METHOD OF PREDICTING BREAST CANCER PROGNOSIS

RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application Nos. 61/557,238, filed November 8, 2011, and 61/597,426, filed February 10, 2012, which are hereby incorporated by reference in their entirety.

FIELD OF THE INVENTION

[0002] The present invention relates to biomarkers associated with breast cancer prognosis. These biomarkers include coding transcripts and their expression products, as well as non-coding transcripts, and are useful for predicting the likelihood of breast cancer recurrence in a breast cancer patient.

INTRODUCTION

[0003] For over a decade, technologies such as DNA microarray and reverse transcription polymerase chain reaction (RT-PCR) have demonstrated that levels of certain RNA transcripts ("gene expression profiles") relate to patient stratification and disease outcomes, especially in a variety of cancers. Several validated and now widely used clinical tests make use of gene expression profiling, such as the Onco*type* DX® RT-PCR test, which measures the levels of 21 biomarker RNAs in archival formalin-fixed paraffin-embedded (FFPE) tissue. The Onco*type* DX® RT-PCR test predicts the risk of recurrence of early estrogen receptor (ER)-positive breast cancer, as well as the likelihood of response to chemotherapy, and is now used to guide treatment decisions for about half of ER+ breast cancer patients in the U.S.

[0004] However, RT-PCR is constrained by the number of transcripts and sequence complexity that can be interrogated, especially given the limited amount of patient FFPE RNA available from many tumor specimens. Recent major advances in DNA sequencing ("next generation sequencing") provide massively parallel throughput and data volumes that eclipse the nucleic acid information content possible with other technologies, such as RT-PCR. Next generation sequencing makes feasible unprecedented extensive genome analysis of groups of individuals, including analyses of sequence differences, polymorphisms, mutations, copy number variations, epigenetic variations and transcript abundance (RNA-Seq).

SUMMARY

[0005] A multiplexed, whole genome sequencing methodology was developed to enable whole transcriptome-wide breast cancer biomarker discovery using low amounts of FFPE tissue. The present invention provides biomarkers that associate, positively or negatively, with a particular clinical outcome in breast cancer. These biomarkers are listed in Tables 1-5 and 15. For example, the clinical outcome could be no cancer recurrence or cancer recurrence. The clinical outcome may be defined by clinical endpoints, such as disease or recurrence free survival, metastasis free survival, overall survival, etc.

[0006] The present invention accommodates the use of archived paraffin-embedded biopsy material for assay of all markers in the set, and therefore is compatible with the most widely available type of biopsy material. It is also compatible with other different methods of tumor tissue harvest, for example, via core biopsy or fine needle aspiration.

[0007] In one aspect, the present invention provides a method of predicting a likelihood of long-term survival without recurrence of breast cancer in a breast cancer patient. The method comprises determining a level of one or more RNA transcripts, or its expression product, in a breast cancer tumor sample obtained from the patient. The RNA transcript or its expression product may be selected from Tables 1 and 15. The likelihood of long-term survival without breast cancer recurrence is then predicted based on the negative or positive correlation of the RNA transcript or its expression product with increased likelihood of long-term survival without breast cancer recurrence. An RNA transcript is negatively correlated with increased long-term survival without recurrence of breast cancer if its direction of association is marked 1 in Tables 1 and 15, and is positively correlated with increased long-term survival without recurrence of breast cancer if its direction of association is marked -1in Tables 1 and 15.

[0008] In another aspect, the present invention provides a method of predicting a likelihood of long-term survival without recurrence of breast cancer in an estrogen receptor (ER)-positive breast cancer patient. The method comprises determining a level of one or more RNA transcripts, or its expression product, in a breast cancer tumor sample obtained from the patient. The RNA transcript or its expression product may be selected from Table 2. The likelihood of long-term survival without breast cancer recurrence is then predicted based on the negative or positive correlation of the RNA transcript or its expression product with increased likelihood of long-term survival without breast cancer recurrence. An RNA transcript is

negatively correlated with increased long-term survival without recurrence of breast cancer if its direction of association is marked 1 in Table 2, and is positively correlated with increased long-term survival without recurrence of breast cancer if its direction of association is marked -1 in Table 2.

[0009] The RNA transcripts, or the expression products, may be grouped into gene networks based on the current understanding of their cellular function. For example, the gene networks include a cell cycle network, ESR1 network, Chr9q22network, Chr17q23-24 network, Chr8q21-24 network, olfactory receptor network, and metabolic-like networks. The present invention therefore also provides a method of predicting a likelihood of long-term survival without breast cancer recurrence in a breast cancer patient by determining a quantitative value, such as a likelihood score, for one or more gene networks based on the level of at least one RNA transcript, or expression product thereof, within the gene network, in a breast cancer tumor sample obtained from the patient. The quantitative value for the gene network may be determined by weighting the contribution of one or more RNA transcripts, or their expression products, to clinical outcome, such as risk of recurrence.

[0010] In yet another aspect, the present invention provides a method of predicting a likelihood of long-term survival without recurrence of breast cancer in a breast cancer patient by determining a level of one or more non-coding sequences in a breast cancer tissue sample obtained from the patient. In one embodiment, the non-coding sequence is one or more intronic RNAs selected from Table 3. In another embodiment, the non-coding sequence is one or more long intergenic non-coding regions (lincRNAs) selected from Table 4. In a further embodiment, the non-coding sequence is one or more intergenic sequences selected from Table 5. In yet another embodiment, the non-coding sequence is one or more intergenic regions 1-69 selected from Table 5. The intergenic region may be comprised of one or more intergenic sequences according to Table 5. The likelihood of long-term survival without breast cancer recurrence is predicted based on the negative or positive correlation of the non-coding sequence with increased likelihood of long-term survival without breast cancer recurrence. A non-coding sequence is negatively correlated with increased long-term survival without recurrence of breast cancer if its direction of association is marked 1 in Tables 3-5, and is positively correlated with increased long-term survival without recurrence of breast cancer if its direction of association is marked -1 in Tables 3-5.

[0011] In a further aspect, the present invention provides a method of predicting a likelihood of long-term survival without recurrence of breast cancer in a breast cancer patient by determining a level of an RNA transcript, or an expression product thereof, from a metabolic-like network in a breast cancer tumor sample obtained from the patient. The metabolic-like networks include a five-gene set comprising ENO1, IDH2, TMSB10, PGK1, and G6PD, and a fourteen-gene set comprising PGD, TKT, TALDO1, G6PD, GP1, SLC1A5, SLC7A5, OGDH, SUCLG1, ENO1, PGK1, IDH2, ACO2, and FBP1. In one aspect, levels of at least three RNA transcripts, or expression products thereof, selected from ENO1, IDH2, TMSB10, PGK1, and G6PD, are determined. In a specific embodiment, the levels of at least IDH2, PGK1, and G6PD are determined. In yet another embodiment, the levels of ENO1, IDH2, TMSB10, PGK1, and G6PD are determined. In another aspect, levels of at least five RNA transcripts, or expression products thereof, selected from PGD, TKT, TALDO1, G6PD, GP1, SLC1A5, SLC7A5, OGDH, SUCLG1, ENO1, PGK1, IDH2, ACO2, and FBP1, are determined. In a specific embodiment, the levels of the RNA transcripts, or expression products thereof, of PGD, TKT, TALDO1, G6PD, GP1, SLC1A5, SLC7A5, OGDH, SUCLG1, ENO1, PGK1, IDH2, ACO2, and FBP1, are determined. The likelihood of long-term survival without breast cancer recurrence is predicted based on the negative or positive correlation of the RNA transcripts, or expression products thereof, with increased likelihood of long-term survival without breast cancer recurrence. Levels of ENO1, IDH2, TMSB10, PGK1, G6PD, PGD, TKT, TALDO1, GP1, SLC1A5, SLC7A5, OGDH, SUCLG1, and ACO2 are all negatively correlated with an increased likelihood of long-term survival without recurrence of breast cancer, while the level of FBP1 is positively correlated with an increased likelihood of long-term survival without recurrence of breast cancer.

[0012] Any of the above methods may utilize a combination of coding and non-coding RNA transcripts for predicting breast cancer prognosis. Moreover, any of the above methods may be performed by whole transcriptome sequencing, reverse transcription polymerase chain reaction (RT-PCR), or by array. Other methods known in the art may be used. In an embodiment of the invention, the breast cancer tumor sample is a fixed, wax-embedded tissue sample or a fine needle biopsy sample. In another embodiment, the level of the RNA transcript, or its expression product, or the level of the non-coding sequence may be normalized.

[0013] In an embodiment of the invention, a likelihood score (e.g., a score predicting a likelihood of long-term survival without breast cancer recurrence) can be calculated based on the

level or normalized level of the coding RNA transcript, or an expression product thereof, and/or non-coding RNA transcript. A score may be calculated using weighted values based on the level or normalized level of the coding RNA transcript (or expression product thereof) and/or the non-coding RNA transcript, and its contribution to clinical outcome, such as long-term survival without breast cancer recurrence.

BRIEF DESCRIPTION OF THE DRAWINGS

[0014] FIG. 1 shows the relationship of increased RNA expression to risk of breast cancer recurrence in 136 breast cancer patients. Each point represents a distinct RNA sequence. The magnitude of the effect size is given by the hazard ratio from Cox proportional hazard analysis and statistical significance by P-Value. Fig. 1A shows an analysis of 192 genes measured by RT-PCR. Tested Onco*type* Dx® genes are indicated. Fig. 1B shows an analysis of assembled RefSeq transcripts as measured by whole transcriptome sequencing.

[0015] FIG. 2 are boxplots of normalized expression values of RNAs in breast cancer patients, stratified by recurrence status. Each point represents a patient tumor. The bottom and top of the box are the 25th and 75th percentiles and the band within the box is the 50th percentile (the median) of the points in the group. The ends of the whiskers represent the lowest datum still within 1.5 interquartile range (IQR) of the lower quartile, and the highest datum still within 1.5 IQR of the upper quartile. Values from RNA-Seq (left panel) and RT-PCR (right panel) are shown: Fig. 2A: BCL2; Fig. 2B: GSTM1; Fig. 2C: AURKA; Fig. 2D: MKI67.

[0016] FIG. 3 is a scatter plot of the breast cancer recurrence risk hazard ratios of 192 RNA sequences comparing the RT-PCR results (x-axis) versus RNA-Seq (assembled RefSeq) results (y axis). Each point represents a distinct RNA.

[0017] FIG. 4 is a comparison of the genes identified using publicly available microarray data and the NGS ("next generation sequencing") data of the present invention. Fig. 4A shows that there is substantial agreement in the genes identified as prognostic between the two platforms (11,659 genes in common, odds ratio = 2.99). Fig. 4B shows that at the low end of RNA-Seq expression (RNAs with mean counts <10.25), the level of agreement among the two platforms is not statistically significant (1620 genes in common, odds ratio = 0.89).

[0018] FIG. 5 is a 2D visualization of the network of gene co-expression (with a Pearson correlation coefficient cutoff of $\geq$0.6) amongst the 1307 identified prognostic RefSeqs generated using Cytoscape 2.8.

DETAILED DESCRIPTION

[0019] Before the present invention and specific exemplary embodiments of the invention are described, it is to be understood that this invention is not limited to particular embodiments described, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

[0020] Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range and any other stated or intervening value in that stated range is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges is also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either both of those included limits are also included in the invention.

[0021] As used herein and in the appended claims, the singular forms "a," "an," and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "an RNA transcript" includes a plurality of such RNA transcripts.

[0022] Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. For example, Singleton *et al.*, Dictionary of Microbiology and Molecular Biology 2nd ed., J. Wiley & Sons (New York, NY 1994), provide one skilled in the art with a general guide to many of the terms used in the present application.

[0023] Additionally, the practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, and biochemistry, which are within the skill of the art. Such techniques are explained fully in the literature, such as, "Molecular Cloning: A Laboratory Manual", 2nd edition (Sambrook et al., 1989); "Oligonucleotide Synthesis" (M.J. Gait, ed., 1984); "Animal Cell Culture" (R.I. Freshney, ed., 1987); "Methods in Enzymology" (Academic Press, Inc.); "Handbook of Experimental Immunology", 4th edition (D.M. Weir & C.C. Blackwell, eds., Blackwell Science Inc., 1987); "Gene Transfer Vectors for Mammalian Cells" (J.M. Miller &

M.P. Calos, eds., 1987); "Current Protocols in Molecular Biology" (F.M. Ausubel et al., eds., 1987); and "PCR: The Polymerase Chain Reaction", (Mullis et al., eds., 1994).

[0024] The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. An example of a cancer is breast cancer.

[0025] The term "co-expressed" as used herein refers to a statistical correlation between the expression level of one sequence and the expression level of another sequence. Pairwise co-expression may be calculated by various methods known in the art, e.g., by calculating a Pearson correlation coefficient or Spearman correlation coefficient. Co-expressed gene cliques or gene networks may also be identified using a graph theory. An analysis of co-expression may be calculated using normalized data.

[0026] The term "correlates" or "correlating" as used herein refers to a statistical association between instances of two events, where events may include numbers, data sets, and the like. For example, when the events involve numbers, a positive correlation (also referred to herein as a "direct correlation") means that as one increases, the other increases as well. A negative correlation (also referred to herein as an "inverse correlation") means that as one increases, the other decreases. The present invention provides coding and non-coding RNA transcripts, or expression products thereof, the levels of which are correlated with a particular outcome measure, such as between the level of an RNA transcript and the likelihood of long-term survival without breast cancer recurrence. For example, the increased level of an RNA transcript may be positively correlated with a likelihood of a good clinical outcome for the patient, such as an increased likelihood of long-term survival without recurrence and/or a positive response to a chemotherapy, and the like. Such a positive correlation may be demonstrated statistically in various ways, e.g. by a low hazard ratio. In another example, the increased level of an RNA transcript may be negatively correlated with a likelihood of good clinical outcome for the patient. In this case, for example, the patient may have a decreased likelihood of long-term survival without recurrence of the cancer and/or a positive response to a chemotherapy, and the like. Such a negative correlation indicates that the patient likely has a poor prognosis or will respond poorly to a chemotherapy, and this may be demonstrated statistically in various ways, e.g., by a high hazard ratio.

[0027] As used herein, the term "exon" refers to any segment of an interrupted gene that is represented in the mature RNA product (B. Lewin. Genes IV Cell Press, Cambridge Mass. 1990). As used herein, the terms "intron" and "intronic sequence" refer to any non-coding region found within genes.

[0028] The term "expression product" as used herein refers to an expression product of a coding RNA transcript. Thus, the term refers to a polypeptide or protein.

[0029] As used herein, the term "intergenic region" refers to a stretch of DNA or RNA sequences located between clusters of genes that contain few or no genes. Intergenic regions are different from intragenic regions (or "introns"), which are non-coding regions that are found between exons within genes. An intergenic region may be comprised of one or more "intergenic sequences." As shown in the Examples below, 69 intergenic regions were found to correlate to long-term survival without breast cancer recurrence, and each intergenic region comprises one or more intergenic sequences. The intergenic sequences are readily available from publicly available information. For example, the UCSC Genome Browser available at http://genome.ucsc.edu/cgi-bin/hgGateway allows inputting of the coordinates, such as the chromosome number and the start/stop positions on the chromosome shown in Tables 4 and 5, to produce an output comprising that sequence.

[0030] As used herein, the terms "long intergenic non-coding RNAs" and "lincRNAs" are used interchangeably and refer to non-coding transcripts that are typically longer than 200 nucleotides. As shown in the Examples below, 22 lincRNAs were found to correlate to long-term survival without breast cancer recurrence. The coordinates of these lincRNAs are publicly available and are also listed in Table 4. The sequences of the lincRNAs may also be obtained from publicly available information, such as the UCSC Genome Browser discussed above.

[0031] As used herein, the term "level" as used herein refers to qualitative or quantitative determination of the number of copies of a coding or non-coding RNA transcript or a polypeptide/protein. An RNA transcript or a polypeptide/protein exhibits an "increased level" when the level of the RNA transcript or polypeptide/protein is higher in a first sample, such as in a clinically relevant subpopulation of patients (e.g., patients who have experienced cancer recurrence), than in a second sample, such as in a related subpopulation (e.g., patients who did not experience cancer recurrence). In the context of an analysis of a level of an RNA transcript

or a polypeptide/protein in a tumor sample obtained from an individual patient, an RNA transcript or polypeptide/protein exhibits "increased level" when the level of the RNA transcript or polypeptide/protein in the subject trends toward, or more closely approximates, the level characteristic of a clinically relevant subpopulation of patients.

[0032] Thus, for example, when the RNA transcript analyzed is an RNA transcript that shows an increased level in subjects that experienced long-term survival without cancer recurrence as compared to subjects that did not experience long-term survival without cancer recurrence, then an "increased" level of a given RNA transcript can be described as being positively correlated with a likelihood of long-term survival without cancer recurrence. If the level of the RNA transcript in an individual patient being assessed trends toward a level characteristic of a subject who experienced long-term survival without cancer recurrence, the level of the RNA transcript supports a determination that the individual patient is more likely to experience long-term survival without cancer recurrence. If the level of the RNA transcript in the individual patient trends toward a level characteristic of a subject who experienced cancer recurrence, then the level of the RNA transcript supports a determination that the individual patient is more likely to experience cancer recurrence.

[0033] The term "likelihood score" is an arithmetically or mathematically calculated numerical value for aiding in simplifying or disclosing or informing the analysis of more complex quantitative information, such as the correlation of certain levels of the disclosed RNA transcripts, their expression products, or gene networks to a likelihood of a certain clinical outcome in a breast cancer patient, such as likelihood of long-term survival without breast cancer recurrence. A likelihood score may be determined by the application of a specific algorithm. The algorithm used to calculate the likelihood score may group the RNA transcripts, or their expression products, into gene networks. A likelihood score may be determined for a gene network by determining the level of one or more RNA transcripts, or an expression product thereof, and weighting their contributions to a certain clinical outcome such as recurrence. A likelihood score may also be determined for a patient. In an embodiment, a likelihood score is a recurrence score, wherein an increase in the recurrence score negatively correlates with an increased likelihood of long-term survival without breast cancer recurrence. In other words, an increase in the recurrence score correlates with bad prognosis. Examples of methods for determining the likelihood score or recurrence score are disclosed in U.S. Patent No. 7,526,387.

[0034] The term "long-term" survival as used herein refers to survival for at least 3 years. In other embodiments, it may refer to survival for at least 5 years, or for at least 10 years following surgery or other treatment.

[0035] As used herein, the term "normalized" with regard to a coding or non-coding RNA transcript, or an expression product of the coding RNA transcript, refers to the level of the RNA transcript, or its expression product, relative to the mean levels of transcript/product of a set of reference RNA transcripts, or their expression products. The reference RNA transcripts, or their expression products, are based on their minimal variation across patients, tissues, or treatments. Alternatively, the coding or non-coding RNA transcript, or its expression product, may be normalized to the totality of tested RNA transcripts, or a subset of such tested RNA transcripts.

