	-0.498977477	7.370697097	7.869674574	NA	NA	NA
233843_at	ZBTB12	ENSG00000204366	0.022611564	-0.519742752	7.218271617	7.738014369	6	p21.33	zinc finger and BTB domain containing 12 [Source:HGNC Symbol;Acc:19066]
1555722_at	SCAMPER	NA	0.022732168	-0.334308255	3.6043183	3.938626555	NA	NA	NA
1553067_a_at	GNRHR2	ENSG00000211451	0.022732168	-0.649001368	7.399753955	8.048755323	1	q21.1	gonadotropin-releasing hormone (type 2) receptor 2 [Source:HGNC Symbol;Acc:16341]
238898_at	LOC101060264	NA	0.023506064	-1.193505286	5.871655735	7.065161021	NA	NA	NA
224166_at	SLC25A2	ENSG00000120329	0.023531188	-0.439944142	4.676270398	5.11621454	5	q31.3	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 2 [Source:HGNC Symbol;Acc:22921]
238239_at	WDR27	ENSG00000184465	0.023677408	-0.865615668	5.475660628	6.341276295	6	q27	WD repeat domain 27 [Source:HGNC Symbol;Acc:21248]
1562089_at	GLYATL1	ENSG00000166840	0.023677408	-0.494191579	3.390583969	3.884775548	11	q12.1	glycine-N-acyltransferase-like 1 [Source:HGNC Symbol;Acc:30519]
207649_at	KRT37	ENSG00000108417	0.023800085	-0.376179216	5.023738968	5.399918184	17	q21.2	keratin 37 [Source:HGNC Symbol;Acc:6455]
1559272_at	EXOC3L1	ENSG00000179044	0.023800085	-0.4129202	8.165645994	8.578566194	16	q22.1	exocyst complex component 3-like 1 [Source:HGNC Symbol;Acc:27540]

1556822_s_at	ZNF837	ENSG00000152475	0.023800085	-0.480490017	6.346952069	6.827442086	19	q13.43	zinc finger protein 837 [Source:HGNC Symbol;Acc:25164]
215328_at	EFR3B	ENSG00000084710	0.023922328	-0.703597987	6.556203567	7.259801553	2	p23.3	EFR3 homolog B {S. cerevisiae} [Source:HGNC Symbol;Acc:29155]
1552932_at	NLRP6	ENSG00000174885	0.024111993	-0.452619884	6.55831599	7.010935874	11	p15.5	NLR family, pyrin domain containing 6 [Source:HGNC Symbol;Acc:22944]

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[00352]

TABLE 3

probeset	gene_ symbol	ensembl_id	q.value	logFC	mean_ nonRef	mean_ Ref	Chromo- some	chrom_ band	gene_description
228754_at	SLC6A6	ENSG00000131389	0	0.975480525	8.981006333	8.005525809	3	p25.1	solute carrier family 6 (neurotransmitter transporter, taurine), member 6 [Source:HGNC Symbol;Acc:11052]
238327_at	ODF38	ENSG00000177989	0.002730266	1.030411696	8.897771439	7.867359743	22	q13.33	outer dense fiber of sperm tails 38 [Source:HGNC Symbol;Acc:34388]
208683_at	CAPN2	ENSG00000162909	0.002730266	2.05913862	9.820197872	7.761059252	1	q41	calpain 2, (m/ii) large subunit [Source:HGNC Symbol;Acc:1479]
218648_at	CRTC3	ENSG00000140577	0.002730266	1.393257272	9.008043592	7.614786319	15	q26.1	CREB regulated transcription coactivator 3 [Source:HGNC Symbol;Acc:26148]
225146_at	FAM219A	ENSG00000164970	0.002730266	0.795746694	8.091945884	7.29619919	9	p13.3	family with sequence similarity 219, member A [Source:HGNC Symbol;Acc:19920]
218589_at	LPAR6	ENSG00000139679	0.002730266	2.422573482	9.17966374	6.757090257	13	q14.2	lysophosphatidic acid receptor 6 [Source:HGNC Symbol;Acc:15520]
217762_s_at	RAB31	ENSG00000168461	0.002730266	1.749576112	10.13226893	8.382692819	18	p11.22	RAB31, member RAS oncogene family [Source:HGNC Symbol;Acc:9771]
201506_at	TGFB1	ENSG00000120708	0.002730266	1.805547727	11.48439996	9.67885223	5	q31.1	transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:11771]
224862_at	GNAQ	ENSG00000156052	0.002730266	2.025363394	6.970609713	4.945246318	9	q21.2	guanine nucleotide binding protein (G protein), q polypeptide [Source:HGNC Symbol;Acc:4390]
201425_at	ALDH2	ENSG00000111275	0.002730266	1.929378657	10.6016455	8.672266847	12	q24.12	aldehyde dehydrogenase 2 family (mitochondrial) [Source:HGNC Symbol;Acc:404]
1555851_s_at	SEPW1	ENSG00000178980	0.003120304	1.533124384	10.54941655	9.016292166	19	q13.33	selenoprotein W, 1 [Source:HGNC Symbol;Acc:10752]
205241_at	SCO2	ENSG00000130489	0.003120304	0.892011788	9.145278369	8.25326658	22	q13.33	SCO2 cytochrome c oxidase assembly protein [Source:HGNC Symbol;Acc:10604]
218552_at	ECHDC2	ENSG00000121310	0.003120304	1.335313564	9.234133085	7.89881952	1	p32.3	enoyl CoA hydratase domain containing 2 [Source:HGNC Symbol;Acc:23408]
55662_at	C10orf76	ENSG00000120029	0.003120304	0.721271142	8.212153422	7.49088228	10	q24.32	chromosome 10 open reading frame 76 [Source:HGNC Symbol;Acc:25788]
204773_at	IL11RA	ENSG00000137070	0.004436682	0.917390241	7.610982979	6.693592738	9	p13.3	interleukin 11 receptor, alpha [Source:HGNC Symbol;Acc:5967]
202600_s_at	NRIP1	ENSG00000180530	0.004436682	1.662365975	7.56245491	5.900088935	21	q21.1	nuclear receptor interacting protein 1 [Source:HGNC Symbol;Acc:8001]
221802_s_at	KIAA1598	ENSG00000187164	0.004818116	1.88945627	8.343765469	6.454309199	10	q25.3	KIAA1598 [Source:HGNC Symbol;Acc:29319]
226000_at	CTTNBP2NL	ENSG00000143079	0.005157169	1.467286291	7.674825326	6.207539034	1	p13.2	CTTNBP2 N-terminal like [Source:HGNC Symbol;Acc:25330]
222484_s_at	CXCL14	ENSG00000145824	0.005173135	3.461735657	11.01983085	7.55809519	5	q31.1	chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;Acc:10640]
201012_at	ANXA1	ENSG00000135046	0.005187505	1.868142161	10.78463604	8.916493883	9	q21.13	annexin A1 [Source:HGNC Symbol;Acc:533]
218854_at	DSE	ENSG00000111817	0.006453355	1.632134259	9.397392236	7.765257977	6	q22.1	dermatan sulfate epimerase [Source:HGNC Symbol;Acc:21144]
214040_s_at	GSN	ENSG00000148180	0.006453355	1.345118377	10.26280296	8.917684579	9	q33.2	gelsolin [Source:HGNC Symbol;Acc:4620]
201302_at	ANXA4	ENSG00000196975	0.006598142	1.701755825	9.377173828	7.675418003	2	p13.3	annexin A4 [Source:HGNC Symbol;Acc:542]
208923_at	CYFIP1	ENSG00000068793	0.006598142	1.418337073	9.308029118	7.889692045	15	q11.2	cytoplasmic FMR1 interacting protein 1 [Source:HGNC Symbol;Acc:13759]
224414_s_at	CARD6	ENSG00000132357	0.007207901	1.29867797	8.497051244	7.198373274	5	p13.1	caspase recruitment domain family, member 6 [Source:HGNC Symbol;Acc:16394]
205945_at	IL6R	ENSG00000160712	0.00809665	1.765992405	8.874117498	7.108125092	1	q21.3	interleukin 6 receptor [Source:HGNC Symbol;Acc:6019]
200765_x_at	CTNNA1	ENSG00000044115	0.00809665	1.117941552	9.630839898	8.512898346	5	q31.2	catenin (cadherin-associated protein), alpha 1, 102kDa

									[Source:HGNC Symbol;Acc:2509]
230325_at	LOC100133985	NA	0.00809665	0.911640912	5.838505821	6.750146733	NA	NA	NA
223228_at	LDOC1L	ENSG00000188636	0.00809665	1.239345994	8.444983654	7.20563766	22	q13.31	leucine zipper, down-regulated in cancer 1-like [Source:HGNC Symbol;Acc:13343]
225842_at	PHLDA1	ENSG00000139289	0.008190797	1.472675991	8.297710351	6.825034361	12	q21.2	pleckstrin homology-like domain, family A, member 1 [Source:HGNC Symbol;Acc:8933]
201348_at	GPX3	ENSG00000211445	0.008351401	2.169917885	11.32422224	9.154304357	5	q33.1	glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Acc:4555]
219885_at	SLFN12	ENSG00000172123	0.008351401	1.235153278	6.097789382	4.862636104	17	q12	schlafen family member 12 [Source:HGNC Symbol;Acc:25500]
212830_at	MEGF9	ENSG00000106780	0.008351401	1.243175161	6.734084575	5.490909414	9	q33.2	multiple EGF-like-domains 9 [Source:HGNC Symbol;Acc:3234]
231463_at	CNTD1	ENSG00000176563	0.008351401	0.538973445	3.84343028	4.382403725	17	q21.31	cyclin N-terminal domain containing 1 [Source:HGNC Symbol;Acc:26847]
202687_s_at	TNFSF10	ENSG00000121858	0.00842482	1.529352742	11.10527322	9.575920476	3	q26.31	tumor necrosis factor (ligand) superfamily, member 10 [Source:HGNC Symbol;Acc:11925]
217731_s_at	ITM2B	ENSG00000136156	0.009100886	1.449335477	10.05152822	8.602192738	13	q14.2	integral membrane protein 2B [Source:HGNC Symbol;Acc:6174]
218694_at	ARMCX1	ENSG00000126947	0.009456042	1.499155444	7.418731757	5.919576313	X	q22.1	armadillo repeat containing, X-linked 1 [Source:HGNC Symbol;Acc:18073]
1558844_at	LOC100506127	NA	0.009456042	0.617533967	6.109066414	6.726600381	NA	NA	NA
202944_at	NAGA	ENSG00000198951	0.009456042	0.994644426	8.604684413	7.610039987	22	q13.2	N-acetylgalactosaminidase, alpha- [Source:HGNC Symbol;Acc:7631]
212522_at	PDE8A	ENSG00000073417	0.009456042	1.212471343	8.751053401	7.538582058	15	q25.3	phosphodiesterase 8A [Source:HGNC Symbol;Acc:8793]
226247_at	PLEKHA1	ENSG00000107679	0.009456042	1.762189016	8.231589342	6.469400327	10	q26.13	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1 [Source:HGNC Symbol;Acc:14335]
243423_at	TNIP1	ENSG00000145901	0.009620936	1.039362698	6.139027011	5.099664313	5	q33.1	TNFAIP3 interacting protein 1 [Source:HGNC Symbol;Acc:16903]
229074_at	EHD4	ENSG00000103966	0.009950302	1.116796029	8.728408949	7.61161292	15	q15.1	EH-domain containing 4 [Source:HGNC Symbol;Acc:3245]
1559507_at	LOC100130357	NA	0.009950302	0.519619931	5.450658035	5.970277966	NA	NA	NA
222154_s_at	SPATS2L	ENSG00000196141	0.009950302	1.239839493	9.90915525	8.669315758	2	q33.1	spermatogenesis associated, serine-rich 2-like [Source:HGNC Symbol;Acc:24574]
200710_at	ACADVL	ENSG00000072778	0.011037244	0.872008393	9.456312268	8.584303875	17	p13.1	acyl-CoA dehydrogenase, very long chain [Source:HGNC Symbol;Acc:92]
228791_at	LOC100129502	NA	0.011037244	1.793891949	8.411266603	6.617374654	NA	NA	NA
208634_s_at	MACF1	ENSG00000127603	0.011768387	1.234625274	10.26299281	9.028367538	1	p34.3	microtubule-actin crosslinking factor 1 [Source:HGNC Symbol;Acc:13664]
242487_at	CC2D1B	ENSG00000154222	0.011768387	0.523814355	6.843606374	6.319792019	1	p32.3	coiled-coil and C2 domain containing 1B [Source:HGNC Symbol;Acc:29386]
218559_s_at	MAFB	ENSG00000204103	0.011768387	1.849122185	11.31545077	9.466328588	20	q12	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B [Source:HGNC Symbol;Acc:6408]
201360_at	CST3	ENSG00000101439	0.011768387	1.353324788	11.64386355	10.29053876	20	p11.21	cystatin C [Source:HGNC Symbol;Acc:2475]
206101_at	ECM2	ENSG00000106823	0.011768387	1.728608593	7.156510825	5.427902231	9	q22.31	extracellular matrix protein 2, female organ and adipocyte specific [Source:HGNC Symbol;Acc:3154]
218004_at	BSDC1	ENSG00000160058	0.011768387	0.541692248	8.948162166	8.406469918	1	p35.1	BSD domain containing 1 [Source:HGNC Symbol;Acc:25501]
36129_at	SGSM2	ENSG00000141258	0.011768387	0.893849973	9.480069571	8.586219598	17	p13.3	small G protein signaling modulator 2 [Source:HGNC Symbol;Acc:29026]
227889_at	LPCAT2	ENSG00000087253	0.011768387	1.982248155	7.953706021	5.971457866	16	q12.2	lysophosphatidylcholine acyltransferase 2 [Source:HGNC Symbol;Acc:26032]
229378_at	STOX1	ENSG00000165730	0.011768387	-	3.913537756	4.507246657	10	q21.3	storkhead box 1 [Source:HGNC Symbol;Acc:23508]

				0.593708902					
218043_s_at	AZI2	ENSG00000163512	0.011768387	0.863898887	6.644284515	5.780385627	3	p24.1	5-azacytidine induced 2 [Source:HGNC Symbol;Acc:24002]
218066_at	SLC12A7	ENSG00000113504	0.011768387	1.005344336	8.912722012	7.907377676	5	p15.33	solute carrier family 12 (potassium/chloride transporters), member 7 [Source:HGNC Symbol;Acc:10915]
58780_s_at	ARHGEF40	ENSG00000165801	0.011846577	1.485982141	7.235422011	5.74943987	14	q11.2	Rho guanine nucleotide exchange factor (GEF) 40 [Source:HGNC Symbol;Acc:25516]
200660_at	S100A11	ENSG00000163191	0.012330232	1.388286368	11.61065539	10.22236902	1	q21.3	S100 calcium binding protein A11 [Source:HGNC Symbol;Acc:10488]
207965_at	NEUROG3	ENSG00000122859	0.012330232	0.438710752	7.869470101	8.308180853	10	q22.1	neurogenin 3 [Source:HGNC Symbol;Acc:13806]
212907_at	SLC30A1	ENSG00000170385	0.012330232	1.171312069	9.350466514	8.179154445	1	q32.3	solute carrier family 30 (zinc transporter), member 1 [Source:HGNC Symbol;Acc:11012]
208999_at	SEPT8	ENSG00000164402	0.012827915	1.11339681	8.412742626	7.299345816	5	q31.1	septin 8 [Source:HGNC Symbol;Acc:16511]
208949_s_at	LGALS3	ENSG00000131981	0.012937259	1.466370381	11.76909335	10.30272297	14	q22.3	lectin, galactoside-binding, soluble, 3 [Source:HGNC Symbol;Acc:6563]
218311_at	MAP4K3	ENSG00000011566	0.012937259	1.467987958	7.560719009	6.092731052	2	p22.1	mitogen-activated protein kinase kinase kinase 3 [Source:HGNC Symbol;Acc:6865]
203518_at	LYST	ENSG00000143669	0.013773579	1.781389247	8.315307394	6.533918147	1	q42.3	lysosomal trafficking regulator [Source:HGNC Symbol;Acc:1968]
1552349_a_at	PRSS33	ENSG00000103355	0.013773579	0.538188858	5.578662199	6.116851057	16	p13.3	protease, serine, 33 [Source:HGNC Symbol;Acc:30405]
1566134_at	CARHSP1	ENSG00000153048	0.014454348	0.556432401	6.9668382	7.523270601	16	p13.2	calcium regulated heat stable protein 1, 24kDa [Source:HGNC Symbol;Acc:17150]
204137_at	GPR137B	ENSG00000077585	0.015679526	2.08875061	9.969766837	7.881016227	1	q42.3	G protein-coupled receptor 137B [Source:HGNC Symbol;Acc:11862]
222217_s_at	SLC27A3	ENSG00000143554	0.015679526	0.901664373	8.452290275	7.550625902	1	q21.3	solute carrier family 27 (fatty acid transporter), member 3 [Source:HGNC Symbol;Acc:10997]
201505_at	LAMB1	ENSG00000091136	0.015689414	1.834716085	9.325407825	7.490691739	7	q31.1	laminin, beta 1 [Source:HGNC Symbol;Acc:6486]
206602_s_at	HOXD3	ENSG00000128652	0.016154072	0.644932774	6.906842818	7.551775592	2	q31.1	homeobox D3 [Source:HGNC Symbol;Acc:5137]
217728_at	S100A6	ENSG00000197956	0.016157189	0.961802592	11.17652114	10.21471854	1	q21.3	S100 calcium binding protein A6 [Source:HGNC Symbol;Acc:10496]
225483_at	VPS26B	ENSG00000151502	0.016160221	0.731464309	8.008598811	7.277134503	11	q25	vacuolar protein sorting 26 homolog B (S. pombe) [Source:HGNC Symbol;Acc:28119]
202686_s_at	AXL	ENSG00000167601	0.016163173	2.164883727	9.749176136	7.584292409	19	q13.2	AXL receptor tyrosine kinase [Source:HGNC Symbol;Acc:905]
236374_at	CTXN3	ENSG00000205279	0.016166047	0.525752287	4.906041398	5.431793686	5	q23.2	cortixin 3 [Source:HGNC Symbol;Acc:31110]
227276_at	PLXDC2	ENSG00000120594	0.016166613	1.969191816	9.857934183	7.888742368	10	p12.31	plexin domain containing 2 [Source:HGNC Symbol;Acc:21013]
228185_at	ZNF25	ENSG00000175395	0.016166613	0.929397523	6.510839476	5.581441953	10	p11.1	zinc finger protein 25 [Source:HGNC Symbol;Acc:13043]
217892_s_at	LIMA1	ENSG00000050405	0.016166613	1.859321745	9.968366162	8.109044417	12	q13.12	LIM domain and actin binding 1 [Source:HGNC Symbol;Acc:24636]
202727_s_at	IFNGR1	ENSG00000027697	0.016166613	1.203322531	9.855227569	8.651905038	6	q23.3	interferon gamma receptor 1 [Source:HGNC Symbol;Acc:5439]
1560963_a_at	LOC100506379	NA	0.016166613	0.647132124	5.446495421	6.093627545	NA	NA	NA
1553837_at	PGAM5	ENSG00000247077	0.016166613	0.466015193	6.896008593	7.362023785	12	q24.33	phosphoglycerate mutase family member 5 [Source:HGNC Symbol;Acc:28763]
1554763_at	UBE2DNL	ENSG00000229547	0.016166613	0.423010772	5.56336289	5.986373662	X	q21.1	ubiquitin-conjugating enzyme E2D N-terminal like (pseudogene) [Source:HGNC Symbol;Acc:28656]
212112_s_at	STX12	ENSG00000117758	0.016166613	0.81158935	8.768046401	7.956457051	1	p35.3	syntaxin 12 [Source:HGNC Symbol;Acc:11430]
203789_s_at	SEMA3C	ENSG00000075223	0.016166613	1.826351818	6.85114482	5.024793002	7	q21.11	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C [Source:HGNC Symbol;Acc:10725]

200677_at	PTTG1IP	ENSG00000183255	0.016166613	0.944308232	10.81552238	9.871214144	21	q22.3	pituitary tumor-transforming 1 interacting protein [Source:HGNC Symbol;Acc:13524]
222876_s_at	ADAP2	ENSG00000184060	0.016166613	1.230284047	9.947909385	8.717625338	17	q11.2	ArfGAP with dual PH domains 2 [Source:HGNC Symbol;Acc:16487]
210145_at	PLA2G4A	ENSG00000116711	0.016166613	1.018586961	5.59768987	4.579102909	1	q31.1	phospholipase A2, group IVA (cytosolic, calcium-dependent) [Source:HGNC Symbol;Acc:9035]
208109_s_at	LINC00597	NA	0.016166613	1.252213786	6.056932621	4.804718835	NA	NA	NA
209651_at	TGFBI1	ENSG00000140682	0.016166613	1.639068946	8.383831001	6.744762056	16	p11.2	transforming growth factor beta 1 induced transcript 1 [Source:HGNC Symbol;Acc:11767]
212698_s_at	SEPT10	ENSG00000186522	0.016166613	2.029386612	6.787501727	4.758115114	2	q13	septin 10 [Source:HGNC Symbol;Acc:14349]
212526_at	SPG20	ENSG00000133104	0.016166613	1.308040982	6.974473237	5.666432255	13	q13.3	spastic paraplegia 20 (Troyer syndrome) [Source:HGNC Symbol;Acc:18514]
209684_at	RIN2	ENSG00000132669	0.016166613	1.948498746	9.250259854	7.301761108	20	p11.23	Ras and Rab interactor 2 [Source:HGNC Symbol;Acc:18750]
223204_at	FAM198B	ENSG00000164125	0.016166613	1.556704699	7.718116717	6.161412018	4	q32.1	family with sequence similarity 198, member B [Source:HGNC Symbol;Acc:25312]
200673_at	LAPTM4A	ENSG00000068697	0.016166613	1.052582957	10.80127759	9.748694636	2	p24.1	lysosomal protein transmembrane 4 alpha [Source:HGNC Symbol;Acc:6924]
219840_s_at	TCL6	ENSG00000187621	0.016166613	-1.34245305	4.185464373	5.527917423	14	q32.13	T-cell leukemia/lymphoma 6 (non-protein coding) [Source:HGNC Symbol;Acc:13463]
222896_at	TMEM38A	ENSG00000072954	0.016166613	0.778177457	6.257085542	7.035262999	19	p13.11	transmembrane protein 38A [Source:HGNC Symbol;Acc:28462]
205688_at	TFAP4	ENSG00000090447	0.016166613	0.616680115	7.99573016	8.612410275	16	p13.3	transcription factor AP-4 (activating enhancer binding protein 4) [Source:HGNC Symbol;Acc:11745]
225384_at	DOCK7	ENSG00000116641	0.016166613	0.820345036	7.335350684	6.515005648	1	p31.3	dedicator of cytokinesis 7 [Source:HGNC Symbol;Acc:19190]
1557021_s_at	LOC100507250	NA	0.016166613	0.767424763	6.40032636	7.167751123	NA	NA	NA
209210_s_at	FERMT2	ENSG00000073712	0.016166613	1.600225002	8.650583066	7.050358064	14	q22.1	fermitin family member 2 [Source:HGNC Symbol;Acc:15767]
201798_s_at	MYOF	ENSG00000138119	0.016166613	1.933721388	9.900889993	7.967168605	10	q23.33	myoferlin [Source:HGNC Symbol;Acc:3656]
225949_at	NRBP2	ENSG00000185189	0.016166613	1.197815793	8.229622618	7.031806824	8	q24.3	nuclear receptor binding protein 2 [Source:HGNC Symbol;Acc:19339]
208924_at	RNF11	ENSG00000123091	0.016166613	1.31265628	7.905885024	6.593228744	1	p32.3	ring finger protein 11 [Source:HGNC Symbol;Acc:10056]
209004_s_at	FBXL5	ENSG00000118564	0.016166613	1.083805753	10.00546225	8.921656499	4	p15.32	F-box and leucine-rich repeat protein 5 [Source:HGNC Symbol;Acc:13602]
237880_at	LOC100506457	NA	0.016166613	0.776375557	6.296009341	7.072384898	NA	NA	NA
226743_at	SLFN11	ENSG00000172716	0.016166613	1.653027622	8.752878393	7.09985077	17	q12	schlafen family member 11 [Source:HGNC Symbol;Acc:26633]
228573_at	ANTXR2	ENSG00000163297	0.016166613	1.223119076	6.502216851	5.279097776	4	q21.21	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
222065_s_at	FLII	ENSG00000177731	0.016166613	0.779423611	9.687503137	8.908079526	17	p11.2	flightless I homolog (Drosophila) [Source:HGNC Symbol;Acc:3750]
210450_at	IGHV5-78	ENSG00000211978	0.016166613	0.929279909	5.444682435	6.373962344	14	q32.33	immunoglobulin heavy variable 5-78 (pseudogene) [Source:HGNC Symbol;Acc:5660]
212989_at	SGMS1	ENSG00000198964	0.016166613	1.180434511	5.341958	4.161523489	10	q11.23	sphingomyelin synthase 1 [Source:HGNC Symbol;Acc:29799]
202228_s_at	NPTN	ENSG00000156642	0.016166613	1.131346073	9.703866415	8.572520342	15	q24.1	neuroplastin [Source:HGNC Symbol;Acc:17867]
227761_at	MYO5A	ENSG00000197535	0.016166613	1.47770878	8.28230981	6.80460103	15	q21.2	myosin VA (heavy chain 12, myoxin) [Source:HGNC Symbol;Acc:7602]
202133_at	WWTR1	ENSG00000018408	0.016166613	1.982540678	8.759155252	6.776614574	3	q25.1	WW domain containing transcription regulator 1 [Source:HGNC Symbol;Acc:24042]
209960_at	HGF	ENSG00000019991	0.016166613	1.216221253	4.738984711	3.522763458	7	q21.11	hepatocyte growth factor (hepatopoietin A; scatter factor) [Source:HGNC Symbol;Acc:4893]
212203_x_at	IFITM3	ENSG00000142089	0.016166613	0.999465366	12.83133036	11.83186499	11	p15.5	interferon induced transmembrane protein 3 [Source:HGNC

									Symbol;Acc:5414]
212158_at	SDC2	ENSG00000169439	0.016166613	1.694879284	8.399184386	6.704305102	8	q22.1	syndecan 2 [Source:HGNC Symbol;Acc:10659]
224797_at	ARRDC3	ENSG00000113369	0.016166613	1.280896615	7.049919874	5.769023259	5	q14.3	arrestin domain containing 3 [Source:HGNC Symbol;Acc:29263]
203124_s_at	SLC11A2	ENSG00000110911	0.016166613	1.314981642	8.210636812	6.895655171	12	q13.12	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 [Source:HGNC Symbol;Acc:10908]
1570336_at	BDH1	ENSG00000161267	0.016166613	0.600927396	5.439307091	6.040234486	3	q29	3-hydroxybutyrate dehydrogenase, type 1 [Source:HGNC Symbol;Acc:1027]
1553034_at	SDCCAG8	ENSG00000054282	0.016166613	0.647985397	7.598443667	6.95045827	1	q43	serologically defined colon cancer antigen 8 [Source:HGNC Symbol;Acc:10671]
219076_s_at	PXMP2	ENSG00000176894	0.016166613	0.603766933	7.746523407	8.35029034	12	q24.33	peroxisomal membrane protein 2, 22kDa [Source:HGNC Symbol;Acc:9716]
230467_at	TMEM52	ENSG00000178821	0.016166613	0.547705024	5.782176283	6.329881307	1	p36.33	transmembrane protein 52 [Source:HGNC Symbol;Acc:27916]
226111_s_at	ZNF385A	ENSG00000161642	0.016166613	1.061296407	9.529821659	8.468525252	12	q13.13	zinc finger protein 385A [Source:HGNC Symbol;Acc:17521]
231579_s_at	TIMP2	ENSG00000035862	0.016166613	1.950902389	11.29034402	9.339441627	17	q25.3	TIMP metalloproteinase inhibitor 2 [Source:HGNC Symbol;Acc:11821]
202007_at	NID1	ENSG00000116962	0.016166613	1.61713841	7.967907666	6.350769257	1	q42.3	nidogen 1 [Source:HGNC Symbol;Acc:7821]
207689_at	TBX10	ENSG00000167800	0.016166613	-0.58354262	5.120413125	5.703955745	11	q13.2	T-box 10 [Source:HGNC Symbol;Acc:11593]
201681_s_at	DLG5	ENSG00000151208	0.016381594	1.584354968	7.6803766	6.096021632	10	q22.3	discs, large homolog 5 (Drosophila) [Source:HGNC Symbol;Acc:2904]
212761_at	TCF7L2	ENSG00000148737	0.016677902	1.565585438	7.595305509	6.029720072	10	q25.2	transcription factor 7-like 2 (T-cell specific, HMG-box) [Source:HGNC Symbol;Acc:11641]
224983_at	SCARB2	ENSG00000138760	0.016923479	1.31926409	9.808332875	8.489068785	4	q21.1	scavenger receptor class B, member 2 [Source:HGNC Symbol;Acc:1665]
218706_s_at	GRAMD3	ENSG00000155324	0.016923479	1.12899438	6.584780567	5.455786187	5	q23.2	GRAM domain containing 3 [Source:HGNC Symbol;Acc:24911]
210165_at	DNASE1	ENSG00000213918	0.0170385	0.638225732	6.797117147	7.435342879	16	p13.3	deoxyribonuclease 1 [Source:HGNC Symbol;Acc:2956]
203595_s_at	IFIT5	ENSG00000152778	0.0170385	1.314122515	8.100950556	6.786828041	10	q23.31	interferon-induced protein with tetratricopeptide repeats 5 [Source:HGNC Symbol;Acc:13328]
1558431_at	NHLRC4	ENSG00000257108	0.017271459	0.440024521	7.110293049	7.55031757	16	p13.3	NHL repeat containing 4 [Source:HGNC Symbol;Acc:26700]
225133_at	KLF3	ENSG00000109787	0.017271459	1.877159888	7.744132654	5.866972766	4	p14	Kruppel-like factor 3 (basic) [Source:HGNC Symbol;Acc:16516]
210122_at	PRM2	ENSG00000122304	0.017305066	0.594945443	6.297604855	6.892550298	16	p13.13	protamine 2 [Source:HGNC Symbol;Acc:9448]
204396_s_at	GRK5	ENSG00000198873	0.017457757	0.977767737	8.13471677	7.156949033	10	q26.11	G protein-coupled receptor kinase 5 [Source:HGNC Symbol;Acc:4544]
1569270_at	LOC100134368	NA	0.017653225	0.524095679	4.998433733	5.522529412	NA	NA	NA
210105_s_at	FYN	ENSG0000010810	0.017653225	1.615658944	10.56933985	8.953680911	6	q21	FYN oncogene related to SRC, FGR, YES [Source:HGNC Symbol;Acc:4037]
201218_at	CTBP2	ENSG00000175029	0.017653225	1.464241977	7.445365995	5.981124019	10	q26.13	C-terminal binding protein 2 [Source:HGNC Symbol;Acc:2495]
203973_s_at	CEBPD	ENSG00000221869	0.017653225	1.614196567	10.46812679	8.853930222	8	q11.21	CCAAT/enhancer binding protein (C/EBP), delta [Source:HGNC Symbol;Acc:1835]
243038_at	RBM43	ENSG00000184898	0.017653225	0.968731593	7.015389524	6.046657931	2	q23.3	RNA binding motif protein 43 [Source:HGNC Symbol;Acc:24790]
212667_at	SPARC	ENSG00000113140	0.017653225	2.038777809	9.760157874	7.721380065	5	q33.1	secreted protein, acidic, cysteine-rich (osteonectin) [Source:HGNC Symbol;Acc:11219]
209341_s_at	IKKB	ENSG00000104365	0.017653225	0.980949734	8.789651207	7.808701473	8	p11.21	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta [Source:HGNC Symbol;Acc:5960]