[0036] As used herein, the term "pathology" of cancer includes all phenomena that comprise the well-being of the patient. This includes, without limitation, abnormal or uncontrollable cell growth, metastasis, interference with the normal functioning of neighboring cells, release of cytokines or other secretory products at abnormal levels, suppression or aggravation of inflammatory or immunological response, neoplasia, premalignancy, malignancy, invasion of surrounding or distant tissues or organs, such as lymph nodes.

[0037] A "patient response" may be assessed using any endpoint indicating a benefit to the patient, including, without limitation, (1) inhibition, to some extent, of tumor growth, including slowing down and complete growth arrest; (2) reduction in the number of tumor cells; (3) reduction in tumor size; (4) inhibition (i.e., reduction, slowing down or complete stopping) of tumor cell infiltration into adjacent peripheral organs and/or tissues; (5) inhibition (i.e. reduction, slowing down or complete stopping) of metastasis; (6) enhancement of anti-tumor immune response, which may, but does not have to, result in the regression or rejection of the tumor; (7) relief, to some extent, of one or more symptoms associated with the cancer; (8) increase in the length of survival following treatment; and/or (9) decreased mortality at a given point of time following treatment.

[0038] The term "prognosis" as used herein, refers to the prediction of the likelihood of cancer-attributable death or progression, including recurrence, metastatic spread, and drug resistance, of neoplastic disease, such as breast cancer. The term "prediction" is used herein to refer to the likelihood that a patient will respond either favorably or unfavorably to a drug or set

of drugs, and also the extent of those responses, or that a patient will survive, following surgical removal of the primary tumor and/or chemotherapy for a certain period of time without cancer recurrence. The methods of the present invention can be used clinically to make treatment decisions by choosing the most appropriate treatment modalities for any particular patient. The methods of the present invention are tools in predicting if a patient is likely to respond favorably to a treatment regimen, such as surgical intervention, chemotherapy with a given drug or drug combination, and/or radiation therapy, or whether long-term survival of the patient without cancer recurrence is likely, following surgery and/or termination of chemotherapy or other treatment modalities.

[0039] The term "breast cancer prognostic biomarker" refers to an RNA transcript, or an expression product thereof, intronic RNA, lincRNA, intergenic sequence, and/or intergenic region found to be associated with long term survival without breast cancer recurrence as disclosed herein.

[0040] The term "reference" RNA transcript or an expression product thereof, as used herein, refers to an RNA transcript or an expression product thereof, whose level can be used to compare the level of an RNA transcript or its expression product in a test sample. In an embodiment of the invention, reference RNA transcripts include housekeeping genes, such as beta-globin, alcohol dehydrogenase, or any other RNA transcript, the level or expression of which does not vary depending on the disease status of the cell containing the RNA transcript or its expression product. In another embodiment, all of the assayed RNA transcripts, or their expression products, or a subset thereof, may serve as reference RNA transcripts or reference RNA expression products.

[0041] As used herein, the term "RefSeq RNA" refers to an RNA that can be found in the Reference Sequence (RefSeq) database, a collection of publicly available nucleotide sequences and their protein products built by the National Center for Biotechnology Information (NCBI). The RefSeq database provides an annotated, non-redundant record for each natural biological molecule (i.e. DNA, RNA or protein) included in the database. Thus, a sequence of a RefSeq RNA is well-known and can be found in the RefSeq database at http://www.ncbi.nlm.nih.gov/RefSeq/. *See also* Pruitt et al., *Nucl. Acids Res.* 33(Supp 1):D501-D504 (2005). Accession numbers for each RefSeq, which include accession numbers for any alternative splice forms, are provided in Tables 1 and 2 and in Table B. The intronic sequences

for a RefSeq are also publicly available. Nonetheless, the coordinates for each intronic sequence listed in Table 3 are provided in Table A. Therefore, the sequence of each RNA sequence in Tables 1-3 and 15 are readily available from publicly available sources.

[0042] As used herein, the term "RNA transcript" refers to the RNA transcription product of DNA and includes coding and non-coding RNA transcripts. RNA transcripts include, for example, mRNA, an unspliced RNA, a splice variant mRNA, a microRNA, fragmented RNA, long intergenic non-coding RNAs (lincRNAs), intergenic RNA sequences or regions, and intronic RNAs.

[0043] The terms "subject," "individual," and "patient" are used interchangeably herein to refer to a mammal being assessed for treatment and/or being treated. In an embodiment, the mammal is a human. The terms "subject," "individual," and "patient" thus encompass individuals having cancer (e.g., breast cancer), including those who have undergone or are candidates for resection (surgery) to remove cancerous tissue.

[0044] As used herein, the term "surgery" applies to surgical methods undertaken for removal of cancerous tissue, including mastectomy, lumpectomy, lymph node removal, sentinel lymph node dissection, prophylactic mastectomy, prophylactic ovary removal, cryotherapy, and tumor biopsy. The tumor samples used for the methods of the present invention may have been obtained from any of these methods.

[0045] The term "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.

[0046] The term "tumor sample" as used herein refers to a sample comprising tumor material obtained from a cancer patient. The term encompasses tumor tissue samples, for example, tissue obtained by surgical resection and tissue obtained by biopsy, such as for example, a core biopsy or a fine needle biopsy. In a particular embodiment, the tumor sample is a fixed, wax-embedded tissue sample, such as a formalin-fixed, paraffin-embedded tissue sample. Additionally, the term "tumor sample" encompasses a sample comprising tumor cells obtained from sites other than the primary tumor, e.g., circulating tumor cells. The term also encompasses cells that are the progeny of the patient's tumor cells, e.g. cell culture samples derived from primary tumor cells or circulating tumor cells. The term further encompasses samples that may comprise protein or nucleic acid material shed from tumor cells *in vivo*, e.g., bone marrow, blood, plasma, serum, and the like. The term also encompasses samples that have

been enriched for tumor cells or otherwise manipulated after their procurement and samples comprising polynucleotides and/or polypeptides that are obtained from a patient's tumor material.

[0047] As used herein, "whole transcriptome sequencing" refers to the use of high throughput sequencing technologies to sequence the entire transcriptome in order to get information about a sample's RNA content. Whole transcriptome sequencing can be done with a variety of platforms for example, the Genome Analyzer (Illumina, Inc., San Diego, CA) and the SOLiD™ Sequencing System (Life Tehcnologies, Carlsbad, CA). However, any platform useful for whole transcriptome sequencing may be used.

[0048] The term "RNA-Seq" or "transcriptome sequencing" refers to sequencing performed on RNA (or cDNA) instead of DNA, where typically, the primary goal is to measure expression levels, detect fusion transcripts, alternative splicing, and other genomic alterations that can be better assessed from RNA. RNA-Seq includes whole transcriptome sequencing as well as target specific sequencing.

[0049] The term "computer-based system," as used herein, refers to the hardware means, software means, and data storage means used to analyze information. The minimum hardware of a patient computer-based system comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that many of the currently available computer-based system are suitable for use in the present invention and may be programmed to perform the specific measurement and/or calculation functions of the present invention.

[0050] To "record" data, programming or other information on a computer readable medium refers to a process for storing information, using any such methods as known in the art. Any convenient data storage structure may be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, e.g. word processing text file, database format, etc.

[0051] A "processor" or "computing means" references any hardware and/or software combination that will perform the functions required of it. For example, any processor herein may be a programmable digital microprocessor such as available in the form of an electronic controller, mainframe, server or personal computer (desktop or portable). Where the processor is programmable, suitable programming can be communicated from a remote location to the

processor, or previously saved in a computer program product (such as a portable or fixed computer readable storage medium, whether magnetic, optical or solid state device based). For example, a magnetic medium or optical disk may carry the programming, and can be read by a suitable reader communicating with each processor at its corresponding station.

[0052] The present invention provides RNA transcripts that are prognostic for breast cancer. These RNA transcripts are listed in Tables 1-5 and 15 and include coding and non-coding RNA transcripts. A subset of the RNA transcripts of Table 1 may be further grouped into gene networks, depending on their known function. For example, the gene networks may include a cell cycle network, ESR1 network, Chr9q22 network, Chr17q23-24 network, Chr8q21-24 network, olfactory receptor network, and metabolic-like networks. The cell cycle network comprises the genes listed in Table 6. The ESR1 network comprises BCL2, SCUBE2, CPEB2, IL6ST, DNALI1, PGR, SLC7A8, C6orf97, RSPH1, EVL, BCL2, NXNL2, GATA3, GFRA1, GFRA1, ZNF740, MKL2, AFF3, ERBB4, RABEP1, KDM4B, ESR1, C4orf32, and CPLX1 as shown in Table 7. The Chr9q22 network comprises ASPN, CENPP, ECM2, OGN, and OMD as shown in Table 8. The Chr17q23-24 network comprises CCDC45, POLG2, SMURF2, CCDC47, CLTC, DCAF7, DDX42, FTSJ3, PSMC5, RPS6KB1, SMARCD2, and TEX2 as shown in Table 9. The Chr8q21-24 network comprises CYC1, DGAT1, GPAA1, GRINA, PUF60, PYCRL, RPL8, SQLE, TSTA3, ESRP1, GRHL2, INTS8, MTDH, and UQCRB as shown in Table 10. The olfactory receptor network comprises 134 genes listed in Table 11. OR10H3, OR14J1, OR2J2, OR2W5, OR5T2, OR7E24, OR7G3, OR8S1, and OR9K2 code for olfactory receptors, and MIR1208, MIR1266, MIR1297, MIR133A1, MIR195, MIR196A1, MIR3170, MIR3183, MIR4267, MIR4275, MIR4318, MIR501, MIR501, MIR539, and MIR542 are microRNA precursors. The metabolic-like network comprises a five gene set of ENO1, IDH2, TMSB10, PGK1, and G6PD, or a fourteen gene set of PGD, TKT, TALDO1, G6PD, GP1, SLC1A5, SLC7A5, OGDH, SUCLG1, ENO1, PGK1, IDH2, ACO2, and FBP1. An RNA transcript, or an expression product thereof, is negatively correlated with an increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the RNA transcript is marked 1 in Tables 1-5 and 15, and is positively correlated with an increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the RNA transcript is marked -1 in Tables 1-5 and 15. Co-expressed RNA transcripts within a gene network may be substituted for other the RNA transcripts within the same gene network.

[0053] The present invention provides methods that utilize the RNA transcripts and associated information. For example, the present invention provides a method of predicting a likelihood that a breast cancer patient will exhibit long-term survival without breast cancer recurrence. The methods of the invention comprise determining the level of at least one RNA transcript, or an expression product thereof, in a tumor sample, and determining the likelihood of long-term survival without breast cancer recurrence based on the correlation between the level of the RNA transcript, or its expression product, and long-term survival without breast cancer recurrence.

[0054] For all aspects of the present invention, the methods may further include determining the level of at least two RNA transcripts, or their expression products. It is further contemplated that the methods of the present invention may further include determining the level of at least three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, or at least fifteen of the RNA transcripts, or their expression products. For example, the levels of at least three RNA transcripts, or their expression products, selected from ENO1, IDH2, TMSB10, PGK1, and G6PD may be determined. In another aspect, the levels of all five of ENO1, IDH2, TMSB10, PGK1, and G6PD RNA transcripts, or their expression products, may be determined. In another example, at least five RNA transcripts, or expression products thereof, selected from PGD, TKT, TALDO1, G6PD, GP1, SLC1A5, SLC7A5, OGDH, SUCLG1, ENO1, PGK1, IDH2, ACO2, and FBP1 may be determined. In yet another example, the levels of all fourteen of PGD, TKT, TALDO1, G6PD, GP1, SLC1A5, SLC7A5, OGDH, SUCLG1, ENO1, PGK1, IDH2, ACO2, and FBP1 may be determined. Coding and non-coding RNA transcripts may be combined in any of the methods described herein.

[0055] The RNA transcripts and associated information provided by the present invention also have utility in the development of therapies to treat cancers and screening patients for inclusion in clinical trials. The RNA transcripts and associated information may further be used to design or produce a reagent that modulates the level or activity of the RNA transcript or its expression product. Such reagents may include, but are not limited to, a drug, an antisense RNA, a small inhibitory RNA (siRNA), a ribozyme, a small molecule, a monoclonal antibody, and a polyclonal antibody.

[0056] In various embodiments of the methods of the present invention, various technological approaches are available for determining the levels of the RNA transcripts,

including, without limitation, whole transcriptome sequencing, RT-PCR, microarrays, and serial analysis of gene expression (SAGE), which are described in more detail below.

CORRELATING LEVEL OF AN RNA TRANSCRIPT OR AN EXPRESSION PRODUCT TO A CLINICAL OUTCOME

[0057] One skilled in the art will recognize that there are many statistical methods that may be used to determine whether there is a correlation between an outcome of interest (e.g., likelihood of survival) and levels of RNA transcripts or their expression products as described here. This relationship can be presented as a continuous recurrence score (RS), or patients may be stratified into risk groups (e.g., low, intermediate, high). For example, a Cox proportional hazards regression model may fit to a particular clinical endpoint (e.g., RFI, DFS, OS). One assumption of the Cox proportional hazards regression model is the proportional hazards assumption, i.e. the assumption that effect parameters multiply the underlying hazard. Assessments of model adequacy may be performed including, but not limited to, examination of the cumulative sum of martingale residuals. One skilled in the art would recognize that there are numerous statistical methods that may be used (e.g., Royston and Parmer (2002), smoothing spline, etc.) to fit a flexible parametric model using the hazard scale and the Weibull distribution with natural spline smoothing of the log cumulative hazards function, with effects for treatment (chemotherapy or observation) and RS allowed to be time-dependent. (*See, e.g.*, P. Royston, M. Parmer, *Statistics in Medicine* 21(15:2175-2197 (2002).)

[0058] In an exemplary embodiment, power calculations are carried out for the Cox proportional hazards model with a single non-binary covariate using the method proposed by F. Hsieh and P. Lavori, *Control Clin Trials* 21:552-560 (2000) as implemented in PASS 2008.

[0059] Any of the methods described may group the levels of RNA transcripts or their expression products. The grouping of the RNA transcripts or expression products may be performed at least in part based on knowledge of the contribution of the RNA transcripts or their expression products according to physiologic functions or component cellular characteristics, such as in the gene networks described herein. The formation of groups, in addition, can facilitate the mathematical weighting of the contribution of various expression levels to the recurrence/likelihood score. The weighting of a gene network representing a physiological process or component cellular characteristic can reflect the contribution of that process or characteristic to the pathology of the cancer and clinical outcome. Accordingly, the present invention provides

gene networks of the RNA transcripts, or their expression products, identified herein for use in the methods disclosed herein.

[0060] The coding and non-coding RNA transcripts, and any expression products thereof, of the present invention are listed in Tables 1-5 and 15. In an embodiment of the invention, a level of one or more RNA transcripts, or an expression product thereof, listed in Tables 1 and 15, is negatively correlated with an increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the RNA transcript is marked 1 in Tables 1 and 15, and is positively correlated with an increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the RNA transcript is marked -1 in Tables 1 and 15.

[0061] In another embodiment of the invention, a level of one or more RNA transcript, or an expression product thereof, listed in Table 2, is negatively correlated with an increased likelihood of long-term survival without recurrence of breast cancer in an ER-positive breast cancer patient if the direction of association of the RNA transcript is marked 1 in Table 2, and is positively correlated with an increased likelihood of long-term survival without recurrence of breast cancer in an ER-positive breast cancer patient if the direction of association of the RNA transcript is marked -1 in Table 2.

[0062] In a further embodiment of the invention, a level of an intronic RNA selected from Table 3 is negatively correlated with an increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the intronic RNA is marked 1 in Table 3, and is positively correlated with an increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the intronic RNA is marked -1 in Table 3.

[0063] In a specific embodiment, a level of one or more long intergenic non-coding region (lincRNA) selected from Table 4 is negatively correlated with an increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the lincRNA is marked 1 in Table 4, and is positively correlated with an increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the lincRNA is marked -1 in Table 4.

[0064] In another embodiment, a level of one or more intergenic sequence or intergenic region selected from intergenic regions 1-69 listed in Table 5 is negatively correlated with an

increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the intergenic sequence or intergenic region is marked 1 in Table 5, and is positively correlated with an increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the intergenic sequence or intergenic region is marked -1 in Table 5.

[0065] In yet another embodiment, a likelihood score is determined for assessing the likelihood of a certain clinical outcome in a breast cancer patient, such as likelihood of long-term survival without breast cancer recurrence. A likelihood score may be calculated by determining the level of one or more RNA transcripts, or its expression product, selected from Tables 1-5 and 15, and mathematically weighting its contribution to the clinical outcome. In a specific embodiment, a likelihood score is determined for a gene network selected from a cell cycle network, ESR1 network, Chr9q22 network, Chr17q23-24 network, Chr8q21-24 network, olfactory receptor network, and metabolic-like networks by determining the level of one or more RNA transcripts, or an expression product thereof, within a gene network. The level of the one or more RNA transcripts, or its expression product, may be weighted by its contribution to a certain clinical outcome, such as recurrence. A likelihood score may also be determined for a gene network based on the likelihood score of one or more RNA transcripts, or an expression product thereof, within the gene network. In another embodiment, a likelihood score may be determined for a patient, based on the likelihood score of one or more RNA transcripts, or an expression product thereof, and/or the likelihood score of one or more gene networks.

METHODS TO PREDICT LIKELIHOOD OF LONG-TERM SURVIVAL WITHOUT BREAST CANCER RECURRENCE

[0066] As described above, a number of coding and non-coding RNA transcripts that correlate with breast cancer prognosis were identified. The levels of these RNA transcripts, or their expression products, can be determined in a tumor sample obtained from an individual patient who has breast cancer and for whom treatment is being contemplated. Depending on the outcome of the assessment, treatment with chemotherapy may be indicated, or an alternative treatment regimen may be indicated.

[0067] In carrying out the method of the present invention, a tumor sample is assayed or measured for a level of an RNA transcript, or its expression product. The tumor sample can be obtained from a solid tumor, e.g., via biopsy, or from a surgical procedure carried out to remove a tumor; or from a tissue or bodily fluid that contains cancer cells. In an embodiment of the

invention, the tumor sample is obtained from a patient with breast cancer, such as ER-positive breast cancer. In another embodiment, the level of an RNA transcript, or its expression product, is normalized relative to the level of one or more reference RNA transcripts, or its expression product.

[0068] In an embodiment of the invention, the likelihood of long-term survival without breast cancer recurrence in an individual patient is predicted by comparing, directly or indirectly, the level or normalized level of the RNA transcript, or its expression product, in the tumor sample from the individual patient to the level or normalized level of the RNA transcript, or its expression product, in a clinically relevant subpopulation of patients. Thus, as explained above, when the RNA transcript, or its expression product, analyzed is an RNA transcript, or an expression product, that shows increased level in subjects that experienced long-term survival without breast cancer recurrence as compared to subjects that experienced breast cancer recurrence, then if the level of the RNA transcript, or its expression product in an individual patient being assessed trends toward a level characteristic of a subject with long-term survival without breast cancer recurrence, then the RNA transcript or its expression product level supports a determination that the individual patient is more likely to experience long-term survival without breast cancer recurrence. Similarly, where the RNA transcript or its expression product analyzed is an RNA transcript or expression product that is increased in subjects who have experienced breast cancer recurrence as compared subjects who have experienced long-term survival without breast cancer recurrence, then if the level of the RNA transcript, or its expression product, in an individual patient being assessed trends toward a level characteristic of a subject with breast cancer recurrence, then RNA transcript or expression product level supports a determination that the individual patient will more likely experience breast cancer recurrence. Thus, the level of a given RNA transcript, or its expression product, can be described as being positively correlated with a likelihood of long-term survival without breast cancer recurrence, or as being negatively correlated with a likelihood of long-term survival without breast cancer recurrence.

[0069] It is understood that the level or normalized level of an RNA transcript, or its expression product, from an individual patient can be compared, directly or indirectly, to the level or normalized level of the RNA transcript, or its expression product, in a clinically relevant subpopulation of patients. For example, when compared indirectly, the level or normalized level of the RNA transcript, or its expression product, from the individual patient may be used to

calculate a likelihood of long-term survival without breast cancer recurrence, such as a likelihood/recurrence score (RS) as described above, and compared to a calculated score in the clinically relevant subpopulation of patients.

METHODS OF ASSAYING LEVELS OF RNA TRANSCRIPTS OR THEIR EXPRESSION PRODUCTS

[0070] Methods of expression profiling include methods based on sequencing of polynucleotides, methods based on hybridization analysis of polynucleotides, and proteomics-based methods. Representative methods for sequencing-based analysis include Massively Parallel Sequencing (*see e.g.*, Tucker et al., *The American J. Human Genetics* 85:142-154, 2009) and Serial Analysis of Gene Expression (SAGE). Exemplary methods known in the art for the quantification of mRNA expression in a sample include northern blotting and *in situ* hybridization (Parker & Barnes, *Methods in Molecular Biology* 106:247-283 (1999)); RNAse protection assays (Hod, *Biotechniques* 13:852-854 (1992)); and PCR-based methods, such as reverse transcription polymerase chain reaction (RT-PCR) (Weis et al., *Trends in Genetics* 8:263-264 (1992)). Antibodies may be employed that can recognize sequence-specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes.

Nucleic Acid Sequencing-Based Methods

[0071] Nucleic acid sequencing technologies are suitable methods for expression analysis. The principle underlying these methods is that the number of times a cDNA sequence is detected in a sample is directly related to the relative RNA levels corresponding to that sequence. These methods are sometimes referred to by the term Digital Gene Expression (DGE) to reflect the discrete numeric property of the resulting data. Early methods applying this principle were Serial Analysis of Gene Expression (SAGE) and Massively Parallel Signature Sequencing (MPSS). *See, e.g.,* S. Brenner, et al., *Nature Biotechnology* 18(6):630-634 (2000).

[0072] More recently, the advent of "next-generation" sequencing technologies has made DGE simpler, higher throughput, and more affordable. As a result, more laboratories are able to utilize DGE to screen the expression of more nucleic acids in more individual patient samples than previously possible. *See, e.g.,* J. Marioni, *Genome Research* 18(9):1509-1517 (2008); R. Morin, *Genome Research* 18(4):610-621 (2008); A. Mortazavi, *Nature Methods* 5(7):621-628 (2008); N. Cloonan, *Nature Methods* 5(7):613-619 (2008). Massively parallel sequencing methods have also enabled whole genome or transcriptome sequencing, allowing the analysis of not only coding but also non-coding sequencees. As reviewed in Tucker et al., *The American J. Human Genetics*

85:142-154 (2009), there are several commercially available massively parallel sequencing platforms, such as the Illumina Genome Analyzer (Illumina, Inc., San Diego, CA), Applied Biosystems SOLiD™ Sequencer (Life Technologies, Carlsbad, CA), Roche GS-FLX 454 Genome Sequencer (Roche Applied Science, Germany), and the Helicos® Genetic Analysis Platform (Helicos Biosciences Corp., Cambridge, MA). Other developing technologies may be used.

Reverse Transcription PCR (RT-PCR)

[0073] The starting material is typically total RNA isolated from a human tumor, usually from a primary tumor. Optionally, normal tissues from the same patient can be used as an internal control. RNA can be extracted from a tissue sample, e.g., from a sample that is fresh, frozen (e.g. fresh frozen), or paraffin-embedded and fixed (e.g. formalin-fixed).

[0074] General methods for RNA extraction are well known in the art and are disclosed in standard textbooks of molecular biology, including Ausubel *et al.*, Current Protocols of Molecular Biology, John Wiley and Sons (1997). Methods for RNA extraction from paraffin embedded tissues are disclosed, for example, in Rupp and Locker, *Lab Invest.* 56:A67 (1987), and De Andrés *et al.*, *BioTechniques* 18:42044 (1995). In particular, RNA isolation can be performed using a purification kit, buffer set and protease from commercial manufacturers, such as Qiagen, according to the manufacturer's instructions. For example, total RNA from cells in culture can be isolated using Qiagen RNeasy mini-columns. Other commercially available RNA isolation kits include MasterPure™ Complete DNA and RNA Purification Kit (EPICENTRE®, Madison, WI), and Paraffin Block RNA Isolation Kit (Ambion, Inc.). Total RNA from tissue samples can be isolated using RNA Stat-60 (Tel-Test). RNA prepared from a tumor sample can be isolated, for example, by cesium chloride density gradient centrifugation. The isolated RNA may then be depleted of ribosomal RNA as described in U.S. Pub. No. 2011/0111409.

[0075] The sample containing the RNA is then subjected to reverse transcription to produce cDNA from the RNA template, followed by exponential amplification in a PCR reaction. The two most commonly used reverse transcriptases are avian myeloblastosis virus reverse transcriptase (AMV-RT) and Moloney murine leukemia virus reverse transcriptase (MMLV-RT). The reverse transcription step is typically primed using specific primers, random hexamers, or oligo-dT primers, depending on the circumstances and the goal of expression profiling. For example, extracted RNA can be reverse-transcribed using a GeneAmp RNA PCR kit (Perkin

Elmer, CA, USA), following the manufacturer's instructions. The derived cDNA can then be used as a template in the subsequent PCR reaction.

[0076] PCR-based methods use a thermostable DNA-dependent DNA polymerase, such as a Taq DNA polymerase. For example, TaqMan® PCR typically utilizes the 5'-nuclease activity of Taq or Tth polymerase to hydrolyze a hybridization probe bound to its target amplicon, but any enzyme with equivalent 5' nuclease activity can be used. Two oligonucleotide primers are used to generate an amplicon typical of a PCR reaction product. A third oligonucleotide, or probe, can be designed to facilitate detection of a nucleotide sequence of the amplicon located between the hybridization sites of the two PCR primers. The probe can be detectably labeled, e.g., with a reporter dye, and can further be provided with both a fluorescent dye, and a quencher fluorescent dye, as in a Taqman® probe configuration. Where a Taqman® probe is used, during the amplification reaction, the Taq DNA polymerase enzyme cleaves the probe in a template-dependent manner. The resultant probe fragments disassociate in solution, and signal from the released reporter dye is free from the quenching effect of the second fluorophore. One molecule of reporter dye is liberated for each new molecule synthesized, and detection of the unquenched reporter dye provides the basis for quantitative interpretation of the data.

[0077] TaqMan® RT-PCR can be performed using commercially available equipment, such as, for example, ABI PRISM 7700™ Sequence Detection System™ (Perkin-Elmer-Applied Biosystems, Foster City, CA, USA), or Lightcycler (Roche Molecular Biochemicals, Mannheim, Germany). In a preferred embodiment, the 5' nuclease procedure is run on a real-time quantitative PCR device such as the ABI PRISM 7700™ Sequence Detection System™. The system consists of a thermocycler, laser, charge-coupled device (CCD), camera and computer. The system amplifies samples in a 384-well format on a thermocycler. The RT-PCR may be performed in triplicate wells with an equivalent of 2ng RNA input per 10 μL-reaction volume. During amplification, laser-induced fluorescent signal is collected in real-time through fiber optics cables for all wells, and detected at the CCD. The system includes software for running the instrument and for analyzing the data.

[0078] 5'-Nuclease assay data are generally initially expressed as a threshold cycle ("C_t"). Fluorescence values are recorded during every cycle and represent the amount of product amplified to that point in the amplification reaction. The threshold cycle (C_t) is generally described as the point when the fluorescent signal is first recorded as statistically significant.

[0079] To minimize errors and the effect of sample-to-sample variation, RT-PCR is usually performed using an internal standard. The ideal internal standard gene (also referred to as a reference gene) is expressed at a constant level among cancerous and non-cancerous tissue of the same origin (i.e., a level that is not significantly different among normal and cancerous tissues), and is not significantly affected by the experimental treatment (i.e., does not exhibit a significant difference in expression level in the relevant tissue as a result of exposure to chemotherapy). RNAs most frequently used to normalize patterns of gene expression are mRNAs for the housekeeping genes glyceraldehyde-3-phosphate-dehydrogenase (GAPDH) and β-actin. Gene expression measurements can be normalized relative to the mean of one or more (e.g., 2, 3, 4, 5, or more) reference genes. Reference-normalized expression measurements can range from 0 to 15, where a one unit increase generally reflects a 2-fold increase in RNA quantity.

[0080] Real time PCR is compatible both with quantitative competitive PCR, where an internal competitor for each target sequence is used for normalization, and with quantitative comparative PCR using a normalization gene contained within the sample, or a housekeeping gene for RT-PCR. For further details see, e.g. Held *et al., Genome Research* 6:986-994 (1996).

Design of PCR Primers and Probes

[0081] PCR primers and probes can be designed based upon exon, intron, or intergenic sequences present in the RNA transcript of interest. Primer/probe design can be performed using publicly available software, such as the DNA BLAT software developed by Kent, W.J., *Genome Res.* 12(4):656-64 (2002), or by the BLAST software including its variations.

[0082] Where necessary or desired, repetitive sequences of the target sequence can be masked to mitigate non-specific signals. Exemplary tools to accomplish this include the Repeat Masker program available on-line through the Baylor College of Medicine, which screens DNA sequences against a library of repetitive elements and returns a query sequence in which the repetitive elements are masked. The masked sequences can then be used to design primer and probe sequences using any commercially or otherwise publicly available primer/probe design packages, such as Primer Express (Applied Biosystems); MGB assay-by-design (Applied Biosystems); Primer3 (Steve Rozen and Helen J. Skaletsky (2000) Primer3 on the WWW for general users and for biologist programmers. In: Rrawetz S, Misener S (eds) *Bioinformatics Methods and Protocols: Methods in Molecular Biology.* Humana Press, Totowa, NJ, pp 365-386).

[0083] Other factors that can influence PCR primer design include primer length, melting temperature (Tm), and G/C content, specificity, complementary primer sequences, and 3 '-end sequence. In general, optimal PCR primers are generally 17-30 bases in length, and contain about 20-80%, such as, for example, about 50-60% G+C bases, and exhibit Tm's between 50 and 80 ^{0}C, e.g. about 50 to 70 ^{0}C.

[0084] For further guidelines for PCR primer and probe design *see, e.g.* Dieffenbach, CW. et al, "General Concepts for PCR Primer Design" in: *PCR Primer, A Laboratory Manual*, Cold Spring Harbor Laboratory Press, New York, 1995, pp. 133-155; Innis and Gelfand, "Optimization of PCRs" in: *PCR Protocols, A Guide to Methods and Applications*, CRC Press, London, 1994, pp. 5-11; and Plasterer, T.N. *Primerselect: Primer and probe design*. Methods Mol. Biol. 70:520-527 (1997), the entire disclosures of which are hereby expressly incorporated by reference.

MassARRAY® System

[0085] In MassARRAY-based methods, such as the exemplary method developed by Sequenom, Inc. (San Diego, CA) following the isolation of RNA and reverse transcription, the obtained cDNA is spiked with a synthetic DNA molecule (competitor), which matches the targeted cDNA region in all positions, except a single base, and serves as an internal standard. The cDNA/competitor mixture is PCR amplified and is subjected to a post-PCR shrimp alkaline phosphatase (SAP) enzyme treatment, which results in the dephosphorylation of the remaining nucleotides. After inactivation of the alkaline phosphatase, the PCR products from the competitor and cDNA are subjected to primer extension, which generates distinct mass signals for the competitor- and cDNA-derived PCR products. After purification, these products are dispensed on a chip array, which is pre-loaded with components needed for analysis with matrix- assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) analysis. The cDNA present in the reaction is then quantified by analyzing the ratios of the peak areas in the mass spectrum generated. For further details see, e.g. Ding and Cantor, *Proc. Natl. Acad. Sci. USA* 100:3059-3064 (2003).

Other PCR-based Methods

[0086] Further PCR-based techniques that can find use in the methods disclosed herein include, for example, BeadArray® technology (Illumina, San Diego, CA; Oliphant et al., *Discovery of Markers for Disease* (Supplement to Biotechniques), June 2002; Ferguson et al., *Analytical Chemistry* 72:5618 (2000)); BeadsArray for Detection of Gene Expression® (BADGE),

using the commercially available LuminexlOO LabMAP® system and multiple color-coded microspheres (Luminex Corp., Austin, TX) in a rapid assay for gene expression (Yang et al., *Genome Res.* 11:1888-1898 (2001)); and high coverage expression profiling (HiCEP) analysis (Fukumura et al., *Nucl. Acids. Res.* 31(16) e94 (2003).

Microarrays

[0087] In this method, polynucleotide sequences of interest (including cDNAs and oligonucleotides) are arrayed on a substrate. The arrayed sequences are then contacted under conditions suitable for specific hybridization with detectably labeled cDNA generated from RNA of a sample. The source of RNA typically is total RNA isolated from a tumor sample, and optionally from normal tissue of the same patient as an internal control or cell lines. RNA can be extracted, for example, from frozen or archived paraffin-embedded and fixed (e.g. formalin-fixed) tissue samples.

[0088] For example, PCR amplified inserts of cDNA clones of a gene to be assayed are applied to a substrate in a dense array. Usually at least 10,000 nucleotide sequences are applied to the substrate. For example, the microarrayed genes, immobilized on the microchip at 10,000 elements each, are suitable for hybridization under stringent conditions. Fluorescently labeled cDNA probes may be generated through incorporation of fluorescent nucleotides by reverse transcription of RNA extracted from tissues of interest. Labeled cDNA probes applied to the chip hybridize with specificity to each spot of DNA on the array. After washing under stringent conditions to remove non-specifically bound probes, the chip is scanned by confocal laser microscopy or by another detection method, such as a CCD camera. Quantitation of hybridization of each arrayed element allows for assessment of corresponding mRNA abundance.

[0089] With dual color fluorescence, separately labeled cDNA probes generated from two sources of RNA are hybridized pair wise to the array. The relative abundance of the transcripts from the two sources corresponding to each specified gene is thus determined simultaneously. The miniaturized scale of the hybridization affords a convenient and rapid evaluation of the expression pattern for large numbers of genes. Such methods have been shown to have the sensitivity required to detect rare transcripts, which are expressed at a few copies per cell, and to reproducibly detect at least approximately two-fold differences in the expression levels (Schena et at, *Proc. Natl. Acad. Sci. USA* 93(2):106-149 (1996)). Microarray analysis can be performed on commercially available

equipment, following the manufacturer's protocols, such as by using the Affymetrix GenChip® technology, or Incyte's microarray technology.

Isolating RNA from Body Fluids

[0090] Methods of isolating RNA for expression analysis from blood, plasma and serum (*see* for example, Tsui NB et al. (2002) *Clin. Chem.* 48,1647-53 and references cited therein) and from urine (*see* for example, Boom R et al. (1990) *J Clin Microbiol.* 28, 495-503 and reference cited therein) have been described.

Immunohistochemistry

[0091] Immunohistochemistry methods are also suitable for detecting the expression levels of genes and applied to the method disclosed herein. Antibodies (e.g., monoclonal antibodies) that specifically bind a gene product of a gene of interest can be used in such methods. The antibodies can be detected by direct labeling of the antibodies themselves, for example, with radioactive labels, fluorescent labels, hapten labels such as biotin, or an enzyme such as horse radish peroxidase or alkaline phosphatase. Alternatively, unlabeled primary antibody can be used in conjunction with a labeled secondary antibody specific for the primary antibody. Immunohistochemistry protocols and kits are well known in the art and are commercially available.

Proteomics

[0092] The term "proteome" is defined as the totality of the proteins present in a sample (e.g. tissue, organism, or cell culture) at a certain point of time. Proteomics includes, among other things, study of the global changes of protein expression in a sample (also referred to as "expression proteomics"). Proteomics typically includes the following steps: (1) separation of individual proteins in a sample by 2-D gel electrophoresis (2-D PAGE); (2) identification of the individual proteins recovered from the gel, e.g. my mass spectrometry or N- terminal sequencing, and (3) analysis of the data using bioinformatics.

GENERAL DESCRIPTION OF THE RNA ISOLATION AND PREPARATION FROM FIXED, PARAFFIN-EMBEDDED SAMPLES FOR WHOLE TRANSCRIPTOME SEQUENCING

[0093] The steps of a representative protocol for profiling gene expression levels using fixed, paraffin-embedded tissues as the RNA source are provided in various published journal articles. (*See, e.g.*, T.E. Godfrey et al,. *J. Molec. Diagnostics* 2: 84-91 (2000); K. Specht et al., *Am. J. Pathol.* 158: 419-29 (2001), M. Cronin, et al., *Am J Pathol* 164:35-42 (2004)). Modified

methods can used for whole transcriptome sequencing as described in the Examples section. Briefly, a representative process starts with cutting a tissue sample section (e.g. about 10 μm thick sections of a paraffin-embedded tumor tissue sample). The RNA is then extracted, and ribosomal RNA may be deleted as described in U.S. Pub. No. 2011/0111409. cDNA sequencing libraries may be prepared that are directional and single or paired-end using commercially available kits such as the ScriptSeq™ mRNA-Seq Library Preparation Kit (Epicenter Biotechnologies, Madison, WI). The libraries may also be barcoded for multiplex sequencing using commercially available barcode primers such as the RNA-Seq Barcode Primers from Epicenter Biotechnologies (Madison, WI). PCR is then carried out to generate the second strand of cDNA to incorporate the barcodes and to amplify the libraries. After the libraries are quantified, the sequencing libraries may be sequenced as described herein.

COEXPRESSION ANALYSIS

[0094] To perform particular biological processes, genes often work together in a concerted way, i.e. they are co-expressed. Co-expressed gene networks identified for a disease process like cancer can also serve as prognostic biomarkers. Such co-expressed genes can be assayed in lieu of, or in addition to, assaying the biomarker with which they co-express.