232781_at	LHX4	ENSG00000121454	0.017653225	0.471163014	6.387893416	6.859056431	1	q25.2	LIM homeobox 4 [Source:HGNC Symbol;Acc:21734]
202336_s_at	PAM	ENSG00000145730	0.017653225	1.318515399	9.289020714	7.970505314	5	q21.1	peptidylglycine alpha-amidating monooxygenase [Source:HGNC Symbol;Acc:8596]
206151_x_at	CELA3B	ENSG00000219073	0.0179046	0.389566615	6.698451608	7.088018223	1	p36.12	chymotrypsin-like elastase family, member 3B [Source:HGNC Symbol;Acc:15945]
1553780_at	LINC00638	ENSG00000258701	0.0179681	0.442959091	5.985279128	6.428238219	14	q32.33	long intergenic non-protein coding RNA 638 [Source:HGNC Symbol;Acc:28325]
212298_at	NRP1	ENSG00000099250	0.018067396	1.779345664	9.257538424	7.47819276	10	p11.22	neuropilin 1 [Source:HGNC Symbol;Acc:8004]
1564386_at	TXNDC8	ENSG00000204193	0.018383789	0.402808114	4.569887895	4.972696009	9	q31.3	thioredoxin domain containing 8 (spermatozoa) [Source:HGNC Symbol;Acc:31454]
221773_at	ELK3	ENSG00000111145	0.018896313	1.62071839	8.175421184	6.554702794	12	q23.1	ELK3, ETS-domain protein (SRF accessory protein 2) [Source:HGNC Symbol;Acc:3325]
207116_s_at	GAPDH5	ENSG00000105679	0.018896313	0.439395893	6.265814968	6.705210861	19	q13.12	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic [Source:HGNC Symbol;Acc:24864]
208816_x_at	ANXA2P2	ENSG00000231991	0.018901839	0.878549333	10.01165886	9.133109525	9	p13.3	annexin A2 pseudogene 2 [Source:HGNC Symbol;Acc:539]
225188_at	RAPH1	ENSG00000173166	0.018901839	2.005188858	7.673175419	5.667986561	2	q33.2	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 [Source:HGNC Symbol;Acc:14436]
1552564_at	NUDT9P1	NA	0.018901839	0.627097479	5.209804097	5.836901576	NA	NA	NA
212779_at	KIAA1109	ENSG00000138688	0.018901839	0.990071878	8.187158776	7.197086899	4	q27	KIAA1109 [Source:HGNC Symbol;Acc:26953]
221748_s_at	TNS1	ENSG00000079308	0.018901839	2.020350883	8.869430402	6.84907952	2	q35	tensin 1 [Source:HGNC Symbol;Acc:11973]
1552811_at	WFIKKN1	ENSG00000127578	0.018901839	0.407943586	7.383936771	7.791880357	16	p13.3	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 1 [Source:HGNC Symbol;Acc:30912]
244543_s_at	BCDIN3D-AS1	ENSG00000258057	0.018901839	0.517606933	6.104813842	6.622420775	12	q13.12	BCDIN3D antisense RNA 1 [Source:HGNC Symbol;Acc:44113]
1555124_at	LOC100129726	NA	0.018901839	0.737667282	6.31928006	7.056947342	NA	NA	NA
213379_at	COQ2	ENSG00000173085	0.018901839	0.52373226	8.028910727	7.505178467	4	q21.23	coenzyme Q2 4-hydroxybenzoate polyprenyltransferase [Source:HGNC Symbol;Acc:25223]
211684_s_at	DYNC1I2	ENSG00000077380	0.018901839	0.822903615	8.910623393	8.087719778	2	q31.1	dynein, cytoplasmic 1, intermediate chain 2 [Source:HGNC Symbol;Acc:2964]
201739_at	SGK1	ENSG00000118515	0.018901839	1.479761374	10.75364976	9.273888386	6	q23.2	serum/glucocorticoid regulated kinase 1 [Source:HGNC Symbol;Acc:10810]
209090_s_at	SH3GLB1	ENSG00000097033	0.018901839	0.961400759	9.96248528	9.001084521	1	p22.3	SH3-domain GRB2-like endophilin B1 [Source:HGNC Symbol;Acc:10833]
225171_at	ARHGAP18	ENSG00000146376	0.018901839	1.537074864	8.677922388	7.140847525	6	q22.33	Rho GTPase activating protein 18 [Source:HGNC Symbol;Acc:21035]
204517_at	PPIC	ENSG00000168938	0.018901839	1.458339897	7.874058821	6.415718925	5	q23.2	peptidylprolyl isomerase C (cyclophilin C) [Source:HGNC Symbol;Acc:9256]
213923_at	RAP2B	ENSG00000181467	0.018901839	1.24137501	10.18514033	8.943765324	3	q25.2	RAP2B, member of RAS oncogene family [Source:HGNC Symbol;Acc:9862]
201590_x_at	ANXA2	ENSG00000182718	0.018901839	1.222362695	12.76741798	11.54505528	15	q22.2	annexin A2 [Source:HGNC Symbol;Acc:537]
202202_s_at	LAMA4	ENSG00000112769	0.018901839	1.095301757	9.350315162	8.255013405	6	q21	laminin, alpha 4 [Source:HGNC Symbol;Acc:6484]
218718_at	PDGFC	ENSG00000145431	0.018921376	2.106384599	7.63389478	5.527510181	4	q32.1	platelet derived growth factor C [Source:HGNC Symbol;Acc:8801]
1553541_at	LMX1A	ENSG00000162761	0.018921376	0.477745764	4.729705201	5.207450965	1	q23.3	LIM homeobox transcription factor 1, alpha [Source:HGNC Symbol;Acc:6653]
206414_s_at	ASAP2	ENSG00000151693	0.018921376	1.474771694	6.713855258	5.239083564	2	p25.1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2

									[Source:HGNC Symbol;Acc:2721]
1553178_a_at	SSTR3	ENSG00000183473	0.019065055	-0.49695403	6.605956381	7.10291041	22	q13.1	somatostatin receptor 3 [Source:HGNC Symbol;Acc:11332]
212169_at	FKBP9	ENSG00000122642	0.019065055	1.110752419	8.896737181	7.785984761	7	p14.3	FK506 binding protein 9, 63 kDa [Source:HGNC Symbol;Acc:3725]
209348_s_at	MAF	ENSG00000178573	0.019065055	2.155786041	8.892163605	6.736377564	16	q23.2	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog [Source:HGNC Symbol;Acc:6776]
202011_at	TJP1	ENSG00000104067	0.019266989	2.093652215	8.408239306	6.314587092	15	q13.1	tight junction protein 1 [Source:HGNC Symbol;Acc:11827]
226823_at	PHACTR4	ENSG00000204138	0.019506232	0.788498176	7.61381437	6.825316194	1	p35.3	phosphatase and actin regulator 4 [Source:HGNC Symbol;Acc:25793]
201375_s_at	PPP2CB	ENSG00000104695	0.019506232	0.883554817	10.00679214	9.123237324	8	p12	protein phosphatase 2, catalytic subunit, beta isozyme [Source:HGNC Symbol;Acc:9300]
1558289_at	RFT1	ENSG00000163933	0.019506232	0.356946278	6.437355142	6.794301421	3	p21.1	RFT1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:30220]
202808_at	WBP1L	ENSG00000166272	0.019506232	0.667279191	9.547031071	8.879751881	10	q24.32	WW domain binding protein 1-like [Source:HGNC Symbol;Acc:23510]
227911_at	ARHGAP28	ENSG00000088756	0.019879747	1.632136074	5.975403546	4.343267472	18	p11.31	Rho GTPase activating protein 28 [Source:HGNC Symbol;Acc:25509]
208034_s_at	PROZ	ENSG00000126231	0.019879747	0.413177596	7.086538428	7.499716024	13	q34	protein Z, vitamin K-dependent plasma glycoprotein [Source:HGNC Symbol;Acc:9460]
1553444_a_at	C1orf127	ENSG00000175262	0.019879747	0.456161699	7.310783447	7.766945146	1	p36.22	chromosome 1 open reading frame 127 [Source:HGNC Symbol;Acc:26730]
220077_at	CCDC134	ENSG00000100147	0.019879747	0.431568198	7.194190518	7.625758716	22	q13.2	coiled-coil domain containing 134 [Source:HGNC Symbol;Acc:26185]
215756_at	LOC730227	NA	0.019879747	0.466760373	5.640296789	6.107057162	NA	NA	NA
206049_at	SELP	ENSG00000174175	0.019879747	1.710090268	7.227626982	5.517536714	1	q24.2	selectin P (granule membrane protein 140kDa, antigen CD62) [Source:HGNC Symbol;Acc:10721]
202357_s_at	CFB	ENSG00000243649	0.019879747	1.157364569	8.626327441	7.468962872	6	p21.33	complement factor B [Source:HGNC Symbol;Acc:1037]
217497_at	TYMP	ENSG00000025708	0.019879747	0.851614407	8.694768908	7.843154501	22	q13.33	thymidine phosphorylase [Source:HGNC Symbol;Acc:3148]
204034_at	ETHE1	ENSG00000105755	0.019879747	0.528926484	8.283720657	7.754794174	19	q13.31	ethylmalonic encephalopathy 1 [Source:HGNC Symbol;Acc:23287]
210139_s_at	PMP22	ENSG00000109099	0.019879747	1.749405657	9.219437323	7.470031666	17	p12	peripheral myelin protein 22 [Source:HGNC Symbol;Acc:9118]
242226_at	LOC100288079	NA	0.019879747	0.466011928	4.501905981	4.967917909	NA	NA	NA
204114_at	NID2	ENSG00000087303	0.019879747	1.635433904	7.748453279	6.113019374	14	q22.1	nidogen 2 (osteonidogen) [Source:HGNC Symbol;Acc:13389]
207159_x_at	CRTC1	ENSG00000105662	0.019974794	0.342848645	8.582700549	8.925549194	19	p13.11	CREB regulated transcription coactivator 1 [Source:HGNC Symbol;Acc:16062]
1564072_at	MYH16	ENSG00000002079	0.020133959	0.513849511	5.117985644	5.631835155	7	q22.1	myosin, heavy chain 16 pseudogene [Source:HGNC Symbol;Acc:31038]
200878_at	EPAS1	ENSG00000116016	0.020133959	1.664350584	10.74528693	9.080936347	2	p21	endothelial PAS domain protein 1 [Source:HGNC Symbol;Acc:3374]
206112_at	ANKRD7	ENSG00000106013	0.020139089	0.584007767	3.631160633	4.2151684	7	q31.31	ankyrin repeat domain 7 [Source:HGNC Symbol;Acc:18588]
202446_s_at	PLSCR1	ENSG00000188313	0.020139089	1.410605009	9.747770469	8.33716546	3	q24	phospholipid scramblase 1 [Source:HGNC Symbol;Acc:9092]
221139_s_at	CSAD	ENSG00000139631	0.020139089	1.103365222	6.326659677	5.223294456	12	q13.13	cysteine sulfinic acid decarboxylase [Source:HGNC Symbol;Acc:18966]
244488_at	LSM14B	ENSG00000149657	0.020139089	0.471204404	5.404535566	5.87573997	20	q13.33	LSM14B, SCD6 homolog B (S. cerevisiae) [Source:HGNC Symbol;Acc:15887]
221012_s_at	TRIM8	ENSG00000171206	0.020139089	0.902154468	9.733515113	8.831360645	10	q24.32	tripartite motif containing 8 [Source:HGNC Symbol;Acc:15579]
1555832_s_at	KLF6	ENSG00000067082	0.020139089	1.505090741	10.49275643	8.987665692	10	p15.1	Kruppel-like factor 6 [Source:HGNC Symbol;Acc:2235]
212859_x_at	MT1E	ENSG00000169715	0.020139089	1.31163782	11.29221774	9.98057992	16	q12.2	metallothionein 1E [Source:HGNC Symbol;Acc:7397]

203729_at	EMP3	ENSG00000142227	0.020691131	1.242611864	10.80078079	9.558168921	19	q13.33	epithelial membrane protein 3 [Source:HGNC Symbol;Acc:3335]
243022_at	LOC100506631	NA	0.020691131	0.472548595	6.586231468	7.058780063	NA	NA	NA
223630_at	C7orf13	ENSG00000244291	0.021317074	0.621418392	6.683076994	7.304495386	7	q36.3	chromosome 7 open reading frame 13 [Source:HGNC Symbol;Acc:17126]
209238_at	STX3	ENSG00000166900	0.021317074	1.047521762	7.816754018	6.769232256	11	q12.1	syntaxin 3 [Source:HGNC Symbol;Acc:11438]
207366_at	KCNS1	ENSG00000124134	0.021317074	0.522556921	5.734453296	6.257010217	20	q13.12	potassium voltage-gated channel, delayed-rectifier, subfamily 5, member 1 [Source:HGNC Symbol;Acc:6300]
1569532_a_at	LCN15	ENSG00000177984	0.021317074	0.463360876	6.730953106	7.194313982	9	q34.3	lipocalin 15 [Source:HGNC Symbol;Acc:33777]
228617_at	XAF1	ENSG00000132530	0.021319587	1.859163345	9.784426104	7.925262758	17	p13.1	XIAP associated factor 1 [Source:HGNC Symbol;Acc:30932]
204436_at	PLEKHO2	ENSG00000241839	0.02166097	0.814909278	9.412794546	8.597885267	15	q22.31	pleckstrin homology domain containing, family O member 2 [Source:HGNC Symbol;Acc:30026]
208291_s_at	TH	ENSG00000180176	0.02166097	0.435400549	5.849357981	6.284758531	11	p15.5	tyrosine hydroxylase [Source:HGNC Symbol;Acc:11782]
1555756_a_at	CLEC7A	ENSG00000172243	0.021739097	1.948701695	9.541407089	7.592705395	12	p13.2	C-type lectin domain family 7, member A [Source:HGNC Symbol;Acc:14558]
202381_at	ADAM9	ENSG00000168615	0.022252306	1.522568908	9.387992162	7.865423254	8	p11.22	ADAM metalloproteinase domain 9 [Source:HGNC Symbol;Acc:216]
202291_s_at	MGP	ENSG00000111341	0.022611564	2.128960252	11.06083826	8.931878011	12	p12.3	matrix Gla protein [Source:HGNC Symbol;Acc:7060]
239119_at	DNAJC3-AS1	ENSG00000247400	0.022611564	0.889794242	6.485868079	7.375662321	13	q32.1	DNAJC3 antisense RNA 1 (head to head) [Source:HGNC Symbol;Acc:39808]
213056_at	FRMD4B	ENSG00000114541	0.022611564	1.741374115	6.023278408	4.281904293	3	p14.1	FERM domain containing 4B [Source:HGNC Symbol;Acc:24886]
218162_at	OLFML3	ENSG00000116774	0.022611564	1.550845738	8.328430141	6.777584404	1	p13.2	olfactomedin-like 3 [Source:HGNC Symbol;Acc:24956]
212845_at	SAMD4A	ENSG0000020577	0.022611564	1.246715477	6.634446869	5.387731392	14	q22.2	sterile alpha motif domain containing 4A [Source:HGNC Symbol;Acc:23023]
240185_at	LOC100147773	NA	0.022611564	0.498977477	7.370697097	7.869674574	NA	NA	NA
233843_at	ZBTB12	ENSG00000204366	0.022611564	0.519742752	7.218271617	7.738014369	6	p21.33	zinc finger and BTB domain containing 12 [Source:HGNC Symbol;Acc:19066]
218541_s_at	C8orf4	ENSG00000176907	0.022732168	1.976295335	6.69374434	4.717449005	8	p11.21	chromosome 8 open reading frame 4 [Source:HGNC Symbol;Acc:1357]
1555722_at	SCAMPER	NA	0.022732168	0.334308255	3.6043183	3.938626555	NA	NA	NA
1559005_s_at	CNTLN	ENSG00000244459	0.022732168	1.390816874	6.512894646	5.122077773	9	p22.2	centilin, centrosomal protein [Source:HGNC Symbol;Acc:23432]
218909_at	RPS6KC1	ENSG00000136643	0.022732168	0.752157812	8.355673576	7.603515764	1	q32.3	ribosomal protein S6 kinase, 52kDa, polypeptide 1 [Source:HGNC Symbol;Acc:10439]
1553067_a_at	GNRHR2	ENSG00000211451	0.022732168	0.649001368	7.399753955	8.048755323	1	q21.1	gonadotropin-releasing hormone (type 2) receptor 2 [Source:HGNC Symbol;Acc:16341]
226384_at	PPAPDC1B	ENSG00000147535	0.022732168	1.211118387	8.15972622	6.948607833	8	p11.23	phosphatidic acid phosphatase type 2 domain containing 1B [Source:HGNC Symbol;Acc:25026]
212509_s_at	MXRA7	ENSG00000182534	0.022732168	1.467475866	9.764658055	8.297182189	17	q25.1	matrix-remodelling associated 7 [Source:HGNC Symbol;Acc:7541]
225975_at	PCDH18	ENSG00000189184	0.023159359	1.779023771	7.236967211	5.45794344	4	q28.3	protocadherin 18 [Source:HGNC Symbol;Acc:14268]
201341_at	ENC1	ENSG00000171617	0.023415903	1.444333682	8.066608054	6.622274373	5	q13.3	ectodermal-neural cortex 1 (with BTB domain) [Source:HGNC Symbol;Acc:3345]
203324_s_at	CAV2	ENSG00000105971	0.023506064	1.952200967	8.152023753	6.199822786	7	q31.2	caveolin 2 [Source:HGNC Symbol;Acc:1528]
238898_at	LOC101060264	NA	0.023506064	1.193505286	5.871655735	7.065161021	NA	NA	NA
212230_at	PPAP2B	ENSG00000162407	0.023506064	1.816510197	9.071697681	7.255187484	1	p32.2	phosphatidic acid phosphatase type 2B [Source:HGNC

									Symbol;Acc:9229]
218632_at	HECTD3	ENSG00000126107	0.023506064	0.736900447	9.627647883	8.890747437	1	p34.1	HECT domain containing E3 ubiquitin protein ligase 3 [Source:HGNC Symbol;Acc:26117]
212204_at	TMEM87A	ENSG00000103978	0.023515139	0.898492789	9.007547211	8.109054422	15	q15.1	transmembrane protein 87A [Source:HGNC Symbol;Acc:24522]
226022_at	SASH1	ENSG00000111961	0.023515139	2.002711158	7.610795761	5.608084603	6	q24.3	SAM and SH3 domain containing 1 [Source:HGNC Symbol;Acc:19182]
224166_at	SLC25A2	ENSG00000120329	0.023531188	0.439944142	4.676270398	5.11621454	5	q31.3	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 2 [Source:HGNC Symbol;Acc:22921]
242800_at	NHS	ENSG00000188158	0.023677408	1.162711533	6.713331023	5.550619491	X	p22.13	Nance-Horan syndrome (congenital cataracts and dental anomalies) [Source:HGNC Symbol;Acc:7820]
203477_at	COL15A1	ENSG00000204291	0.023677408	1.614306704	8.436883195	6.822576491	9	q22.33	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
200857_s_at	NCOR1	ENSG00000141027	0.023677408	0.709194263	8.662953014	7.95375875	17	p11.2	nuclear receptor corepressor 1 [Source:HGNC Symbol;Acc:7672]
238239_at	WDR27	ENSG00000184465	0.023677408	0.865615668	5.475660628	6.341276295	6	q27	WD repeat domain 27 [Source:HGNC Symbol;Acc:21248]
1562089_at	GLYATL1	ENSG00000166840	0.023677408	0.494191579	3.390583969	3.884775548	11	q12.1	glycine-N-acyltransferase-like 1 [Source:HGNC Symbol;Acc:30519]
224996_at	ASPH	ENSG00000198363	0.023699601	1.523017401	7.874015884	6.350998483	8	q12.3	aspartate beta-hydroxylase [Source:HGNC Symbol;Acc:757]
223562_at	PARVG	ENSG00000138964	0.023699601	1.500914846	9.669889441	8.168974594	22	q13.31	parvin, gamma [Source:HGNC Symbol;Acc:14654]
213353_at	ABCA5	ENSG00000154265	0.023699601	0.996243159	8.332970994	7.336727836	17	q24.3	ATP-binding cassette, sub-family A (ABC1), member 5 [Source:HGNC Symbol;Acc:35]
209593_s_at	TOR1B	ENSG00000136816	0.023800085	0.46611305	7.855147944	7.389034893	9	q34.11	torsin family 1, member B (torsin B) [Source:HGNC Symbol;Acc:11995]
207649_at	KRT37	ENSG00000108417	0.023800085	0.376179216	5.023738968	5.399918184	17	q21.2	keratin 37 [Source:HGNC Symbol;Acc:6455]
35626_at	SGSH	ENSG00000181523	0.023800085	0.781709479	9.793809878	9.012100399	17	q25.3	N-sulfoglucosamine sulfohydrolase [Source:HGNC Symbol;Acc:10818]
1559272_at	EXOC3L1	ENSG00000179044	0.023800085	-0.4129202	8.165645994	8.578566194	16	q22.1	exocyst complex component 3-like 1 [Source:HGNC Symbol;Acc:27540]
234994_at	TMEM200A	ENSG00000164484	0.023800085	1.612047423	6.524547814	4.91250039	6	q23.1	transmembrane protein 200A [Source:HGNC Symbol;Acc:21075]
1556822_s_at	ZNF837	ENSG00000152475	0.023800085	0.480490017	6.346952069	6.827442086	19	q13.43	zinc finger protein 837 [Source:HGNC Symbol;Acc:25164]
211456_x_at	MT1P2	NA	0.023800085	1.026714169	11.3370169	10.31030273	NA	NA	NA
215328_at	EFR3B	ENSG00000084710	0.023922328	0.703597987	6.556203567	7.259801553	2	p23.3	EFR3 homolog B (S. cerevisiae) [Source:HGNC Symbol;Acc:29155]
203501_at	CPQ	ENSG00000104324	0.024111993	0.986206289	7.824447671	6.838241383	8	q22.1	carboxypeptidase Q [Source:HGNC Symbol;Acc:16910]
226155_at	FAM160B1	ENSG00000151553	0.024111993	0.94991516	8.161808151	7.21189299	10	q25.3	family with sequence similarity 160, member B1 [Source:HGNC Symbol;Acc:29320]
1552932_at	NLRP6	ENSG00000174885	0.024111993	0.452619884	6.55831599	7.010935874	11	p15.5	NLR family, pyrin domain containing 6 [Source:HGNC Symbol;Acc:22944]
1552258_at	LINC00152	ENSG00000222041	0.024124457	1.12452576	8.139434844	7.014909085	2	p11.2	long intergenic non-protein coding RNA 152 [Source:HGNC Symbol;Acc:28717]
238025_at	MLKL	ENSG00000168404	0.02486642	1.215990498	8.756992858	7.54100236	16	q23.1	mixed lineage kinase domain-like [Source:HGNC Symbol;Acc:26617]
219460_s_at	TMEM127	ENSG00000135956	0.02486642	0.454625359	8.62922137	8.174596011	2	q11.2	transmembrane protein 127 [Source:HGNC Symbol;Acc:26038]
225522_at	AAK1	ENSG00000115977	0.02486642	1.172801595	8.65290817	7.480106575	2	p13.3	AP2 associated kinase 1 [Source:HGNC Symbol;Acc:19679]
217757_at	A2M	ENSG00000175899	0.024980362	1.576462299	12.02894127	10.45247897	12	p13.31	alpha-2-macroglobulin [Source:HGNC Symbol;Acc:7]
223168_at	RHOU	ENSG00000116574	0.025426902	1.560384918	7.215568938	5.655184019	1	q42.13	ras homolog family member U [Source:HGNC Symbol;Acc:17794]
1561615_s_at	SLC8A1	ENSG00000183023	0.025807759	1.56503616	8.855136737	7.290100577	2	p22.1	solute carrier family 8 (sodium/calcium exchanger), member 1

									[Source:HGNC Symbol;Acc:11068]
203758_at	CTSO	ENSG00000256043	0.02606631	1.156055866	9.31162358	8.155567714	4	q32.1	cathepsin O [Source:HGNC Symbol;Acc:2542]
226552_at	IER5L	ENSG00000188483	0.026467277	0.93672703	7.611941271	6.675214241	9	q34.11	immediate early response 5-like [Source:HGNC Symbol;Acc:23679]
202766_s_at	FBN1	ENSG00000166147	0.027121311	1.374537951	7.745362428	6.370824476	15	q21.1	fibrillin 1 [Source:HGNC Symbol;Acc:3603]
225629_s_at	ZBTB4	ENSG00000174282	0.027121311	1.019746013	9.543580585	8.523834572	17	p13.1	zinc finger and BTB domain containing 4 [Source:HGNC Symbol;Acc:23847]
212136_at	ATP2B4	ENSG00000058668	0.027282655	1.526692329	8.833219126	7.306526797	1	q32.1	ATPase, Ca ²⁺ transporting, plasma membrane 4 [Source:HGNC Symbol;Acc:817]
1555881_s_at	LZTS2	ENSG00000107816	0.027517178	0.440221226	7.841075386	7.400854161	10	q24.31	leucine zipper, putative tumor suppressor 2 [Source:HGNC Symbol;Acc:29381]
57715_at	CALHM2	ENSG00000138172	0.027517178	0.696007379	8.099815478	7.403808099	10	q24.33	calcium homeostasis modulator 2 [Source:HGNC Symbol;Acc:23493]
226601_at	SLC30A7	ENSG00000162695	0.027517178	0.937218503	8.338967731	7.401749228	1	p21.2	solute carrier family 30 (zinc transporter), member 7 [Source:HGNC Symbol;Acc:19306]
217890_s_at	PARVA	ENSG00000197702	0.027517178	1.563831784	9.16028555	7.596453867	11	p15.3	parvin, alpha [Source:HGNC Symbol;Acc:14652]
207624_s_at	RPGR	ENSG00000156313	0.027571838	0.526289635	7.293504241	6.767214606	X	p11.4	retinitis pigmentosa GTPase regulator [Source:HGNC Symbol;Acc:10295]
212372_at	MYH10	ENSG00000133026	0.027571838	1.055713787	8.323251043	7.267537256	17	p13.1	myosin, heavy chain 10, non-muscle [Source:HGNC Symbol;Acc:7568]
226820_at	ZNF352	ENSG00000160094	0.027571838	0.806241318	8.807479051	8.001237733	1	p35.1	zinc finger protein 362 [Source:HGNC Symbol;Acc:18079]
202551_s_at	CRIM1	ENSG00000150938	0.027571838	1.425695658	8.947673951	7.521978294	2	p22.3	cysteine rich transmembrane BMP regulator 1 (chordin-like) [Source:HGNC Symbol;Acc:2359]
208030_s_at	ADD1	ENSG00000087274	0.027642759	0.584654998	9.931156175	9.346501177	4	p16.3	adducin 1 (alpha) [Source:HGNC Symbol;Acc:243]
206618_at	IL18R1	ENSG00000115604	0.027642759	1.481537358	7.518533037	6.03699568	2	q12.1	interleukin 18 receptor 1 [Source:HGNC Symbol;Acc:5988]
201212_at	LGMN	ENSG00000100600	0.027659186	2.066812025	10.1698232	8.103011174	14	q32.12	legumain [Source:HGNC Symbol;Acc:9472]
208782_at	FSTL1	ENSG00000163430	0.027736606	1.32524447	10.08689397	8.761649497	3	q13.33	folliculin-like 1 [Source:HGNC Symbol;Acc:3972]
209191_at	TUBB6	ENSG00000176014	0.027736606	1.657527449	9.832241239	8.17471379	18	p11.21	tubulin, beta 6 class V [Source:HGNC Symbol;Acc:20776]
206875_s_at	SLK	ENSG00000065613	0.027736606	1.064373439	8.057717065	6.993343627	10	q24.33	STE20-like kinase [Source:HGNC Symbol;Acc:11088]
212990_at	SYNJ1	ENSG00000159082	0.027736606	1.044260381	7.114954309	6.070693928	21	q22.11	synaptojanin 1 [Source:HGNC Symbol;Acc:11503]
204193_at	CHKB	ENSG00000100288	0.027736606	0.899813254	9.518634166	8.618820912	22	q13.33	choline kinase beta [Source:HGNC Symbol;Acc:1938]
203243_s_at	PDZIM5	ENSG00000163110	0.028029546	1.142844616	7.842659274	6.699814657	4	q22.3	PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:17468]
227554_at	MAGI2-AS3	ENSG00000234456	0.028029546	1.583516525	7.049678455	5.46616193	7	q21.11	MAGI2 antisense RNA 3 [Source:HGNC Symbol;Acc:40862]
224616_at	DYNLC1L2	ENSG00000135720	0.028029546	0.795711906	10.00717568	9.211463776	16	q22.1	dynein, cytoplasmic 1, light intermediate chain 2 [Source:HGNC Symbol;Acc:2966]
218901_at	PLSCR4	ENSG00000114698	0.028186238	1.641200848	5.938606594	4.297405747	3	q24	phospholipid scramblase 4 [Source:HGNC Symbol;Acc:16497]
209050_s_at	RALGDS	ENSG00000160271	0.028198657	0.830143523	9.509798483	8.67965496	9	q34.2	ral guanine nucleotide dissociation stimulator [Source:HGNC Symbol;Acc:9842]
209472_at	CCBL2	ENSG00000137944	0.028198657	0.791465989	9.348801739	8.55733575	1	p22.2	cysteine conjugate-beta lyase 2 [Source:HGNC Symbol;Acc:33238]
227542_at	SOCS6	ENSG00000170677	0.028198657	1.310031965	6.680388823	5.370356858	18	q22.2	suppressor of cytokine signaling 6 [Source:HGNC Symbol;Acc:16833]
204039_at	CEBPA	ENSG00000245848	0.028198657	0.929871866	8.572792639	7.642920773	19	q13.11	CCAAT/enhancer binding protein (C/EBP), alpha [Source:HGNC Symbol;Acc:1833]
212586_at	CAST	ENSG00000153113	0.028198657	0.741294527	9.204773928	8.463479401	5	q15	calpastatin [Source:HGNC Symbol;Acc:1515]
201280_s_at	DAB2	ENSG00000153071	0.028198657	1.77978079	8.603166646	6.823385856	5	p13.1	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:2662]
201599_at	OAT	ENSG00000065154	0.028198657	0.889981447	9.474237119	8.584255672	10	q26.13	ornithine aminotransferase [Source:HGNC Symbol;Acc:8091]
225334_at	C10orf32	ENSG00000166275	0.028198657	0.781438768	8.253485336	7.472046568	10	q24.32	chromosome 10 open reading frame 32 [Source:HGNC Symbol;Acc:23516]