[0095] One skilled in the art will recognize that many co-expression analysis methods now known or later developed will fall within the scope and spirit of the present invention. These methods may incorporate, for example, correlation coefficients, co-expression network analysis, clique analysis, etc., and may be based on expression data from RT-PCR, microarrays, sequencing, and other similar technologies. For example, gene expression clusters can be identified using pair-wise analysis of correlation based on Pearson or Spearman correlation coefficients. (*See e.g*, Pearson K. and Lee A., *Biometrika* 2:357 (1902); C. Spearman, *Amer. J. Psychol.* 15:72-101 (1904); J. Myers, A. Well, *Research Design and Statistical Analysis*, p. 508 (2nd Ed., 2003).) In general, a correlation coefficient of equal to or greater than 0.3 is considered to be statistically significant in a sample size of at least 20. (*See e.g.*, G. Norman, D. Streiner, *Biostatistics: The Bare Essentials*, 137-138 (3rd Ed. 2007).)

REFERENCE NORMALIZATION

[0096] In order to minimize expression measurement variations due to non-biological variations in samples, e.g., the amount and quality of product to be measured, the level of an RNA transcript or its expression product may be normalized relative to the mean levels obtained for one

or more reference RNA transcripts or their expression products. Examples of reference RNA transcripts or expression products include housekeeping genes, such as GAPDH. Alternatively, all of the assayed RNA transcripts or expression products, or a subset thereof, may also serve as reference. On a transcript (or protein)-by-transcript (or protein) basis, measured normalized amount of a patient tumor RNA or protein may be compared to the amount found in a cancer tissue reference set. *See e.g.*, Cronin, M. et al., *Am. Soc. Investigative Pathology* 164:35-42 (2004). The normalization may be carried out such that a one unit increase in normalized level of an RNA transcript or expression product generally reflects a 2-fold increase in quantity present in the sample.

KITS OF THE INVENTION

[0097] The materials for use in the methods of the present invention are suited for preparation of kits produced in accordance with well known procedures. The present invention thus provides kits comprising agents, which may include primers and/or probes, for quantitating the level of the disclosed RNA transcripts or their expression products via methods such as whole transcriptome sequencing or RT-PCR for predicting prognostic outcome. Such kits may optionally contain reagents for the extraction of RNA from tumor samples, in particular, fixed paraffin-embedded tissue samples and/or reagents for whole transcriptome sequencing. In addition, the kits may optionally comprise the reagent(s) with an identifying description or label or instructions relating to their use in the methods of the present invention. The kits may comprise containers (including microliter plates suitable for use in an automated implementation of the method), each with one or more of the various reagents (typically in concentrated form) utilized in the methods, including, for example, pre-fabricated microarrays, buffers, the appropriate nucleotide triphosphates (e.g., dATP, dCTP, dGTP and dTTP; or rATP, rCTP, rGTP and UTP), reverse transcriptase, DNA polymerase, RNA polymerase, and one or more probes and primers of the present invention (e.g., appropriate length poly(T) or random primers linked to a promoter reactive with the RNA polymerase). Mathematical algorithms used to estimate or quantify prognostic information are also potential components of kits.

REPORTS

[0098] The methods of this invention are suited for the preparation of reports summarizing the predictions resulting from the methods of the present invention. A "report" as described herein, is an electronic or tangible document that includes elements that provide information of

interest relating to a likelihood assessment and its results. A subject report includes at least a likelihood assessment, e.g., an indication as to the likelihood that a cancer patient will exhibit long-term survival without breast cancer recurrence. A subject report can be completely or partially electronically generated, e.g., presented on an electronic display (e.g., computer monitor). A report can further include one or more of: 1) information regarding the testing facility; 2) service provider information; 3) patient data; 4) sample data; 5) an interpretive report, which can include various information including: a) indication; b) test data, where test data can include a normalized level of one or more RNA transcripts of interest, and 6) other features.

[0099] The present invention therefore provides methods of creating reports and the reports resulting therefrom. The report may include a summary of the levels of the RNA transcripts, or the expression products of such RNA transcripts, in the cells obtained from the patient's tumor sample. The report may include a prediction that the patient has an increased likelihood of long-term survival without breast cancer recurrence or the report may include a prediction that the subject has a decreased likelihood of long-term survival without breast cancer recurrence. The report may include a recommendation for a treatment modality such as surgery alone or surgery in combination with chemotherapy. The report may be presented in electronic format or on paper.

[00100] Thus, in some embodiments, the methods of the present invention further include generating a report that includes information regarding the patient's likelihood of long-term survival without breast cancer recurrence. For example, the methods of the present invention can further include a step of generating or outputting a report providing the results of a patient response likelihood assessment, which can be provided in the form of an electronic medium (e.g., an electronic display on a computer monitor), or in the form of a tangible medium (e.g., a report printed on paper or other tangible medium).

[00101] A report that includes information regarding the likelihood that a patient will exhibit long-term survival without breast cancer recurrence, is provided to a user. An assessment as to the likelihood that a cancer patient will exhibit long-term survival without breast cancer reucrrence, is referred to as a "likelihood assessment." A person or entity who prepares a report ("report generator") may also perform the likelihood assessment. The report generator may also perform one or more of sample gathering, sample processing, and data generation, e.g., the report generator may also perform one or more of: a) sample gathering; b) sample processing; c) measuring a level of an RNA transcript or its expression product; d) measuring a level of a

reference RNA transcript or its expression product; and e) determining a normalized level of an RNA transcript or its expression product. Alternatively, an entity other than the report generator can perform one or more sample gathering, sample processing, and data generation.

[00102] The term "user" or "client" refers to a person or entity to whom a report is transmitted, and may be the same person or entity who does one or more of the following: a) collects a sample; b) processes a sample; c) provides a sample or a processed sample; and d) generates data for use in the likelihood assessment. In some cases, the person or entity who provides sample collection and/or sample processing and/or data generation, and the person who receives the results and/or report may be different persons, but are both referred to as "users" or "clients." In certain embodiments, e.g., where the methods are completely executed on a single computer, the user or client provides for data input and review of data output. A "user" can be a health professional (e.g., a clinician, a laboratory technician, a physician (e.g., an oncologist, surgeon, pathologist), etc.).

[00103] In embodiments where the user only executes a portion of the method, the individual who, after computerized data processing according to the methods of the invention, reviews data output (e.g., results prior to release to provide a complete report, a complete, or reviews an "incomplete" report and provides for manual intervention and completion of an interpretive report) is referred to herein as a "reviewer." The reviewer may be located at a location remote to the user (e.g., at a service provided separate from a healthcare facility where a user may be located).

[00104] Where government regulations or other restrictions apply (e.g., requirements by health, malpractice, or liability insurance), all results, whether generated wholly or partially electronically, are subjected to a quality control routine prior to release to the user.

COMPUTER-BASED SYSTEMS AND METHODS

[00105] The methods and systems described herein can be implemented in numerous ways. In one embodiment of the invention, the methods involve use of a communications infrastructure, for example, the internet. Several embodiments of the invention are discussed below. The present invention may also be implemented in various forms of hardware, software, firmware, processors, or a combination thereof. The methods and systems described herein can be implemented as a combination of hardware and software. The software can be implemented as an application program tangibly embodied on a program storage device, or different portions of the

software implemented in the user's computing environment (e.g., as an applet) and on the reviewer's computing environment, where the reviewer may be located at a remote site (e.g., at a service provider's facility).

[00106] In an embodiment of the invention, during or after data input by the user, portions of the data processing can be performed in the user-side computing environment. For example, the user-side computing environment can be programmed to provide for defined test codes to denote a likelihood "score," where the score is transmitted as processed or partially processed responses to the reviewer's computing environment in the form of test code for subsequent execution of one or more algorithms to provide a result and/or generate a report in the reviewer's computing environment. The score can be a numerical score (representative of a numerical value) or a non-numerical score representative of a numerical value or range of numerical values (e.g., "A": representative of a 90-95% likelihood of a positive response; "High": representative of a greater than 50% chance of a positive response (or some other selected threshold of likelihood); "Low": representative of a less than 50% chance of a positive response (or some other selected threshold of likelihood), and the like.

[00107] As a computer system, the system generally includes a processor unit. The processor unit operates to receive information, which can include test data (e.g., level of an RNA transcript or its expression product; level of a reference RNA transcript or its expression product; normalized level of an RNA transcript or its expression product) and may also include other data such as patient data. This information received can be stored at least temporarily in a database, and data analyzed to generate a report as described above.

[00108] Part or all of the input and output data can also be sent electronically. Certain output data (e.g., reports) can be sent electronically or telephonically (e.g., by facsimile, using devices such as fax back). Exemplary output receiving devices can include a display element, a printer, a facsimile device and the like. Electronic forms of transmission and/or display can include email, interactive television, and the like. In an embodiment of the invention, all or a portion of the input data and/or output data (e.g., usually at least the final report) are maintained on a web server for access, preferably confidential access, with typical browsers. The data may be accessed or sent to health professionals as desired. The input and output data, including all or a portion of the final report, can be used to populate a patient's medical record that may exist in a confidential database as the healthcare facility.

[00109] The present invention also contemplates a computer-readable storage medium (e.g., CD-ROM, memory key, flash memory card, diskette, etc.) having stored thereon a program which, when executed in a computing environment, provides for implementation of algorithms to carry out all or a portion of the results of a likelihood assessment as described herein. Where the computer-readable medium contains a complete program for carrying out the methods described herein, the program includes program instructions for collecting, analyzing and generating output, and generally includes computer readable code devices for interacting with a user as described herein, processing that data in conjunction with analytical information, and generating unique printed or electronic media for that user.

[00110] Where the storage medium includes a program that provides for implementation of a portion of the methods described herein (e.g., the user-side aspect of the methods (e.g., data input, report receipt capabilities, etc.)), the program provides for transmission of data input by the user (e.g., via the internet, via an intranet, etc.) to a computing environment at a remote site. Processing or completion of processing of the data is carried out at the remote site to generate a report. After review of the report, and completion of any needed manual intervention, to provide a complete report, the complete report is then transmitted back to the user as an electronic document or printed document (e.g., fax or mailed paper report). The storage medium containing a program according to the invention can be packaged with instructions (e.g., for program installation, use, etc.) recorded on a suitable substrate or a web address where such instructions may be obtained. The computer-readable storage medium can also be provided in combination with one or more reagents for carrying out a likelihood assessment (e.g., primers, probes, arrays, or such other kit components).

[00111] Having described the invention, the same will be more readily understood through reference to the following Examples, which are provided by way of illustration, and are not intended to limit the invention in any way. All citations through the disclosure are hereby expressly incorporated by reference.

EXAMPLE 1

Materials and Methods

[00112] Patients

[00113] One hundred and thirty-six primary breast cancer FFPE tumor specimens with clinical outcomes were provided by Providence St. Joseph Medical Center (Burbank, CA), with institutional review board approval. The time to first recurrence of breast cancer or death due to breast cancer (including death due to unknown cause) was determined from these records. Patients who were still alive without breast cancer recurrence or who died due to known other causes were considered censored at the time of last follow-up or death. These tumor specimens were used for biomarker discovery in the development of the Onco*type* DX® assay. *See e.g.*, U.S. Patent No. 7,081,340; S. Paik et al., *The New England Journal of Medicine* 351, 2817 (2004). For the present study, 136 specimens had adequate RNA remaining. Among the 136 patients, 26 experienced breast cancer recurrence or death due to breast cancer.

[00114] RNA-Seq Sample Preparation and Sequencing

[00115] Total RNA was prepared from three 10-μm-thick sections of FFPE tumor tissue as previously described using the MasterPure™ Purification Kit (Epicentre® Biotechnologies, Madison, WI). M. Cronin *et al.*, *The American Journal of Pathology* **164**, 35 (Jan, 2004). One hundred nanograms of the isolated RNA were depleted of ribosomal RNA as described. *See* U.S. Pub. No. 2011/0111409. Sequencing libraries for whole transcriptome analysis were prepared using ScriptSeq™ mRNA-Seq Library Preparation Kits (Epicentre® Biotechnologies, Madison, WI). During the cDNA synthesis step, additional incubation for 90 minutes at 37°C was implemented in the reverse transcription step to increase library yield. After 3'-terminal tagging, the di-tagged cDNA was purified using MinElute® PCR Purification Kits (Qiagen, Valencia, CA). Two 6 base index sequences were used to prepare barcoded libraries for duplex sequencing (RNA-Seq Barcode Primers; Epicentre® Biotechnologies, Madison, WI). PCR was carried out through 16 cycles to generate the second strand of cDNA, incorporate barcodes, and amplify libraries. The amplified libraries were size-selected by a solid phase reversible immobilization, paramagnetic bead-based process (Agencourt® AMPure® XP System; Beckman Coulter Genomics, Danvers, MA). Libraries were quantified by PicoGreen® assay (Life Technologies, Carlsbad, CA) and visualized with an Agilent Bioanalyzer using a DNA 1000 kit (Agilent Technologies, Waldbronn, Germany).

[00116] TruSeq™ SR Cluster Kits v2 (Illumina Inc.; San Diego, CA) were used for cluster generation in an Illumina cBOT™ instrument following the manufacturer's protocol. Two indexed libraries were loaded into each lane of flow cells. Sequencing was performed on an Illumina HiSeq®2000 instrument (Illumina, Inc.) by the manufacturer's protocol. Multiplexed single-read runs were carried out with a total of 57 cycles per run (including 7 cycles for the index sequences).

[00117] Data Quality Assessment

[00118] Each sequencing lane was duplexed with two patient sample libraries using a 6 base barcode to differentiate between them. The mean read ratio +/-SD between the two samples in each lane was 1.05±0.38 and the mean +/-SD percentage of un-discerned barcodes was 2.08%±1.63% . Using principal components analysis and other exploratory data analysis methods, no systematic differences were found among samples associated with flow cell or barcode.

[00119] In a run-in phase of the study, duplicate libraries were prepared for 8 samples selected at random from the study set of 136. RefSeq RNA coverage for these libraries ranged between 3.1M and 6.7M uniquely mapped reads. Log count Pearson correlations among duplicate libraries ranged between 0.947 and 0.985. Single libraries were prepared for the remaining 128 samples and distributed in duplex mode among the lanes of 8 flow-cells. Sequencing in 3 lanes failed. Two libraries had low yield, resulting in low coverage. Three lanes were flagged by various Illumina process monitoring indices: low Q30 (coverage = 2.8M and 4.2M), high cluster density (coverage = 1.6M and 1.8M), or inadequate imaging (coverage = 3.3M and 3.1M). For the remaining lanes, sample coverage ranged between 2.5M and 7.3M reads. New libraries for the samples that had low yield were prepared and sequenced. Libraries in the failed and flagged lanes, as well as some of the low coverage samples, were re-sequenced. Replicate correlations among all sequenced samples were very high, 0.985 for the samples with the high cluster density in the original run, and over 0.990 for all others. For the analysis data set, data for one of each of the duplicate libraries from the run-in experiment were kept. For the samples for which new libraries were prepared and for the samples in the failed and flagged lanes, the reads from the subsequent run were used. For the samples with low coverage for which the library was reprocessed, reads from the two runs were pooled. For the rest of the samples, the reads from the single lane were used. Results differed little when other data analysis procedures were used, for example, using only the second run when libraries were reprocessed.

[00120] Statistics and Bioinformatics

[00121] With the exception noted below, all primary analysis of sequence data was performed in CASAVA 1.7, the standard data processing package from Illumina. De-multiplexing of sample indices was set with 1 mismatch tolerance to separate the two samples within each lane. Raw FASTQ sequences were trimmed from both ends before mapping to the human genome (UCSC release, version 19), to address 3' end adapter contamination and random RT primer artifacts, and 5' end terminal-tagging oligonucleotide artifacts. The libraries as prepared contain strand-of-origin (directional) sequence information. Annotated RNA counts (defined by refFlat.txt from UCSC) were calculated by CASAVA 1.7 both with and without consideration of strand-of-origin information. Although retained in the mapping process, CASAVA does not provide directional counts by default. These counts were obtained by splitting the mapped (export.txt) file into two parts, one with sense strand counts, the other with antisense strand counts, and processing them independently. Raw FASTQ sequence was mapped with Bowtie (B. Langmead et al., *Genome Biology* **10**, R25 (2009)) in parallel with CASAVA to count ribosomal RNA transcripts.

[00122] Data were analyzed in 3 categories: first, RefSeq RNAs, about 80% of which are exon sequences, consolidated for each gene; second, intronic RNA sequences, consolidated for each gene; third, intergenic sequences. RNAs with maximum counts less than 5 among the 136 patients were excluded from analysis. Of 21,283 total RefSeq transcripts counted by CASAVA, 821 had a maximum count less than 5, leaving 20,462 RefSeq transcripts for analysis. Similar to a recently published procedure described by Bullard et al. (*BMC Bioinformatics* **11**, 94 (2010)), $\log_2$ raw RNA counts (setting the log2 for a 0 count to 0) were normalized by subtracting the 3rd quartile of the $\log_2$ RefSeq RNA counts and adding the cohort mean 3rd quartile ("Q3 normalization"). For analysis of RefSeq and intergenic RNAs normalization, RefSeq RNA data were used. For analysis of intronic RNAs normalization, intronic RNA data were used.

[00123] Standardized hazard ratios for breast cancer recurrence for each RNA, that is, the proportional change in the hazard with a 1-standard deviation increase in the normalized level of the RNA, were calculated using univariate Cox proportional hazard regression analyses (Cox, *Journal of the Royal Statistical Society: Series B (Methodological)* **34**, 187 (1972)). The robust standard error estimate of Lin and Wei (*Journal of the American Statistical Society*, **84**, 1074 (1989)) was used to accommodate possible departures from the assumptions of Cox

regression, including nonlinearity of the relationship of gene expression with log hazard and nonproportional hazards. False discovery rates (FDR, q-values) were assessed using the method of Storey (*Journal of the Royal Statistical Society, Series B* **64**, 479 (2002)) with a "tuning parameter" of λ=0.5. Analyses were conducted to identify true discovery degree of association (TDRDA) sets of RNAs with absolute standardized hazard ratio greater than a specified lower bound while controlling the FDR at 10% (Crager, *Statistics in Medicine* **29**, 33 (2010). Taking individual RNAs identified at this FDR, the analysis finds the maximum lower bound for which the RNA is included in a TDRDA set. Also computed was an estimate of each RNA's actual standardized hazard ratio corrected for regression to the mean. *Id.*

[00124] Expression of 192 transcripts in the same tumor RNAs was measured using previously described RT-PCR methods (Cronin et al., *The American Journal of Pathology* **164**, 35 (Jan, 2004); Cronin et al., *Clinical Chemistry* **50**, 1464 (Aug, 2004)). Standardized hazard ratios associating the expression of each gene (normalized by subtracting each gene's crossing threshold (C_T) from the cohort median C_T) with cancer recurrence were computed using the same methods used for evaluation of the RNA-Seq data.

[00125] Identifying Intergenic Sequences

[00126] Intergenic regions were identified by a novel program that evaluates genomic regions that vary widely in length and on a population basis. This program was developed to evaluate intergenic regions having wide variations in length, and to use data from a population of subjects rather than an individual subject. The uniquely mapped reads from all 136 patients were analyzed to identify clusters of reads that might arise from intergenic transcripts. Genomic regions containing less than 2 mapped reads of genomic sequence were not counted to eliminate potential noise from mis-mapping orgenomic DNA contamination. The remaining reads were clustered into individual read "islands" based on the overlap of their mapped coordinates to the hg 19 reference human genome, which resulted in 12,750,071 islands in all 136 patient samples. Any islands within 30 base pairs (bp) of each other were grouped together as regions of interest (ROI) producing a total of 6,633,258 ROIs. The number of ROIs were further reduced by the following criteria: 1) The average number of reads mapped to the ROI was $\geq$ 5 across all 136 patients, 2) the length of the ROI was at least 100 bp, and 3) the read depth (average read number divided by the length of the ROI) was $\geq$ 0.075. Applying these criteria reduced the number of ROIs to 23,024. ROIs were classified as intergenic regions if they

did not overlap with the transcripts (including non-coding ones) annotated in the refFlat.txt file obtained from UCSC, thereby eliminating overlap with known exons and introns of protein-coding genes and well annotated non-protein coding transcripts. A total of 2,101 intergenic regions were identified by this computational procedure.

EXAMPLE 2

Evaluation of whole transcriptome RNA-Seq as a platform for biomarker discovery

[00127] Patient clinical characteristics are shown in Table 12. One-hundred and ten patients (81%) had no involved nodes. There was a mixture of chemotherapy and hormonal therapy usage. Estrogen receptor (ER) status was not included in patient records. Therefore, normalized ESR1 mRNA levels obtained in the present RNA-Seq study were used to identify 111 tumors as estrogen-receptor positive and 25 as estrogen-receptor negative. Use of RT-PCR rather than RNA-Seq for this purpose yielded similar but not identical results, identifying as ER+ two more patients, for a total of 113. Archive ages of FFPE tumor blocks ranged from 5 to 12.4 years (median 8.5 years).

[00128] RNA-Seq results were successfully generated for all 136 patients, with an average of 43 million median reads per patient (86 million median reads per Illumina Hiseq 2000 flow cell lane). Sixty-nine percent of these uniquely mapped to the human genome: 19.2% to exons, 64.9 % to introns, and 15.9% to intergenic regions. Ribosomal RNA accounted for less than 0.3% of the total reads. On average, 17,248 Refseq transcripts were detected per patient, 66% with greater than 10 counts, and 47% with greater than 100 counts.

[00129] Use of third quartile normalization effectively mitigated trends in overall coverage related to sample age and produced stable estimates of expression with relative log expression (RLE, individual gene $\log_2$ count minus within-patient median $\log_2$ count) values that were centered on zero and relatively tightly distributed around 0, an indicator of effective normalization.

[00130] Figure 1A displays results from the historical RT-PCR 192 candidate gene screen of the Providence 136 patient cohort, relating increasing mRNA expression to recurrence risk hazard ratios and statistical significance. As shown, fourteen of the sixteen cancer-related genes in the Onco*type* DX® panel were assayed, and most were identified with Hazard Ratios greater than 1.2 or less than 0.8 and P values <0.05.

[00131] The effect sizes and statistical significance of Oncotype DX® genes were similar when screening was carried out by whole transcriptome RNA-Seq rather than RT-PCR (compare Figures 1A and 1B). This is shown in detail on a gene by gene basis in box plots (Figure 2). A scatter plot of log hazard ratios demonstrates overall concordance between the 192 gene RT-PCR results with the RNA-Seq analyses (Lin et al., *Journal of the Royal Statistical Society, Series B* **84**, 1074 (1989)) (Lin concordance correlation: 0.810; Pearson correlation coefficient: 0.813; Figure 3). Significantly, RNA-Seq further associates many RefSeq RNAs with disease recurrence: a total of 1307 at FDR<10% (Table 1), hereafter referred to as "identified RefSeq RNAs." In contrast, the 192 gene RT-PCR study identified 32 RNAs at FDR<10%, and consumed five-fold more input RNA. Together, these results indicate that RNA-Seq can provide a practical, sensitive and precise platform for genome-wide biomarker discovery in FFPE tissue.

EXAMPLE 3

RefSeq Transcripts and Gene Networks that Associate with Risk of Breast Recurrence

[00132] There were 1307 RefSeqs associated with disease recurrence outcome at FDR <10% (Table 1). Because the reproducibility of within-sample transcript counts inevitably decreases as transcript abundance decreases, the impact of transcript abundance on initial biomarker discovery was evaluated. These 1307 RNAs were binned with respect to count abundance. Accounting for the 821 transcripts with maximum counts less than 5, which were deliberately excluded from analysis, rare transcripts (with less than 10 median counts) represent 28% of all RefSeq transcripts. The percent of RNAs identified decreases but is not dramatically different as median counts decrease from greater than 1,000 to 10-99. Even at median counts less than 10, the percent of RNAs identified fell by less than half compared to sequences present at higher abundance.

[00133] Among the 1307 identified RefSeq RNAs, many relate to recurrence with very high statistical significance (Table 1). TDRDA analysis identified 144 with standardized hazard ratio greater than 1.1, controlling FDR at 10%. Estimated standardized hazard ratios corrected for regression to the mean are as high as 1.66. Uncorrected hazard ratios range from approximately 0.4 to 2.5. The ratio of RNAs for which high expression associates with increased risk of cancer recurrence, versus decreased risk is approximately 1.

[00134] The library chemistry used in this study provides DNA strand-of-origin information for transcripts. The analysis that identifies 1307 prognostic RefSeq RNAs is not filtered for directionality. When this is done, 1023 of these RefSeq transcripts are still associated with disease recurrence at FDR<10% when only sense strand counts are analyzed. Less than 10% of the total RefSeq counts locate in the anti-sense direction. Nevertheless, 798 anti-sense transcripts associate with recurrence risk.

Validation of the Association of RefSeq transcripts with Breast Cancer Prognosis in an Independent Cohort

[00135] The performance of these identified RNAs was further evaluated using public gene expression data from an independent cohort of breast cancer patient tumors that had been assayed by DNA microarray technology. The microarray data set was assembled by merging patient sets published in two articles (M. J. van de Vijver *et al.*, *New England Journal of Medicine* **347**, 1999 (2002); L. J. Van't Veer *et al.*, *Nature* **415**, 530 (2002)), providing data on 337 patients ("NKI dataset"). Metastasis-free survival information was available for 319 patients. Standardized hazard ratios for cancer recurrence were estimated for each gene targeted by the microarray using univariate Cox proportional hazard regression analysis. Genes were identified as prognostic using a 10% FDR threshold as was done with the RNA-Seq data. Among the 11,659 genes common to both platforms, there is highly significant agreement in the classification of genes as prognostic (Figure 4) but concordance falls off as transcript abundance decreases. For RNA-Seq RNAs present at >100 counts, 44% were identified as prognostic in the NKI dataset.

Gene Networks

[00136] Hierarchical clustering (Eisen et al., *Proceedings of the National Academy of Sciences* **95**, 14863 (1998)) of the 1307 identified RefSeq RNAs (Table 1) suggests the presence of co-expressed gene networks. Cytoscape (P. Shannon *et al.*, *Genome Research* **13**, 2498 (2003); M. E. Smoot et al., *Bioinformatics* **27**, 431 (2011)) was used to evaluate the subset of these RNAs for which each member correlates in its expression with at least one other RNA at $R \geq 0.6$. Figure 5 graphically represents the resulting correlation matrix of 597 genes and 4011 interactions. One prominent (51 member) RefSeq RNA network represented in Figure 5 is enriched in RNAs with Reactome database annotations (G. Joshi-Tope *et al.*, *Nucleic Acids Res* **33**, D428 (2005)) that are functionally related to regulation of the cell cycle and mitosis, and

associates with poor prognosis ("cell cycle network") (Table 6). This network includes three of the five proliferation-associated Onco*type* DX® genes (BIRC5, MYBL2, MKI67). A second network is enriched in RNAs that co-express with the estrogen receptor gene (ESR1) ("ESR1 network") and associate with reduced recurrence risk, including the Onco*type* DX® genes, BCL2 and SCUBE2. The other ESR1 network genes include CPEB2, IL6ST, DNALI1, PGR, SLC7A8, C6orf97, RSPH1, EVL, BCL2, NXNL2, GATA3, GFRA1, GFRA1, ZNF740, MKL2, AFF3, ERBB4, RABEP1, KDM4B, ESR1, C4orf32, and CPLX1 (Table 7). ESR1 itself is not statistically associated with disease outcome in our RNA-Seq results, nor was it previously found to be significant in this cohort by RT-PCR analysis.

[00137] This analysis also reveals several novel RNA networks, three of which map to discrete cytogenetic bands (Figure 5): 1) a network of five poor prognosis RNAs mapping to a 289 kilobase region located at Chr9q22 ("Chr9q22 network"), which includes ASPN, CENPP, ECM2, OGN, and OMD (Table 8); 2) a network of twelve RNAs mapping to a 6.6 megabase region of Chr17q23-24 ("Chr17q23-24 network"), which includes CCDC45, POLG2, SMURF2, CCDC47, CLTC, DCAF7, DDX42, FTSJ3, PSMC5, RPS6KB1, SMARCD2, and TEX2 (Table 9); and 3) a fourteen RNA network mapping to a 47 megabase span on Chr8q21-24 ("Chr8q21-24 network"), which includes CYC1, DGAT1, GPAA1, GRINA, PUF60, PYCRL, RPL8, SQLE, TSTA3, ESRP1, GRHL2, INTS8, MTDH, and UQCRB (Table 10). Finally, Figure 5 represents a large (134 member) RNA network that has strong Gene Ontology and Biocarta annotations to olfactory signaling, glucose metabolism, and glucuronidation ("olfactory receptor network") (Table 11). Nine of the transcripts in this novel network encode olfactory receptors. (OR10H3, OR14J1, OR2J2, OR2W5, OR5T2, OR7E24, OR7G3, OR8S1, and OR9K2). Fifteen are microRNA precursors (MIR1208, MIR1266, MIR1297, MIR133A1, MIR195, MIR196A1, MIR3170, MIR3183, MIR4267, MIR4275, MIR4318, MIR501, MIR501, MIR539, and MIR542). Most of the RNAs in this network are rare (raw median counts less than 10). All but 2 of them associate with poor prognosis as shown in Table 1.

TABLE 6: Cell cycle network

ANLN	CDC25C	EPR1	KIF18B	NUSAP1
ASPM	CDCA2	EXO1	KIF20A	PGK1
BIRC5	CENPE	FAM83D	KIF23	PRC1
BLM	CENPF	GTSE1	KIF2C	PRR11
BUB1	CENPN	HIST1H2AH	KPNA2	RRM2
BUB1B	CENPO	HJURP	MELK	SGOL1
C15orf23	CEP55	HMMR	MKI67	TRIP13
CASC5	DLGAP5	INCENP	MYBL2	TROAP
CCNA2	E2F1	KIF11	NEK2	TUBA1B
CCNB2	ECT2	KIF14	NUP93	UBE2C
				ZNF695

TABLE 7: ESR1 network

BCL2	SCUBE2	CPEB2	IL6ST	DNALI1	PGR
SLC7A8	C6orf97	RSPH1	EVL	BCL2	NXNL2
GATA3	GFRA1	GFRA1	ZNF740	MKL2	AFF3
ERBB4	RABEP1	KDM4B	ESR1	C4orf32	CPLX1

TABLE 8: Chr9q22 network

ASPN	CENPP	ECM2	OGN	OMD

TABLE 9: Chr17q23-24 network

CCDC45	POLG2	SMURF2	CCDC47	CLTC	DCAF7
DDX42	FTSJ3	PSMC5	RPS6KB1	SMARCD2	TEX2

TABLE 10: Chr8q21-24 network

CYC1	DGAT1	GPAA1	GRINA	PUF60	PYCRL	RPL8
SQLE	TSTA3	ESRP1	GRHL2	INTS8	MTDH	UQCRB

TABLE 11: Olfactory receptor network

AFM	F11	LOC285577	NR1H4	SLC30A10
APCS	F9	LOC401177	OCM	SLC30A3
APOBEC1	FAM131C	LOC401242	OPALIN	SNAR-G1
ATOH7	FAM169B	LOC642006	OR10H3	SNCB
ATXN3L	FAM9C	LOC646960	OR14J1	SNORD116
BARHL2	FEZF1	LOC729966	OR2J2	SNORD18B
C17orf64	FOXD4L5	LRIT2	OR2W5	SP8
C18orf26	FTMT	LYPD2	OR5T2	SPRR3
C19orf75	FZD9	MAGEB2	OR7E24	SPRYD5
C20orf185	GBX2	MIR1208	OR7G3	STATH
C7orf72	GPR33	MIR1266	OR8S1	TAAR6
C9orf27	GPX5	MIR1297	OR9K2	TFAP2D
CA5A	GSTA2	MIR133A1	PABPC1L2B	TRIM10
CAMKV	GSTTP1	MIR195	PACRGL	TRYX3
CHAT	HBZ	MIR196A1	PCDH11Y	TSPAN19
CLCN1	HCRTR2	MIR3170	PGA3	TXNDC8
CLEC18B	HMX1	MIR3183	PNLIP	UGT2A1
COL20A1	HMX3	MIR4267	POM121L10	UGT2B10
COL9A1	KCNJ4	MIR4275	POTEG	UGT2B7
COX8C	KCNV1	MIR4318	POU3F4	VWC2
CRYZ	KRT20	MIR501	PRSS41	ZFP42
DEFB133	KRT72	MIR539	RAB28	ZNF705D
DEFB135	KRT78	MIR542	RAB9BP1	
DNAJC5G	KRT83	MOXD2P	RP1-177G6	
DOC2GP	LHX5	NCRNA0020	RXFP2	
DSCR10	LOC100129	NCRNA0022	SCRT2	
EVX1	LOC100133	NPFFR1	SERPINB10	
EVX2	LOC144742	NPPB	SI	

Table 12. Case characteristics and outcomes

Characteristic	No. patients/no. analyzed (%)
Tumor size (cm)	
0-2	81/136 (60%)
2-5	49/136 (36%)
>5	6/136 (4%)
No. lymph nodes at primary diagnosis	
0	110/136 (81%)
1-9	11/136 (8%)
10-15	9/136 (7%)
16-20	6/136 (4%)
Adjuvant tamoxifen	
Yes	54/136 (40%)
No	77/136 (57%)
Unknown	5/136 (4%)
Adjuvant chemotherapy	
Yes	51/136 (38%)
No	79/136 (58%)
Unknown	6/136 (4%)
ER Status*	
ER positive	111/136 (82%)
ER negative	25/136 (18%)
Vital Status	
Distant recurrence, death due to breast cancer, or death due to unknown cause	
Total	26/136 (19%)
ER positive	16/136 (12%)
ER negative	10/136 (7%)
Alive without distant recurrence or death due to other cause	
Total	110/136 (81%)
ER positive	95/136 (70%)
ER negative	15/136 (11%)

*ER status determined by RNA-Seq analysis as described

EXAMPLE 4
Risk of recurrence in ER+ patients

[00138] ER status, which is often described in clinical practice in binary terms as ER+ and ER- via immunohistochemistry evaluation of breast tumors, dichotomizes breast cancer with respect to clinical outcome and gene expression profiles. While ER status information was not part of patient records for this study cohort, RNA-Seq ESR1 counts were used to separate patients. This analysis is presented in Table 2. This is a novel method of defining ER status but note the small population size (10 recurrence events) and the absence of hormonal therapy in a significant fraction of those patients that were defined as ER+. Administration of hormonal therapy (e.g., tamoxifen or an aromatase inhibitor) is current standard clinical practice, and both significantly decreases recurrence risk and influences the nature of biomarkers that predict recurrence. Nevertheless, this analysis does identify the expected cell cycle gene signature as a marker of high recurrence risk (exemplified by the genes CCNA2; CENPN, KIF20, ARPP19 and BUB3). In all, expression of 363 RefSeq transcripts relate to recurrence risk at FDR<10% (Table 2). Within this set of transcripts, the most prominent RefSeq RNA network found using Cytoscape as described above is similar to the rare "olfactory receptor network" that was identified in the analysis of the entire 136 patient cohort. In the ESR1+ patients, this olfactory receptor network consists of 86 RefSeq RNAs (see Table 13), 6 of which are olfactory receptors (OR14J1, OR2B3, OR2J2, OR2W5, OR5T2, OR8S1) and 8 pre-microRNAs (MIR1208, MIR1251, MIR1266, MIR195, MIR4275, MIR4318, MIR542, MIR548I2). All RNAs in this network associate with increased risk of disease recurrence as shown in Table 2.

TABLE 13: Olfactory receptor network in ER-positive patients

APCS	APOBEC1	ATXN3L	BAGE	C17orf88
C18orf26	C19orf75	C9orf27	CA5A	CCDC105
CHAT	COL20A1	COX7B2	COX8C	DEFB133
DKFZp779M	DSCR10	DUSP13	EVX1	EVX2
FAM169B	FEZF1	GAB4	GDF7	GPR50
GPX5	GSTA2	GUCY2F	HCRTR2	HMX1
HMX3	KRT78	KRT83	LOC100129	LOC144742
LOC285577	LOC286186	LOC401177	LOC642345	LOC645971
LOC647107	LOC729966	LPO	LRIT2	LYPD2
MAGEA10	MAGEB10	MIR1208	MIR1251	MIR1266
MIR195	MIR4275	MIR4318	MIR542	MIR548I2
NCRNA0020	NCRNA0022	NKX1-2	NPPB	OR14J1

OR2B3	OR2J2	OR2W5	OR5T2	OR8S1
PCDH11Y	PGA3	POTEG	PRDM9	PRSS41
RAB9BP1	RAET1L	RNASE9	RP1-177G6	SCRT2
SERPINB10	SLC17A6	SNAR-G1	SNCB	SNORD115
SNORD116	SNORD18C	SOST	SPRR3	TPTE
WFDC9				

EXAMPLE 5

Association of Intronic Sequences with Breast Cancer Prognosis

[00139] Reads mapping to intronic regions of the genome account for ~65% of all of the sequence data. Introns tend to co-express with exons of the same genes (median R = 0.67), although these correlations vary over a wide range, from roughly zero to over 0.9. The percent of intronic RNAs that map in the antisense direction is slightly higher than in the case of RefSeq RNAs (median: ~7.5% versus ~5%, respectively). A large number (1698) of intronic RNAs associate with breast cancer recurrence (at FDR < 10%; non-directional analysis; Table 3), with ranges of hazard ratios and p-values are similar to those of the above-identified 1307 RefSeq RNAs.

[00140] Over two thirds (1154) of the identified intronic transcripts do not lie within the prognostic RefSeq RNAs listed in Table 1 above. That is, their cognate assembled exons are not also discovered. (Among the 100 most highly statistically significant intronic RNAs this fraction is 0.44.) This subset of the identified intronic RNAs is particularly likely to contain prognostic information that is not captured by the RefSeq RNAs. The basis for these might be statistical: average counts for all intronic RNAs are more than threefold higher than for all exons, so signal to noise ratio is more favorable for discovery of intronic RNAs. Nevertheless, in the population of exons that are not discovered along with discovered cognate introns, average exon abundance is just a little lower than in the entire population of discovered exons (mean counts (244, versus 312 average counts, respectively). This result is consistent with these intronic RNAs carrying prognostic information that is not carried in their corresponding exons.