201334_s_at	ARHGEF12	ENSG00000196914	0.028226747	1.120752315	9.211231463	8.090479148	11	q23.3	Rho guanine nucleotide exchange factor (GEF) 12 [Source:HGNC Symbol;Acc:14193]
229041_s_at	ITGB2-AS1	ENSG00000227039	0.028919999	1.834305085	9.515397779	7.681092694	21	q22.3	ITGB2 antisense RNA 1 [Source:HGNC Symbol;Acc:44304]
212124_at	ZMIZ1	ENSG00000108175	0.028919999	1.472001753	10.25152688	8.779525132	10	q22.3	zinc finger, MIZ-type containing 1 [Source:HGNC Symbol;Acc:16493]
204863_s_at	IL6ST	ENSG00000134352	0.028919999	1.145080811	9.161299338	8.016218527	5	q11.2	interleukin 6 signal transducer (gp130, oncostatin M receptor) [Source:HGNC Symbol;Acc:6021]
215235_at	SPTAN1	ENSG00000197694	0.028919999	0.687712354	10.61620713	9.928494779	9	q34.11	spectrin, alpha, non-erythrocytic 1 [Source:HGNC Symbol;Acc:11273]
212606_at	WDFY3	ENSG00000163625	0.028919999	1.687587613	6.840272287	5.152684674	4	q21.23	WD repeat and FYVE domain containing 3 [Source:HGNC Symbol;Acc:20751]
212601_at	ZZEF1	ENSG00000074755	0.028919999	0.462251252	8.027308146	7.565056894	17	p13.2	zinc finger, ZZ-type with EF-hand domain 1 [Source:HGNC Symbol;Acc:29027]
228577_x_at	ODF2L	ENSG00000122417	0.028919999	0.928335466	7.134280411	6.205944945	1	p22.3	outer dense fiber of sperm tails 2-like [Source:HGNC Symbol;Acc:29225]
227776_at	ACER3	ENSG00000078124	0.028919999	1.179421743	7.521437369	6.342015626	11	q13.5	alkaline ceramidase 3 [Source:HGNC Symbol;Acc:16066]
201146_at	NFE2L2	ENSG00000116044	0.028919999	0.970559163	10.2023661	9.231806934	2	q31.2	nuclear factor (erythroid-derived 2)-like 2 [Source:HGNC Symbol;Acc:7782]
214807_at	LOC100509635	NA	0.028919999	1.839892443	8.320892858	6.481000416	NA	NA	NA
201185_at	HTRA1	ENSG00000166033	0.028919999	1.815072013	9.750466378	7.935394366	10	q26.13	Htra serine peptidase 1 [Source:HGNC Symbol;Acc:9476]
209120_at	NR2F2	ENSG00000185551	0.029112343	2.191435636	8.372704969	6.181269333	15	q26.2	nuclear receptor subfamily 2, group F, member 2 [Source:HGNC Symbol;Acc:7976]
226021_at	RDH10	ENSG00000121039	0.029112343	1.181075712	6.837596657	5.656520945	8	q21.11	retinol dehydrogenase 10 (all-trans) [Source:HGNC Symbol;Acc:19975]
224480_s_at	AGPAT9	ENSG00000138678	0.029340633	1.110871028	4.910358231	3.799487203	4	q21.23	1-acylglycerol-3-phosphate O-acyltransferase 9 [Source:HGNC Symbol;Acc:28157]
212077_at	CALD1	ENSG00000122786	0.029340633	1.724790131	10.17919504	8.454404905	7	q33	caldesmon 1 [Source:HGNC Symbol;Acc:1441]
204745_x_at	MT1G	ENSG00000125144	0.029340633	1.041896811	10.90300528	9.861108467	16	q13	metallothionein 1G [Source:HGNC Symbol;Acc:7399]
227930_at	AGO4	ENSG00000134698	0.029585591	1.105352072	6.925534304	5.820182232	1	p34.3	argonaute RISC catalytic component 4 [Source:HGNC Symbol;Acc:18424]
212636_at	QKI	ENSG00000112531	0.029710813	1.378340651	8.509471015	7.131130365	6	q26	QKI, KH domain containing, RNA binding [Source:HGNC Symbol;Acc:21100]
202609_at	EPS8	ENSG00000151491	0.029743118	2.016395991	8.302002557	6.285606566	12	p12.3	epidermal growth factor receptor pathway substrate 8 [Source:HGNC Symbol;Acc:3420]
207791_s_at	RAB1A	ENSG00000138069	0.029761404	0.834242654	9.926540665	9.092298011	2	p14	RAB1A, member RAS oncogene family [Source:HGNC Symbol;Acc:9758]
226377_at	NFIC	ENSG00000141905	0.029761404	1.124935006	8.785641229	7.660706223	19	p13.3	nuclear factor I/C (CCAAT-binding transcription factor) [Source:HGNC Symbol;Acc:7786]
212607_at	AKT3	ENSG00000117020	0.029761404	1.28613632	8.86790134	7.58176502	1	q44	v-akt murine thymoma viral oncogene homolog 3 [Source:HGNC Symbol;Acc:393]
220122_at	MCTP1	ENSG00000175471	0.029807901	1.579458936	7.121595256	5.54213632	5	q15	multiple C2 domains, transmembrane 1 [Source:HGNC Symbol;Acc:26183]
225941_at	EIF4E3	ENSG00000163412	0.029807901	1.364241317	7.790818489	6.426577172	3	p13	eukaryotic translation initiation factor 4E family member 3 [Source:HGNC Symbol;Acc:31837]
65635_at	ENGASE	ENSG00000167280	0.029836343	0.549126535	9.240446513	8.691319977	17	q25.3	endo-beta-N-acetylglucosaminidase [Source:HGNC Symbol;Acc:24622]
202897_at	SIRPA	ENSG00000198053	0.029836343	1.079213131	9.722842102	8.643628972	20	p13	signal-regulatory protein alpha [Source:HGNC Symbol;Acc:9662]

213817_at	IRAK3	ENSG00000090376	0.029836343	1.432000131	6.594781364	5.162781233	12	q14.3	interleukin-1 receptor-associated kinase 3 [Source:HGNC Symbol;Acc:17020]
204703_at	IFT88	ENSG00000032742	0.029836343	0.555626502	7.914095211	7.358468709	13	q12.11	intraflagellar transport 88 homolog (Chlamydomonas) [Source:HGNC Symbol;Acc:20606]
201029_s_at	CD99	ENSG00000002586	0.029836343	1.179550753	11.79489029	10.61533954	X	p22.33	CD99 molecule [Source:HGNC Symbol;Acc:7082]
201105_at	LGA1S1	ENSG00000100097	0.029836343	1.067969519	12.55395514	11.48598563	22	q13.1	lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:6561]
228666_at	C15orf38	ENSG00000242498	0.029836343	0.965528767	8.632863432	7.667334665	15	q26.1	chromosome 15 open reading frame 38 [Source:HGNC Symbol;Acc:28782]
213733_at	MYO1F	ENSG00000142347	0.029836343	1.212020923	9.0479833	7.835962377	19	p13.2	myosin 1F [Source:HGNC Symbol;Acc:7600]
225162_at	SH3D19	ENSG00000109686	0.029836343	1.697719881	6.304495587	4.606775706	4	q31.3	SH3 domain containing 19 [Source:HGNC Symbol;Acc:30418]
221766_s_at	FAM46A	ENSG00000112773	0.030025868	1.307438215	9.102394105	7.79495589	6	q14.1	family with sequence similarity 46, member A [Source:HGNC Symbol;Acc:18345]
235256_s_at	GALM	ENSG00000143891	0.030025868	1.3208648	7.939207095	6.618342295	2	p22.1	galactose mutarotase (aldose 1-epimerase) [Source:HGNC Symbol;Acc:24063]
201417_at	SOX4	ENSG00000124766	0.030025868	1.094353867	7.314555393	6.220201526	6	p22.3	SRY (sex determining region Y)-box 4 [Source:HGNC Symbol;Acc:11200]
201963_at	ACSL1	ENSG00000151726	0.030025868	1.026257459	9.481284578	8.455027119	4	q35.1	acyl-CoA synthetase long-chain family member 1 [Source:HGNC Symbol;Acc:3569]
218983_at	C1RL	ENSG00000139178	0.030025868	1.053541158	6.970689021	5.917147863	12	p13.31	complement component 1, r subcomponent-like [Source:HGNC Symbol;Acc:21265]
225442_at	DDR2	ENSG00000162733	0.030025868	1.204158025	8.120903012	6.916744987	1	q23.3	discoidin domain receptor tyrosine kinase 2 [Source:HGNC Symbol;Acc:2731]
225128_at	KDELC2	ENSG00000178202	0.030088928	0.839868955	7.886197408	7.046328453	11	q22.3	KDEL (Lys-Asp-Glu-Leu) containing 2 [Source:HGNC Symbol;Acc:28496]
225913_at	PEAK1	NA	0.030088928	0.877481347	8.926047545	8.048566198	NA	NA	NA
238477_at	KIF1C	ENSG00000129250	0.030088928	0.514313913	6.616651948	6.102338035	17	p13.2	kinesin family member 1C [Source:HGNC Symbol;Acc:6317]
1557236_at	APOL6	ENSG00000221963	0.030333182	1.353018745	6.588334921	5.235316176	22	q12.3	apolipoprotein L, 6 [Source:HGNC Symbol;Acc:14870]
224764_at	ARHGAP21	ENSG00000107863	0.030504136	0.72625482	8.341027571	7.614772751	10	p12.1	Rho GTPase activating protein 21 [Source:HGNC Symbol;Acc:23725]
204568_at	ATG14	ENSG00000126775	0.030504136	0.68255677	7.833224815	7.150668045	14	q22.3	autophagy related 14 [Source:HGNC Symbol;Acc:19962]
202598_at	S100A13	ENSG00000189171	0.030504136	0.905469594	10.25862756	9.353157962	1	q21.3	S100 calcium binding protein A13 [Source:HGNC Symbol;Acc:10490]
218815_s_at	TMEM51	ENSG00000171729	0.030529954	0.821120093	9.101393989	8.280273897	1	p36.21	transmembrane protein 51 [Source:HGNC Symbol;Acc:25488]
204214_s_at	RAB32	ENSG00000118508	0.030529954	0.974779135	8.206092346	7.231313211	6	q24.3	RAB32, member RAS oncogene family [Source:HGNC Symbol;Acc:9772]
226152_at	TTC7B	ENSG00000165914	0.030555177	1.225826179	7.058997136	5.833170957	14	q32.11	tetratricopeptide repeat domain 7B [Source:HGNC Symbol;Acc:19858]
205590_at	RASGRP1	ENSG00000172575	0.030555177	1.811511239	10.05801133	8.246500094	15	q14	RAS guanyl releasing protein 1 (calcium and DAG-regulated) [Source:HGNC Symbol;Acc:9878]
1555579_s_at	PTPRM	ENSG00000173482	0.030555177	1.133321622	7.834017042	6.70069542	18	p11.23	protein tyrosine phosphatase, receptor type, M [Source:HGNC Symbol;Acc:9675]
218486_at	KLF11	ENSG00000172059	0.030555177	1.276283669	7.737115935	6.460832266	2	p25.1	Kruppel-like factor 11 [Source:HGNC Symbol;Acc:11811]
204451_at	FZD1	ENSG00000157240	0.030555177	1.280052899	7.241574346	5.961521446	7	q21.13	frizzled family receptor 1 [Source:HGNC Symbol;Acc:4038]
226186_at	TMOD2	ENSG00000128872	0.030555177	1.362546177	6.78422602	5.421679843	15	q21.2	tropomodulin 2 (neuronal) [Source:HGNC Symbol;Acc:11872]
225288_at	COL27A1	ENSG00000196739	0.030691053	1.40544216	7.835001659	6.429559499	9	q32	collagen, type XXVII, alpha 1 [Source:HGNC Symbol;Acc:22986]
225163_at	FRMD4A	ENSG00000151474	0.030947129	1.137531712	7.41162528	6.274093568	10	p13	FERM domain containing 4A [Source:HGNC Symbol;Acc:25491]
221541_at	CRISP1D2	ENSG00000103196	0.030947129	1.757392292	8.718881123	6.961488831	16	q24.1	cysteine-rich secretory protein LCCL domain containing 2

									[Source:HGNC Symbol;Acc:25248]
230480_at	PIWIL4	ENSG00000134627	0.030947129	0.657514674	6.112214345	5.45469967	11	q21	piwi-like RNA-mediated gene silencing 4 [Source:HGNC Symbol;Acc:18444]
227444_at	ARMCX4	ENSG00000196440	0.030947129	0.976979963	6.028166519	5.051186556	X	q22.1	armadillo repeat containing, X-linked 4 [Source:HGNC Symbol;Acc:28615]
218285_s_at	BDH2	ENSG00000164039	0.030947129	0.724767228	8.942667027	8.217899799	4	q24	3-hydroxybutyrate dehydrogenase, type 2 [Source:HGNC Symbol;Acc:32389]
209687_at	CXCL12	ENSG00000107562	0.030947129	2.225058448	9.716134003	7.491075555	10	q11.21	chemokine (C-X-C motif) ligand 12 [Source:HGNC Symbol;Acc:10672]
203261_at	DCTN6	ENSG00000104671	0.030947129	0.806565337	10.35688135	9.550316016	8	p12	dynactin 6 [Source:HGNC Symbol;Acc:16964]
227001_at	NIPAL2	ENSG00000104361	0.030947129	1.385419946	8.211606253	6.826186308	8	q22.2	NIPA-like domain containing 2 [Source:HGNC Symbol;Acc:25854]
213119_at	SLC36A1	ENSG00000123643	0.030947129	0.527649011	8.188390174	7.660741163	5	q33.1	solute carrier family 36 (proton/amino acid symporter), member 1 [Source:HGNC Symbol;Acc:18761]
201089_at	ATP6V1B2	ENSG00000147416	0.030947129	0.97966903	10.05201136	9.072342335	8	p21.3	ATPase, H transporting, lysosomal 56/58kDa, V1 subunit B2 [Source:HGNC Symbol;Acc:854]
228937_at	LACC1	ENSG00000179630	0.030947129	1.434772368	7.870868743	6.436096375	13	q14.11	laccase (multicopper oxidoreductase) domain containing 1 [Source:HGNC Symbol;Acc:26789]
219666_at	MS4A6A	ENSG00000110077	0.031011469	2.158907191	10.17588351	8.016976319	11	q12.2	membrane-spanning 4-domains, subfamily A, member 6A [Source:HGNC Symbol;Acc:13375]
209160_at	AKR1C3	ENSG00000196139	0.031011469	1.558340801	6.702549633	5.144208832	10	p15.1	aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:386]
203688_at	PKD2	ENSG00000118762	0.031011469	1.22466397	8.101780908	6.877116938	4	q22.1	polycystic kidney disease 2 (autosomal dominant) [Source:HGNC Symbol;Acc:9009]
209379_s_at	CCSER2	ENSG00000107771	0.031011469	0.895302988	6.749214848	5.85391186	10	q23.1	coiled-coil serine-rich protein 2 [Source:HGNC Symbol;Acc:29197]
202973_x_at	FAM13A	ENSG00000138640	0.031011469	1.509075891	6.614676319	5.105600428	4	q22.1	family with sequence similarity 13, member A [Source:HGNC Symbol;Acc:19367]
222999_s_at	CCNL2	ENSG00000221978	0.031011469	0.586307213	9.418617885	8.832310673	1	p36.33	cyclin L2 [Source:HGNC Symbol;Acc:20570]
32811_at	MYO1C	ENSG00000197879	0.031087661	0.640476944	9.336456528	8.695979584	17	p13.3	myosin IC [Source:HGNC Symbol;Acc:7597]
213737_x_at	GOLGA8I	ENSG00000153666	0.031114275	1.284101363	9.220785563	7.9366842	15	q11.2	golgin A8 family, member I [Source:HGNC Symbol;Acc:26660]
202351_at	ITGAV	ENSG00000138448	0.031169046	1.360408955	9.310596989	7.950188034	2	q32.1	integrin, alpha V [Source:HGNC Symbol;Acc:6150]
226066_at	MITF	ENSG00000187098	0.031203036	1.394602359	8.259922404	6.865320045	3	p14.1	microphthalmia-associated transcription factor [Source:HGNC Symbol;Acc:7105]
212453_at	KIAA1279	ENSG00000198954	0.031374519	0.701033594	7.66960335	6.968569756	10	q22.1	KIAA1279 [Source:HGNC Symbol;Acc:23419]
223276_at	SMIM3	ENSG00000256235	0.031482467	1.057195825	7.313511684	6.256315859	5	q33.1	small integral membrane protein 3 [Source:HGNC Symbol;Acc:30248]
63825_at	ABHD2	ENSG00000140526	0.031482467	1.051003553	8.787774645	7.736771092	15	q26.1	abhydrolase domain containing 2 [Source:HGNC Symbol;Acc:18717]
203817_at	GUCY1B3	ENSG00000061918	0.031482467	1.374252812	7.677665745	6.303412934	4	q32.1	guanylate cyclase 1, soluble, beta 3 [Source:HGNC Symbol;Acc:4687]
232090_at	DNM3OS	ENSG00000230630	0.031482467	1.876637903	6.738189882	4.861551979	1	q24.3	DNM3 opposite strand/antisense RNA [Source:HGNC Symbol;Acc:41228]
218292_s_at	PRKAG2	ENSG00000106617	0.03162987	0.737763701	7.332144993	6.594381292	7	q36.1	protein kinase, AMP-activated, gamma 2 non-catalytic subunit [Source:HGNC Symbol;Acc:9386]
1558173_a_at	LUZP1	ENSG00000169641	0.03162987	0.796546664	9.005566311	8.209019647	1	p36.12	leucine zipper protein 1 [Source:HGNC Symbol;Acc:14985]
201438_at	COL6A3	ENSG00000163359	0.03162987	1.673097599	11.52000403	9.846906433	2	q37.3	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
235458_at	HAVCR2	ENSG00000135077	0.03162987	1.567140584	9.031225144	7.46408456	5	q33.3	hepatitis A virus cellular receptor 2 [Source:HGNC Symbol;Acc:18437]
223393_s_at	TSHZ3	ENSG00000121297	0.03162987	1.323992867	7.607905295	6.283912428	19	q12	teashirt zinc finger homeobox 3 [Source:HGNC Symbol;Acc:30700]

215706_x_at	ZYX	ENSG00000159840	0.031657402	0.877362553	10.7162578	9.838895242	7	q34	zyxin [Source:HGNC Symbol;Acc:13200]
219315_s_at	TMEM204	ENSG00000131634	0.031799565	0.945133516	7.656936821	6.711803305	16	p13.3	transmembrane protein 204 [Source:HGNC Symbol;Acc:14158]
201296_s_at	WSB1	ENSG00000109046	0.031799565	1.262242726	10.19943828	8.937195558	17	q11.1	WD repeat and SOCS box containing 1 [Source:HGNC Symbol;Acc:19221]
232231_at	RUNX2	ENSG00000124813	0.031799565	2.284394978	8.680094375	6.395699398	6	p21.1	runx-related transcription factor 2 [Source:HGNC Symbol;Acc:10472]
226225_at	MCC	ENSG00000171444	0.031799565	1.796214442	5.490904796	3.694690354	5	q22.2	mutated in colorectal cancers [Source:HGNC Symbol;Acc:6935]
214660_at	ITGA1	ENSG00000213949	0.031799565	0.935911859	4.662646523	3.726734663	5	q11.2	integrin, alpha 1 [Source:HGNC Symbol;Acc:6134]
216903_s_at	MICU1	ENSG00000107745	0.031799565	0.517945824	8.82526293	8.307317106	10	q22.1	mitochondrial calcium uptake 1 [Source:HGNC Symbol;Acc:1530]
215111_s_at	TSC22D1	ENSG00000102804	0.031799565	1.489649253	9.321974172	7.832324919	13	q14.11	TSC22 domain family, member 1 [Source:HGNC Symbol;Acc:16826]
200782_at	ANXA5	ENSG00000164111	0.031799565	0.961354796	10.84305118	9.881696385	4	q27	annexin A5 [Source:HGNC Symbol;Acc:543]
226771_at	ATP8B2	ENSG00000143515	0.031799565	1.091181637	8.208903918	7.117722281	1	q21.3	ATPase, aminophospholipid transporter, class I, type 8B, member 2 [Source:HGNC Symbol;Acc:13534]
212185_x_at	MT2A	ENSG00000125148	0.031799565	1.014640934	12.3668934	11.35225247	16	q12.2	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
200986_at	SERPING1	ENSG00000149131	0.031970706	1.239835886	10.45704492	9.217209036	11	q12.1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 [Source:HGNC Symbol;Acc:1228]
221269_s_at	SH3BGR13	ENSG00000142669	0.031970706	0.564410347	11.47106325	10.9066529	1	p36.11	SH3 domain binding glutamic acid-rich protein like 3 [Source:HGNC Symbol;Acc:15568]
202081_at	IER2	ENSG00000160888	0.031970706	1.223949737	10.27326737	9.049317631	19	p13.2	immediate early response 2 [Source:HGNC Symbol;Acc:28871]
206995_x_at	SCARF1	ENSG00000074660	0.0324388	0.731394685	6.493193087	5.761798402	17	p13.3	scavenger receptor class F, member 1 [Source:HGNC Symbol;Acc:16820]
204963_at	SSPN	ENSG00000123096	0.032493399	1.977402115	7.971609463	5.994207348	12	p12.1	sarcospan [Source:HGNC Symbol;Acc:11322]
202192_s_at	GAS7	ENSG00000007237	0.032688533	1.055406528	9.145390855	8.089984326	17	p13.1	growth arrest-specific 7 [Source:HGNC Symbol;Acc:4169]
224747_at	UBE2Q2	ENSG00000140367	0.032688533	1.004434491	8.252426793	7.247992302	15	q24.2	ubiquitin-conjugating enzyme E2Q family member 2 [Source:HGNC Symbol;Acc:19248]
202136_at	ZMYND11	ENSG00000015171	0.032688533	1.001702173	9.778629696	8.776927523	10	p15.3	zinc finger, MYND-type containing 11 [Source:HGNC Symbol;Acc:16966]
209970_x_at	CASP1	ENSG00000137752	0.032709967	1.260485478	9.149474702	7.888989224	11	q22.3	caspase 1, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:1499]
234987_at	SAMHD1	ENSG00000101347	0.032726724	1.416504141	9.200321126	7.783816985	20	q11.23	SAM domain and HD domain 1 [Source:HGNC Symbol;Acc:15925]
205173_x_at	CD58	ENSG00000116815	0.032726724	1.604544482	9.908500357	8.303955875	1	p13.1	CD58 molecule [Source:HGNC Symbol;Acc:1688]
229732_at	ZNF823	ENSG00000197933	0.032726724	0.521251726	4.981580656	4.46032893	19	p13.2	zinc finger protein 823 [Source:HGNC Symbol;Acc:30936]
37408_at	MRC2	ENSG0000011028	0.032726724	0.976917275	9.119459522	8.142542247	17	q23.2	mannose receptor, C type 2 [Source:HGNC Symbol;Acc:16875]
208922_s_at	NXF1	ENSG00000162231	0.032726724	0.716558245	10.10896656	9.392408317	11	q12.3	nuclear RNA export factor 1 [Source:HGNC Symbol;Acc:8071]
200766_at	CTSD	ENSG00000117984	0.032726724	1.031649441	11.05559476	10.02394532	11	p15.5	cathepsin D [Source:HGNC Symbol;Acc:2529]
209129_at	TRIP6	ENSG00000087077	0.032726724	0.614395443	8.270124739	7.655729295	7	q22.1	thyroid hormone receptor interactor 6 [Source:HGNC Symbol;Acc:12311]
228728_at	CPED1	ENSG00000106034	0.032726724	1.325706695	6.216332514	4.890625819	7	q31.31	cadherin-like and PC-esterase domain containing 1 [Source:HGNC Symbol;Acc:26159]
223028_s_at	SNX9	ENSG00000130340	0.032726724	1.546959073	9.600897425	8.053938352	6	q25.3	sorting nexin 9 [Source:HGNC Symbol;Acc:14973]
214464_at	CDC42BPA	ENSG00000143776	0.032726724	1.59035691	8.71190947	7.12155256	1	q42.13	CDC42 binding protein kinase alpha (DMPK-like) [Source:HGNC Symbol;Acc:1737]
204059_s_at	ME1	ENSG00000065833	0.032726724	2.130953781	7.883910609	5.752956829	6	q14.2	malic enzyme 1, NADP(+)-dependent, cytosolic [Source:HGNC Symbol;Acc:6983]
202481_at	DHRS3	ENSG00000162496	0.032726724	1.355717458	9.373900183	8.018182725	1	p36.22	dehydrogenase/reductase (SDR family) member 3 [Source:HGNC Symbol;Acc:17693]
201426_s_at	VIM	ENSG00000026025	0.032726724	0.861969983	13.16643703	12.30446705	10	p13	vimentin [Source:HGNC Symbol;Acc:12692]
214177_s_at	PBXIP1	ENSG00000163346	0.032726724	0.643944864	8.558973921	7.915029058	1	q21.3	pre-B-cell leukemia homeobox interacting protein 1 [Source:HGNC