EXAMPLE 6

Association of Intergenic Sequences with Breast Cancer Prognosis

[00141] Two approaches were used to search for biomarkers within the population of intergenic RNAs, first by interrogating reads that map to 2,500 well-documented long

intergenic non-coding RNAs (lincRNAs) (A. M. Khalil *et al.*, *Proceedings of the National Academy of Sciences of the United States of America* **106**, 11667 (Jul 14, 2009)). Twenty-two of these (Table 4), associate with breast cancer recurrence risk at FDR<10%. Second, intergenic transcripts were screened more broadly by using a novel computational algorithm described in Example 1 to identify clusters of reads that map to intergenic regions of the genome in one or more of the tumor specimens. The number of reads mapped to these clusters was used as a measure of the relative expression of putative intergenic transcripts. Altogether, 2101 putative intergenic transcripts were identified, 775 of which are contained in or overlap with lincRNAs that have been identified previously in one or more previous studies of non-coding transcripts and their expression was tested for association with recurrence of breast cancer in the cohort of 136 patients. Expression of 194 (9%) of these transcripts correlates with breast cancer recurrence at FDR < 10%. This list of 194 transcripts was further condensed by merging clusters of reads separated by < 1000 bp to produce a set of 69 intergenic transcripts associated with recurrence of breast cancer (Table 5). Thirty-two of these 69 associate with decreased recurrence risk. The criterion for merging of clusters (< 1000 bp) is supported by the observation that the median correlation coefficient for co-expression of the merged clusters is extraordinarily high (median R = 0.94). Non-merged transcripts exhibited weak co-expression (median R = 0.27).

EXAMPLE 7

[00142] In a second study, 78 patient samples as described in Cobleigh et al., *Clin. Cancer Res.* 11:8623-8631 (2005) and in U.S. Patent No. 7,569,345 were obtained from women with invasive breast cancer and ≥ 10 positive nodes with no evidence of metastatic disease who had surgery at Rush University Medical Center from 1979 to 1999. Clinical outcome data were available for all patients. Patients who were still alive without breast cancer recurrence or who died due to known other causes were considered censored at the time of last follow-up or death. For the present study, 76 specimens had adequate RNA remaining for RNA-Seq.

[00143] Clinical characteristics of the 78 patients are shown in Table 14. RNA preparation, sequencing, and data analyses were performed as described in Example 1. Table 15 shows 125 RefSeq genes identified by RNA-Seq that were associated with breast cancer recurrence at FDR <10%. RefSeqs marked with "1" were associated with an increased likelihood of breast cancer recurrence and those marked with "-1" were associated with a

decreased likelihood of breast cancer recurrence. Table 15 shows the maximum lower bound, greater or equal to 0 for identified genes at 10% FDR; StdHR, which is the estimated standardized Hazard Ratio from the proportional hazards model; StdHR.qvalue, which is the q-value computed from the set of StdHR p-values derived from the robust estimate of standard errors and using Storey's procedure as implemented in R qvalue package with lambda=0.5; and StdHR.pv, which is the p-value of the estimated standardized coefficient for null hypothesis coeff=0 or HR (hazard ratio)=1. The accession numbers of each of the 125 RefSeqs are shown in Table B. Twenty of these genes were also associated with recurrence in the first study described in Example 1. This overlap is unlikely to occur by chance ($p<2.5 \times 10^{-5}$).

TABLE 14. Case characteristics and outcomes

Characteristic	No. patients/no. analyzed (%)
Mean age ± SD (range), years	57±13 (33-86)
Tumor size (cm)	
0-2	26/78 (33%)
2-5	28/78 (36%)
>5	24/78 (31%)
No. lymph nodes at primary diagnosis	
0-9	0/78 (0%)
10-15	40/78 (51%)
15-20	18/78 (23%)
20-30	12/78 (15%)
>30	8/78 (10%)
Adjuvant tamoxifen	
Yes	42/78 (54%)
No	36/78 (46%)
Adjuvant chemotherapy	
Yes	62/78 (80%)
No	16/78 (20%)
Tumor grade	
1	11/78 (14%)
2	37/78 (47%)
3	30/78 (38%)
Vital Status	
Distant recurrence, death due to breast cancer, or death due to unknown cause	55/78 (71%)
Alive without distant recurrence or death due to other cause	23/78 (29%)

Table 15. List of Assembled RefSeq RNAs Associated with Risk of Breast Cancer Recurrence in 76 Breast Cancer Patients

Gene	Direction of Association (1=Higher Expression means Higher Risk)	Maximum lower bound ≥0 @ 10% FDR	StdHR	StdHR.qvalue	StdHR.pv
TRPS1	-1	0.05	0.600271454	0.013404626	3.19E-06
SHROOM3	-1	0.05	0.592316052	0.013404626	4.52E-06
GREB1L	-1	0.05	0.589787342	0.013404626	4.78E-06
MICA	-1	0.05	0.53495849	0.013404626	6.17E-06
PIP4K2B	1	0.05	1.766657976	0.013404626	1.26E-06
CWC25	1	0.05	1.710144609	0.013404626	3.99E-06
SLITRK2	1	0.05	1.742894004	0.013404626	4.77E-06
C3orf18	-1	0.049	0.603537151	0.013404626	6.91E-06
C3orf15	-1	0.049	0.56549207	0.014911144	8.54E-06
DIS3L	-1	0.049	0.467081559	0.017557656	1.31E-05
PSMD8	1	0.048	1.584581143	0.013404626	6.47E-06
B4GALT5	1	0.047	1.722034237	0.015499558	1.07E-05
ARPC1B	1	0.046	1.621399637	0.015499558	9.90E-06
SLC26A5	-1	0.04	0.616339501	0.018957169	1.52E-05
ZNF837	-1	0.04	0.548382663	0.023868625	2.13E-05
BEND5	-1	0.038	0.589144544	0.023868625	2.38E-05
LOC100128675	-1	0.038	0.565506214	0.023868625	2.55E-05
GRTP1	-1	0.038	0.545883691	0.023868625	2.60E-05
AP1M1	1	0.035	1.600383771	0.023868625	2.43E-05
RTN4RL2	-1	0.03	0.610998068	0.029939316	3.43E-05
MAGI1	-1	0.03	0.616876931	0.030777252	3.93E-05
ENPP5	-1	0.03	0.595416002	0.031338122	4.31E-05
BZRAP1	-1	0.03	0.584798633	0.030777252	4.06E-05
DDB1	1	0.03	1.870965036	0.033898745	5.06E-05
NEDD4L	-1	0.029	0.606690251	0.031907709	4.57E-05
TMEM56	-1	0.028	0.68559784	0.030777252	3.91E-05
LRRC49	-1	0.028	0.525377682	0.036410064	6.25E-05
CYBASC3	1	0.028	1.661030039	0.033898745	5.44E-05
CLINT1	1	0.028	1.671589497	0.033898745	5.38E-05
CLCA2	1	0.027	1.703214484	0.036410064	6.44E-05
RPRD1A	-1	0.026	0.588692979	0.038013045	7.05E-05
TSPAN10	-1	0.026	0.571930206	0.038013045	7.19E-05
BCL2	-1	0.023	0.607244603	0.038114312	7.57E-05
BBS5	-1	0.022	0.706595678	0.036410064	6.47E-05

LOC100128640	-1	0.022	0.611210083	0.039413064	8.14E-05
CAMK2G	1	0.022	1.577924166	0.039413064	8.36E-05
TSPAN14	1	0.022	1.677559326	0.042870801	9.33E-05
RWDD3	-1	0.021	0.712509834	0.038114312	7.64E-05
TRAK1	-1	0.021	0.584711667	0.047369248	0.000117029
LOC730668	-1	0.021	0.545574613	0.047369248	0.000122501
ZNF621	-1	0.021	0.53393884	0.047369248	0.000120123
PELI3	-1	0.021	0.536673514	0.047369248	0.00012757
NCOA3	1	0.021	1.602212601	0.047369248	0.000107001
PSMB3	1	0.021	1.835670697	0.047369248	0.00012513
ZNF763	-1	0.018	0.646608385	0.047369248	0.000114793
CHDH	-1	0.018	0.625931486	0.047369248	0.000123182
SUSD4	-1	0.017	0.681812692	0.047369248	0.000117816
DNAH14	-1	0.017	0.568526034	0.051201952	0.000149628
KRT4	1	0.016	1.544128591	0.048843319	0.000137137
STK3	1	0.015	1.577969259	0.051201952	0.000148028
CCDC24	-1	0.014	0.711374716	0.048843319	0.000135924
IQCH	-1	0.013	0.690451374	0.05619298	0.000167433
NCRNA00173	-1	0.013	0.636905593	0.05928902	0.000183576
GTPBP10	-1	0.013	0.607771723	0.05928902	0.000200438
EML2	-1	0.013	0.594614968	0.05928902	0.000197289
LAPTM4B	1	0.013	1.559498582	0.057278344	0.000173949
SLC38A2	1	0.013	1.663522257	0.05928902	0.000197664
SCARNA15	1	0.013	1.873906539	0.05928902	0.000194249
MID2	-1	0.011	0.675617922	0.05928902	0.000196751
SLC26A8	-1	0.01	0.662530005	0.063180343	0.000220834
NKAPP1	-1	0.01	0.610606787	0.063891002	0.000226979
CLN5	-1	0.009	0.728165906	0.062238826	0.000213977
TLR5	-1	0.009	0.622951299	0.067031927	0.000241979
NPY5R	-1	0.009	0.574139163	0.070777897	0.000259557
LOC402778	-1	0.008	0.678984812	0.070973513	0.000272475
RPL14	-1	0.008	0.656553359	0.070836186	0.00026788
C6orf155	-1	0.008	0.643543245	0.071686076	0.000283425
ABCA3	-1	0.008	0.635422012	0.070836186	0.000267888
LOC723809	1	0.008	1.659680175	0.071686076	0.000282431
EPB49	-1	0.006	0.682134101	0.076840825	0.000308209
PLEKHA7	-1	0.006	0.631608043	0.077339749	0.000314641
RNU6ATAC	1	0.006	1.879268984	0.081043767	0.000334354
LAMC2	-1	0.004	0.692500587	0.082276981	0.000357633
MST1	-1	0.004	0.680494962	0.082276981	0.000353331
GSTM2	-1	0.004	0.631940594	0.082276981	0.000348608
ZNF337	-1	0.004	0.605531534	0.082276981	0.0003583

MTR	-1	0.004	0.601352242	0.083092569	0.000372137
WBSCR27	-1	0.004	0.574418341	0.083092569	0.000372492
LOC100130093	-1	0.003	0.727169905	0.083092569	0.000376135
FGFRL1	-1	0.003	0.684954343	0.086078557	0.000409381
TSNAXIP1	-1	0.003	0.667743065	0.086078557	0.000397407
BAIAP3	-1	0.003	0.657836003	0.086078557	0.000401136
TSC1	-1	0.003	0.635691021	0.086078557	0.000406333
LDLRAD3	-1	0.003	0.609908608	0.087926789	0.000430472
NPY1R	-1	0.003	0.536099497	0.087926789	0.000433424
IKBIP	1	0.003	1.630733535	0.087926789	0.000438324
WDR67	1	0.003	1.660073877	0.087926789	0.000434133
HMGCR	1	0.003	1.692917307	0.089657364	0.000452088
ZNF415	-1	0.002	0.702493074	0.092515604	0.000493007
LMX1B	-1	0.002	0.644058753	0.090095896	0.000459462
RBBP8	-1	0.002	0.611872583	0.093229516	0.000511211
SORBS2	-1	0.002	0.57041462	0.091505704	0.000474625
LASP1	1	0.002	1.577783177	0.092781758	0.000499741
PLCB3	1	0.002	1.591205516	0.092515604	0.000491513
CKAP4	1	0.002	1.608591213	0.093229516	0.000520375
RPPH1	1	0.002	1.722187729	0.093229516	0.000523521
SCARNA16	1	0.002	1.796667248	0.091505704	0.000477138
MFSD2A	1	0.002	1.81578939	0.093229516	0.000517013
ICA1	-1	0.001	0.713463664	0.095431649	0.000611726
OPLAH	-1	0.001	0.689897885	0.095431649	0.000620497
C2orf55	-1	0.001	0.674335475	0.094641728	0.000573056
ZNF48	-1	0.001	0.669187687	0.095431649	0.000618057
APC2	-1	0.001	0.66649698	0.095431649	0.000633369
PSD	-1	0.001	0.641610877	0.094641728	0.000555159
FAM201A	-1	0.001	0.635911763	0.095431649	0.000634315
C9orf156	-1	0.001	0.607820806	0.094641728	0.000567374
LOC644759	-1	0.001	0.593692626	0.094641728	0.000578394
PPP1R9A	-1	0.001	0.572844709	0.094641728	0.000585681
LRRN2	-1	0.001	0.569366964	0.094641728	0.000582567
OGFRL1	-1	0.001	0.542834434	0.095431649	0.000597706
OGDHL	1	0.001	1.506439856	0.094641728	0.000542532
G6PD	1	0.001	1.527692381	0.094641728	0.000539162
TMSB10	1	0.001	1.517112962	0.094641728	0.000579912
VASP	1	0.001	1.553404873	0.095431649	0.000632006
SEC23A	1	0.001	1.563911218	0.095431649	0.000608307
TMEM86A	1	0.001	1.655435111	0.094641728	0.000568909
ZNF774	-1	0	0.714351245	0.09802593	0.000674027
CLIC6	-1	0	0.691206304	0.098757456	0.000691447

ATL1	-1	0	0.686405034	0.098757456	0.000695989
C3orf23	-1	0	0.657672146	0.097719921	0.000663413
CHKB	-1	0	0.627745021	0.097719921	0.000666323
ARMCX6	-1	0	0.614708597	0.097719921	0.000661617
PTPN18	-1	0	0.600263531	0.098757456	0.000701692
ENTPD8	-1	0	0.589002346	0.098757456	0.000696835
MTFR1	1	0	1.470708659	0.099147778	0.000710146

EXAMPLE 8

Identification of Metabolic-Like Gene Networks Associated with Breast Cancer Prognosis

[00144] IDH2 was identified as a gene that associated with recurrence risk in the "Providence" patient cohort described in Example 1 (see Table 1) but did not belong to either the proliferation or estrogen receptor gene groups of the Onco*type* DX® Breast Cancer Assay. In fact, IDH2 encodes a key central metabolism gene, isocitrate dehydrogenase 2. It was discovered that IDH2 co-expresses with four other genes (ENO1, TMSB10, PGK1, and G6PD) that also co-express with each other, as show in Table 16. All but TMSB10 have known associations with metabolic pathways.

Table 16. Expression Correlation Matrix (R values) for give genes from the Providence patient cohort

	Chr~1~ENO1	**Chr~15~IDH2**	**Chr~2~TMSB10**	**Chr~x~PGK1**	**Chr~x~G6PD**
Chr~1~ENO1	1	0.5793053	0.67591657	0.79870882	0.468844448
Chr~15~IDH2	0.5793053	1	0.454417575	0.60309254	0.528542452
Chr~2~TMSB10	0.67591657	0.454417575	1	0.61952893	0.401039076
Chr~x~PGK1	0.798708824	0.603092544	0.619528934	1	0.50257563
Chr~x~G6PD	0.468844448	0.528542452	0.401039076	0.50257563	1

IDH2

[00145] IDH1 encodes isocitrate dehydrogenase 2, which is an NADP(+)-dependent isocitrate dehydrogenase found in the mitochondria. It plays a role in intermediary metabolism and energy production. The protein may tightly associate or interact with the pyruvate dehydrogenase complex.

ENO1

[00146] ENO1 encodes alpha-enolase, one of three enolase isoenzymes found in mammals. Each isoenzyme is a homodimer composed of 2 alpha, 2 gamma, or 2 beta subunits, and functions as a glycolytic enzyme. Alternative splicing of this gene results in a shorter isoform that has been shown to bind to the c-myc promoter and function as a tumor suppressor. Several pseudogenes have been identified, including one on the long arm of chromosome 1. Alpha-enolase has also been identified as an autoantigen in Hashimoto encephalopathy.

PGK1

[00147] The PGK1 gene encodes phosphoglycerate kinase, another glycolytic enzyme, which converts 1,3-diphosphoglycerate to 3-phosphoglycerate. This reaction generates one molecule of adenosine triphosphate (ATP), which is the main energy source in cells.

G6PD

[00148] G6PD encodes glucose-6-phosphate dehydrogenase, a cytosolic enzyme whose main function is to produce NADPH in the pentose phosphate pathway. This pathway generates both energy and molecular building blocks for nucleic acids and aromatic amino acids.

TMSB10

[00149] TMSB10 encodes thymosin beta-10, which plays an important role in the organization of the cytoskeleton. It binds to and sequesters actin monomers (G actin) and therefore inhibits actin polymerization.

[00150] The association of these five genes with recurrence rate was explored in the Providence patient cohort (see Example 1), "Rush" patient cohort (see Example 7), and the Netherlands Cancer Institute ("NKI") patient cohort (van de Vijver et al., *N. Engl. J. Med.* 347:1999-2009, 2002). As shown in Table 17, all five genes independently significantly associated with increased risk of recurrence in all three patient cohorts.

Table 17. Association of Five Genes with Recurrence Risk in Three Patient Cohorts

NKI			Providence			Rush		
Gene	**StdHR**	**StdHR.pv**	**Gene**	**StdHR**	**StdHR.pv**	**Gene**	**StdHR**	**StdHR.pv**
ENO1	1.411864	0.001155	**ENO1**	1.814954	0.001364	**ENO1**	1.404991	0.01904
G6PD	1.324279	0.005794	**G6PD**	1.544944	1.18E-06	**G6PD**	1.527692	0.000539

IDH2	1.291325	0.011292	**IDH2**	1.639955	1.35E-08	**IDH2**	1.382299	0.018213
PGK1	1.507714	1.24E-05	**PGK1**	1.69818	0.00737	**PGK1**	1.381217	0.038252
TMSB10	1.249215	0.032488	**TMSB10**	1.776591	0.004188	**TMSB10**	1.517113	0.00058

[00151] The expression cohesion of the five genes was compared with the cohesion of expression of the proliferation gene group (comprising Ki-67, STK15, SURV, CCNB1, MYBL2) and estrogen receptor gene group (comprising ER, PR, BCL2, SCUBE2) of the Onco*type* DX® Breast Cancer Assay. , The Pearson R value averages and ranges from the Providence cohort were as follows: five genes: R=0.56 (range 0.48-0.63); proliferation gene group: R=0.67 (range 0.62-0.70); estrogen receptor gene group: R=0.58 (range 0.55-0.62). Moreover, the five genes also co-expressed with the five proliferation genes with a Pearson correlation of R=0.44 (range 0.31-0.60). However, the cohesion of expression of each of the five genes with the five-gene cluster is higher than with the proliferation gene group. This analysis indicates that the five genes do belong to a co-expressed gene module that is approximately as cohesive as the previously defined proliferation and estrogen receptor co-expressed gene modules and that can justifiably be considered a distinct co-expressed gene module. This suggests that inclusion of one or more of the five genes (ENO1, G6PD, IDH2, PGK1, TMSB10) may provide additional prognostic information to the Onco*type* DX® Recurrence Score® result.