									Symbol;Acc:21199]
218793_s_at	SCML1	ENSG00000047634	0.032726724	1.794930413	7.348371208	5.553440795	X	p22.13	sex comb on midleg-like 1 (Drosophila) [Source:HGNC Symbol;Acc:10580]
201163_s_at	IGFBP7	ENSG000000163453	0.032726724	1.277289099	11.02178563	9.744496534	4	q12	insulin-like growth factor binding protein 7 [Source:HGNC Symbol;Acc:5476]
225406_at	TWSG1	ENSG000000128791	0.032726724	1.015495797	8.499218476	7.483722679	18	p11.22	twisted gastrulation homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:12429]
209071_s_at	RG55	ENSG000000143248	0.032726724	1.999256143	9.334305908	7.335049765	1	q23.3	regulator of G-protein signaling 5 [Source:HGNC Symbol;Acc:10001]
204206_at	MNT	ENSG00000070444	0.032726724	0.454316598	8.034279619	7.579963021	17	p13.3	MNT, MAX dimerization protein [Source:HGNC Symbol;Acc:7188]
226026_at	DIRC2	ENSG000000138463	0.032726724	1.212593407	8.349561256	7.136967849	3	q21.1	disrupted in renal carcinoma 2 [Source:HGNC Symbol;Acc:16628]
214683_s_at	CLK1	ENSG00000013441	0.032726724	0.921509328	10.05348313	9.131973801	2	q33.1	CDC-like kinase 1 [Source:HGNC Symbol;Acc:2068]
218095_s_at	TMEM165	ENSG000000134851	0.032726724	0.788171748	10.38714798	9.598976234	4	q12	transmembrane protein 165 [Source:HGNC Symbol;Acc:30760]
219316_s_at	FLVCR2	ENSG000000119686	0.032726724	0.85580157	7.371184456	6.515382886	14	q24.3	feline leukemia virus subgroup C cellular receptor family, member 2 [Source:HGNC Symbol;Acc:20105]
226763_at	SESTD1	ENSG000000187231	0.032726724	1.059647685	9.5497248	8.490077115	2	q31.2	SEC14 and spectrin domains 1 [Source:HGNC Symbol;Acc:18379]
227361_at	HS3ST3B1	ENSG000000125430	0.032726724	1.522718422	7.752502237	6.229783816	17	p12	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 [Source:HGNC Symbol;Acc:5198]
205248_at	DOPEY2	ENSG000000142197	0.032726724	0.619809007	7.178374889	6.558366882	21	q22.12	dopey family member 2 [Source:HGNC Symbol;Acc:1291]
211026_s_at	MGLL	ENSG00000074416	0.032726724	1.34626057	9.704250583	8.357990013	3	q21.3	monoglyceride lipase [Source:HGNC Symbol;Acc:17038]
212224_at	ALDH1A1	ENSG000000165092	0.032726724	2.327986623	9.644018097	7.316031474	9	q21.13	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC Symbol;Acc:402]
201215_at	PLS3	ENSG000000102024	0.032726724	1.846069002	7.903700354	6.057631352	X	q23	plastin 3 [Source:HGNC Symbol;Acc:9091]
218432_at	FBXO3	ENSG000000110429	0.032726724	0.969202811	6.759587278	5.790384467	11	p13	F-box protein 3 [Source:HGNC Symbol;Acc:13582]
212428_at	KIAA0368	ENSG000000136813	0.032726724	0.502712224	8.880960464	8.37824824	9	q31.3	KIAA0368 [Source:HGNC Symbol;Acc:29020]
203394_s_at	HES1	ENSG000000114315	0.032726724	1.18052545	9.074966195	7.894440745	3	q29	hair and enhancer of split 1, (Drosophila) [Source:HGNC Symbol;Acc:5192]
235125_x_at	FAM73A	ENSG000000180488	0.032726724	0.78900753	6.551390988	5.762383458	1	p31.1	family with sequence similarity 73, member A [Source:HGNC Symbol;Acc:24741]
224690_at	FAM210B	ENSG000000124098	0.032726724	1.21859774	8.947455594	7.728857855	20	q13.2	family with sequence similarity 210, member B [Source:HGNC Symbol;Acc:16102]
219991_at	SLC2A9	ENSG000000109667	0.032726724	0.745206521	7.42728002	6.6820735	4	p16.1	solute carrier family 2 (facilitated glucose transporter), member 9 [Source:HGNC Symbol;Acc:13446]
214560_at	FPR3	ENSG000000187474	0.032726724	1.552547402	10.11158701	8.559039603	19	q13.41	formyl peptide receptor 3 [Source:HGNC Symbol;Acc:3828]
210946_at	PPAP2A	ENSG000000067113	0.032726724	0.869426384	8.48212043	7.612694046	5	q11.2	phosphatidic acid phosphatase type 2A [Source:HGNC Symbol;Acc:9228]
210817_s_at	CALCOCO2	ENSG000000136436	0.032726724	0.901072122	10.04861929	9.147547173	17	q21.32	calcium binding and coiled-coil domain 2 [Source:HGNC Symbol;Acc:29912]
208636_at	ACTN1	ENSG000000072110	0.032726724	1.492130835	9.059966788	7.567835952	14	q24.1	actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
1561226_at	XCR1	ENSG000000173578	0.032726724	0.928038272	4.98061814	4.052579867	3	p21.31	chemokine (C motif) receptor 1 [Source:HGNC Symbol;Acc:1625]
229256_at	PGM2L1	ENSG000000165434	0.032726724	0.950253856	6.806744083	5.856490226	11	q13.4	phosphoglucomutase 2-like 1 [Source:HGNC Symbol;Acc:20898]
228131_at	ERCC1	ENSG00000012061	0.032726724	0.698680629	8.644377717	7.945697089	19	q13.32	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence) [Source:HGNC Symbol;Acc:3433]
209310_s_at	CASP4	ENSG000000196954	0.032735931	0.910389382	10.59028021	9.679890826	11	q22.3	caspase 4, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:1505]
218729_at	LXN	ENSG00000079257	0.032735931	1.373435682	9.36297787	7.989542188	3	q25.32	latexin [Source:HGNC Symbol;Acc:13347]
227274_at	SYNJ2BP	ENSG000000213463	0.032835037	0.945655293	8.969654087	8.023998795	14	q24.2	synaptojanin 2 binding protein [Source:HGNC Symbol;Acc:18955]

219147_s_at	NMRK1	ENSG00000106733	0.032835037	1.031303038	8.134786202	7.103483164	9	q21.13	nicotinamide riboside kinase 1 [Source:HGNC Symbol;Acc:26057]
205083_at	AOX1	ENSG00000138356	0.032835037	1.344757535	6.346468615	5.001711108	2	q33.1	aldehyde oxidase 1 [Source:HGNC Symbol;Acc:553]
209109_s_at	TSPAN6	ENSG00000000003	0.032869735	1.316302616	7.197532473	5.881229857	X	q22.1	tetraspanin 6 [Source:HGNC Symbol;Acc:11858]
225303_at	KIRREL	ENSG00000183853	0.032869735	1.284466775	7.658036153	6.373569378	1	q23.1	kin of IRRE like (Drosophila) [Source:HGNC Symbol;Acc:15734]
225185_at	MRAS	ENSG00000158186	0.032869735	1.037700745	7.834458987	6.796758242	3	q22.3	muscle RAS oncogene homolog [Source:HGNC Symbol;Acc:7227]
203716_s_at	DPP4	ENSG00000197635	0.032869735	1.50992049	8.788771757	7.278851267	2	q24.2	dipeptidyl-peptidase 4 [Source:HGNC Symbol;Acc:3009]
204342_at	SLC25A24	ENSG00000085491	0.032869735	0.999800872	8.623812513	7.624011641	1	p13.3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24 [Source:HGNC Symbol;Acc:20662]
202948_at	IL1R1	ENSG00000115594	0.033187995	1.749785268	8.584052713	6.834267445	2	q11.2	interleukin 1 receptor, type I [Source:HGNC Symbol;Acc:5993]
212511_at	PICALM	ENSG00000073921	0.033187995	0.742253285	6.915631282	6.173377997	11	q14.2	phosphatidylinositol binding clathrin assembly protein [Source:HGNC Symbol;Acc:15514]
214429_at	MTMR6	ENSG00000139505	0.033465507	0.769730363	8.954554788	8.184824425	13	q12.13	myotubularin related protein 6 [Source:HGNC Symbol;Acc:7453]
214021_x_at	ITGB5	ENSG00000082781	0.033488347	1.43597723	6.631668819	5.19569159	3	q21.2	integrin, beta 5 [Source:HGNC Symbol;Acc:6160]
227624_at	TET2	ENSG00000168769	0.033488347	1.07690976	7.558846267	6.481936507	4	q24	tet methylcytosine dioxygenase 2 [Source:HGNC Symbol;Acc:25941]
225093_at	UTRN	ENSG00000152818	0.033488347	1.565715389	10.04128739	8.475571999	6	q24.2	utrophin [Source:HGNC Symbol;Acc:12635]
227379_at	MBOAT1	ENSG00000172197	0.033637219	1.226714416	7.197726855	5.971012439	6	p22.3	membrane bound O-acyltransferase domain containing 1 [Source:HGNC Symbol;Acc:21579]
213139_at	SNAI2	ENSG0000019549	0.033800859	1.549581679	6.953320081	5.403738401	8	q11.21	snail family zinc finger 2 [Source:HGNC Symbol;Acc:11094]
212099_at	RHOB	ENSG00000143878	0.033800859	1.563197657	9.851472658	8.288275001	2	p24.1	ras homolog family member B [Source:HGNC Symbol;Acc:668]
204894_s_at	AOC3	ENSG00000131471	0.033800859	1.488715186	6.950874216	5.46215903	17	q21.31	amine oxidase, copper containing 3 [Source:HGNC Symbol;Acc:550]
219432_at	EVC	ENSG00000072840	0.033800859	0.973495437	7.657380766	6.683885329	4	p16.2	Ellis van Creveld syndrome [Source:HGNC Symbol;Acc:3497]
55065_at	MARK4	ENSG00000007047	0.033800859	0.450131769	7.655069099	7.204937331	19	q13.32	MAP/microtubule affinity-regulating kinase 4 [Source:HGNC Symbol;Acc:13538]
226353_at	SPPL2A	ENSG00000138600	0.034000797	1.086036284	9.82423751	8.738201226	15	q21.2	signal peptide peptidase like 2A [Source:HGNC Symbol;Acc:30227]
216598_s_at	CCL2	ENSG00000108691	0.034000797	1.574100327	11.80437366	10.23027333	17	q12	chemokine (C-C motif) ligand 2 [Source:HGNC Symbol;Acc:10618]
226568_at	FAM102B	ENSG00000162636	0.034000797	1.19493473	7.320320998	6.125386268	1	p13.3	family with sequence similarity 102, member B [Source:HGNC Symbol;Acc:27637]
218764_at	PRKCH	ENSG00000027075	0.034090749	1.324224837	8.842467348	7.518242511	14	q23.1	protein kinase C, eta [Source:HGNC Symbol;Acc:9403]
225984_at	PRKAA1	ENSG00000132356	0.034117995	0.761625478	6.863441712	6.101816234	5	p13.1	protein kinase, AMP-activated, alpha 1 catalytic subunit [Source:HGNC Symbol;Acc:9376]
201542_at	SAR1A	ENSG00000079332	0.034117995	0.735645671	9.772431133	9.036785462	10	q22.1	SAR1 homolog A (S. cerevisiae) [Source:HGNC Symbol;Acc:10534]
203455_s_at	SAT1	ENSG00000130066	0.034117995	1.316520019	11.13299333	9.816473307	X	p22.11	spermidine/spermine N1-acetyltransferase 1 [Source:HGNC Symbol;Acc:10540]
225922_at	FNIP2	ENSG00000052795	0.034117995	1.519527523	8.166224411	6.646696888	4	q32.1	folliculin interacting protein 2 [Source:HGNC Symbol;Acc:29280]
218665_at	FZD4	ENSG00000174804	0.034117995	1.021163189	7.416230764	6.395067575	11	q14.2	frizzled family receptor 4 [Source:HGNC Symbol;Acc:4042]
221666_s_at	PYCARD	ENSG00000103490	0.034190831	0.606108157	9.397235781	8.791127624	16	p11.2	PYD and CARD domain containing [Source:HGNC Symbol;Acc:16608]
201058_s_at	MYL9	ENSG00000101335	0.034190831	1.2676991	10.37627198	9.108572878	20	q11.23	myosin, light chain 9, regulatory [Source:HGNC Symbol;Acc:15754]
203397_s_at	GALNT3	ENSG00000115339	0.034190831	1.306640305	5.45104883	4.144408525	2	q24.3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3) [Source:HGNC Symbol;Acc:4125]
222453_at	CYBRD1	ENSG00000071967	0.034190831	1.315727811	9.001391772	7.685663961	2	q31.1	cytochrome b reductase 1 [Source:HGNC Symbol;Acc:20797]
208146_s_at	CPVL	ENSG00000106066	0.034190831	1.943264679	9.534937034	7.591672354	7	p14.3	carboxypeptidase, vitellogenic-like [Source:HGNC Symbol;Acc:14399]
227334_at	USP54	ENSG00000166348	0.034190831	0.595004786	7.632456518	7.037451732	10	q22.2	ubiquitin specific peptidase 54 [Source:HGNC Symbol;Acc:23513]
226534_at	KITLG	ENSG00000049130	0.034190831	1.687120279	6.504808499	4.81768822	12	q21.32	KIT ligand [Source:HGNC Symbol;Acc:6343]
229120_s_at	CDC42SE1	ENSG00000197622	0.034190831	1.026120843	9.039741792	8.013620949	1	q21.3	CDC42 small effector 1 [Source:HGNC Symbol;Acc:17719]

225066_at	PPP2R2D	ENSG00000175470	0.034190831	0.410023152	6.51512502	6.105101868	10	q26.3	protein phosphatase 2, regulatory subunit B, delta [Source:HGNC Symbol;Acc:23732]
211977_at	GPR107	ENSG00000148358	0.034190831	0.41506351	7.323330309	6.908266799	9	q34.11	G protein-coupled receptor 107 [Source:HGNC Symbol;Acc:17830]
217967_s_at	FAM129A	ENSG00000135842	0.034190831	1.631617618	9.361851904	7.730234286	1	q25.3	family with sequence similarity 129, member A [Source:HGNC Symbol;Acc:16784]
207705_s_at	NINL	ENSG00000101004	0.034190831	0.458032479	7.469271682	7.011239203	20	p11.21	ninein-like [Source:HGNC Symbol;Acc:29163]
230029_x_at	UBR3	ENSG00000144357	0.034212391	0.713232741	7.406813979	6.693581237	2	q31.1	ubiquitin protein ligase E3 component n-recogin 3 (putative) [Source:HGNC Symbol;Acc:30467]
227236_at	TSPAN2	ENSG00000134198	0.034240086	1.160525883	6.827257615	5.666731733	1	p13.2	tetraspanin 2 [Source:HGNC Symbol;Acc:20659]
202510_s_at	TNFAIP2	ENSG00000185215	0.034240086	1.611311545	10.98695296	9.375641416	14	q32.32	tumor necrosis factor, alpha-induced protein 2 [Source:HGNC Symbol;Acc:11895]
202450_s_at	CTSK	ENSG00000143387	0.034333589	2.058768294	10.34330275	8.284534455	1	q21.3	cathepsin K [Source:HGNC Symbol;Acc:2536]
226395_at	HOOK3	ENSG00000168172	0.034360811	0.907384172	9.099732802	8.192348631	8	p11.21	hook homolog 3 (Drosophila) [Source:HGNC Symbol;Acc:23576]
219403_s_at	HPSE	ENSG00000173083	0.034374363	1.273377491	7.073411349	5.800033858	4	q21.23	heparanase [Source:HGNC Symbol;Acc:5164]
227623_at	CACNA2D1	ENSG00000153956	0.034401348	1.509374159	5.523191348	4.013817189	7	q21.11	calcium channel, voltage-dependent, alpha 2/delta subunit 1 [Source:HGNC Symbol;Acc:1399]
202239_at	PARP4	ENSG00000102699	0.034401348	0.920213526	9.568361079	8.648147553	13	q12.12	poly (ADP-ribose) polymerase family, member 4 [Source:HGNC Symbol;Acc:271]
204646_at	DPYD	ENSG00000188641	0.034480931	1.716538106	8.184742	6.468203894	1	p21.3	dihydropyrimidine dehydrogenase [Source:HGNC Symbol;Acc:3012]
209335_at	DCN	ENSG00000011465	0.034606801	2.0562205	8.106748111	6.050527611	12	q21.33	decorin [Source:HGNC Symbol;Acc:2705]
202341_s_at	TRIM2	ENSG00000109654	0.034606801	1.154998273	7.682678312	6.527680038	4	q31.3	tripartite motif containing 2 [Source:HGNC Symbol;Acc:15974]
203386_at	TBC1D4	ENSG00000136111	0.034611968	1.59863556	9.927925002	8.329289442	13	q22.2	TBC1 domain family, member 4 [Source:HGNC Symbol;Acc:19165]
202465_at	PCOLCE	ENSG00000106333	0.034687227	1.110793856	9.858341328	8.747547472	7	q22.1	procollagen C-endopeptidase enhancer [Source:HGNC Symbol;Acc:8738]
218501_at	ARHGEF3	ENSG00000163947	0.034710054	1.211901006	9.645778775	8.433877769	3	p14.3	Rho guanine nucleotide exchange factor (GEF) 3 [Source:HGNC Symbol;Acc:683]
203935_at	ACVR1	ENSG00000115170	0.034710054	0.929748525	7.592939572	6.663191047	2	q24.1	activin A receptor, type I [Source:HGNC Symbol;Acc:171]
227726_at	RNF166	ENSG00000158717	0.034778201	0.765255386	6.490241897	5.724986511	16	q24.3	ring finger protein 166 [Source:HGNC Symbol;Acc:28856]
225351_at	FAM45A	ENSG00000119979	0.034778201	0.712687022	7.985558444	7.272871422	10	q26.11	family with sequence similarity 45, member A [Source:HGNC Symbol;Acc:31793]
209967_s_at	CREM	ENSG00000095794	0.034778201	1.498708212	8.008162888	6.509454676	10	p11.21	cAMP responsive element modulator [Source:HGNC Symbol;Acc:2352]
217767_at	C3	ENSG00000125730	0.034901896	1.610302964	11.06255643	9.452253469	19	p13.3	complement component 3 [Source:HGNC Symbol;Acc:1318]
202377_at	LEPROT	ENSG00000213625	0.034901896	0.958758279	8.927718442	7.968960164	1	p31.3	leptin receptor overlapping transcript [Source:HGNC Symbol;Acc:29477]
212067_s_at	C1R	ENSG00000159403	0.034901896	1.095883775	10.97729778	9.881414002	12	p13.31	complement component 1, r subcomponent [Source:HGNC Symbol;Acc:1246]
206461_x_at	MT1H	ENSG00000205358	0.034906504	0.937479848	10.94110484	10.00362499	16	q13	metallothionein 1H [Source:HGNC Symbol;Acc:7400]
212651_at	RHOBTB1	ENSG00000072422	0.034920435	1.278051787	5.30325947	4.025207683	10	q21.2	Rho-related BTB domain containing 1 [Source:HGNC Symbol;Acc:18738]
213077_at	YTHDC2	ENSG00000047188	0.034920435	1.082274718	7.160912963	6.078638245	5	q22.2	YTH domain containing 2 [Source:HGNC Symbol;Acc:24721]
238617_at	KIF26B	ENSG00000162849	0.034920435	1.816726723	7.548086863	5.73136014	1	q44	kinesin family member 26B [Source:HGNC Symbol;Acc:25484]
201540_at	FHL1	ENSG00000022267	0.034920435	2.090914464	8.481468308	6.390553844	X	q26.3	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:3702]
227325_at	PRR24	ENSG00000257704	0.034920435	0.590098253	7.823937835	7.233839582	19	q13.32	proline rich 24 [Source:HGNC Symbol;Acc:27406]
208093_s_at	NDEL1	ENSG00000166579	0.034947401	0.741034838	8.576080766	7.835045928	17	p13.1	nudE nuclear distribution E homolog (A. nidulans)-like 1 [Source:HGNC Symbol;Acc:17620]
202006_at	PTPN12	ENSG00000127947	0.035088557	1.018262804	9.540273742	8.522010938	7	q11.23	protein tyrosine phosphatase, non-receptor type 12 [Source:HGNC

									Symbol;Acc:9645]
209216_at	WDR45	ENSG00000196998	0.035088557	0.696795004	8.826888223	8.130093219	X	p11.23	WD repeat domain 45 [Source:HGNC Symbol;Acc:28912]
225782_at	MSRB3	ENSG00000174099	0.035088557	1.444375496	6.51471588	5.070340384	12	q14.3	methionine sulfoxide reductase B3 [Source:HGNC Symbol;Acc:27375]
200602_at	APP	ENSG00000142192	0.035088557	1.325930012	9.055534642	7.729604631	21	q21.3	amyloid beta (A4) precursor protein [Source:HGNC Symbol;Acc:620]
226939_at	CPEB2	ENSG00000137449	0.035264082	1.226498712	7.611624387	6.385125675	4	p15.33	cytoplasmic polyadenylation element binding protein 2 [Source:HGNC Symbol;Acc:21745]
218986_s_at	DDX60	ENSG00000137628	0.035316356	1.486021371	8.318531076	6.832509705	4	q32.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 [Source:HGNC Symbol;Acc:25942]
203139_at	DAPK1	ENSG00000196730	0.035316356	1.707948936	8.912548269	7.204599333	9	q21.33	death-associated protein kinase 1 [Source:HGNC Symbol;Acc:2674]
213764_s_at	MFAP5	ENSG00000197614	0.035434896	1.297982185	5.790529452	4.492547267	12	p13.31	microfibrillar associated protein 5 [Source:HGNC Symbol;Acc:29673]
202565_s_at	SVIL	ENSG00000197321	0.035639458	1.389051153	8.635444721	7.246393568	10	p11.23	supervillin [Source:HGNC Symbol;Acc:11480]
210968_s_at	RTN4	ENSG00000115310	0.035770121	0.829593112	10.69653249	9.866939383	2	p16.1	reticulin 4 [Source:HGNC Symbol;Acc:14085]
225562_at	RASA3	ENSG00000185989	0.035779896	0.972127539	9.062084532	8.089956993	13	q34	RAS p21 protein activator 3 [Source:HGNC Symbol;Acc:20331]
218454_at	PLBD1	ENSG00000121316	0.03578637	1.441982401	10.25391754	8.81193514	12	p13.1	phospholipase B domain containing 1 [Source:HGNC Symbol;Acc:26215]
209467_s_at	MKNK1	ENSG00000079277	0.035868055	0.783294393	8.294847035	7.511552642	1	p33	MAP kinase interacting serine/threonine kinase 1 [Source:HGNC Symbol;Acc:7110]
226869_at	MEGF6	ENSG00000162591	0.035950269	1.265043406	7.859101342	6.594057936	1	p36.32	multiple EGF-like-domains 6 [Source:HGNC Symbol;Acc:3232]
221569_at	AHI1	ENSG00000135541	0.035950269	1.076140591	7.793652098	6.717511506	6	q23.3	Abelson helper integration site 1 [Source:HGNC Symbol;Acc:21575]
1569157_s_at	ZNF846	ENSG00000196605	0.035950269	0.774623333	6.057018085	5.282394752	19	p13.2	zinc finger protein 846 [Source:HGNC Symbol;Acc:27260]
218132_s_at	TSEN34	ENSG00000170892	0.035950269	0.438866613	8.237398535	7.798531921	19	q13.42	tRNA splicing endonuclease 34 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:15506]
201591_s_at	NISCH	ENSG0000010322	0.036284071	0.405648171	8.996513107	8.590864936	3	p21.1	nischarin [Source:HGNC Symbol;Acc:18006]
227098_at	DUSP18	ENSG00000167065	0.036417437	0.482163643	7.203923142	6.721759499	22	q12.2	dual specificity phosphatase 18 [Source:HGNC Symbol;Acc:18484]
203910_at	ARHGAP29	ENSG00000137962	0.036417437	1.513169879	7.336341356	5.823171477	1	p21.3	Rho GTPase activating protein 29 [Source:HGNC Symbol;Acc:30207]
1555847_a_at	LOC284454	NA	0.036417437	0.929013425	9.021958303	8.092944878	NA	NA	NA
241353_s_at	LOC100507507	NA	0.036417437	0.563123987	6.938191846	6.375067858	NA	NA	NA
202225_at	CRK	ENSG00000167193	0.036417437	0.76604843	9.380487824	8.614439395	17	p13.3	v-crk avian sarcoma virus CT10 oncogene homolog [Source:HGNC Symbol;Acc:2362]
212915_at	PDZRN3	ENSG00000121440	0.036490985	1.312579319	6.719045192	5.406465873	3	p13	PDZ domain containing ring finger 3 [Source:HGNC Symbol;Acc:17704]
202920_at	ANK2	ENSG00000145362	0.036490985	1.463394123	8.12462823	6.661234107	4	q25	ankyrin 2, neuronal [Source:HGNC Symbol;Acc:493]
235391_at	FAM92A1	ENSG00000188343	0.036548329	0.621136179	7.223438844	6.602302665	8	q22.1	family with sequence similarity 92, member A1 [Source:HGNC Symbol;Acc:30452]
224906_at	ANO6	ENSG00000177119	0.036675313	0.877112362	8.66468344	7.787571078	12	q12	anoctamin 6 [Source:HGNC Symbol;Acc:25240]
227087_at	INPP4A	ENSG00000040933	0.036675313	1.026789448	8.031874294	7.005084846	2	q11.2	inositol polyphosphate-4-phosphatase, type I, 107kDa [Source:HGNC Symbol;Acc:6074]
225931_s_at	RNF213	ENSG00000173821	0.036802205	1.10725232	9.749178104	8.641925784	17	q25.3	ring finger protein 213 [Source:HGNC Symbol;Acc:14539]
212690_at	DDHD2	ENSG00000085788	0.036831284	0.878356205	9.176866822	8.298510616	8	p11.23	DDHD domain containing 2 [Source:HGNC Symbol;Acc:29106]
209003_at	SLC25A11	ENSG00000108528	0.036890888	0.43772317	7.954667222	7.516944052	17	p13.2	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 [Source:HGNC Symbol;Acc:10981]
202206_at	ARL4C	ENSG00000188042	0.036890888	1.389805117	9.321386817	7.9315817	2	q37.1	ADP-ribosylation factor-like 4C [Source:HGNC Symbol;Acc:698]
232000_at	TTC39B	ENSG00000155158	0.037068478	1.356512637	4.978732932	3.622220295	9	p22.3	tetratricopeptide repeat domain 39B [Source:HGNC

									Symbol;Acc:23704]
225386_s_at	HNRPLL	NA	0.037068478	1.459395359	9.121601553	7.662206194	NA	NA	NA
226409_at	TBC1D20	ENSG00000125875	0.037068478	0.505585753	8.965323908	8.459738154	20	p13	TBC1 domain family, member 20 [Source:HGNC Symbol;Acc:16133]
204066_s_at	AGAP1	ENSG00000157985	0.037087501	1.078941551	6.075080058	4.996138507	2	q37.2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 [Source:HGNC Symbol;Acc:16922]
212441_at	KIAA0232	ENSG00000170871	0.037087501	0.590210466	8.606785896	8.01657543	4	p16.1	KIAA0232 [Source:HGNC Symbol;Acc:28992]
225726_s_at	PLEKHH1	ENSG00000054690	0.037087501	0.952695106	5.964957706	5.0122626	14	q24.1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 [Source:HGNC Symbol;Acc:17733]
232094_at	KATNBL1	ENSG00000134152	0.037087501	0.5971703	7.264443135	6.667272835	15	q14	katanin p80 subunit B-like 1 [Source:HGNC Symbol;Acc:26199]
225604_s_at	GLIPR2	ENSG00000122694	0.037323559	0.853910711	7.844159209	6.990248499	9	p13.3	GLI pathogenesis-related 2 [Source:HGNC Symbol;Acc:18007]
205225_at	ESR1	ENSG00000091831	0.037323559	1.382468278	6.467921229	5.085452951	6	q25.1	estrogen receptor 1 [Source:HGNC Symbol;Acc:3467]
218838_s_at	TTC31	ENSG00000115282	0.037323559	0.672650224	8.524158479	7.851508256	2	p13.1	tetratricopeptide repeat domain 31 [Source:HGNC Symbol;Acc:25759]
227961_at	CTSB	ENSG00000164733	0.037323559	1.338139585	10.24117448	8.903034892	8	p23.1	cathepsin B [Source:HGNC Symbol;Acc:2527]
1558041_a_at	KIAA0895L	ENSG00000196123	0.037412554	0.876742459	7.925106663	7.048364204	16	q22.1	KIAA0895-like [Source:HGNC Symbol;Acc:34408]
209540_at	IGF1	ENSG00000017427	0.037412554	1.522509458	8.256633376	6.734123918	12	q23.2	insulin-like growth factor 1 (somatomedin C) [Source:HGNC Symbol;Acc:5464]
203651_at	ZFYVE16	ENSG00000039319	0.037412554	1.025141601	8.527484121	7.502342519	5	q14.1	zinc finger, FYVE domain containing 16 [Source:HGNC Symbol;Acc:20756]
224900_at	ANKFY1	ENSG00000185722	0.037546087	0.532952956	8.581470479	8.048517523	17	p13.2	ankyrin repeat and FYVE domain containing 1 [Source:HGNC Symbol;Acc:20763]
223441_at	SLC17A5	ENSG00000119899	0.037627191	0.645005952	6.824616025	6.179610072	6	q13	solute carrier family 17 (anion/sugar transporter), member 5 [Source:HGNC Symbol;Acc:10933]
204294_at	AMT	ENSG00000145020	0.037627191	0.399434215	8.335213696	7.935779481	3	p21.31	aminomethyltransferase [Source:HGNC Symbol;Acc:473]
204040_at	RNF144A	ENSG00000151692	0.037681586	1.481347774	6.933003595	5.451655821	2	p25.2	ring finger protein 144A [Source:HGNC Symbol;Acc:20457]
225272_at	SAT2	ENSG00000141504	0.037706134	0.618612094	9.078150553	8.459538459	17	p13.1	spermidine/spermine N1-acetyltransferase family member 2 [Source:HGNC Symbol;Acc:23160]
204464_s_at	EDNRA	ENSG00000151617	0.037706134	1.424834074	7.176770385	5.751936311	4	q31.22	endothelin receptor type A [Source:HGNC Symbol;Acc:3179]
205011_at	VWA5A	ENSG00000110002	0.037706134	1.501068828	8.178126937	6.677058109	11	q24.2	von Willebrand factor A domain containing 5A [Source:HGNC Symbol;Acc:6658]
212765_at	CAMSAP2	ENSG00000118200	0.037713812	1.070277586	7.585165033	6.514887447	1	q32.1	calmodulin regulated spectrin-associated protein family, member 2 [Source:HGNC Symbol;Acc:29188]
212624_s_at	CHN1	ENSG00000128656	0.037754756	1.199366569	8.339419696	7.140053127	2	q31.1	chimerin 1 [Source:HGNC Symbol;Acc:1943]
209213_at	CBR1	ENSG00000159228	0.037828214	0.716339962	9.378175666	8.661835705	21	q22.12	carbonyl reductase 1 [Source:HGNC Symbol;Acc:1548]
207738_s_at	NCKAP1	ENSG00000061676	0.037828214	1.742016807	5.909031575	4.167014768	2	q32.1	NCK-associated protein 1 [Source:HGNC Symbol;Acc:7666]
206856_at	LILRB5	ENSG00000105609	0.037950057	1.58731928	8.757091921	7.169772641	19	q13.42	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 [Source:HGNC Symbol;Acc:6609]
200697_at	HK1	ENSG00000156515	0.03798879	0.497080421	10.98016503	10.48308461	10	q22.1	hexokinase 1 [Source:HGNC Symbol;Acc:4922]
219134_at	ELTD1	ENSG00000162618	0.038039799	1.633116993	7.99727279	6.364155796	1	p31.1	EGF, latrophilin and seven transmembrane domain containing 1 [Source:HGNC Symbol;Acc:20822]
222294_s_at	RAB27A	ENSG00000069974	0.038154279	1.512875635	7.227372685	5.71449705	15	q21.3	RAB27A, member RAS oncogene family [Source:HGNC Symbol;Acc:9766]
201057_s_at	GOLGB1	ENSG00000173230	0.038450193	0.639618056	9.22083416	8.581216104	3	q13.33	golgin B1 [Source:HGNC Symbol;Acc:4429]
218017_s_at	HGSNAT	ENSG00000165102	0.038566561	1.101893048	8.583362968	7.48146992	8	p11.21	heparan-alpha-glucosaminide N-acetyltransferase [Source:HGNC Symbol;Acc:26527]
226905_at	FAM101B	ENSG00000183688	0.038659566	1.355638698	8.83238214	7.476743442	17	p13.3	family with sequence similarity 101, member B [Source:HGNC Symbol;Acc:28705]
226616_s_at	NDUFV3	ENSG00000160194	0.038671508	0.66206984	10.46600414	9.803934298	21	q22.3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa

									[Source:HGNC Symbol;Acc:7719]
215127_s_at	RBMS1	ENSG00000153250	0.038707721	0.985761408	9.060146035	8.074384626	2	q24.2	RNA binding motif, single stranded interacting protein 1 [Source:HGNC Symbol;Acc:9907]
212373_at	FEM1B	ENSG00000169018	0.03889702	0.961868668	8.42816521	7.466295542	15	q23	fem-1 homolog b (C. elegans) [Source:HGNC Symbol;Acc:3649]
222750_s_at	SRD5A3	ENSG00000128039	0.03889702	0.762605382	8.2518174	7.489212018	4	q12	steroid 5 alpha-reductase 3 [Source:HGNC Symbol;Acc:25812]
236006_s_at	AKAP10	ENSG00000108599	0.039007321	0.655037688	7.828287091	7.173249402	17	p11.2	A kinase (PRKA) anchor protein 10 [Source:HGNC Symbol;Acc:368]
224733_at	CMTM3	ENSG00000140931	0.039181923	0.690269684	9.982739003	9.292469319	16	q21	CKLF-like MARVEL transmembrane domain containing 3 [Source:HGNC Symbol;Acc:19174]
204981_at	SLC22A18	ENSG00000110628	0.039181923	0.561183888	7.589939798	7.028755911	11	p15.4	solute carrier family 22, member 18 [Source:HGNC Symbol;Acc:10964]
223077_at	TMOD3	ENSG00000138594	0.039239917	1.092206647	7.964720713	6.872514066	15	q21.2	tropomodulin 3 (ubiquitous) [Source:HGNC Symbol;Acc:11873]
209686_at	S100B	ENSG00000160307	0.039241475	0.901290569	6.761868136	5.860577567	21	q22.3	S100 calcium binding protein B [Source:HGNC Symbol;Acc:10500]
225325_at	MFSD6	ENSG00000151690	0.039241475	0.839407884	8.69192971	7.852521826	2	q32.2	major facilitator superfamily domain containing 6 [Source:HGNC Symbol;Acc:24711]
205236_x_at	SOD3	ENSG00000109610	0.03957993	0.891900627	8.45163302	7.559732393	4	p15.2	superoxide dismutase 3, extracellular [Source:HGNC Symbol;Acc:11181]
228220_at	FCHO2	ENSG00000157107	0.03957993	1.563762465	8.795856173	7.232093708	5	q13.2	FCH domain only 2 [Source:HGNC Symbol;Acc:25180]
205904_at	MICA	ENSG00000204520	0.03957993	0.427228475	7.684753887	7.257525412	6	p21.33	MHC class I polypeptide-related sequence A [Source:HGNC Symbol;Acc:7090]
226777_at	ADAM12	ENSG00000148848	0.03957993	1.943247065	7.771445066	5.828198001	10	q26.2	ADAM metalloproteinase domain 12 [Source:HGNC Symbol;Acc:190]
213618_at	ARAP2	ENSG00000047365	0.03957993	1.028082071	7.620559319	6.592477248	4	p14	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2 [Source:HGNC Symbol;Acc:16924]
205624_at	CPA3	ENSG00000163751	0.03957993	2.151198872	6.492961642	4.34176277	3	q24	carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:2298]
215268_at	KIAA0754	ENSG00000255103	0.03957993	0.809104773	6.285140538	5.476035765	1	p34.3	KIAA0754 [Source:HGNC Symbol;Acc:29111]
203672_x_at	TPMT	ENSG00000137364	0.03957993	0.554375735	9.623390267	9.069014532	6	p22.3	thiopurine S-methyltransferase [Source:HGNC Symbol;Acc:12014]
1555229_a_at	C1S	ENSG00000182326	0.03957993	1.562833271	10.46271064	8.899877365	12	p13.31	complement component 1, s subcomponent [Source:HGNC Symbol;Acc:1247]
203855_at	WDR47	ENSG00000085433	0.03957993	0.715002164	7.128000627	6.412998464	1	p13.3	WD repeat domain 47 [Source:HGNC Symbol;Acc:29141]
207072_at	IL18RAP	ENSG00000115607	0.03957993	0.981690585	7.548943432	6.567252847	2	q12.1	interleukin 18 receptor accessory protein [Source:HGNC Symbol;Acc:5989]
221935_s_at	EOGT	ENSG00000163378	0.03960808	0.83587661	7.127103969	6.291227359	3	p14.1	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase [Source:HGNC Symbol;Acc:28526]
203232_s_at	ATXN1	ENSG00000124788	0.03960808	1.486472653	8.293823116	6.807350464	6	p22.3	ataxin 1 [Source:HGNC Symbol;Acc:10548]
202096_s_at	TSPQ	ENSG00000100300	0.039769597	0.618613605	9.561586207	8.942972602	22	q13.2	translocator protein (18kDa) [Source:HGNC Symbol;Acc:1158]
224813_at	WASL	ENSG00000106299	0.039769597	0.810234478	8.822272437	8.012037959	7	q31.32	Wiskott-Aldrich syndrome-like [Source:HGNC Symbol;Acc:12735]
213455_at	FAM114A1	ENSG00000197712	0.039797292	0.841637956	7.947071796	7.10543384	4	p14	family with sequence similarity 114, member A1 [Source:HGNC Symbol;Acc:25087]
226873_at	FAM63B	ENSG00000128923	0.039877715	0.781681687	7.054055786	6.272374099	15	q21.3	family with sequence similarity 63, member B [Source:HGNC Symbol;Acc:26954]
1554503_a_at	OSCAR	ENSG00000170909	0.040082873	0.481594381	6.652982594	6.171388213	19	q13.42	osteoclast associated, immunoglobulin-like receptor [Source:HGNC Symbol;Acc:29960]
206118_at	STAT4	ENSG00000138378	0.040381182	1.642843342	7.76374389	6.120900548	2	q32.3	signal transducer and activator of transcription 4 [Source:HGNC Symbol;Acc:11365]
210970_s_at	IBTK	ENSG00000005700	0.040543289	0.753886475	8.260872375	7.506985901	6	q14.1	inhibitor of Bruton agammaglobulinemia tyrosine kinase [Source:HGNC Symbol;Acc:17853]
227113_at	ADHFE1	ENSG00000147576	0.040543289	0.706136194	8.382822434	7.67668624	8	q13.1	alcohol dehydrogenase, iron containing, 1 [Source:HGNC Symbol;Acc:16354]

202949_s_at	FHL2	ENSG00000115641	0.040593602	1.403182627	7.613598294	6.210415667	2	q12.2	four and a half LIM domains 2 [Source:HGNC Symbol;Acc:3703]
225579_at	PQLC3	ENSG00000162976	0.040596862	1.113667847	9.537872547	8.4242047	2	p25.1	PQ loop repeat containing 3 [Source:HGNC Symbol;Acc:28503]
235291_s_at	FLJ32255	NA	0.040715697	1.119695897	7.867314072	6.747618175	NA	NA	NA
203939_at	NT5E	ENSG00000135318	0.040733387	0.806179248	7.42523104	6.619051792	6	q14.3	5'-nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:8021]
214274_s_at	ACAA1	ENSG00000060971	0.040793718	0.502419076	9.465451705	8.963032628	3	p22.2	acetyl-CoA acyltransferase 1 [Source:HGNC Symbol;Acc:82]
204046_at	PLCB2	ENSG00000137841	0.040802463	0.533783551	8.533797162	8.000013611	15	q15.1	phospholipase C, beta 2 [Source:HGNC Symbol;Acc:9055]
202392_s_at	PISD	ENSG00000241878	0.041073186	0.356364153	8.566583027	8.210218874	22	q12.2	phosphatidylserine decarboxylase [Source:HGNC Symbol;Acc:8999]
218326_s_at	LGR4	ENSG00000205213	0.041073186	1.255121429	5.022109926	3.766988497	11	p14.1	leucine-rich repeat containing G protein-coupled receptor 4 [Source:HGNC Symbol;Acc:13299]
229119_s_at	ZSWIM7	ENSG00000214941	0.041073186	1.024786314	7.910530196	6.885743882	17	p12	zinc finger, SWIM-type containing 7 [Source:HGNC Symbol;Acc:26993]
206491_s_at	NAPA	ENSG00000105402	0.041414647	0.495436416	9.333764247	8.838327831	19	q13.33	N-ethylmaleimide-sensitive factor attachment protein, alpha [Source:HGNC Symbol;Acc:7641]
227450_at	ERP27	ENSG00000139055	0.041414647	0.966196682	6.328914416	5.362717734	12	p12.3	endoplasmic reticulum protein 27 [Source:HGNC Symbol;Acc:26495]
200866_s_at	PSAP	ENSG00000197746	0.041414647	1.085359838	11.69848738	10.61312755	10	q22.1	prosaposin [Source:HGNC Symbol;Acc:9498]
200720_s_at	ACTR1A	ENSG00000138107	0.041414647	0.496753402	8.824861676	8.328108274	10	q24.32	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast) [Source:HGNC Symbol;Acc:167]
232064_at	FER	ENSG00000151422	0.041414647	0.656054594	7.136386009	6.480331415	5	q21.3	fer (fps/fes related) tyrosine kinase [Source:HGNC Symbol;Acc:3655]
217922_at	MAN1A2	ENSG00000198162	0.04144504	0.69736844	8.202283201	7.504914761	1	p12	mannosidase, alpha, class 1A, member 2 [Source:HGNC Symbol;Acc:6822]
201944_at	HEXB	ENSG00000049860	0.041569794	1.010944746	11.59320288	10.58225814	5	q13.3	hexosaminidase B (beta polypeptide) [Source:HGNC Symbol;Acc:4879]
210986_s_at	TPM1	ENSG00000140416	0.041569794	1.650337469	9.944608224	8.294270755	15	q22.2	tropomyosin 1 (alpha) [Source:HGNC Symbol;Acc:12010]
227568_at	HECTD2	ENSG00000165338	0.041569794	1.119931753	6.685060885	5.565129131	10	q23.32	HECT domain containing E3 ubiquitin protein ligase 2 [Source:HGNC Symbol;Acc:26736]
200645_at	GABARAP	ENSG00000170296	0.041569794	0.631747342	11.38104358	10.74929624	17	p13.1	GABA(A) receptor-associated protein [Source:HGNC Symbol;Acc:4067]
219892_at	TM6SF1	ENSG00000136404	0.041569794	1.518719736	7.818958694	6.300238959	15	q25.2	transmembrane 6 superfamily member 1 [Source:HGNC Symbol;Acc:11860]
222431_at	SPIN1	ENSG00000106723	0.041569794	0.70282485	9.186280228	8.483455378	9	q22.1	spindlin 1 [Source:HGNC Symbol;Acc:11243]
203665_at	HMOX1	ENSG00000100292	0.041569794	1.019908548	9.506813677	8.486905129	22	q12.3	heme oxygenase (decycling) 1 [Source:HGNC Symbol;Acc:5013]
202506_at	SSFA2	ENSG00000138434	0.041569794	0.947553911	8.018471473	7.070917562	2	q31.3	sperm specific antigen 2 [Source:HGNC Symbol;Acc:11319]
221899_at	N4BP2L2	ENSG00000244754	0.041569794	0.865335269	9.046774211	8.181438942	13	q13.1	NEDD4 binding protein 2-like 2 [Source:HGNC Symbol;Acc:26916]
203668_at	MAN2C1	ENSG00000140400	0.041690206	0.633916604	8.663669977	8.029753373	15	q24.2	mannosidase, alpha, class 2C, member 1 [Source:HGNC Symbol;Acc:6827]
206295_at	IL18	ENSG00000150782	0.041916833	1.292174393	9.298735781	8.006561388	11	q23.1	interleukin 18 (interferon-gamma-inducing factor) [Source:HGNC Symbol;Acc:5986]
228152_s_at	DDX60L	ENSG00000181381	0.041916833	1.421343576	7.853791688	6.432448112	4	q32.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like [Source:HGNC Symbol;Acc:26429]
228341_at	NUDT16	ENSG00000198585	0.041916833	0.813285601	6.707601846	5.894316245	3	q22.1	nudix (nucleoside diphosphate linked moiety X)-type motif 16 [Source:HGNC Symbol;Acc:26442]
218164_at	SPATA20	ENSG00000006282	0.041916833	0.587929592	9.02333374	8.435404148	17	q21.33	spermatogenesis associated 20 [Source:HGNC Symbol;Acc:26125]
227070_at	GLT8D2	ENSG00000120820	0.041916833	1.757351115	5.840317565	4.082966449	12	q23.3	glycosyltransferase 8 domain containing 2 [Source:HGNC Symbol;Acc:24890]
213083_at	SLC35D2	ENSG00000130958	0.041916833	0.829365427	7.315854336	6.486488909	9	q22.32	solute carrier family 35 (UDP-GlcNAc/UDP-glucose transporter), member D2 [Source:HGNC Symbol;Acc:20799]

224772_at	NAV1	ENSG00000134369	0.041916833	1.051478872	7.602145754	6.550666882	1	q32.1	neuron navigator 1 [Source:HGNC Symbol;Acc:15989]
229287_at	PCNX	ENSG00000100731	0.041916833	0.943930482	7.566201547	6.622271065	14	q24.2	pecanex homolog (Drosophila) [Source:HGNC Symbol;Acc:19740]
201200_at	CREG1	ENSG00000143162	0.041916833	1.058155445	11.10068635	10.0425309	1	q24.2	cellular repressor of E1A-stimulated genes 1 [Source:HGNC Symbol;Acc:2351]
229450_at	IFIT3	ENSG00000119917	0.041916833	1.6631975	9.084234826	7.421037327	10	q23.31	interferon-induced protein with tetratricopeptide repeats 3 [Source:HGNC Symbol;Acc:5411]
228249_at	C11orf74	ENSG00000166352	0.041916833	0.848798181	5.174338696	4.325540515	11	p12	chromosome 11 open reading frame 74 [Source:HGNC Symbol;Acc:25142]
38487_at	STAB1	ENSG00000010327	0.04205946	1.090580398	9.310990038	8.22040964	3	p21.1	stabilin 1 [Source:HGNC Symbol;Acc:18628]
202974_at	MPP1	ENSG00000130830	0.04205946	1.062976134	9.614559777	8.551583643	X	q28	membrane protein, palmitoylated 1, 55kDa [Source:HGNC Symbol;Acc:7219]
226510_at	HEATR5A	ENSG00000129493	0.04205946	0.7510398	7.259760589	6.508720789	14	q12	HEAT repeat containing 5A [Source:HGNC Symbol;Acc:20276]
228282_at	MFSB8	ENSG00000164073	0.04205946	0.819273204	7.582661234	6.763388029	4	q28.2	major facilitator superfamily domain containing 8 [Source:HGNC Symbol;Acc:28486]
203675_at	NUCB2	ENSG00000070081	0.04205946	0.905774662	9.751698376	8.845923714	11	p15.1	nucleobindin 2 [Source:HGNC Symbol;Acc:8044]
228384_s_at	PYROXD2	ENSG00000119943	0.04205946	0.304011115	6.385890727	6.081879612	10	q24.2	pyridine nucleotide-disulphide oxidoreductase domain 2 [Source:HGNC Symbol;Acc:23517]
229367_s_at	GIMAP6	ENSG00000133561	0.04205946	1.409013647	8.888667615	7.479653968	7	q36.1	GTPase, IMAP family member 6 [Source:HGNC Symbol;Acc:21918]
218309_at	CAMK2N1	ENSG00000162545	0.04205946	1.260533336	7.868836571	6.608303235	1	p36.12	calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC Symbol;Acc:24190]
34726_at	CACNB3	ENSG00000167535	0.04205946	0.413630799	6.934617087	6.520986288	12	q13.12	calcium channel, voltage-dependent, beta 3 subunit [Source:HGNC Symbol;Acc:1403]
212670_at	ELN	ENSG00000049540	0.04205946	1.231152927	8.81370025	7.582547323	7	q11.23	elastin [Source:HGNC Symbol;Acc:3327]
229800_at	DCLK1	ENSG00000133083	0.04205946	1.498592436	6.412070979	4.913478542	13	q13.3	doublecortin-like kinase 1 [Source:HGNC Symbol;Acc:2700]
201975_at	CUP1	ENSG00000130779	0.042246192	1.028511221	8.482482941	7.453971719	12	q24.31	CAP-GLY domain containing linker protein 1 [Source:HGNC Symbol;Acc:10461]
224413_s_at	TM2D2	ENSG00000169490	0.042247538	0.61300573	9.024042453	8.411036723	8	p11.22	TM2 domain containing 2 [Source:HGNC Symbol;Acc:24127]
204011_at	SPRY2	ENSG00000136158	0.042331876	1.318852631	7.198128454	5.879275822	13	q31.1	sprouty homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:11270]
235033_at	NPEPL1	ENSG00000215440	0.042331876	0.763205701	5.890585229	5.127379527	20	q13.32	aminopeptidase-like 1 [Source:HGNC Symbol;Acc:16244]
228348_at	LIN5	ENSG00000140471	0.042350925	0.889830233	8.824668316	7.934838083	15	q26.3	lines homolog (Drosophila) [Source:HGNC Symbol;Acc:30922]
227628_at	GPX8	ENSG00000164294	0.042351094	1.180447997	6.970795245	5.790347248	5	q11.2	glutathione peroxidase 8 (putative) [Source:HGNC Symbol;Acc:33100]
1557112_a_at	VPS53	ENSG00000141252	0.042351094	0.518032516	7.975808016	7.4577755	17	p13.3	vacuolar protein sorting 53 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:25608]
228071_at	GIMAP7	ENSG00000179144	0.042351094	1.647364043	8.992108891	7.344744848	7	q36.1	GTPase, IMAP family member 7 [Source:HGNC Symbol;Acc:22404]
209264_s_at	TSPAN4	ENSG00000214063	0.042351094	0.681754755	9.006699575	8.32494482	11	p15.5	tetraspanin 4 [Source:HGNC Symbol;Acc:11859]
208892_s_at	DUSP6	ENSG00000139318	0.042351094	1.228973817	7.992040123	6.763066305	12	q21.33	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:3072]
201315_x_at	IFITM2	ENSG00000185201	0.042351094	0.739392199	11.67358479	10.9341926	11	p15.5	interferon induced transmembrane protein 2 [Source:HGNC Symbol;Acc:5413]
222802_at	EDN1	ENSG00000078401	0.042351094	1.460541762	6.322746092	4.86220433	6	p24.1	endothelin 1 [Source:HGNC Symbol;Acc:3176]
1553395_a_at	CD200R1	ENSG00000163606	0.042351094	1.256910265	6.464778546	5.207868281	3	q13.2	CD200 receptor 1 [Source:HGNC Symbol;Acc:24235]
226399_at	DNAJB14	ENSG00000164031	0.042351094	0.849947729	8.162884294	7.312936565	4	q23	DnaJ (Hsp40) homolog, subfamily B, member 14 [Source:HGNC Symbol;Acc:25881]
226490_at	NHSL1	ENSG00000135540	0.042351094	1.194665858	7.117630828	5.92296497	6	q24.1	NHS-like 1 [Source:HGNC Symbol;Acc:21021]
222513_s_at	SORBS1	ENSG00000095637	0.042351094	1.325460985	8.112293431	6.786832446	10	q24.1	sorbin and SH3 domain containing 1 [Source:HGNC Symbol;Acc:14565]
218705_s_at	SNX24	ENSG00000064652	0.042351094	0.90943161	7.531422028	6.621990418	5	q23.2	sorting nexin 24 [Source:HGNC Symbol;Acc:21533]
226837_at	SPRED1	ENSG00000166068	0.042351094	1.212871192	7.561561543	6.348690351	15	q14	sprouty-related, EVH1 domain containing 1 [Source:HGNC

									Symbol;Acc:20249]
225338_at	ZYG11B	ENSG00000162378	0.042351094	0.624478143	7.313789874	6.689311731	1	p32.3	zyg-11 family member B, cell cycle regulator [Source:HGNC Symbol;Acc:25820]
204955_at	SRPX	ENSG00000101955	0.042351094	1.769176749	7.330012241	5.560835493	X	p11.4	sushi-repeat containing protein, X-linked [Source:HGNC Symbol;Acc:11309]
210840_s_at	IQGAP1	ENSG00000140575	0.042351094	0.815667827	10.6038101	9.788142278	15	q26.1	IQ motif containing GTPase activating protein 1 [Source:HGNC Symbol;Acc:6110]
201494_at	PRCP	ENSG00000137509	0.042351094	0.880611665	10.84225026	9.961638596	11	q14.1	prolylcarboxypeptidase (angiotensinase C) [Source:HGNC Symbol;Acc:9344]
204415_at	IFI6	ENSG00000126709	0.042351094	1.113083585	9.36647792	8.253394336	1	p36.11	interferon, alpha-inducible protein 6 [Source:HGNC Symbol;Acc:4054]
209290_s_at	NFIB	ENSG00000147862	0.042351094	1.655774494	8.40919634	6.753421846	9	p22.3	nuclear factor I/B [Source:HGNC Symbol;Acc:7785]
221474_at	MYL12B	ENSG00000118680	0.042419604	0.586131101	10.97279348	10.38666238	18	p11.31	myosin, light chain 12B, regulatory [Source:HGNC Symbol;Acc:29827]
235747_at	SLC25A16	ENSG00000122912	0.042419604	0.546049363	7.042744928	6.496695565	10	q21.3	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16 [Source:HGNC Symbol;Acc:10986]
201924_at	AFF1	ENSG00000172493	0.042419604	0.952063778	10.2416206	9.289556827	4	q21.3	AF4/FMR2 family, member 1 [Source:HGNC Symbol;Acc:7135]
218045_x_at	PTMS	ENSG00000159335	0.042596049	0.607162357	9.924387924	9.317225567	12	p13.31	parathyroid hormone-related protein [Source:HGNC Symbol;Acc:9629]
213943_at	TWIST1	ENSG00000122691	0.042596049	1.16873421	7.271938017	6.103203807	7	p21.1	twist basic helix-loop-helix transcription factor 1 [Source:HGNC Symbol;Acc:12428]
226752_at	FAM174A	ENSG00000174132	0.042596049	0.92871631	5.776448605	4.847732296	5	q21.1	family with sequence similarity 174, member A [Source:HGNC Symbol;Acc:24943]
201876_at	PON2	ENSG00000105854	0.042719768	1.187571081	9.054738216	7.867167135	7	q21.3	paraoxonase 2 [Source:HGNC Symbol;Acc:9205]
1554240_a_at	ITGAL	ENSG00000005844	0.042881947	1.302505376	9.317162745	8.014657369	16	p11.2	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) [Source:HGNC Symbol;Acc:6148]
203989_x_at	F2R	ENSG00000181104	0.042891128	1.246519921	7.440038684	6.193518762	5	q13.3	coagulation factor II (thrombin) receptor [Source:HGNC Symbol;Acc:3537]
226425_at	CLIP4	ENSG00000115295	0.042891128	1.499860122	7.783328081	6.28346796	2	p23.2	CAP-GLY domain containing linker protein family, member 4 [Source:HGNC Symbol;Acc:26108]
200762_at	DPYSL2	ENSG00000092964	0.042891128	1.159171793	9.328123535	8.168951742	8	p21.2	dihydropyrimidinase-like 2 [Source:HGNC Symbol;Acc:3014]
223681_s_at	INADL	ENSG00000132849	0.042891128	1.250998756	6.181876637	4.930877881	1	p31.3	InaD-like (Drosophila) [Source:HGNC Symbol;Acc:28881]
211986_at	AHNAK	ENSG00000124942	0.042891128	1.334146601	11.47855827	10.14441167	11	q12.3	AHNAK nucleoprotein [Source:HGNC Symbol;Acc:347]
204112_s_at	HNMT	ENSG00000150540	0.042891128	1.303474995	8.681932953	7.378457958	2	q22.1	histamine N-methyltransferase [Source:HGNC Symbol;Acc:5028]
235360_at	PLEKHM3	ENSG00000178385	0.042891128	0.436326441	7.481077573	7.044751132	2	q33.3	pleckstrin homology domain containing, family M, member 3 [Source:HGNC Symbol;Acc:34006]
209276_s_at	GLRX	ENSG00000173221	0.042939851	1.153352768	10.46513253	9.311779765	5	q15	glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:4330]
226113_at	ZNF436	ENSG00000125945	0.042950747	0.967635125	7.934452645	6.96681752	1	p36.12	zinc finger protein 436 [Source:HGNC Symbol;Acc:20814]
201694_s_at	EGR1	ENSG00000120738	0.04303339	2.356208235	9.680723259	7.324515023	5	q31.2	early growth response 1 [Source:HGNC Symbol;Acc:3238]
204417_at	GALC	ENSG00000054983	0.043091339	1.18197166	9.186049316	8.004077656	14	q31.3	galactosylceramidase [Source:HGNC Symbol;Acc:4115]
211178_s_at	PSTPIP1	ENSG00000140368	0.043103445	0.558040078	8.764374999	8.206334921	15	q24.3	proline-serine-threonine phosphatase interacting protein 1 [Source:HGNC Symbol;Acc:9580]
203088_at	FBLN5	ENSG00000140092	0.043103445	1.57461041	8.128331591	6.553721182	14	q32.12	fibulin 5 [Source:HGNC Symbol;Acc:3602]
218450_at	HEBP1	ENSG0000013583	0.043103445	0.756321096	8.459513001	7.703191905	12	p13.1	heme binding protein 1 [Source:HGNC Symbol;Acc:17176]
210113_s_at	NLRP1	ENSG00000091592	0.043127824	0.654465183	7.398936818	6.744471635	17	p13.2	NLR family, pyrin domain containing 1 [Source:HGNC Symbol;Acc:14374]
225673_at	MYADM	ENSG00000179820	0.043127824	1.185973479	9.460657173	8.274683693	19	q13.42	myeloid-associated differentiation marker [Source:HGNC Symbol;Acc:7544]