[00152] Because the five gene set described above included at least three genes involved in central metabolism, the results of Table 1 were analyzed to identify additional genes that belong to the glycolysis, the citric acid (TCA) cycle, and the pentose phosphate pathways and that associate with risk of breast cancer recurrence. Fourteen (14) genes were found to have a $p<0.005$: PGD; TKT; TALD01; G6PD; GPI; SLC1A5; SLC7A5; OGDH; SUCLG1; ENO1; PGK1; IDH2; ACO2; and FBP1. As shown in Table 1, all of these genes except for FBP1, was associated with increased likelihood of cancer recurrence. This latter result is consistent with the fact that the FBP1gene product is anabolic (catalyzes gluconeogenesis), whereas the others are catabolic (generate energy).

[00153] The 14 gene set and 5 gene set were subjected to a gene set analysis ("GSA") by the method of Efron and Tibshirani (*The Annals of Applied Statistics* 1:107-129, 2007), which assesses the significance of pre-defined gene sets, rather than individual genes.

The GSA scores for the 14 gene set and 5 gene set were evaluated in the Providence, Rush, and NKI cohorts, and compared to GSA scores of >800 canonical pathway ("CP") gene sets from the larger C2 ("curated gene sets") collection developed at the Broad Institute (*see* Molecular Signatures Database (MgSigDB) v3.0 on the Gene Set Enrichment Analysis website of the Broad (*see also* Subramanian et al. *PNAS* 102:15545-15550, 2005). The GSA scores, p values, and rank among all the gene sets are shown in Table 18.

Table 18.

	Providence			Rush			NKI		
GeneSet.Names	GSA.Scores	GSA.pvalue	Rank	GSA.Scores	GSA.pvalue	Rank	GSA.Scores	GSA.pvalue	Rank
GHI_5_GENES	3.194815511	0	1	2.875067912	0	1	1.602688891	0.035	10
GHI_14_GENES	2.642470237	0	2	1.345232468	0.025	4	0.988332268	0.035	49
REACTOME UNWINDING OF DNA	1.1	0.1	20	0.5	0.2	69	2.7	0	1
REACTOME-E2F-TRANSCRIPTIONAL TARGETS	1.0	0.06	21	0.7	0.05	27	1.8	0	2

[00154] As can be seen from Table 18, the 5 gene set and the 14 gene set both exhibited high GSA scores in all three patient cohorts, as indicated by their ranks among GSA scores for all >800 canonical gene sets. Also, the p values of the 5 gene and 14 gene metabolic gene modules were statistically significant across all three patient cohorts ($(p<0.05)$.

[00155] All references cited throughout the disclosure, including the examples, are hereby expressly incorporated by reference for their entire disclosure.

[00156] While the present invention has been described with reference to what is considered to be specific embodiments, it is to be understood that the invention is not so limited. To the contrary, the invention is intended to cover various modifications and equivalents included within the spirit and scope of the appended claims.

Table 1. List of Assembled RefSeq RNAs Associated with Risk of Breast Cancer Recurrence in 136 Breast Cancer Patients

Gene	Accession No.	Direction of Association (1=Higher Expression Means Higher Risk)	p-value	Standardized Hazard Ratio Estimate (95% Confidence Interval)	q-value (FDR)	Maximum Lower Bound Std HR @ 10% FDR	Regression-to-the-Mean-Corrected Std HR
KIF1B	NM_183416	1	5.88E-10	2.43 (1.84, 3.23)	<0.1%	1.29	1.66
KIF1B	NM_015074	1	5.88E-10	2.43 (1.84, 3.23)	<0.1%	1.29	1.66
ZFP3	NM_153018	-1	3.99E-09	0.36 (0.26, 0.51)	<0.1%	1.29	1.62
FAM21C	NM_015262	-1	1.20E-10	0.51 (0.41, 0.62)	<0.1%	1.25	1.62
FAM21C	NM_001169107	-1	1.20E-10	0.51 (0.41, 0.62)	<0.1%	1.25	1.62
FAM21C	NM_001169106	-1	1.20E-10	0.51 (0.41, 0.62)	<0.1%	1.25	1.62
FLJ14186	NR_037596	-1	4.41E-09	0.44 (0.33, 0.58)	<0.1%	1.25	1.61
DAP	NM_004394	1	1.43E-08	2.27 (1.71, 3.02)	<0.1%	1.24	1.59
P2RX4	NM_002560	-1	2.29E-09	0.49 (0.39, 0.62)	<0.1%	1.24	1.6
GGCT	NR_037669	1	7.24E-11	1.68 (1.43, 1.96)	<0.1%	1.21	1.52
GGCT	NM_001199815	1	7.24E-11	1.68 (1.43, 1.96)	<0.1%	1.21	1.52
GGCT	NM_001199817	1	7.24E-11	1.68 (1.43, 1.96)	<0.1%	1.21	1.52
GGCT	NM_001199816	1	7.24E-11	1.68 (1.43, 1.96)	<0.1%	1.21	1.52
GGCT	NM_024051	1	7.24E-11	1.68 (1.43, 1.96)	<0.1%	1.21	1.52
TMEM91	NM_001098823	-1	2.68E-08	0.48 (0.37, 0.62)	<0.1%	1.21	1.56
TMEM91	NM_001042595	-1	2.68E-08	0.48 (0.37, 0.62)	<0.1%	1.21	1.56
TMEM91	NM_001098821	-1	2.68E-08	0.48 (0.37, 0.62)	<0.1%	1.21	1.56
TMEM91	NM_001098822	-1	2.68E-08	0.48 (0.37, 0.62)	<0.1%	1.21	1.56
TMEM91	NM_001098825	-1	2.68E-08	0.48 (0.37, 0.62)	<0.1%	1.21	1.56
TMEM91	NM_001098824	-1	2.68E-08	0.48 (0.37, 0.62)	<0.1%	1.21	1.56
ANKRD27	NM_032139	1	2.87E-10	1.69 (1.43, 1.99)	<0.1%	1.2	1.52
CDK20	NM_001170639	-1	1.33E-09	0.60 (0.50, 0.70)	<0.1%	1.19	1.5
CDK20	NM_178432	-1	1.33E-09	0.60 (0.50, 0.70)	<0.1%	1.19	1.5
CDK20	NM_001170640	-1	1.33E-09	0.60 (0.50, 0.70)	<0.1%	1.19	1.5
CDK20	NM_001039803	-1	1.33E-09	0.60 (0.50, 0.70)	<0.1%	1.19	1.5
CDK20	NM_012119	-1	1.33E-09	0.60 (0.50, 0.70)	<0.1%	1.19	1.5
GKAP1	NM_001135953	-1	2.68E-08	0.55 (0.45, 0.68)	<0.1%	1.19	1.52
GKAP1	NM_025211	-1	2.68E-08	0.55 (0.45, 0.68)	<0.1%	1.19	1.52
NAA35	NM_024635	-1	6.53E-07	0.43 (0.30, 0.60)	<0.1%	1.19	1.5
OMD	NM_005014	-1	4.64E-07	0.41 (0.29, 0.58)	<0.1%	1.19	1.51
OR10H3	NM_013938	1	5.26E-09	1.78 (1.47, 2.16)	<0.1%	1.19	1.53
TSPAN17	NM_012171	1	5.21E-08	1.88 (1.50, 2.37)	<0.1%	1.19	1.53
TSPAN17	NM_130465	1	5.21E-08	1.88 (1.50, 2.37)	<0.1%	1.19	1.53
TSPAN17	NM_001006616	1	5.21E-08	1.88 (1.50, 2.37)	<0.1%	1.19	1.53
IDH2	NM_002168	1	1.34E-08	1.64 (1.38, 1.95)	<0.1%	1.17	1.47
KCNV1	NM_014379	1	3.04E-08	1.74 (1.43, 2.12)	<0.1%	1.17	1.5
SPTAN1	NM_003127	-1	6.87E-07	0.47 (0.34, 0.63)	<0.1%	1.17	1.5
SPTAN1	NM_001130438	-1	6.87E-07	0.47 (0.34, 0.63)	<0.1%	1.17	1.5
SPTAN1	NM_001195532	-1	6.87E-07	0.47 (0.34, 0.63)	<0.1%	1.17	1.5
CANX	NM_001746	1	1.14E-06	2.08 (1.55, 2.80)	<0.1%	1.16	1.49
CANX	NM_001024649	1	1.14E-06	2.08 (1.55, 2.80)	<0.1%	1.16	1.49

CENPP	NM_001012267	-1	1.82E-07	0.55 (0.44, 0.69)	<0.1%	1.16	1.49
CYB5D2	NR_023346	-1	4.13E-07	0.55 (0.44, 0.69)	<0.1%	1.16	1.48
CYB5D2	NR_023347	-1	4.13E-07	0.55 (0.44, 0.69)	<0.1%	1.16	1.48
CYB5D2	NM_144611	-1	4.13E-07	0.55 (0.44, 0.69)	<0.1%	1.16	1.48
MMP15	NM_002428	1	3.19E-06	2.46 (1.68, 3.59)	0.10%	1.16	1.46
RANBP10	NM_020850	1	1.79E-07	1.84 (1.46, 2.31)	<0.1%	1.16	1.5
RTN1	NM_021136	-1	1.15E-06	0.47 (0.35, 0.64)	<0.1%	1.16	1.49
RTN1	NM_206852	-1	1.15E-06	0.47 (0.35, 0.64)	<0.1%	1.16	1.49
RTN1	NM_206857	-1	1.15E-06	0.47 (0.35, 0.64)	<0.1%	1.16	1.49
STK32B	NM_018401	-1	9.39E-07	0.49 (0.37, 0.65)	<0.1%	1.16	1.49
TKT	NM_001135055	1	7.52E-07	1.94 (1.49, 2.53)	<0.1%	1.16	1.49
TKT	NM_001064	1	7.52E-07	1.94 (1.49, 2.53)	<0.1%	1.16	1.49
TRABD	NM_025204	1	5.97E-09	1.53 (1.32, 1.76)	<0.1%	1.16	1.43
UBXN11	NM_183008	-1	9.88E-09	0.64 (0.55, 0.74)	<0.1%	1.16	1.44
UBXN11	NM_145345	-1	9.88E-09	0.64 (0.55, 0.74)	<0.1%	1.16	1.44
UBXN11	NM_001077262	-1	9.88E-09	0.64 (0.55, 0.74)	<0.1%	1.16	1.44
ULBP3	NM_024518	1	1.34E-06	2.02 (1.52, 2.69)	<0.1%	1.16	1.49
ADAMTS16	NM_139056	-1	2.10E-06	0.54 (0.42, 0.70)	0.10%	1.15	1.46
ARMCX1	NM_016608	-1	8.63E-09	0.67 (0.59, 0.77)	<0.1%	1.15	1.4
CCDC68	NM_001143829	-1	4.63E-06	0.44 (0.31, 0.63)	0.10%	1.15	1.46
CCDC68	NM_025214	-1	4.63E-06	0.44 (0.31, 0.63)	0.10%	1.15	1.46
CDC25B	NM_004358	1	6.27E-06	2.10 (1.52, 2.91)	0.10%	1.15	1.45
CDC25B	NM_021873	1	6.27E-06	2.10 (1.52, 2.91)	0.10%	1.15	1.45
CDC25B	NM_021872	1	6.27E-06	2.10 (1.52, 2.91)	0.10%	1.15	1.45
GAN	NM_022041	1	4.35E-06	2.18 (1.56, 3.04)	0.10%	1.15	1.46
GLIS2	NM_032575	-1	3.86E-07	0.57 (0.46, 0.71)	<0.1%	1.15	1.47
GPR126	NM_198569	1	5.93E-06	2.14 (1.54, 2.98)	0.10%	1.15	1.45
GPR126	NM_020455	1	5.93E-06	2.14 (1.54, 2.98)	0.10%	1.15	1.45
GPR126	NM_001032395	1	5.93E-06	2.14 (1.54, 2.98)	0.10%	1.15	1.45
GPR126	NM_001032394	1	5.93E-06	2.14 (1.54, 2.98)	0.10%	1.15	1.45
INTU	NM_015693	-1	4.31E-07	0.57 (0.46, 0.71)	<0.1%	1.15	1.47
LIPT1	NM_145197	-1	1.50E-08	0.66 (0.57, 0.76)	<0.1%	1.15	1.42
LIPT1	NM_145196	-1	1.50E-08	0.66 (0.57, 0.76)	<0.1%	1.15	1.42
LIPT1	NM_015929	-1	1.50E-08	0.66 (0.57, 0.76)	<0.1%	1.15	1.42
LIPT1	NM_145198	-1	1.50E-08	0.66 (0.57, 0.76)	<0.1%	1.15	1.42
LIPT1	NM_145199	-1	1.50E-08	0.66 (0.57, 0.76)	<0.1%	1.15	1.42
MEGF9	NM_001080497	-1	5.50E-06	0.48 (0.35, 0.66)	0.10%	1.15	1.45
OR7E24	NM_001079935	1	1.56E-08	1.50 (1.30, 1.72)	<0.1%	1.15	1.41
PHOSPHO2	NM_001008489	-1	1.27E-07	0.63 (0.54, 0.75)	<0.1%	1.15	1.43
PHOSPHO2	NM_001199287	-1	1.27E-07	0.63 (0.54, 0.75)	<0.1%	1.15	1.43
PHOSPHO2	NM_001199288	-1	1.27E-07	0.63 (0.54, 0.75)	<0.1%	1.15	1.43
PHOSPHO2	NM_001199285	-1	1.27E-07	0.63 (0.54, 0.75)	<0.1%	1.15	1.43
PHOSPHO2	NM_001199286	-1	1.27E-07	0.63 (0.54, 0.75)	<0.1%	1.15	1.43
TEX2	NM_018469	1	1.34E-07	1.68 (1.38, 2.03)	<0.1%	1.15	1.47
TXNDC16	NM_020784	-1	2.75E-08	0.66 (0.57, 0.77)	<0.1%	1.15	1.41
TXNDC16	NM_001160047	-1	2.75E-08	0.66 (0.57, 0.77)	<0.1%	1.15	1.41
ZNF141	NM_003441	-1	3.45E-08	0.63 (0.54, 0.74)	<0.1%	1.15	1.44
ZNF239	NM_001099282	-1	9.30E-08	0.63 (0.53, 0.74)	<0.1%	1.15	1.44
ZNF239	NM_005674	-1	9.30E-08	0.63 (0.53, 0.74)	<0.1%	1.15	1.44

ZNF239	NM_001099284	-1	9.30E-08	0.63 (0.53, 0.74)	<0.1%	1.15	1.44
ZNF239	NM_001099283	-1	9.30E-08	0.63 (0.53, 0.74)	<0.1%	1.15	1.44
ZNF429	NM_001001415	-1	5.67E-09	0.67 (0.58, 0.77)	<0.1%	1.15	1.41
ACP1	NM_004300	1	3.01E-06	1.80 (1.41, 2.31)	0.10%	1.14	1.45
ACP1	NM_007099	1	3.01E-06	1.80 (1.41, 2.31)	0.10%	1.14	1.45
ACP1	NR_024080	1	3.01E-06	1.80 (1.41, 2.31)	0.10%	1.14	1.45
ACP1	NM_001040649	1	3.01E-06	1.80 (1.41, 2.31)	0.10%	1.14	1.45
C17orf96	NM_001130677	1	1.84E-06	1.69 (1.36, 2.10)	<0.1%	1.14	1.44
C7orf30	NM_138446	1	6.82E-06	2.08 (1.51, 2.86)	0.10%	1.14	1.45
CCDC40	NM_017950	-1	8.80E-06	0.50 (0.37, 0.68)	0.10%	1.14	1.44
CENPN	NM_001100625	1	1.37E-05	2.27 (1.57, 3.29)	0.20%	1.14	1.43
CENPN	NM_018455	1	1.37E-05	2.27 (1.57, 3.29)	0.20%	1.14	1.43
CENPN	NM_001100624	1	1.37E-05	2.27 (1.57, 3.29)	0.20%	1.14	1.43
CLINT1	NM_014666	1	6.00E-06	1.98 (1.47, 2.66)	0.10%	1.14	1.45
CLINT1	NM_001195556	1	6.00E-06	1.98 (1.47, 2.66)	0.10%	1.14	1.45
CLINT1	NM_001195555	1	6.00E-06	1.98 (1.47, 2.66)	0.10%	1.14	1.45
FAM131C	NM_182623	1	3.59E-06	1.87 (1.43, 2.43)	0.10%	1.14	1.46
FZD9	NM_003508	1	4.24E-07	1.60 (1.33, 1.92)	<0.1%	1.14	1.43
GPRIN1	NM_052899	1	1.21E-05	2.27 (1.57, 3.27)	0.20%	1.14	1.43
HMGCS1	NM_002130	1	2.74E-07	1.59 (1.33, 1.89)	<0.1%	1.14	1.43
HMGCS1	NM_001098272	1	2.74E-07	1.59 (1.33, 1.89)	<0.1%	1.14	1.43
KIF20A	NM_005733	1	3.69E-05	2.62 (1.66, 4.14)	0.40%	1.14	1.38
KRT83	NM_002282	1	6.89E-07	1.66 (1.36, 2.04)	<0.1%	1.14	1.45
MEX3B	NM_032246	1	1.37E-05	2.25 (1.56, 3.25)	0.20%	1.14	1.43
NUDT19	NM_001105570	1	7.72E-06	2.03 (1.49, 2.77)	0.10%	1.14	1.45
RNF145	NM_001199383	1	6.56E-06	1.96 (1.46, 2.62)	0.10%	1.14	1.45
RNF145	NM_001199382	1	6.56E-06	1.96 (1.46, 2.62)	0.10%	1.14	1.45
RNF145	NM_144726	1	6.56E-06	1.96 (1.46, 2.62)	0.10%	1.14	1.45
RNF145	NM_001199381	1	6.56E-06	1.96 (1.46, 2.62)	0.10%	1.14	1.45
RNF145	NM_001199380	1	6.56E-06	1.96 (1.46, 2.62)	0.10%	1.14	1.45
RPS23	NM_001025	-1	2.24E-06	0.56 (0.44, 0.71)	0.10%	1.14	1.45
SDAD1	NM_018115	1	2.98E-07	1.54 (1.31, 1.82)	<0.1%	1.14	1.41
SNAR-G1	NR_004383	1	8.18E-07	1.59 (1.32, 1.92)	<0.1%	1.14	1.42
TBX4	NM_018488	1	1.12E-06	1.68 (1.36, 2.06)	<0.1%	1.14	1.44
ULK4	NM_017886	-1	1.18E-05	0.48 (0.34, 0.66)	0.20%	1.14	1.43
USO1	NM_003715	1	1.01E-07	1.51 (1.30, 1.76)	<0.1%	1.14	1.4
ZNF214	NM_013249	-1	9.49E-06	0.51 (0.38, 0.68)	0.10%	1.14	1.44
ZNF540	NM_152606	-1	4.66E-07	0.64 (0.54, 0.76)	<0.1%	1.14	1.41
ZNF540	NM_001172225	-1	4.66E-07	0.64 (0.54, 0.76)	<0.1%	1.14	1.41
ZNF540	NM_001172226	-1	4.66E-07	0.64 (0.54, 0.76)	<0.1%	1.14	1.41
ZNF823	NM_001080493	-1	1.72E-08	0.70 (0.62, 0.79)	<0.1%	1.14	1.37
ADC	NM_052998	-1	4.67E-07	0.67 (0.57, 0.78)	<0.1%	1.13	1.38
ADHFE1	NM_144650	-1	1.40E-05	0.53 (0.40, 0.71)	0.20%	1.13	1.42
C3orf15	NM_033364	-1	1.71E-05	0.47 (0.34, 0.67)	0.20%	1.13	1.42
CYB5B	NM_030579	1	4.23E-05	2.44 (1.59, 3.73)	0.40%	1.13	1.39
DCDC5	NM_020869	-1	3.07E-05	0.45 (0.31, 0.65)	0.30%	1.13	1.4
DNAH6	NM_001370	-1	6.69E-06	0.58 (0.46, 0.73)	0.10%	1.13	1.42
ECM2	NM_001393	-1	2.26E-05	0.45 (0.31, 0.65)	0.30%	1.13	1.41
ECM2	NM_001197295	-1	2.26E-05	0.45 (0.31, 0.65)	0.30%	1.13	1.41