31874_at	GAS2L1	ENSG00000185340	0.043127824	0.959125758	7.063627768	6.10450201	22	q12.2	growth arrest-specific 2 like 1 [Source:HGNC Symbol;Acc:16955]
222597_at	SNAP29	ENSG00000099940	0.043127824	0.523137969	8.682269428	8.159131459	22	q11.21	synaptosomal-associated protein, 29kDa [Source:HGNC Symbol;Acc:11133]
226279_at	PRSS23	ENSG00000150687	0.043152778	1.36043671	7.67513518	6.31469847	11	q14.2	protease, serine, 23 [Source:HGNC Symbol;Acc:14370]
235570_at	RBMS3	ENSG00000144642	0.043152778	1.782327906	7.335632998	5.553305092	3	p24.1	RNA binding motif, single stranded interacting protein 3 [Source:HGNC Symbol;Acc:13427]
214830_at	SLC38A6	ENSG00000139974	0.043249838	1.276930786	7.341342657	6.064411871	14	q23.1	solute carrier family 38, member 6 [Source:HGNC Symbol;Acc:19863]
201366_at	ANXA7	ENSG00000138279	0.043259906	0.763011677	8.850377121	8.087365443	10	q22.2	annexin A7 [Source:HGNC Symbol;Acc:545]
203179_at	GALT	ENSG00000213930	0.043316491	0.410171519	8.83328444	8.423112921	9	p13.3	galactose-1-phosphate uridylyltransferase [Source:HGNC Symbol;Acc:4135]
225919_s_at	C9orf72	ENSG00000147894	0.04347548	0.855251908	8.181409697	7.326157789	9	p21.2	chromosome 9 open reading frame 72 [Source:HGNC Symbol;Acc:28337]
36711_at	MAFF	ENSG00000185022	0.04347548	1.042386023	5.605979018	4.563592995	22	q13.1	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F [Source:HGNC Symbol;Acc:6780]
205174_s_at	QPCT	ENSG00000115828	0.043531412	1.261724497	8.418598958	7.156874461	2	p22.2	glutaminy-peptide cyclotransferase [Source:HGNC Symbol;Acc:9753]
225032_at	FND3B	ENSG00000075420	0.043656579	1.148111719	9.690617367	8.542505648	3	q26.31	fibronectin type III domain containing 3B [Source:HGNC Symbol;Acc:24670]
225283_at	ARRDC4	ENSG00000140450	0.043675035	1.263277402	6.919418159	5.656140757	15	q26.2	arrestin domain containing 4 [Source:HGNC Symbol;Acc:28087]
212820_at	DMXL2	ENSG00000104093	0.043693329	1.723755285	9.098753998	7.374998712	15	q21.2	Dmx-like 2 [Source:HGNC Symbol;Acc:2938]
202411_at	IFI27	ENSG00000165949	0.043693329	1.419904538	10.65301374	9.233109201	14	q32.12	interferon, alpha-inducible protein 27 [Source:HGNC Symbol;Acc:5397]
201444_s_at	ATP6AP2	ENSG00000182220	0.043693329	0.848128217	9.927790973	9.079662756	X	p11.4	ATPase, H transporting, lysosomal accessory protein 2 [Source:HGNC Symbol;Acc:18305]
212209_at	MED13L	ENSG00000123066	0.043693329	0.718689048	7.683203365	6.964514318	12	q24.21	mediator complex subunit 13-like [Source:HGNC Symbol;Acc:22962]
228082_at	CLMP	ENSG00000166250	0.043693329	0.811085985	8.019360923	7.208274938	11	q24.1	CXADR-like membrane protein [Source:HGNC Symbol;Acc:24039]
201579_at	FAT1	ENSG00000083857	0.043693329	1.199696602	6.984437994	5.784741393	4	q35.2	FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
201050_at	PLD3	ENSG00000105223	0.043738675	0.872712957	11.22150754	10.34879458	19	q13.2	phospholipase D family, member 3 [Source:HGNC Symbol;Acc:17158]
205726_at	DIAPH2	ENSG00000147202	0.043865363	0.824323825	7.524441934	6.700118109	X	q21.33	diaphanous-related formin 2 [Source:HGNC Symbol;Acc:2877]
212717_at	PLEKHM1	ENSG00000225190	0.04386943	0.350082673	8.468551352	8.118468679	17	q21.31	pleckstrin homology domain containing, family M (with RUN domain) member 1 [Source:HGNC Symbol;Acc:29017]
202827_s_at	MMP14	ENSG00000157227	0.043950069	1.093430274	9.702737954	8.60930768	14	q11.2	matrix metalloproteinase 14 (membrane-inserted) [Source:HGNC Symbol;Acc:7160]
201594_s_at	PPP4R1	ENSG00000154845	0.043950069	0.81803938	9.27411864	8.456079261	18	p11.22	protein phosphatase 4, regulatory subunit 1 [Source:HGNC Symbol;Acc:9320]
203460_s_at	PSEN1	ENSG00000080815	0.043950069	0.81390235	8.845796903	8.031894553	14	q24.2	presenilin 1 [Source:HGNC Symbol;Acc:9508]
221840_at	PTPRE	ENSG00000132334	0.044016553	1.294850625	8.885637792	7.590787167	10	q26.2	protein tyrosine phosphatase, receptor type, E [Source:HGNC Symbol;Acc:9669]
203410_at	AP3M2	ENSG00000070718	0.044042681	0.768339069	7.036583	6.268243931	8	p11.21	adaptor-related protein complex 3, mu 2 subunit [Source:HGNC Symbol;Acc:570]
226582_at	LOC400043	NA	0.044042681	0.869479209	6.73443097	5.864951761	NA	NA	NA
209600_s_at	ACOX1	ENSG00000161533	0.044042681	0.648332519	8.512058318	7.863725799	17	q25.1	acyl-CoA oxidase 1, palmitoyl [Source:HGNC Symbol;Acc:119]
221814_at	GPR124	ENSG00000020181	0.044042681	1.095880575	8.488647675	7.3927671	8	p11.23	G protein-coupled receptor 124 [Source:HGNC Symbol;Acc:17849]
230836_at	ST8SIA4	ENSG00000113532	0.044042681	1.017497807	7.57919038	6.561692573	5	q21.1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4 [Source:HGNC Symbol;Acc:10871]

204270_at	SKI	ENSG00000157933	0.044042681	0.896035069	9.220481497	8.324446427	1	p36.33	v-ski avian sarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:10896]
200872_at	S100A10	ENSG00000197747	0.044042681	0.862231392	12.14558315	11.28335176	1	q21.3	S100 calcium binding protein A10 [Source:HGNC Symbol;Acc:10487]
219761_at	CLEC1A	ENSG00000150048	0.044042681	1.291289338	6.704345965	5.413056627	12	p13.2	C-type lectin domain family 1, member A [Source:HGNC Symbol;Acc:24355]
212708_at	MSL1	ENSG00000188895	0.044042681	0.856069768	9.529726222	8.673656454	17	q21.1	male-specific lethal 1 homolog (Drosophila) [Source:HGNC Symbol;Acc:27905]
204326_x_at	MTIX	ENSG00000187193	0.044070216	1.001729342	10.8648548	9.863125458	16	q13	metallothionein 1X [Source:HGNC Symbol;Acc:7405]
241392_at	TMEM39A	ENSG00000176142	0.044070216	0.341471009	6.928601856	6.587130847	3	q13.33	transmembrane protein 39A [Source:HGNC Symbol;Acc:25600]
205771_s_at	AKAP7	ENSG00000118507	0.044070216	0.731995834	6.526724778	5.794728944	6	q23.2	A kinase (PRKA) anchor protein 7 [Source:HGNC Symbol;Acc:377]
206227_at	CILP	ENSG00000138615	0.044070216	2.257502766	8.735997724	6.478494958	15	q22.31	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase [Source:HGNC Symbol;Acc:1980]
204158_s_at	TCIRG1	ENSG00000110719	0.044070216	0.593079771	9.597157124	9.004077354	11	q13.2	T-cell, immune regulator 1, ATPase, H transporting, lysosomal V0 subunit A3 [Source:HGNC Symbol;Acc:11647]
212948_at	CAMTA2	ENSG00000108509	0.044070216	0.538388211	9.486336458	8.947948247	17	p13.2	calmodulin binding transcription activator 2 [Source:HGNC Symbol;Acc:18807]
218241_at	GOLGA5	ENSG00000066455	0.044078355	0.503478348	7.912463839	7.408985491	14	q32.12	golgin A5 [Source:HGNC Symbol;Acc:4428]
203042_at	LAMP2	ENSG00000005893	0.044078355	1.386613769	9.189891489	7.80327772	X	q24	lysosomal-associated membrane protein 2 [Source:HGNC Symbol;Acc:6501]
223264_at	MESDC1	ENSG00000140406	0.044215499	0.658578285	8.66869473	8.010116444	15	q25.1	mesoderm development candidate 1 [Source:HGNC Symbol;Acc:13519]
243141_at	SGMS2	ENSG00000164023	0.044312646	1.085634594	5.816519276	4.730884682	4	q25	sphingomyelin synthase 2 [Source:HGNC Symbol;Acc:28395]
212513_s_at	USP33	ENSG00000077254	0.044312646	0.869205809	8.910601155	8.041395346	1	p31.1	ubiquitin specific peptidase 33 [Source:HGNC Symbol;Acc:20059]
44111_at	VPS33B	ENSG00000184056	0.044312646	0.71852938	7.769682095	7.051152715	15	q26.1	vacuolar protein sorting 33 homolog B (yeast) [Source:HGNC Symbol;Acc:12712]
203044_at	CHSY1	ENSG00000131873	0.044778087	0.860312924	9.374891415	8.514578491	15	q26.3	chondroitin sulfate synthase 1 [Source:HGNC Symbol;Acc:17198]
201133_s_at	PJA2	ENSG00000198961	0.045063391	0.928851445	8.789327346	7.860475902	5	q21.3	praja ring finger 2, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:17481]
238478_at	BNC2	ENSG00000173068	0.04510855	1.581928937	6.500666236	4.918737299	9	p22.2	basonuclein 2 [Source:HGNC Symbol;Acc:30988]
207121_s_at	MAPK6	ENSG00000069956	0.045216957	0.971961406	9.250325309	8.278363904	15	q21.2	mitogen-activated protein kinase 6 [Source:HGNC Symbol;Acc:6879]
226757_at	IFIT2	ENSG00000119922	0.045216957	1.258163287	7.398381051	6.140217764	10	q23.31	interferon-induced protein with tetratricopeptide repeats 2 [Source:HGNC Symbol;Acc:5409]
224929_at	TMEM173	ENSG00000184584	0.045216957	0.976901806	8.795661513	7.818759707	5	q31.2	transmembrane protein 173 [Source:HGNC Symbol;Acc:27962]
219013_at	GALNT11	ENSG00000178234	0.045216957	0.624765223	8.111616397	7.486851174	7	q36.1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11) [Source:HGNC Symbol;Acc:19875]
203732_at	TRIP4	ENSG00000103671	0.045216957	0.534991672	8.282763586	7.747771914	15	q22.31	thyroid hormone receptor interactor 4 [Source:HGNC Symbol;Acc:12310]
206991_s_at	CCR5	ENSG00000160791	0.045321132	1.498899795	8.807195729	7.308295934	3	p21.31	chemokine (C-C motif) receptor 5 (gene/pseudogene) [Source:HGNC Symbol;Acc:1606]
212192_at	KCTD12	ENSG00000178695	0.045321132	1.241111969	11.04261631	9.801504337	13	q22.3	potassium channel tetramerization domain containing 12 [Source:HGNC Symbol;Acc:14678]
212071_s_at	SPTBN1	ENSG00000115306	0.045389085	1.148298747	10.50838671	9.360087962	2	p16.2	spectrin, beta, non-erythrocytic 1 [Source:HGNC Symbol;Acc:11275]
204194_at	BACH1	ENSG00000156273	0.045389085	0.684495403	7.331339629	6.646844226	21	q21.3	BTB and CNC homology 1, basic leucine zipper transcription factor 1 [Source:HGNC Symbol;Acc:935]

213469_at	PGAP1	ENSG00000197121	0.045389085	0.801387927	4.677932308	3.876544381	2	q33.1	post-GPI attachment to proteins 1 [Source:HGNC Symbol;Acc:25712]
207173_x_at	CDH11	ENSG00000140937	0.045389085	1.855491998	9.112092659	7.256600661	16	q21	cadherin 11, type 2, OB-cadherin (osteoblast) [Source:HGNC Symbol;Acc:1750]
202020_s_at	LANCL1	ENSG00000115365	0.045389085	0.72258943	9.184946138	8.462356708	2	q34	LanC lantibiotic synthetase component C-like 1 (bacterial) [Source:HGNC Symbol;Acc:6508]
201384_s_at	NBR1	ENSG00000188554	0.045622403	0.69719383	9.452833592	8.755639763	17	q21.31	neighbor of BRCA1 gene 1 [Source:HGNC Symbol;Acc:6746]
213004_at	ANGPTL2	ENSG00000136859	0.045650379	1.488271363	9.435206476	7.946935113	9	q33.3	angiopoietin-like 2 [Source:HGNC Symbol;Acc:490]
203310_at	STXBP3	ENSG00000116266	0.045775429	0.770798736	7.72163929	6.950840554	1	p13.3	syntaxin binding protein 3 [Source:HGNC Symbol;Acc:11446]
212239_at	PIK3R1	ENSG00000145675	0.045775429	0.737750823	9.025386358	8.287635535	5	q13.1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) [Source:HGNC Symbol;Acc:8979]
225864_at	FAM84B	ENSG00000168672	0.045775429	1.677914651	6.194231305	4.516316654	8	q24.21	family with sequence similarity 84, member B [Source:HGNC Symbol;Acc:24166]
218679_s_at	VPS28	ENSG00000160948	0.045809883	0.390907854	9.691259817	9.300351963	8	q24.3	vacuolar protein sorting 28 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:18178]
211964_at	COL4A2	ENSG00000134871	0.045856854	1.232811948	10.70556132	9.472749367	13	q34	collagen, type IV, alpha 2 [Source:HGNC Symbol;Acc:2203]
212501_at	CEBPB	ENSG00000172216	0.045856854	0.738238476	10.55473241	9.816493929	20	q13.13	CCAAT/enhancer binding protein (C/EBP), beta [Source:HGNC Symbol;Acc:1834]
215596_s_at	LTN1	ENSG00000198862	0.045856854	0.600695092	9.12314625	8.522451158	21	q21.3	listerin E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc:13082]
235306_at	GIMAP8	ENSG00000171115	0.045948778	1.141523234	7.866981655	6.725458421	7	q36.1	GTPase, IMAP family member 8 [Source:HGNC Symbol;Acc:21792]
213746_s_at	FLNA	ENSG00000196924	0.045983205	0.670976446	10.55453024	9.883553792	X	q28	filamin A, alpha [Source:HGNC Symbol;Acc:3754]
200982_s_at	ANXA6	ENSG00000197043	0.045983205	0.967756544	9.852305278	8.884548734	5	q33.1	annexin A6 [Source:HGNC Symbol;Acc:544]
227029_at	FAM177A1	ENSG00000151327	0.046043333	0.833008817	6.455041674	5.622032856	14	q13.2	family with sequence similarity 177, member A1 [Source:HGNC Symbol;Acc:19829]
225695_at	SLC35F6	ENSG00000213699	0.046225372	0.724610376	9.024413478	8.299803103	2	p23.3	solute carrier family 35, member F6 [Source:HGNC Symbol;Acc:26055]
230263_s_at	DOCK5	ENSG00000147459	0.046636223	0.984168534	5.975225342	4.991056808	8	p21.2	dedicator of cytokinesis 5 [Source:HGNC Symbol;Acc:23476]
219860_at	LY6G5C	ENSG00000204428	0.046660118	0.498836907	6.319773104	5.820936197	6	p21.33	lymphocyte antigen 6 complex, locus G5C [Source:HGNC Symbol;Acc:13932]
216620_s_at	ARHGEF10	ENSG00000104728	0.046660118	1.005916383	8.01557698	7.009660598	8	p23.3	Rho guanine nucleotide exchange factor (GEF) 10 [Source:HGNC Symbol;Acc:14103]
209298_s_at	ITSN1	ENSG00000205726	0.046711592	1.277202537	5.88081823	4.603615693	21	q22.11	intersectin 1 (SH3 domain protein) [Source:HGNC Symbol;Acc:6183]
219383_at	PRR5L	ENSG00000135362	0.046711592	0.874143565	4.475309631	3.601166066	11	p13	proline rich 5 like [Source:HGNC Symbol;Acc:25878]
218204_s_at	FYCO1	ENSG00000163820	0.046711592	0.475324889	7.841059718	7.36573483	3	p21.31	FYVE and coiled-coil domain containing 1 [Source:HGNC Symbol;Acc:14673]
212637_s_at	WWP1	ENSG00000123124	0.046711592	0.922349431	7.411309223	6.488959792	8	q21.3	WW domain containing E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc:17004]
200784_s_at	LRP1	ENSG00000123384	0.046711592	0.835469409	10.71172473	9.876255321	12	q13.3	low density lipoprotein receptor-related protein 1 [Source:HGNC Symbol;Acc:6692]
202668_at	EFNB2	ENSG00000125266	0.046711592	1.300618622	7.729295355	6.428676733	13	q33.3	ephrin-B2 [Source:HGNC Symbol;Acc:3227]
211926_s_at	MYH9	ENSG00000100345	0.046850713	0.514027812	10.37283665	9.85880884	22	q12.3	myosin, heavy chain 9, non-muscle [Source:HGNC Symbol;Acc:7579]
207181_s_at	CASP7	ENSG00000165806	0.046856444	0.877318568	8.172928021	7.295609453	10	q25.3	caspase 7, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:1508]
203940_s_at	VASH1	ENSG00000071246	0.046903847	0.759053043	8.993567489	8.234514446	14	q24.3	vasohibin 1 [Source:HGNC Symbol;Acc:19964]
225046_at	LOC389831	NA	0.046903847	1.209299028	9.502744298	8.29344527	NA	NA	NA

229699_at	LOC100129550	NA	0.046903847	0.787522797	7.252124657	6.46460186	NA	NA	NA
1555997_s_at	IGFBP5	ENSG00000115461	0.046903847	2.089302737	9.039541189	6.950238452	2	q35	insulin-like growth factor binding protein 5 [Source:HGNC Symbol;Acc:5474]
221858_at	TBC1D12	ENSG00000108239	0.046903847	0.975449344	6.730088398	5.754639554	10	q23.33	TBC1 domain family, member 12 [Source:HGNC Symbol;Acc:29082]
202123_s_at	ABL1	ENSG00000097007	0.046903847	0.535932838	8.956464172	8.420531334	9	q34.12	c-abl oncogene 1, non-receptor tyrosine kinase [Source:HGNC Symbol;Acc:76]
209189_at	FOS	ENSG00000170345	0.046903847	2.311395259	8.928569361	6.617174102	14	q24.3	FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:3796]
231697_s_at	VMP1	ENSG00000062716	0.046903847	1.337676729	9.338248758	8.000572029	17	q23.1	vacuole membrane protein 1 [Source:HGNC Symbol;Acc:29559]
231823_s_at	SH3PXD2B	ENSG00000174705	0.046907121	1.342190597	8.749657487	7.40746689	5	q35.1	SH3 and PX domains 2B [Source:HGNC Symbol;Acc:29242]
226917_s_at	ANAPC4	ENSG00000053900	0.046907121	0.7157989	9.420943217	8.705144317	4	p15.2	anaphase promoting complex subunit 4 [Source:HGNC Symbol;Acc:19990]
213135_at	TIAM1	ENSG00000156299	0.046959774	1.432495967	8.128730835	6.696234868	21	q22.11	T-cell lymphoma invasion and metastasis 1 [Source:HGNC Symbol;Acc:11805]
222793_at	DDX58	ENSG00000107201	0.046977274	0.793030854	6.897065298	6.104034445	9	p21.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 [Source:HGNC Symbol;Acc:19102]
235059_at	RAB12	ENSG00000206418	0.047160578	0.736169692	8.288455057	7.552285365	18	p11.22	RAB12, member RAS oncogene family [Source:HGNC Symbol;Acc:31332]
213364_s_at	SNX1	ENSG00000028528	0.047357556	0.941321551	7.632325883	6.691004333	15	q22.31	sorting nexin 1 [Source:HGNC Symbol;Acc:11172]
213194_at	ROBO1	ENSG00000169855	0.047357556	1.202364784	8.299204466	7.096839682	3	p12.2	roundabout, axon guidance receptor, homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:10249]
223434_at	GBP3	ENSG00000117226	0.047368037	1.767006321	8.155929476	6.388923155	1	p22.2	guanylate binding protein 3 [Source:HGNC Symbol;Acc:4184]
201464_x_at	JUN	ENSG00000177606	0.047576751	1.411647741	9.379205572	7.967557831	1	p32.1	jun proto-oncogene [Source:HGNC Symbol;Acc:6204]
228325_at	KIAA0146	NA	0.047576751	1.637115768	6.87876789	5.241652122	NA	NA	NA
226639_at	SFT2D3	ENSG00000173349	0.047769829	0.402970073	7.472242013	7.06927194	2	q14.3	SFT2 domain containing 3 [Source:HGNC Symbol;Acc:28767]
204204_at	SLC31A2	ENSG00000136867	0.04778455	1.078146963	7.858561834	6.78041487	9	q32	solute carrier family 31 (copper transporter), member 2 [Source:HGNC Symbol;Acc:11017]
213659_at	ZNF75D	ENSG00000186376	0.04778455	0.665495605	7.859603651	7.194108047	X	q26.3	zinc finger protein 75D [Source:HGNC Symbol;Acc:13145]
219165_at	PDLIM2	ENSG00000120913	0.047788444	0.537830248	8.659828829	8.12199858	8	p21.3	PDZ and LIM domain 2 (mystique) [Source:HGNC Symbol;Acc:13992]
202704_at	TOB1	ENSG00000141232	0.047841124	1.157733162	7.864872509	6.707139347	17	q21.33	transducer of ERBB2, 1 [Source:HGNC Symbol;Acc:11979]
201059_at	CTTN	ENSG00000085733	0.047841124	1.132979997	8.126828979	6.993848982	11	q13.3	cortactin [Source:HGNC Symbol;Acc:3338]
208626_s_at	VAT1	ENSG00000108828	0.047842986	0.94552568	10.23981289	9.294287208	17	q21.31	vesicle amine transport protein 1 homolog (T. californica) [Source:HGNC Symbol;Acc:16919]
224285_at	GPR174	ENSG00000147138	0.047886452	1.19745705	7.961716488	6.764259438	X	q21.1	G protein-coupled receptor 174 [Source:HGNC Symbol;Acc:30245]
202746_at	ITM2A	ENSG00000078596	0.047974392	1.756296873	8.555659235	6.799362362	X	q21.1	integral membrane protein 2A [Source:HGNC Symbol;Acc:6173]
1557749_at	EHBP1L1	ENSG00000173442	0.047976051	1.300818836	7.376097806	6.07527897	11	q13.1	EH domain binding protein 1-like 1 [Source:HGNC Symbol;Acc:30682]
208671_at	SERINC1	ENSG00000111897	0.047976051	0.972609476	8.578870199	7.606260723	6	q22.31	serine incorporator 1 [Source:HGNC Symbol;Acc:13464]
235199_at	RNF125	ENSG00000101695	0.048038754	1.064207451	7.065692015	6.001484564	18	q12.1	ring finger protein 125, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:21150]
236565_s_at	LARP6	ENSG00000166173	0.048102844	0.684300387	5.230392066	4.546091679	15	q23	La ribonucleoprotein domain family, member 6 [Source:HGNC Symbol;Acc:24012]
204575_s_at	MMP19	ENSG00000123342	0.048164884	0.946555962	7.578626866	6.632070904	12	q13.2	matrix metalloproteinase 19 [Source:HGNC Symbol;Acc:7165]
221653_x_at	APO12	ENSG00000128335	0.048164884	0.588583201	10.11616798	9.527584778	22	q12.3	apolipoprotein L, 2 [Source:HGNC Symbol;Acc:619]
224804_s_at	FAM219B	ENSG00000178761	0.048164884	0.651562841	8.895175581	8.24361274	15	q24.1	family with sequence similarity 219, member B [Source:HGNC Symbol;Acc:24695]

202820_at	AHR	ENSG00000106546	0.048164884	1.191425195	8.433260381	7.241835186	7	p21.1	aryl hydrocarbon receptor [Source:HGNC Symbol;Acc:348]
204082_at	PBX3	ENSG00000167081	0.048164884	0.63580907	8.576776457	7.940967387	9	q33.3	pre-B-cell leukemia homeobox 3 [Source:HGNC Symbol;Acc:8634]
218109_s_at	MFSD1	ENSG00000118855	0.048304996	1.139673302	10.13940908	8.999735777	3	q25.32	major facilitator superfamily domain containing 1 [Source:HGNC Symbol;Acc:25874]
231897_at	PTGR1	ENSG00000106853	0.048304996	1.154891244	7.789450843	6.634559598	9	q31.3	prostaglandin reductase 1 [Source:HGNC Symbol;Acc:18429]
205786_s_at	ITGAM	ENSG00000169896	0.048305577	1.137807787	8.121972126	6.984164339	16	p11.2	integrin, alpha M (complement component 3 receptor 3 subunit) [Source:HGNC Symbol;Acc:6149]
203510_at	MET	ENSG00000105976	0.048305577	1.650209197	7.842578732	6.192369534	7	q31.2	met proto-oncogene [Source:HGNC Symbol;Acc:7029]
224896_s_at	TTL	ENSG00000114999	0.048305577	0.56036721	8.810442042	8.250074832	2	q13	tubulin tyrosine ligase [Source:HGNC Symbol;Acc:21586]
232645_at	LOC153684	NA	0.048305577	0.888956991	7.159878318	6.270921327	NA	NA	NA
226576_at	ARHGAP26	ENSG00000145819	0.048305577	0.822588192	6.112705611	5.290117419	5	q31.3	Rho GTPase activating protein 26 [Source:HGNC Symbol;Acc:17073]
219191_s_at	BIN2	ENSG00000110934	0.048305577	1.097818549	9.34065692	8.242838371	12	q13.13	bridging integrator 2 [Source:HGNC Symbol;Acc:1053]
214853_s_at	SHC1	ENSG00000160691	0.048305577	0.580661886	10.02587289	9.445211	1	q21.3	SHC (Src homology 2 domain containing) transforming protein 1 [Source:HGNC Symbol;Acc:10840]
224358_s_at	MS4A7	ENSG00000166927	0.048314327	2.066880998	8.506524406	6.439643408	11	q12.2	membrane-spanning 4-domains, subfamily A, member 7 [Source:HGNC Symbol;Acc:13378]
209164_s_at	CYB561	ENSG00000008283	0.04855986	0.862673302	8.334774098	7.472100797	17	q23.3	cytochrome b561 [Source:HGNC Symbol;Acc:2571]
222175_s_at	MED15	ENSG00000099917	0.04855986	0.445190149	9.603400247	9.158210098	22	q11.21	mediator complex subunit 15 [Source:HGNC Symbol;Acc:14248]
219469_at	DYNC2H1	ENSG00000187240	0.048569792	0.659598577	6.555849742	5.896251165	11	q22.3	dynein, cytoplasmic 2, heavy chain 1 [Source:HGNC Symbol;Acc:2962]
226143_at	RAI1	ENSG00000108557	0.048569792	1.208393363	8.541447862	7.333054499	17	p11.2	retinoic acid induced 1 [Source:HGNC Symbol;Acc:9834]
212681_at	EPB41L3	ENSG00000082397	0.048619009	1.347291945	8.071548526	6.724256581	18	p11.31	erythrocyte membrane protein band 4.1-like 3 [Source:HGNC Symbol;Acc:3380]
215784_at	CD1E	ENSG00000158488	0.048710337	1.145368323	5.448260924	4.302892601	1	q23.1	CD1e molecule [Source:HGNC Symbol;Acc:1638]
211161_s_at	COL3A1	ENSG00000168542	0.048710337	2.029466261	11.58325522	9.553788957	2	q32.2	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
209906_at	C3AR1	ENSG00000171860	0.048810009	1.181583182	9.98497067	8.803387488	12	p13.31	complement component 3a receptor 1 [Source:HGNC Symbol;Acc:1319]
200625_s_at	CAP1	ENSG00000131236	0.048951883	0.838593198	11.78722536	10.94863217	1	p34.2	CAP, adenylate cyclase-associated protein 1 (yeast) [Source:HGNC Symbol;Acc:20040]
209550_at	NDN	ENSG00000182636	0.048952014	0.889205149	8.585921026	7.696715877	15	q11.2	neddin, melanoma antigen (MAGE) family member [Source:HGNC Symbol;Acc:7675]
214039_s_at	LAPTM4B	ENSG00000104341	0.048974372	1.662825915	7.882223505	6.21939759	8	q22.1	lysosomal protein transmembrane 4 beta [Source:HGNC Symbol;Acc:13646]
209356_x_at	EFEMP2	ENSG00000172638	0.049063503	0.758705207	8.0078881	7.249182893	11	q13.1	EGF containing fibulin-like extracellular matrix protein 2 [Source:HGNC Symbol;Acc:3219]
207276_at	CDR1	ENSG00000184258	0.049177921	1.892594551	9.606611577	7.714017027	X	q27.1	cerebellar degeneration-related protein 1, 34kDa [Source:HGNC Symbol;Acc:1798]
209955_s_at	FAP	ENSG00000078098	0.049177921	1.477706269	8.251596445	6.773890176	2	q24.2	fibroblast activation protein, alpha [Source:HGNC Symbol;Acc:3590]
226844_at	MOB3B	ENSG00000120162	0.049203301	1.163764789	6.922109848	5.758345059	9	p21.2	MOB kinase activator 3B [Source:HGNC Symbol;Acc:23825]
222468_at	KIAA0319L	ENSG00000142687	0.049203301	0.30117243	8.203036313	7.901863883	1	p34.3	KIAA0319-like [Source:HGNC Symbol;Acc:30071]
226056_at	ARHGAP31	ENSG00000031081	0.049246985	0.787516152	8.433132327	7.645616175	3	q13.33	Rho GTPase activating protein 31 [Source:HGNC Symbol;Acc:29216]
226695_at	PRRX1	ENSG00000116132	0.049316222	1.762734658	9.803780005	8.041045346	1	q24.2	paired related homeobox 1 [Source:HGNC Symbol;Acc:9142]
204844_at	ENPEP	ENSG00000138792	0.049441905	0.659515691	4.49151479	3.831999099	4	q25	glutamyl aminopeptidase (aminopeptidase A) [Source:HGNC Symbol;Acc:3355]
200612_s_at	AP2B1	ENSG00000006125	0.049441905	0.595747097	8.555795692	7.960048594	17	q12	adaptor-related protein complex 2, beta 1 subunit [Source:HGNC

									Symbol;Acc:563]
200923_at	LGALS3BP	ENSG00000108679	0.049441905	0.921133422	10.07362245	9.152489033	17	q25.3	lectin, galactoside-binding, soluble, 3 binding protein [Source:HGNC Symbol;Acc:6564]
208074_s_at	AP2S1	ENSG00000042753	0.049593197	0.59579328	10.51238698	9.9165937	19	q13.32	adaptor-related protein complex 2, sigma 1 subunit [Source:HGNC Symbol;Acc:565]
200897_s_at	PALLD	ENSG00000129116	0.049598626	1.601894471	9.526128512	7.924234041	4	q32.3	palladin, cytoskeletal associated protein [Source:HGNC Symbol;Acc:17068]
209667_at	CES2	ENSG00000172831	0.049598626	0.512790855	8.055153847	7.542362992	16	q22.1	carboxylesterase 2 [Source:HGNC Symbol;Acc:1864]
225785_at	REEP3	ENSG00000165476	0.049648667	1.112993317	7.249649028	6.136655711	10	q21.3	receptor accessory protein 3 [Source:HGNC Symbol;Acc:23711]
227265_at	FGL2	ENSG00000127951	0.049648667	1.768021672	9.464203046	7.696181374	7	q11.23	fibrinogen-like 2 [Source:HGNC Symbol;Acc:3696]
226679_at	SLC26A11	ENSG00000181045	0.049648667	1.377482675	8.622059873	7.244577198	17	q25.3	solute carrier family 26, member 11 [Source:HGNC Symbol;Acc:14471]
202441_at	ERLIN1	ENSG00000107566	0.049690836	0.585414195	8.619248306	8.033834111	10	q24.31	ER lipid raft associated 1 [Source:HGNC Symbol;Acc:16947]
227758_at	RERG	ENSG00000134533	0.049697612	1.130937723	5.789853181	4.658915458	12	p12.3	RAS-like, estrogen-regulated, growth inhibitor [Source:HGNC Symbol;Acc:15980]
204036_at	LPAR1	ENSG00000198121	0.049813564	1.444039399	6.674595378	5.230555979	9	q31.3	lysophosphatidic acid receptor 1 [Source:HGNC Symbol;Acc:3166]
225755_at	KLHDC8B	ENSG00000185909	0.049849481	0.85120088	8.00569222	7.15449134	3	p21.31	kelch domain containing 8B [Source:HGNC Symbol;Acc:28557]
209571_at	CIR1	ENSG00000138433	0.049849481	0.376268664	8.299113302	7.922844638	2	q31.1	corepressor interacting with RBPI, 1 [Source:HGNC Symbol;Acc:24217]
210184_at	ITGAX	ENSG00000140678	0.049853347	1.112779508	8.872883821	7.760104313	16	p11.2	integrin, alpha X (complement component 3 receptor 4 subunit) [Source:HGNC Symbol;Acc:6152]
217940_s_at	CARKD	ENSG00000213995	0.049853347	0.480686702	8.908728186	8.428041484	13	q34	carbohydrate kinase domain containing [Source:HGNC Symbol;Acc:25576]
212993_at	NACC2	ENSG00000148411	0.050114999	1.114963871	7.888031769	6.773067899	9	q34.3	NACC family member 2, BEN and BTB (POZ) domain containing [Source:HGNC Symbol;Acc:23846]
1562876_s_at	LOC541471	NA	0.050218071	0.682562423	3.603677506	2.921115083	NA	NA	NA
242268_at	CELF2	ENSG00000048740	0.050218071	1.553668129	7.210053313	5.656385183	10	p14	CUGBP, Elav-like family member 2 [Source:HGNC Symbol;Acc:2550]
213125_at	OLFML2B	ENSG00000162745	0.050218071	0.787465426	8.741575545	7.954110119	1	q23.3	olfactomedin-like 2B [Source:HGNC Symbol;Acc:24558]
221257_x_at	FBXO38	ENSG00000145868	0.050300966	0.597625209	7.698194987	7.100569778	5	q32	F-box protein 38 [Source:HGNC Symbol;Acc:28844]
236782_at	SAMD3	ENSG00000164483	0.050399558	1.072740707	7.590990221	6.518249514	6	q23.1	sterile alpha motif domain containing 3 [Source:HGNC Symbol;Acc:21574]
1554690_a_at	TACC1	ENSG00000147526	0.050505576	1.079368013	9.700334844	8.620966831	8	p11.22	transforming, acidic coiled-coil containing protein 1 [Source:HGNC Symbol;Acc:11522]
203431_s_at	ARHGAP32	ENSG00000134909	0.050518588	1.238339866	6.793820795	5.555480928	11	q24.3	Rho GTPase activating protein 32 [Source:HGNC Symbol;Acc:17399]
226711_at	FOXN2	ENSG00000170802	0.050635583	0.937101457	9.838675692	8.901574235	2	p16.3	forkhead box N2 [Source:HGNC Symbol;Acc:5281]
203562_at	FEZ1	ENSG00000149557	0.050635583	1.424636375	7.169090802	5.744454428	11	q24.2	fasciculation and elongation protein zeta 1 (zyglin I) [Source:HGNC Symbol;Acc:3659]
201508_at	IGFBP4	ENSG00000141753	0.050635583	1.218153348	10.95048091	9.732327564	17	q21.2	insulin-like growth factor binding protein 4 [Source:HGNC Symbol;Acc:5473]
209933_s_at	CD300A	ENSG00000167851	0.050838453	1.063950828	8.653599864	7.589649035	17	q25.1	CD300a molecule [Source:HGNC Symbol;Acc:19319]
226751_at	CNRIP1	ENSG00000119865	0.05098315	1.046366586	7.446206604	6.399840018	2	p14	cannabinoid receptor interacting protein 1 [Source:HGNC Symbol;Acc:24546]
203303_at	DYNLT3	ENSG00000165169	0.05098315	0.838978072	9.479702344	8.640724272	X	p11.4	dynein, light chain, Tctex-type 3 [Source:HGNC Symbol;Acc:11694]
1556698_a_at	GPRIN3	ENSG00000185477	0.05098315	1.215337617	6.331782061	5.116444444	4	q22.1	GPRIN family member 3 [Source:HGNC Symbol;Acc:27733]
223454_at	CXCL16	ENSG00000161921	0.05098315	0.987094685	9.755064685	8.76797	17	p13.2	chemokine (C-X-C motif) ligand 16 [Source:HGNC Symbol;Acc:16642]
202032_s_at	MAN2A2	ENSG00000196547	0.05098315	0.885891887	9.56468737	8.678795483	15	q26.1	mannosidase, alpha, class 2A, member 2 [Source:HGNC

									Symbol;Acc:6825]
205779_at	RAMP2	ENSG00000131477	0.051156378	0.933822492	8.483654672	7.54983218	17	q21.31	receptor (G protein-coupled) activity modifying protein 2 [Source:HGNC Symbol;Acc:9844]
209110_s_at	RGL2	ENSG00000237441	0.051156378	0.662542944	8.743821756	8.081278812	6	p21.32	ral guanine nucleotide dissociation stimulator-like 2 [Source:HGNC Symbol;Acc:9769]
209935_at	ATP2C1	ENSG00000017260	0.051156378	0.657015693	6.368275466	5.711259774	3	q22.1	ATPase, Ca ²⁺ transporting, type 2C, member 1 [Source:HGNC Symbol;Acc:13211]
214453_s_at	IFI44	ENSG00000137965	0.051156378	1.633185311	9.486683614	7.853498302	1	p31.1	interferon-induced protein 44 [Source:HGNC Symbol;Acc:16938]
201063_at	RCN1	ENSG00000049449	0.051233232	0.702809737	9.216222535	8.513412798	11	p13	reticulocalbin 1, EF-hand calcium binding domain [Source:HGNC Symbol;Acc:9934]
213222_at	PLCB1	ENSG00000182621	0.051361434	0.700475436	4.535979887	3.835504451	20	p12.3	phospholipase C, beta 1 (phosphoinositide-specific) [Source:HGNC Symbol;Acc:15917]
201069_at	MMP2	ENSG00000087245	0.051361434	1.691353818	10.01928343	8.327929615	16	q12.2	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) [Source:HGNC Symbol;Acc:7166]
200661_at	CTSA	ENSG00000064601	0.051361434	0.720607027	10.64337094	9.922763911	20	q13.12	cathepsin A [Source:HGNC Symbol;Acc:9251]
213258_at	TFPI	ENSG00000003436	0.051378943	1.419437821	8.029849535	6.610411714	2	q32.1	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) [Source:HGNC Symbol;Acc:11760]
225414_at	RNF149	ENSG00000163162	0.05142224	0.804672421	9.112269744	8.307597324	2	q11.2	ring finger protein 149 [Source:HGNC Symbol;Acc:23137]
219397_at	COQ10B	ENSG00000115520	0.05142224	0.654479835	7.359951703	6.705471868	2	q33.1	coenzyme Q10 homolog B (S. cerevisiae) [Source:HGNC Symbol;Acc:25819]
222127_s_at	EXOC1	ENSG00000090989	0.051602523	0.754363501	9.746303928	8.991940427	4	q12	exocyst complex component 1 [Source:HGNC Symbol;Acc:30380]
223220_s_at	PARP9	ENSG00000138496	0.051602523	0.979949321	9.260981734	8.281032413	3	q21.1	poly (ADP-ribose) polymerase family, member 9 [Source:HGNC Symbol;Acc:24118]
213422_s_at	MXRA8	ENSG00000162576	0.051602523	1.242243727	8.999253285	7.757009558	1	p36.33	matrix-remodelling associated 8 [Source:HGNC Symbol;Acc:7542]
203153_at	IFIT1	ENSG00000185745	0.051753444	1.528926589	7.71997217	6.191045582	10	q23.31	interferon-induced protein with tetratricopeptide repeats 1 [Source:HGNC Symbol;Acc:5407]
202100_at	RALB	ENSG00000144118	0.051843475	0.671402473	8.880755781	8.209353307	2	q14.2	v-ral simian leukemia viral oncogene homolog B [Source:HGNC Symbol;Acc:9840]
224895_at	YAP1	ENSG00000137693	0.051946417	1.490945911	7.474062759	5.983116848	11	q22.1	Yes-associated protein 1 [Source:HGNC Symbol;Acc:16262]
201368_at	ZFP36L2	ENSG00000152518	0.052319048	0.964711787	10.56868804	9.603976254	2	p21	ZFP36 ring finger protein-like 2 [Source:HGNC Symbol;Acc:1108]
212027_at	RBM25	ENSG00000119707	0.052384081	0.678190641	9.494823888	8.816633247	14	q24.2	RNA binding motif protein 25 [Source:HGNC Symbol;Acc:23244]
221942_s_at	GUCY1A3	ENSG00000164116	0.052439589	1.367770663	7.987538556	6.619767893	4	q32.1	guanylate cyclase 1, soluble, alpha 3 [Source:HGNC Symbol;Acc:4685]
213800_at	CFH	ENSG00000000971	0.052439589	1.232286055	7.757236819	6.524950764	1	q31.3	complement factor H [Source:HGNC Symbol;Acc:4883]
1554999_at	RASGEF1B	ENSG00000138670	0.052613981	1.417397531	6.341497404	4.924099873	4	q21.22	RasGEF domain family, member 1B [Source:HGNC Symbol;Acc:24881]
218606_at	ZDHC7	ENSG00000153786	0.052736978	0.390537911	8.928963607	8.538425696	16	q24.1	zinc finger, DHHC-type containing 7 [Source:HGNC Symbol;Acc:18459]
204083_s_at	TPM2	ENSG00000198467	0.052793888	1.005641012	10.06504289	9.059401879	9	p13.3	tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:12011]
1553955_at	PPP1R21	ENSG00000162869	0.052932924	0.83883015	8.379910468	7.541080318	2	p16.3	protein phosphatase 1, regulatory subunit 21 [Source:HGNC Symbol;Acc:30595]
228083_at	CACNA2D4	ENSG00000151062	0.052932924	0.833099044	7.25294855	6.419849507	12	p13.33	calcium channel, voltage-dependent, alpha 2/delta subunit 4 [Source:HGNC Symbol;Acc:20202]
227304_at	SMCR8	ENSG00000176994	0.052932924	0.799991418	8.377826966	7.577835548	17	p11.2	Smith-Magenis syndrome chromosome region, candidate 8 [Source:HGNC Symbol;Acc:17921]
225710_at	GNB4	ENSG00000114450	0.052932924	1.087540407	8.393034502	7.305494096	3	q26.33	guanine nucleotide binding protein (G protein), beta polypeptide 4 [Source:HGNC Symbol;Acc:20731]
204154_at	CDO1	ENSG00000129596	0.052983909	1.192918606	5.120926441	3.928007836	5	q22.3	cysteine dioxygenase type 1 [Source:HGNC Symbol;Acc:1795]

228318_s_at	CRIPAK	ENSG00000179979	0.05300806	0.531106343	6.682490506	6.151384164	4	p16.3	cysteine-rich PAK1 inhibitor [Source:HGNC Symbol;Acc:26619]
227013_at	LAT52	ENSG00000150457	0.05300806	1.10106835	7.79320732	6.692138971	13	q12.11	large tumor suppressor kinase 2 [Source:HGNC Symbol;Acc:6515]
1558692_at	C1orf85	ENSG00000198715	0.053110207	0.572438959	5.400511953	4.828072994	1	q22	chromosome 1 open reading frame 85 [Source:HGNC Symbol;Acc:29436]
213238_at	ATP10D	ENSG00000145246	0.053110207	1.051038069	8.615730447	7.564692379	4	p12	ATPase, class V, type 10D [Source:HGNC Symbol;Acc:13549]
201850_at	CAPG	ENSG00000042493	0.053135419	0.809383904	10.75410257	9.944718664	2	p11.2	capping protein (actin filament), gelsolin-like [Source:HGNC Symbol;Acc:1474]
209717_at	EVI5	ENSG00000067208	0.053140372	0.711449575	7.081763345	6.37031377	1	p22.1	ecotropic viral integration site 5 [Source:HGNC Symbol;Acc:3501]
227388_at	TUSC1	ENSG00000198680	0.053261035	1.564367321	8.139272536	6.574905215	9	p21.2	tumor suppressor candidate 1 [Source:HGNC Symbol;Acc:31010]
200771_at	LAMC1	ENSG00000135862	0.053546476	0.885804076	8.418291529	7.532487453	1	q25.3	laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;Acc:6492]
229055_at	GPR68	ENSG00000119714	0.053546476	0.837700456	9.226090778	8.388390321	14	q32.11	G protein-coupled receptor 68 [Source:HGNC Symbol;Acc:4519]
200927_s_at	RAB14	ENSG00000119396	0.053623502	0.522640122	8.220465934	7.697825812	9	q33.2	RAB14, member RAS oncogene family [Source:HGNC Symbol;Acc:16524]
225447_at	GPD2	ENSG00000115159	0.053623502	0.967759668	8.485215298	7.51745563	2	q24.1	glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Source:HGNC Symbol;Acc:4456]
225525_at	KIAA1671	ENSG00000197077	0.053800235	1.446748208	7.312947558	5.866199349	22	q11.23	KIAA1671 [Source:HGNC Symbol;Acc:29345]
209649_at	STAM2	ENSG00000115145	0.053803885	0.757498312	7.629711981	6.872213668	2	q23.3	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2 [Source:HGNC Symbol;Acc:11358]
219492_at	CHIC2	ENSG00000109220	0.054091605	0.67290252	8.38646188	7.71355936	4	q12	cysteine-rich hydrophobic domain 2 [Source:HGNC Symbol;Acc:1935]
1560060_s_at	VPS37C	ENSG00000167987	0.054133103	0.55757033	8.463033953	7.905463623	11	q12.2	vacuolar protein sorting 37 homolog C (S. cerevisiae) [Source:HGNC Symbol;Acc:26097]
217947_at	CMTM6	ENSG00000091317	0.054171637	0.70230484	10.47748323	9.775178387	3	p22.3	CKLF-like MARVEL transmembrane domain containing 6 [Source:HGNC Symbol;Acc:19177]
219078_at	GPATCH2	ENSG00000092978	0.054197198	0.95185617	7.045735811	6.093879641	1	q41	G patch domain containing 2 [Source:HGNC Symbol;Acc:25499]
203854_at	CFI	ENSG00000205403	0.05429229	1.205739531	6.704059047	5.498319516	4	q25	complement factor I [Source:HGNC Symbol;Acc:5394]
209637_s_at	RGS12	ENSG00000159788	0.054327713	0.502100289	7.515977537	7.013877248	4	p16.3	regulator of G-protein signaling 12 [Source:HGNC Symbol;Acc:9994]
202252_at	RAB13	ENSG00000143545	0.054335009	0.913757531	9.579585924	8.665828393	1	q21.3	RAB13, member RAS oncogene family [Source:HGNC Symbol;Acc:9762]
227373_at	ATXN1L	ENSG00000224470	0.054335009	0.759716522	8.404084446	7.644367924	16	q22.2	ataxin 1-like [Source:HGNC Symbol;Acc:33279]
207469_s_at	PIR	ENSG00000087842	0.054460455	0.663778954	6.265059241	5.601280287	X	p22.2	pirin (iron-binding nuclear protein) [Source:HGNC Symbol;Acc:30048]
212543_at	AIM1	ENSG00000112297	0.054463686	0.788119117	9.682280231	8.894161115	6	q21	absent in melanoma 1 [Source:HGNC Symbol;Acc:356]
208983_s_at	PECAM1	NA	0.054523626	1.305077039	10.69253604	9.387459	NA	NA	NA
226438_at	SNTB1	ENSG00000172164	0.054649274	0.809609573	6.953942186	6.144332613	8	q24.12	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) [Source:HGNC Symbol;Acc:11168]
201567_s_at	GOLGA4	ENSG00000144674	0.054736968	0.544061301	8.834091632	8.290030331	3	p22.2	golgin A4 [Source:HGNC Symbol;Acc:4427]
204520_x_at	BRD1	ENSG00000100425	0.05484599	0.438369852	9.008739811	8.570369959	22	q13.33	bromodomain containing 1 [Source:HGNC Symbol;Acc:1102]
217828_at	SLTM	ENSG00000137776	0.05484599	0.830702603	8.864809369	8.034106766	15	q22.1	SAFB-like, transcription modulator [Source:HGNC Symbol;Acc:20709]
224689_at	MANBAL	ENSG00000101363	0.05484599	0.340215626	9.457076055	9.11686043	20	q11.23	mannosidase, beta A, lysosomal-like [Source:HGNC Symbol;Acc:15799]
219157_at	KLHL2	ENSG00000109466	0.054892546	0.636752761	8.271660585	7.634907824	4	q32.3	kelch-like family member 2 [Source:HGNC Symbol;Acc:6353]
232024_at	GIMAP2	ENSG00000106560	0.055019604	1.162132159	7.593742729	6.431610571	7	q36.1	GTPase, IMAP family member 2 [Source:HGNC Symbol;Acc:21789]
219087_at	ASPN	ENSG00000106819	0.05508081	1.844431057	7.912112086	6.06768103	9	q22.31	asporin [Source:HGNC Symbol;Acc:14872]
213010_at	PRKCDBP	ENSG00000170955	0.05508081	0.666737424	7.157466	6.490728576	11	p15.4	protein kinase C, delta binding protein [Source:HGNC

									Symbol;Acc:9400]
219570_at	KIF16B	ENSG00000089177	0.05508081	0.939524718	6.792995577	5.853470859	20	p12.1	kinesin family member 16B [Source:HGNC Symbol;Acc:15869]
214066_x_at	NPR2	ENSG000000159899	0.05508081	0.499560523	7.871514788	7.371954265	9	p13.3	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B) [Source:HGNC Symbol;Acc:7944]
228372_at	C10orf128	ENSG000000204161	0.05508081	1.228253425	8.331788019	7.103534595	10	q11.23	chromosome 10 open reading frame 128 [Source:HGNC Symbol;Acc:27274]
230276_at	FAM49A	ENSG000000197872	0.05508081	1.286488945	6.31293966	5.026450715	2	p24.2	family with sequence similarity 49, member A [Source:HGNC Symbol;Acc:25373]
203002_at	AMOTL2	ENSG000000114019	0.05508081	1.381170498	7.607053309	6.225882812	3	q22.2	angiomin like 2 [Source:HGNC Symbol;Acc:17812]
225688_s_at	PHLDB2	ENSG000000144824	0.05508081	1.642110715	7.415401954	5.773291239	3	q13.2	pleckstrin homology-like domain, family B, member 2 [Source:HGNC Symbol;Acc:29573]
1553678_a_at	ITGB1	ENSG000000150093	0.05508081	0.762328098	9.60484688	8.842518782	10	p11.22	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) [Source:HGNC Symbol;Acc:6153]
203476_at	TPBG	ENSG000000146242	0.05508081	1.402870201	8.397859019	6.994988818	6	q14.1	trophoblast glycoprotein [Source:HGNC Symbol;Acc:12004]
201180_s_at	GNAI3	ENSG000000065135	0.05508081	0.716484855	9.753542862	9.037058006	1	p13.3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 [Source:HGNC Symbol;Acc:4387]
220141_at	C11orf63	ENSG000000109944	0.05508081	0.530289066	5.631726383	5.101437317	11	q24.1	chromosome 11 open reading frame 63 [Source:HGNC Symbol;Acc:26288]
227923_at	SHANK3	ENSG000000251322	0.05508081	1.175626141	7.738817565	6.563191424	22	q13.33	SH3 and multiple ankyrin repeat domains 3 [Source:HGNC Symbol;Acc:14294]
235334_at	ST6GALNAC3	ENSG000000184005	0.05508081	0.832570926	5.744060873	4.911489947	1	p31.1	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylglactosaminide alpha-2,6-sialyltransferase 3 [Source:HGNC Symbol;Acc:19343]
235411_at	PGBD1	ENSG000000137338	0.05508081	0.454906286	5.741778418	5.286872132	6	p22.1	piggyBac transposable element derived 1 [Source:HGNC Symbol;Acc:19398]
216689_x_at	ARHGAP1	ENSG000000175220	0.055086404	0.521010788	9.747525869	9.226515081	11	p11.2	Rho GTPase activating protein 1 [Source:HGNC Symbol;Acc:673]
202932_at	YES1	ENSG000000176105	0.055086404	1.212404455	6.259729591	5.047325136	18	p11.32	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 [Source:HGNC Symbol;Acc:12841]
212293_at	HIPK1	ENSG000000163349	0.055094773	0.690816647	7.914422373	7.223605727	1	p13.2	homeodomain interacting protein kinase 1 [Source:HGNC Symbol;Acc:19006]
225618_at	ARHGAP27	ENSG000000159314	0.055334195	0.473020908	7.935836992	7.462816084	17	q21.31	Rho GTPase activating protein 27 [Source:HGNC Symbol;Acc:31813]
201242_s_at	ATP1B1	ENSG000000143153	0.055334195	1.283149532	7.126474102	5.84332457	1	q24.2	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide [Source:HGNC Symbol;Acc:804]
203583_at	UNC50	ENSG000000115446	0.055334195	0.452783056	8.989706349	8.536923292	2	q11.2	unc-50 homolog (C. elegans) [Source:HGNC Symbol;Acc:16046]
1557938_s_at	PTRF	ENSG000000177469	0.055334195	0.894352142	8.261399661	7.367047519	17	q21.2	polymerase I and transcript release factor [Source:HGNC Symbol;Acc:9688]
242321_at	PTPN14	ENSG000000152104	0.055341667	1.326981686	5.787995241	4.461013556	1	q41	protein tyrosine phosphatase, non-receptor type 14 [Source:HGNC Symbol;Acc:9647]
212950_at	GPR116	ENSG000000069122	0.055341667	1.466287536	6.762014415	5.295726879	6	p12.3	G protein-coupled receptor 116 [Source:HGNC Symbol;Acc:19030]
205639_at	AOAH	ENSG000000136250	0.055341667	0.654520054	9.612122833	8.957602778	7	p14.2	acyloxyacyl hydrolase (neutrophil) [Source:HGNC Symbol;Acc:548]
223209_s_at	VIMP	ENSG000000131871	0.055341667	0.83813242	9.523564232	8.685431812	15	q26.3	VCP-interacting membrane protein [Source:HGNC Symbol;Acc:30396]
208131_s_at	PTGIS	ENSG000000124212	0.055389281	1.321200027	7.490939927	6.1697399	20	q13.13	prostaglandin I2 (prostacyclin) synthase [Source:HGNC Symbol;Acc:9603]
227833_s_at	MBD6	ENSG000000166987	0.055396564	0.751922649	10.51819974	9.766277089	12	q13.3	methyl-CpG binding domain protein 6 [Source:HGNC Symbol;Acc:20445]
208991_at	STAT3	ENSG000000168610	0.055396564	0.946587005	9.530424681	8.583837676	17	q21.2	signal transducer and activator of transcription 3 (acute-phase

									response factor) [Source:HGNC Symbol;Acc:11364]
216361_s_at	KAT6A	ENSG00000083168	0.055396564	0.651745657	7.927871972	7.276126315	8	p11.21	K(iysine) acetyltransferase 6A [Source:HGNC Symbol;Acc:13013]
1554106_at	NBEAL1	ENSG000000144426	0.055396564	0.661916069	7.462248226	6.800332157	2	q33.2	neurobeachin-like 1 [Source:HGNC Symbol;Acc:20681]
209357_at	CITED2	ENSG000000164442	0.055396564	1.232382537	9.303494571	8.071112033	6	q24.1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 [Source:HGNC Symbol;Acc:1987]
53720_at	C19orf66	ENSG000000130813	0.055431756	0.967375092	9.679981688	8.712606595	19	p13.2	chromosome 19 open reading frame 66 [Source:HGNC Symbol;Acc:25649]
228964_at	PRDM1	ENSG000000057657	0.055431756	1.955052921	9.250667771	7.295614851	6	q21	PR domain containing 1, with ZNF domain [Source:HGNC Symbol;Acc:9346]
228624_at	TMEM144	ENSG000000164124	0.055512399	0.888115651	6.82051307	5.932397419	4	q32.1	transmembrane protein 144 [Source:HGNC Symbol;Acc:25633]
225626_at	PAG1	ENSG000000076641	0.055625052	1.648320718	9.726492347	8.07817163	8	q21.13	phosphoprotein associated with glycosphingolipid microdomains 1 [Source:HGNC Symbol;Acc:30043]
225885_at	EEA1	ENSG000000102189	0.055625052	0.727821543	7.739962682	7.012141139	12	q22	early endosome antigen 1 [Source:HGNC Symbol;Acc:3185]
236172_at	LTBR	ENSG000000213903	0.055654381	1.08404573	7.38748053	6.3034348	14	q12	leukotriene B4 receptor [Source:HGNC Symbol;Acc:6713]
201953_at	CIB1	ENSG000000185043	0.055677119	0.709254173	9.414667247	8.705413075	15	q26.1	calcium and integrin binding 1 (calmyrin) [Source:HGNC Symbol;Acc:16920]
213069_at	HEG1	ENSG000000173706	0.055677119	1.058297106	9.011754037	7.953456931	3	q21.2	heart development protein with EGF-like domains 1 [Source:HGNC Symbol;Acc:29227]
226885_at	RNF217	ENSG000000146373	0.055687877	1.507951738	5.917910835	4.409959097	6	q22.31	ring finger protein 217 [Source:HGNC Symbol;Acc:21487]
203038_at	PTPRK	ENSG000000152894	0.055687877	1.549533171	8.029702811	6.48016964	6	q22.33	protein tyrosine phosphatase, receptor type, K [Source:HGNC Symbol;Acc:9674]
240703_s_at	HERC1	ENSG000000103657	0.055700396	0.961787237	6.445277876	5.48349064	15	q22.31	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1 [Source:HGNC Symbol;Acc:4867]
221641_s_at	ACOT9	ENSG000000123130	0.055791741	0.592409727	9.037040731	8.444631004	X	p22.11	acyl-CoA thioesterase 9 [Source:HGNC Symbol;Acc:17152]
210845_s_at	PLAUR	ENSG000000011422	0.055813214	0.996379681	8.86607143	7.869691749	19	q13.31	plasminogen activator, urokinase receptor [Source:HGNC Symbol;Acc:9053]
212097_at	CAV1	ENSG000000105974	0.055813214	1.72714647	8.888796375	7.161649906	7	q31.2	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;Acc:1527]
243198_at	TEX9	ENSG000000151575	0.055813214	1.558466496	6.115528068	4.557061571	15	q21.3	testis expressed 9 [Source:HGNC Symbol;Acc:29585]
204122_at	TYROBP	ENSG000000011600	0.055813214	1.153345531	11.48995674	10.33661121	19	q13.12	TYRO protein tyrosine kinase binding protein [Source:HGNC Symbol;Acc:12449]
226343_at	DPP8	ENSG000000074603	0.055813214	0.667567668	8.292781672	7.625214004	15	q22.31	dipeptidyl-peptidase 8 [Source:HGNC Symbol;Acc:16490]
205715_at	BST1	ENSG000000109743	0.056095876	0.344955791	7.18626587	6.841310079	4	p15.32	bone marrow stromal cell antigen 1 [Source:HGNC Symbol;Acc:1118]
211980_at	COL4A1	ENSG000000187498	0.056095876	1.223646645	10.90017588	9.676529238	13	q34	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
213572_s_at	SERPINB1	ENSG000000021355	0.056095876	0.852583509	9.447180216	8.594596707	6	p25.2	serpin peptidase inhibitor, clade B (ovalbumin), member 1 [Source:HGNC Symbol;Acc:3311]
209047_at	AQP1	ENSG000000240583	0.056095876	1.711689396	8.767180781	7.055491386	7	p14.3	aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc:633]
214077_x_at	MEIS3P1	ENSG000000179277	0.056095876	0.924586393	8.655448343	7.730861949	17	p12	Meis homeobox 3 pseudogene 1 [Source:HGNC Symbol;Acc:7002]
202946_s_at	BTBD3	ENSG000000132640	0.056281665	1.008164542	5.025902254	4.017737712	20	p12.2	BTB (POZ) domain containing 3 [Source:HGNC Symbol;Acc:15854]
242953_at	ZNF234	ENSG000000263002	0.056315736	0.863642317	6.410969189	5.547326872	19	q13.31	zinc finger protein 234 [Source:HGNC Symbol;Acc:13027]
218380_at	LOC728392	NA	0.056642523	0.659862844	8.050295783	7.390432938	NA	NA	NA
215000_s_at	FEZ2	ENSG000000171055	0.056642523	0.895521867	9.749836768	8.854314901	2	p22.2	fasciculation and elongation protein zeta 2 (zyglin II) [Source:HGNC Symbol;Acc:3660]
229238_at	C17orf97	ENSG000000187624	0.056642523	0.793626222	7.026857654	6.233231432	17	p13.3	chromosome 17 open reading frame 97 [Source:HGNC Symbol;Acc:33800]
219700_at	PLXDC1	ENSG000000161381	0.056642523	1.303729295	7.282377392	5.978648097	17	q12	plexin domain containing 1 [Source:HGNC Symbol;Acc:20945]
202432_at	PPP3CB	ENSG000000107758	0.056855469	0.594665801	8.654289616	8.059623814	10	q22.2	protein phosphatase 3, catalytic subunit, beta isozyme

									[Source:HGNC Symbol;Acc:9315]
1558711_at	FAM13A-AS1	ENSG00000248019	0.05685832	0.663485851	6.443455817	5.779969966	4	q22.1	FAM13A antisense RNA 1 [Source:HGNC Symbol;Acc:19370]
202304_at	FNDCA	ENSG00000102531	0.05685832	0.958277594	8.951195819	7.992919225	13	q14.2	fibronectin type III domain containing 3A [Source:HGNC Symbol;Acc:20296]
213429_at	BICC1	ENSG00000122870	0.05685832	1.455435599	5.911436667	4.456001068	10	q21.1	bicaudal C homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:19351]
203388_at	ARRB2	ENSG00000141480	0.05685832	0.790037084	8.830550615	8.040513531	17	p13.2	arrestin, beta 2 [Source:HGNC Symbol;Acc:712]
205140_at	FPGT	ENSG00000254685	0.056862868	0.746130122	7.424392378	6.678262256	1	p31.1	fucose-1-phosphate guanylyltransferase [Source:HGNC Symbol;Acc:3825]
226594_at	ENTPD5	ENSG00000187097	0.056942273	0.5571412	7.32471655	6.767575351	14	q24.3	ectonucleoside triphosphate diphosphohydrolase 5 [Source:HGNC Symbol;Acc:3367]
219506_at	C1orf54	ENSG00000118292	0.056942273	1.14432295	10.50282075	9.358497804	1	q21.2	chromosome 1 open reading frame 54 [Source:HGNC Symbol;Acc:26258]
209230_s_at	NUPR1	ENSG00000176046	0.056996975	1.108100553	11.12843917	10.02033862	16	p11.2	nuclear protein, transcriptional regulator, 1 [Source:HGNC Symbol;Acc:29990]
205498_at	GHR	ENSG00000112964	0.057095384	1.399155512	5.181886139	3.782730626	5	p13.1	growth hormone receptor [Source:HGNC Symbol;Acc:4263]

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[00353]

TABLE 4

Gene	cox.pvalues	cox.coefficients	ensembl_gene_id	Chromosome	band	description
CAMTA2	0.00000203	-4.668235881	ENSG00000108509	17	p13.2	calmodulin binding transcription activator 2 [Source:HGNC Symbol;Acc:18807]
ODF3B	0.00003813	-2.506221601	ENSG00000177989	22	q13.33	outer dense fiber of sperm tails 3B [Source:HGNC Symbol;Acc:34388]
SCO2	0.00005664	-2.545936327	ENSG00000130489	22	q13.33	SCO2 cytochrome c oxidase assembly protein [Source:HGNC Symbol;Acc:10604]
PSTPIP1	0.00005675	-3.099610719	ENSG00000140368	15	q24.3	proline-serine-threonine phosphatase interacting protein 1 [Source:HGNC Symbol;Acc:9580]
ZNF25	0.00006246	-2.650047611	ENSG00000175395	10	p11.1	zinc finger protein 25 [Source:HGNC Symbol;Acc:13043]
PHLDA1	0.00008490	-1.39157215	ENSG00000139289	12	q21.2	pleckstrin homology-like domain, family A, member 1 [Source:HGNC Symbol;Acc:8933]
LOC100509205	0.00008899	3.284490596	NA	NA	NA	NA
NINL	0.00009498	-3.750225037	ENSG00000101004	20	p11.21	ninein-like [Source:HGNC Symbol;Acc:29163]
IL11RA	0.00011009	-2.428243399	ENSG00000137070	9	p13.3	interleukin 11 receptor, alpha [Source:HGNC Symbol;Acc:5967]
IL18RAP	0.00013238	-2.002156881	ENSG00000115607	2	q12.1	interleukin 18 receptor accessory protein [Source:HGNC Symbol;Acc:5989]
CC2D1B	0.00013484	-3.165981531	ENSG00000154222	1	p32.3	coiled-coil and C2 domain containing 1B [Source:HGNC Symbol;Acc:29386]
FAM219A	0.00016883	-2.594263538	ENSG00000164970	9	p13.3	family with sequence similarity 219, member A [Source:HGNC Symbol;Acc:19920]
IL18R1	0.00019551	-1.244126139	ENSG00000115604	2	q12.1	interleukin 18 receptor 1 [Source:HGNC Symbol;Acc:5988]
CASP7	0.00019755	-1.567912334	ENSG00000165806	10	q25.3	caspase 7, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:1508]
CD5	0.00022052	-2.463614971	ENSG00000110448	11	q12.2	CD5 molecule [Source:HGNC Symbol;Acc:1685]
COX10	0.00023739	-2.388350273	ENSG00000006695	17	p12	cytochrome c oxidase assembly homolog 10 (yeast) [Source:HGNC Symbol;Acc:2260]
LYST	0.00033014	-0.979162015	ENSG00000143669	1	q42.3	lysosomal trafficking regulator [Source:HGNC Symbol;Acc:1968]
LOC100507507	0.00036569	-2.223497444	NA	NA	NA	NA
TRIP6	0.00037027	-2.212398882	ENSG00000087077	7	q22.1	thyroid hormone receptor interactor 6 [Source:HGNC Symbol;Acc:12311]
WDR27	0.00037479	2.047182081	ENSG00000184465	6	q27	WD repeat domain 27 [Source:HGNC Symbol;Acc:21248]
SLFN12	0.00037578	-1.198035184	ENSG00000172123	17	q12	schlafen family member 12 [Source:HGNC Symbol;Acc:25500]
TBC1D4	0.00038960	-0.865903169	ENSG00000136111	13	q22.2	TBC1 domain family, member 4 [Source:HGNC Symbol;Acc:19165]
ACADVL	0.00040722	-1.831475638	ENSG00000072778	17	p13.1	acyl-CoA dehydrogenase, very long chain [Source:HGNC Symbol;Acc:92]
PHEX	0.00042337	-1.148081776	ENSG00000102174	X	p22.11	phosphate regulating endopeptidase homolog, X-linked [Source:HGNC Symbol;Acc:8918]
TOR1B	0.00048257	-2.788588939	ENSG00000136816	9	q34.11	torsin family 1, member B (torsin B) [Source:HGNC Symbol;Acc:11995]
KIF26B	0.00050893	-0.820664008	ENSG00000162849	1	q44	kinesin family member 26B [Source:HGNC Symbol;Acc:25484]
COQ2	0.00052599	-2.524800127	ENSG00000173085	4	q21.23	coenzyme Q2 4-hydroxybenzoate polyprenyltransferase [Source:HGNC Symbol;Acc:25223]
NDUFV3	0.00054696	-2.206346662	ENSG00000160194	21	q22.3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa [Source:HGNC Symbol;Acc:7719]
CNTLN	0.00056050	-1.199738102	ENSG00000044459	9	p22.2	centlein, centrosomal protein [Source:HGNC Symbol;Acc:23432]
SLC6A6	0.00056079	-1.66525648	ENSG00000131389	3	p25.1	solute carrier family 6 (neurotransmitter transporter, taurine), member 6 [Source:HGNC Symbol;Acc:11052]
TUBG2	0.00057975	-2.766415519	ENSG00000037042	17	q21.2	tubulin, gamma 2 [Source:HGNC Symbol;Acc:12419]
LPAR6	0.00059706	-0.810738084	ENSG00000139679	13	q14.2	lysophosphatidic acid receptor 6 [Source:HGNC Symbol;Acc:15520]
SLC12A7	0.00060983	-1.723437657	ENSG00000113504	5	p15.33	solute carrier family 12 (potassium/chloride transporters), member 7 [Source:HGNC Symbol;Acc:10915]
TYMP	0.00061216	-1.832645096	ENSG00000025708	22	q13.33	thymidine phosphorylase [Source:HGNC Symbol;Acc:3148]
TMOD2	0.00062660	-1.291604457	ENSG00000128872	15	q21.2	tropomodulin 2 (neuronal) [Source:HGNC Symbol;Acc:11872]
SUN2	0.00063540	-5.074770677	ENSG00000100242	22	q13.1	Sad1 and UNC84 domain containing 2 [Source:HGNC Symbol;Acc:14210]
NRBP2	0.00066284	-1.371485291	ENSG00000185189	8	q24.3	nuclear receptor binding protein 2 [Source:HGNC Symbol;Acc:19339]
ZSWIM7	0.00067007	-1.458321834	ENSG000000214941	17	p12	zinc finger, SWIM-type containing 7 [Source:HGNC Symbol;Acc:26993]
S100B	0.00067297	-1.792059143	ENSG00000160307	21	q22.3	S100 calcium binding protein B [Source:HGNC Symbol;Acc:10500]
ITGB2-AS1	0.00067370	-0.863312228	ENSG000000227039	21	q22.3	ITGB2 antisense RNA 1 [Source:HGNC Symbol;Acc:44304]
LOC730227	0.00067711	3.052297063	NA	NA	NA	NA
ALLC	0.00070484	1.173487594	ENSG00000151360	2	p25.3	allantoicase [Source:HGNC Symbol;Acc:17377]
ECHDC2	0.00074255	-1.182987095	ENSG00000121310	1	p32.3	enoyl CoA hydratase domain containing 2 [Source:HGNC Symbol;Acc:23408]

VPS26B	0.00076061	-1.959803305	ENSG00000151502	11	q25	vacuolar protein sorting 26 homolog B (S. pombe) [Source:HGNC Symbol;Acc:28119]
MGC16142	0.00081730	3.447869406	NA	NA	NA	NA
ADAP2	0.00085355	-1.423623909	ENSG00000184060	17	q11.2	ArfGAP with dual PH domains 2 [Source:HGNC Symbol;Acc:16487]
TCL6	0.00085843	1.001037623	ENSG00000187621	14	q32.13	T-cell leukemia/lymphoma 6 (non-protein coding) [Source:HGNC Symbol;Acc:13463]
IFIT5	0.00086743	-1.127640551	ENSG00000152778	10	q23.31	interferon-induced protein with tetratricopeptide repeats 5 [Source:HGNC Symbol;Acc:13328]
LDOC1L	0.00088004	-1.303614625	ENSG00000188636	22	q13.31	leucine zipper, down-regulated in cancer 1-like [Source:HGNC Symbol;Acc:13343]
NUDT16	0.00091516	-1.407527098	ENSG00000198585	3	q22.1	nudix (nucleoside diphosphate linked moiety X)-type motif 16 [Source:HGNC Symbol;Acc:26442]
FLII	0.00093525	-1.671920539	ENSG00000177731	17	p11.2	flightless I homolog (Drosophila) [Source:HGNC Symbol;Acc:3750]
HEXIM1	0.00096902	-1.893455283	ENSG00000186834	17	q21.31	hexamethylene bis-acetamide inducible 1 [Source:HGNC Symbol;Acc:24953]
SGSM2	0.00099078	-1.460523274	ENSG00000141258	17	p13.3	small G protein signaling modulator 2 [Source:HGNC Symbol;Acc:29026]
FXVD2	0.00100378	-1.494412258	ENSG00000137731	11	q23.3	FXVD domain containing ion transport regulator 2 [Source:HGNC Symbol;Acc:4026]
RDH10	0.00100828	-1.263627433	ENSG00000121039	8	q21.11	retinol dehydrogenase 10 (all-trans) [Source:HGNC Symbol;Acc:19975]
RHOBTB2	0.00100852	1.443814978	ENSG00000008853	8	p21.3	Rho-related BTB domain containing 2 [Source:HGNC Symbol;Acc:18756]
PDE8A	0.00103756	-1.366305067	ENSG00000073417	15	q25.3	phosphodiesterase 8A [Source:HGNC Symbol;Acc:8793]
KIAA1598	0.00106273	-0.883804986	ENSG00000187164	10	q25.3	KIAA1598 [Source:HGNC Symbol;Acc:29319]
ACSL1	0.00106684	-1.1398898	ENSG00000151726	4	q35.1	acyl-CoA synthetase long-chain family member 1 [Source:HGNC Symbol;Acc:3569]
CAPN2	0.00111892	-0.673819472	ENSG00000162909	1	q41	calpain 2, (m/II) large subunit [Source:HGNC Symbol;Acc:1479]
EPM2A	0.00112005	2.042733065	ENSG00000112425	6	q24.3	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin) [Source:HGNC Symbol;Acc:3413]
SPG20	0.00112318	-1.345465148	ENSG00000133104	13	q13.3	spastic paraplegia 20 (Troyer syndrome) [Source:HGNC Symbol;Acc:18514]
NUDT9P1	0.00113163	1.948144791	NA	NA	NA	NA
FHOD1	0.00116819	-2.500243302	ENSG00000135723	16	q22.1	formin homology 2 domain containing 1 [Source:HGNC Symbol;Acc:17905]
OSCAR	0.00118671	-2.271018361	ENSG00000170909	19	q13.42	osteoclast associated, immunoglobulin-like receptor [Source:HGNC Symbol;Acc:29960]
ARMCX1	0.00119573	-1.079753587	ENSG00000126947	X	q22.1	armadillo repeat containing, X-linked 1 [Source:HGNC Symbol;Acc:18073]
SELP	0.00122190	-0.903200375	ENSG00000174175	1	q24.2	selectin P (granule membrane protein 140kDa, antigen CD62) [Source:HGNC Symbol;Acc:10721]
CD200R1	0.00126705	-0.920571979	ENSG00000163606	3	q13.2	CD200 receptor 1 [Source:HGNC Symbol;Acc:24235]
PLEKHA7	0.00128422	-1.287862112	ENSG00000166689	11	p15.1	pleckstrin homology domain containing, family A member 7 [Source:HGNC Symbol;Acc:27049]
GNAQ	0.00133109	-0.799757937	ENSG00000156052	9	q21.2	guanine nucleotide binding protein (G protein), q polypeptide [Source:HGNC Symbol;Acc:4390]
ZBTB4	0.00135017	-1.220347435	ENSG00000174282	17	p13.1	zinc finger and BTB domain containing 4 [Source:HGNC Symbol;Acc:23847]
CLEC12A	0.00136635	-1.624654383	ENSG00000172322	12	p13.2	C-type lectin domain family 12, member A [Source:HGNC Symbol;Acc:31713]
PISD	0.00139038	-3.41677807	ENSG00000241878	22	q12.2	phosphatidylserine decarboxylase [Source:HGNC Symbol;Acc:8999]
ALDH2	0.00141785	-0.672902178	ENSG00000111275	12	q24.12	aldehyde dehydrogenase 2 family (mitochondrial) [Source:HGNC Symbol;Acc:404]
IL6R	0.00142894	-0.755163035	ENSG00000160712	1	q21.3	interleukin 6 receptor [Source:HGNC Symbol;Acc:6019]
MRC2	0.00144402	-1.526866671	ENSG00000011028	17	q23.2	mannose receptor, C type 2 [Source:HGNC Symbol;Acc:16875]
TSEN34	0.00145956	-2.689190004	ENSG00000170892	19	q13.42	tRNA splicing endonuclease 34 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:15506]
GALM	0.00147988	-0.995059373	ENSG00000143891	2	p22.1	galactose mutarotase (aldose 1-epimerase) [Source:HGNC Symbol;Acc:24063]
EMP3	0.00148006	-1.056401849	ENSG00000142227	19	q13.33	epithelial membrane protein 3 [Source:HGNC Symbol;Acc:3335]
SAT2	0.00157137	-2.792215867	ENSG00000141504	17	p13.1	spermidine/spermine N1-acetyltransferase family member 2 [Source:HGNC Symbol;Acc:23160]
TTC31	0.00157244	-1.63766409	ENSG00000115282	2	p13.1	tetratricopeptide repeat domain 31 [Source:HGNC Symbol;Acc:25759]
CES2	0.00159167	-2.024818272	ENSG00000172831	16	q22.1	carboxylesterase 2 [Source:HGNC Symbol;Acc:1864]
AGPAT9	0.00159441	-1.35239458	ENSG00000138678	4	q21.23	1-acylglycerol-3-phosphate O-acyltransferase 9 [Source:HGNC Symbol;Acc:28157]
RBM43	0.00161986	-1.428737679	ENSG00000184898	2	q23.3	RNA binding motif protein 43 [Source:HGNC Symbol;Acc:24790]
CXCL14	0.00162663	-0.467340849	ENSG00000145824	5	q31.1	chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;Acc:10640]
PLEKHA1	0.00167197	-0.919870988	ENSG00000107679	10	q26.13	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1 [Source:HGNC Symbol;Acc:14335]
SLC35D2	0.00168394	-1.418796477	ENSG00000130958	9	q22.32	solute carrier family 35 (UDP-GlcNAc/UDP-glucose transporter), member D2 [Source:HGNC Symbol;Acc:20799]
LOC654841	0.00170773	4.303627408	NA	NA	NA	NA
RFPL35	0.00171657	-2.35571089	ENSG00000205853	22	q12.3	RFPL3 antisense [Source:HGNC Symbol;Acc:9981]

PLCB2	0.00175948	-2.173217301	ENSG00000137841	15	q15.1	phospholipase C, beta 2 [Source:HGNC Symbol;Acc:9055]
DPP4	0.00176325	-1.056413733	ENSG00000197635	2	q24.2	dipeptidyl-peptidase 4 [Source:HGNC Symbol;Acc:3009]
FAM219B	0.00181328	-1.464593174	ENSG00000178761	15	q24.1	family with sequence similarity 219, member B [Source:HGNC Symbol;Acc:24695]
TSPAN2	0.00181539	-1.024722523	ENSG00000134198	1	p13.2	tetraspanin 2 [Source:HGNC Symbol;Acc:20659]
SLC2A4RG	0.00183651	-2.092522041	ENSG00000125520	20	q13.33	SLC2A4 regulator [Source:HGNC Symbol;Acc:15930]
TCF7L2	0.00183773	-1.072368328	ENSG00000148737	10	q25.2	transcription factor 7-like 2 (T-cell specific, HMG-box) [Source:HGNC Symbol;Acc:11641]
C10orf76	0.00184603	-1.832924913	ENSG00000120029	10	q24.32	chromosome 10 open reading frame 76 [Source:HGNC Symbol;Acc:25788]
NAGA	0.00187105	-1.371486854	ENSG00000198951	22	q13.2	N-acetylgalactosaminidase, alpha- [Source:HGNC Symbol;Acc:7631]
RIPK3	0.00190047	-3.462098915	ENSG00000129465	14	q12	receptor-interacting serine-threonine kinase 3 [Source:HGNC Symbol;Acc:10021]
CD1E	0.00197070	-1.121895164	ENSG00000158488	1	q23.1	CD1e molecule [Source:HGNC Symbol;Acc:1638]
HAVCR2	0.00202258	-0.729699479	ENSG00000135077	5	q33.3	hepatitis A virus cellular receptor 2 [Source:HGNC Symbol;Acc:18437]

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[00354] From the foregoing, it will be appreciated that, although specific embodiments have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of what is provided herein. All of the references referred to above are incorporated herein by reference in their entireties.

What is claimed is:

1. A method for predicting the clinical sensitivity of a diffuse large B-cell lymphoma (DLBCL) to treatment with lenalidomide comprising:
 - (a) obtaining a first biological sample from a first patient having a DLBCL;
 - (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 3;
 - (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 3 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having a DLBCL, wherein the DLBCL in the second patient is clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and wherein the differential expression of the one, two, three, four, five or more of the genes in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample indicates that the DLBCL in the first patient will be clinical sensitive to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof.
2. A method for predicting the clinical sensitivity of a DLBCL to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, comprising:
 - (a) obtaining a first biological sample from a first patient having a DLBCL;
 - (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 4;
 - (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 4 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having a DLBCL, wherein the DLBCL in the second patient is clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and wherein the differential expression of the one, two, three, four, five or more of the genes in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample indicates that the DLBCL in the first patient will be clinical sensitive to treatment with lenalidomide.

3. A method for predicting the clinical sensitivity of a DLBCL to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, comprising:
 - (a) obtaining a first biological sample from a first patient having a DLBCL;
 - (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 1; and
 - (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 1 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having a DLBCL, wherein the DLBCL cancer in the second patient is clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and wherein a higher level of expression of the one, two, three, four, five or more of the genes in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample indicates that the DLBCL in the first patient will be clinical sensitive to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof.
4. A method for predicting the clinical sensitivity of a DLBCL to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, comprising:
 - (a) obtaining a first biological sample from a first patient having a DLBCL;
 - (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 2; and
 - (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 2 in the first biological sample with the level of expression of the same genes in a second biological sample is from a second patient having a DLBCL, wherein the DLBCL in the second patient is clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and wherein a lower level of expression of the one, two, three, four, five or more of the genes in the first biological sample relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample indicates that the DLBCL in the first patient will be clinical sensitive to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof.

5. A method for predicting the clinical sensitivity of a DLBCL to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, comprising:
- obtaining a first tumor sample from a first patient having a DLBCL;
 - measuring the proportion of dendritic cells in the first tumor sample; and
 - comparing the proportion of dendritic cells in the first tumor sample with the proportion of dendritic cells in a second tumor sample from a second patient having a DLBCL, wherein the second patient's DLBCL is clinically insensitive to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and
- wherein a higher proportion of dendritic cells in the first tumor sample relative the proportion of dendritic cells in the second tumor sample indicates that the DLBCL in the first patient will be clinical sensitive to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof.
6. A methods for predicting the clinical sensitivity of a DLBCL to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, comprising:
- obtaining a first tumor sample from a first patient having a DLBCL;
 - measuring the proportion of plasma cells in the first tumor sample; and
 - comparing the proportion of plasma cells in the first tumor sample with the proportion of plasma cells in a second tumor sample from a second patient having a DLBCL, wherein the second patient's DLBCL is clinically insensitive to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and
- wherein a higher proportion of plasma cells in the first tumor sample relative the proportion of plasma cells in the second tumor sample indicates that the DLBCL in the first patient will be clinical sensitive to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof.
7. A method for predicting the clinical sensitivity of a DLBCL to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, comprising:
- obtaining a first biological sample from a first patient having a DLBCL
 - measuring the expression of the genes or a certain subset of genes set forth in Table 1, 2, 3, or 4 in the first biological sample; and

- (c) comparing the gene expression profile of the genes or subset of genes in the first biological sample to (i) the gene expression profile of the genes or subset of genes in tumor samples from patients having DLBCL which are clinically sensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and (ii) the gene expression of the genes or subset of genes in tumor samples from patients having DLBCL which are clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof,

wherein a gene expression profile for the genes or subset of genes in the first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having DLBCL which are clinically sensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, indicates that the DLBCL in the first patient will be clinical sensitive to treatment with lenalidomide, and a gene expression profile for the genes or subset of genes in first biological sample similar to the gene expression profile for the genes or subset of genes in tumor samples from patients having DLBCL which are clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, indicates that the DLBCL of the first patient will be clinically insensitive to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof.

8. A method for predicting the clinical sensitivity of a DLBCL to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, comprising:
 - (a) obtaining a first tumor sample from a first patient having a hematological cancer;
 - (b) measuring the proportion of immune cells in the first tumor sample; and
 - (c) comparing the proportion of the immune cells in the first tumor sample to (i) the proportion of the same immune cells in tumor samples from patients having DLBCL which are clinically sensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and (ii) the proportion of the same immune cells in tumor samples from patients having DLBCL which are clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof,
 wherein a proportion of the immune cells in the first tumor sample similar to the proportion of the same immune cells in tumor samples from patients having DLBCL which are clinically sensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, indicates that the DLBCL in the first patient will be clinical sensitive to treatment

with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and a proportion of the immune cells in the first tumor sample similar to the proportion of the same immune cells in tumor samples from patients having DLBCL which are clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, indicates that the DLBCL in the first patient will be clinical insensitive to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof.

9. A method for managing or treating a DLBCL comprising:
 - (a) obtaining a first biological sample from a first patient having a DLBCL;
 - (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 3;
 - (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 3 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having a DLBCL, wherein the DLBCL in the second patient is clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof; and
 - (d) administering lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, to the first patient if the one, two, three, four, five or more of the genes in the first biological sample are differentially expressed relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample.
10. A method for managing or treating a DLBCL comprising:
 - (a) obtaining a first biological sample from a first patient having a DLBCL;
 - (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 4;
 - (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 4 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having a DLBCL, wherein the DLBCL in the second patient is clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof; and
 - (d) administering lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, to the first patient if the one, two, three, four, five or more of the genes in the

first biological sample are differentially expressed relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample.

11. A method for managing or treating a DLBCL comprising:
 - (a) obtaining a first biological sample from a first patient having a DLBCL;
 - (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 1;
 - (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 1 in the first biological sample with the level of expression of the same genes in a second biological sample from a second patient having a DLBCL, wherein the DLBCL in the second patient is clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof; and
 - (d) administering lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, to the first patient if a higher level of expression of the one, two, three, four, five or more of the genes in the first biological sample is measured relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample.
12. A method for managing or treating a DLBCL comprising:
 - (a) obtaining a first biological sample from a first patient having a DLBCL;
 - (b) measuring the level of expression of one, two, three, four, five or more of the genes identified in Table 2;
 - (c) comparing the level of expression of the one, two, three, four, five or more of the genes identified in Table 2 in the first biological sample with the level of expression of the same genes in a second biological sample is from a second patient having a DLBCL, wherein the DLBCL in the second patient is clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof; and
 - (d) administering lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, to the first patient if a lower level of expression of the one, two, three, four, five or more of the genes in the first biological sample is measured relative to the level of expression of the one, two, three, four, five or more of the genes in the second biological sample.

13. A method for managing or treating a DLBCL:
- (a) obtaining a first biological sample from a first patient having a DLBCL;
 - (b) measuring the expression of a certain subset of genes set forth in Table 1, 2, 3 or 4, or any combination thereof in the first biological sample,
 - (c) comparing the gene expression profile of the subset of genes in the first biological sample to (i) the gene expression profile of the subset of genes in tumor samples from patients having DLBCL which are clinically sensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and (ii) the gene expression of the subset of genes in tumor samples from patients having DLBCL which are clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof; and
 - (d) administering lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, to the first patient if: (i) the gene expression profile for the subset of genes in the first biological sample is similar to the gene expression profile for the subset of genes in tumor samples from patients having DLBCL which are clinically sensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and (ii) the gene expression profile for the subset of genes in first biological sample is not similar to the gene expression profile for the subset of genes in tumor samples from patients having DLBCL which are clinically insensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof.
14. A method for managing or treating a DLBCL comprising:
- (a) obtaining a first tumor sample from a first patient having a DLBCL;
 - (b) measuring the proportion of dendritic cells in the first tumor sample;
 - (c) comparing the proportion of dendritic cells in the first tumor sample with the proportion of dendritic cells in a second tumor sample from a second patient having a DLBCL, wherein the second patient's DLBCL is clinically insensitive to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof; and
 - (d) administering lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, to the first patient if a higher proportion of dendritic cells in the first tumor sample is measured relative the proportion of dendritic cells in the second tumor sample.

15. A method for managing or treating a DLBCL comprising:
- (a) obtaining a first tumor sample from a first patient having a DLBCL;
 - (b) measuring the proportion of plasma cells in the first tumor sample;
 - (c) comparing the proportion of plasma cells in the first tumor sample with the proportion of plasma cells in a second tumor sample from a second patient having a DLBCL, wherein the second patient's DLBCL is clinically insensitive to treatment with lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof; and
 - (d) administering lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, to the first patient if a higher proportion of plasma cells in the first tumor sample is measured relative the proportion of plasma cells in the second tumor sample.
16. A method for managing or treating a DLBCL comprising:
- (a) obtaining a first tumor sample from a first patient having a DLBCL;
 - (b) measuring the proportion of immune cells in the first tumor sample; and
 - (c) comparing the proportion of the immune cells in the first tumor sample to (i) the proportion of the same immune cells in tumor samples from patients having DLBCL which are clinically sensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and (ii) the proportion of the same immune cells in tumor samples from patients having DLBCL which are clinically insensitive to the lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof; and
 - (d) administering lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, to the first patient if the proportion of the immune cells in the first tumor sample is (i) similar to the proportion of the same immune cells in tumor samples from patients having DLBCL which are clinically sensitive to lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof, and (ii) not similar to the proportion of the same immune cells in tumor samples from patients having DLBCL which are clinically insensitive to the lenalidomide, or pharmaceutically acceptable salts, solvates or isomers thereof.
17. The method of any one of claims 1 to 16, wherein the DLBCL is refractory.
18. The method of any one of claims 1 to 16, wherein the DLBCL is relapsed in the first patient.

19. The method of any one of claims 1 to 16, wherein the DLBCL is a germinal center B-cell-like subtype.
20. The method of any one of claims 1 to 16, wherein the DLBCL is an activated B-cell-like subtype.