ECM2	NM_001197296	-1	2.26E-05	0.45 (0.31, 0.65)	0.30%	1.13	1.41
G6PD	NM_000402	1	1.18E-06	1.54 (1.30, 1.84)	<0.1%	1.13	1.4
G6PD	NM_001042351	1	1.18E-06	1.54 (1.30, 1.84)	<0.1%	1.13	1.4
GRHL2	NM_024915	1	2.62E-05	2.07 (1.47, 2.91)	0.30%	1.13	1.42
GTSE1	NM_016426	1	3.48E-05	2.45 (1.60, 3.75)	0.40%	1.13	1.39
HTR7P1	NR_002774	-1	1.10E-05	0.52 (0.39, 0.69)	0.20%	1.13	1.43
LOC100133308	NR_024472	1	1.27E-06	1.54 (1.30, 1.84)	<0.1%	1.13	1.4
LOC400657	NR_024484	-1	1.20E-08	0.72 (0.64, 0.80)	<0.1%	1.13	1.34
MAGEA10	NM_021048	1	1.09E-06	1.54 (1.30, 1.83)	<0.1%	1.13	1.4
MAGEA10	NM_001011543	1	1.09E-06	1.54 (1.30, 1.83)	<0.1%	1.13	1.4
MPP6	NM_016447	1	1.45E-05	2.05 (1.48, 2.83)	0.20%	1.13	1.43
RAB28	NM_001017979	-1	4.43E-10	0.74 (0.68, 0.82)	<0.1%	1.13	1.31
RAB28	NM_001159601	-1	4.43E-10	0.74 (0.68, 0.82)	<0.1%	1.13	1.31
RAB28	NM_004249	-1	4.43E-10	0.74 (0.68, 0.82)	<0.1%	1.13	1.31
SMURF2	NM_022739	1	3.92E-06	1.76 (1.38, 2.23)	0.10%	1.13	1.44
TXNRD1	NM_182742	1	2.99E-05	2.13 (1.49, 3.03)	0.30%	1.13	1.41
TXNRD1	NM_003330	1	2.99E-05	2.13 (1.49, 3.03)	0.30%	1.13	1.41
TXNRD1	NM_001093771	1	2.99E-05	2.13 (1.49, 3.03)	0.30%	1.13	1.41
TXNRD1	NM_182743	1	2.99E-05	2.13 (1.49, 3.03)	0.30%	1.13	1.41
TXNRD1	NM_182729	1	2.99E-05	2.13 (1.49, 3.03)	0.30%	1.13	1.41
ZNF44	NM_016264	-1	2.33E-05	0.48 (0.34, 0.67)	0.30%	1.13	1.41
ZNF44	NM_001164276	-1	2.33E-05	0.48 (0.34, 0.67)	0.30%	1.13	1.41
BBS5	NM_152384	-1	8.81E-06	0.60 (0.47, 0.75)	0.10%	1.12	1.41
C14orf45	NM_025057	-1	3.59E-05	0.49 (0.35, 0.69)	0.40%	1.12	1.4
CAMTA2	NM_001171166	-1	2.25E-05	0.53 (0.39, 0.71)	0.30%	1.12	1.41
CAMTA2	NM_001171168	-1	2.25E-05	0.53 (0.39, 0.71)	0.30%	1.12	1.41
CAMTA2	NM_001171167	-1	2.25E-05	0.53 (0.39, 0.71)	0.30%	1.12	1.41
CAMTA2	NM_015099	-1	2.25E-05	0.53 (0.39, 0.71)	0.30%	1.12	1.41
CRYZ	NM_001130042	-1	3.86E-08	0.73 (0.65, 0.81)	<0.1%	1.12	1.33
CRYZ	NM_001130043	-1	3.86E-08	0.73 (0.65, 0.81)	<0.1%	1.12	1.33
CRYZ	NM_001889	-1	3.86E-08	0.73 (0.65, 0.81)	<0.1%	1.12	1.33
CRYZ	NM_001134759	-1	3.86E-08	0.73 (0.65, 0.81)	<0.1%	1.12	1.33
FDX1	NM_004109	-1	3.82E-06	0.63 (0.52, 0.77)	0.10%	1.12	1.4
G3BP2	NM_203504	1	2.29E-06	1.54 (1.29, 1.83)	0.10%	1.12	1.39
G3BP2	NM_203505	1	2.29E-06	1.54 (1.29, 1.83)	0.10%	1.12	1.39
G3BP2	NM_012297	1	2.29E-06	1.54 (1.29, 1.83)	0.10%	1.12	1.39
GARS	NM_002047	1	6.42E-06	1.67 (1.34, 2.09)	0.10%	1.12	1.42
HYDIN	NM_032821	-1	1.37E-05	0.54 (0.41, 0.71)	0.20%	1.12	1.42
HYDIN	NM_017558	-1	1.37E-05	0.54 (0.41, 0.71)	0.20%	1.12	1.42
HYDIN	NM_001198542	-1	1.37E-05	0.54 (0.41, 0.71)	0.20%	1.12	1.42
HYDIN	NM_001198543	-1	1.37E-05	0.54 (0.41, 0.71)	0.20%	1.12	1.42
IFT74	NM_001099222	-1	1.72E-05	0.55 (0.42, 0.72)	0.20%	1.12	1.42
IFT74	NM_025103	-1	1.72E-05	0.55 (0.42, 0.72)	0.20%	1.12	1.42
IFT74	NM_001099224	-1	1.72E-05	0.55 (0.42, 0.72)	0.20%	1.12	1.42
IFT74	NM_001099223	-1	1.72E-05	0.55 (0.42, 0.72)	0.20%	1.12	1.42
KCNJ4	NM_152868	1	3.50E-06	1.59 (1.31, 1.93)	0.10%	1.12	1.4
KCNJ4	NM_004981	1	3.50E-06	1.59 (1.31, 1.93)	0.10%	1.12	1.4
MAPK6	NM_002748	1	3.70E-08	1.37 (1.22, 1.53)	<0.1%	1.12	1.32
MYOF	NM_133337	-1	8.78E-06	0.60 (0.48, 0.75)	0.10%	1.12	1.41

MYOF	NM_013451	-1	8.78E-06	0.60 (0.48, 0.75)	0.10%	1.12	1.41
SH3GLB2	NM_020145	-1	1.89E-05	0.52 (0.39, 0.70)	0.20%	1.12	1.42
TRIM45	NM_001145635	-1	2.13E-05	0.54 (0.40, 0.71)	0.30%	1.12	1.41
TRIM45	NM_025188	-1	2.13E-05	0.54 (0.40, 0.71)	0.30%	1.12	1.41
VDAC1	NM_003374	1	7.01E-05	2.45 (1.57, 3.80)	0.60%	1.12	1.37
VDAC1	NR_036625	1	7.01E-05	2.45 (1.57, 3.80)	0.60%	1.12	1.37
VDAC1	NR_036624	1	7.01E-05	2.45 (1.57, 3.80)	0.60%	1.12	1.37
BCL2	NM_000657	-1	3.28E-05	0.54 (0.40, 0.72)	0.30%	1.11	1.4
BCL2	NM_000633	-1	3.28E-05	0.54 (0.40, 0.72)	0.30%	1.11	1.4
C9orf3	NM_001193329	-1	1.59E-05	0.60 (0.48, 0.76)	0.20%	1.11	1.4
C9orf3	NM_001193331	-1	1.59E-05	0.60 (0.48, 0.76)	0.20%	1.11	1.4
C9orf3	NM_032823	-1	1.59E-05	0.60 (0.48, 0.76)	0.20%	1.11	1.4
CEP72	NM_018140	1	9.55E-05	2.27 (1.50, 3.43)	0.70%	1.11	1.37
DNALI1	NM_003462	-1	9.88E-06	0.63 (0.51, 0.77)	0.10%	1.11	1.39
ECEL1	NM_004826	1	7.48E-06	1.54 (1.28, 1.86)	0.10%	1.11	1.38
FAM179B	NM_015091	-1	6.45E-05	0.45 (0.31, 0.67)	0.50%	1.11	1.38
HEATR2	NM_017802	1	2.70E-05	1.83 (1.38, 2.43)	0.30%	1.11	1.41
IRAK4	NM_001145256	-1	0.000036189	0.51 (0.37, 0.70)	0.40%	1.11	1.4
IRAK4	NM_001114182	-1	0.000036189	0.51 (0.37, 0.70)	0.40%	1.11	1.4
IRAK4	NM_001145258	-1	0.000036189	0.51 (0.37, 0.70)	0.40%	1.11	1.4
IRAK4	NM_001145257	-1	0.000036189	0.51 (0.37, 0.70)	0.40%	1.11	1.4
IRAK4	NM_016123	-1	0.000036189	0.51 (0.37, 0.70)	0.40%	1.11	1.4
LOC147804	NR_003148	-1	5.76E-05	0.51 (0.36, 0.71)	0.50%	1.11	1.39
LOC645323	NR_015436	1	0.000032725	1.83 (1.38, 2.43)	0.30%	1.11	1.41
LOC645323	NR_024384	1	0.000032725	1.83 (1.38, 2.43)	0.30%	1.11	1.41
LOC645323	NR_024383	1	0.000032725	1.83 (1.38, 2.43)	0.30%	1.11	1.41
LRGUK	NM_144648	-1	5.37E-05	0.51 (0.37, 0.71)	0.50%	1.11	1.39
LRRC46	NM_033413	-1	3.76E-05	0.51 (0.37, 0.70)	0.40%	1.11	1.4
NOL8	NM_017948	-1	4.65E-05	0.53 (0.39, 0.72)	0.40%	1.11	1.4
NOL8	NR_024020	-1	4.65E-05	0.53 (0.39, 0.72)	0.40%	1.11	1.4
OR2J2	NM_030905	1	4.20E-06	1.53 (1.28, 1.84)	0.10%	1.11	1.38
PERP	NM_022121	1	2.52E-05	1.73 (1.34, 2.23)	0.30%	1.11	1.4
PHB	NM_002634	1	1.15E-05	1.63 (1.31, 2.03)	0.20%	1.11	1.4
SCRN3	NM_024583	-1	8.57E-06	0.62 (0.50, 0.76)	0.10%	1.11	1.4
SCRN3	NM_001193528	-1	8.57E-06	0.62 (0.50, 0.76)	0.10%	1.11	1.4
SLC35D2	NM_007001	-1	4.26E-05	0.53 (0.39, 0.72)	0.40%	1.11	1.4
SMARCD2	NM_001098426	1	6.36E-06	1.60 (1.30, 1.96)	0.10%	1.11	1.4
SPIN1	NM_006717	-1	0.000050879	0.47 (0.32, 0.67)	0.50%	1.11	1.39
STARD3NL	NM_032016	1	3.16E-05	1.91 (1.41, 2.59)	0.30%	1.11	1.41
TUBB1	NM_030773	-1	1.63E-05	0.60 (0.48, 0.76)	0.20%	1.11	1.4
ZNF211	NM_198855	-1	2.09E-05	0.60 (0.47, 0.76)	0.20%	1.11	1.4
ZNF211	NM_006385	-1	2.09E-05	0.60 (0.47, 0.76)	0.20%	1.11	1.4
ZNF227	NM_182490	-1	0.000077689	0.47 (0.32, 0.68)	0.60%	1.11	1.38
ZNF626	NM_145297	-1	1.76E-05	0.58 (0.46, 0.75)	0.20%	1.11	1.41
ZNF626	NM_001076675	-1	1.76E-05	0.58 (0.46, 0.75)	0.20%	1.11	1.41
ACAP2	NM_012287	1	5.36E-05	1.81 (1.36, 2.41)	0.50%	1.1	1.39
COL9A1	NM_078485	1	2.06E-07	1.32 (1.19, 1.47)	<0.1%	1.1	1.29
COL9A1	NM_001851	1	2.06E-07	1.32 (1.19, 1.47)	<0.1%	1.1	1.29
IQCD	NM_138451	-1	6.49E-05	0.51 (0.37, 0.71)	0.50%	1.1	1.39

LOC100131726	NR_024479	1	6.29E-05	1.98 (1.42, 2.76)	0.50%	1.1	1.39
LOC401242	NR_033379	1	5.07E-06	1.44 (1.23, 1.68)	0.10%	1.1	1.34
MTHFSD	NR_027490	1	7.01E-05	1.87 (1.37, 2.54)	0.60%	1.1	1.39
MTHFSD	NR_027489	1	7.01E-05	1.87 (1.37, 2.54)	0.60%	1.1	1.39
MTHFSD	NM_022764	1	7.01E-05	1.87 (1.37, 2.54)	0.60%	1.1	1.39
MTHFSD	NM_001159379	1	7.01E-05	1.87 (1.37, 2.54)	0.60%	1.1	1.39
MTHFSD	NM_001159378	1	7.01E-05	1.87 (1.37, 2.54)	0.60%	1.1	1.39
MTHFSD	NM_001159377	1	7.01E-05	1.87 (1.37, 2.54)	0.60%	1.1	1.39
MTHFSD	NM_001159380	1	7.01E-05	1.87 (1.37, 2.54)	0.60%	1.1	1.39
NCRNA00200	NR_015376	1	1.02E-06	1.37 (1.21, 1.55)	<0.1%	1.1	1.31
NMNAT3	NM_178177	-1	6.81E-05	0.52 (0.38, 0.72)	0.60%	1.1	1.39
RAI2	NM_021785	-1	6.18E-05	0.52 (0.37, 0.71)	0.50%	1.1	1.39
RAI2	NR_033348	-1	6.18E-05	0.52 (0.37, 0.71)	0.50%	1.1	1.39
RAI2	NR_033349	-1	6.18E-05	0.52 (0.37, 0.71)	0.50%	1.1	1.39
RAI2	NM_001172732	-1	6.18E-05	0.52 (0.37, 0.71)	0.50%	1.1	1.39
RAI2	NM_001172739	-1	6.18E-05	0.52 (0.37, 0.71)	0.50%	1.1	1.39
RAI2	NM_001172743	-1	6.18E-05	0.52 (0.37, 0.71)	0.50%	1.1	1.39
RCHY1	NM_001009922	1	5.97E-06	1.45 (1.23, 1.70)	0.10%	1.1	1.35
RCHY1	NM_015436	1	5.97E-06	1.45 (1.23, 1.70)	0.10%	1.1	1.35
RCHY1	NM_001008925	1	5.97E-06	1.45 (1.23, 1.70)	0.10%	1.1	1.35
SI	NM_001041	1	1.46E-08	1.27 (1.17, 1.38)	<0.1%	1.1	1.25
SNORD18B	NR_002442	1	1.73E-05	1.55 (1.27, 1.90)	0.20%	1.1	1.38
TMOD3	NM_014547	1	3.74E-07	1.32 (1.19, 1.47)	<0.1%	1.1	1.29
UGT2B7	NM_001074	1	8.45E-06	1.49 (1.25, 1.77)	0.10%	1.1	1.36
ZNF433	NM_001080411	-1	5.49E-05	0.53 (0.39, 0.72)	0.50%	1.1	1.39
AACSP1	NR_024035	1	1.38E-05	1.46 (1.23, 1.73)	0.20%	1.09	1.35
AKD1	NM_001145128	-1	1.23E-05	0.70 (0.60, 0.82)	0.20%	1.09	1.33
AKD1	NM_145025	-1	1.23E-05	0.70 (0.60, 0.82)	0.20%	1.09	1.33
ANKFN1	NM_153228	1	0.000106619	1.73 (1.31, 2.28)	0.80%	1.09	1.37
ANKRD54	NR_036556	1	0.000155771	1.98 (1.39, 2.82)	1.00%	1.09	1.37
ANKRD54	NM_138797	1	0.000155771	1.98 (1.39, 2.82)	1.00%	1.09	1.37
ASB13	NM_024701	-1	4.43E-06	0.72 (0.62, 0.83)	0.10%	1.09	1.32
ASB13	NR_037164	-1	4.43E-06	0.72 (0.62, 0.83)	0.10%	1.09	1.32
ASB13	NR_024581	-1	4.43E-06	0.72 (0.62, 0.83)	0.10%	1.09	1.32
C17orf64	NM_181707	1	4.20E-06	1.38 (1.20, 1.58)	0.10%	1.09	1.31
C17orf68	NM_025099	-1	0.000123317	0.52 (0.38, 0.73)	0.90%	1.09	1.37
C5	NM_001735	-1	0.00013293	0.55 (0.40, 0.75)	0.90%	1.09	1.37
C7orf72	NM_001161834	1	4.05E-07	1.30 (1.17, 1.43)	<0.1%	1.09	1.27
CASC1	NM_018272	-1	8.53E-05	0.58 (0.44, 0.76)	0.70%	1.09	1.38
CASC1	NM_001082972	-1	8.53E-05	0.58 (0.44, 0.76)	0.70%	1.09	1.38
CASC1	NM_001082973	-1	8.53E-05	0.58 (0.44, 0.76)	0.70%	1.09	1.38
CCDC47	NM_020198	1	2.73E-05	1.57 (1.27, 1.94)	0.30%	1.09	1.37
CCDC66	NM_001141947	-1	9.67E-05	0.54 (0.40, 0.74)	0.70%	1.09	1.38
CCDC66	NR_024460	-1	9.67E-05	0.54 (0.40, 0.74)	0.70%	1.09	1.38
CCDC66	NM_001012506	-1	9.67E-05	0.54 (0.40, 0.74)	0.70%	1.09	1.38
CCNA2	NM_001237	1	0.000135444	2.06 (1.42, 3.00)	0.90%	1.09	1.37
COL20A1	NM_020882	1	1.40E-05	1.45 (1.23, 1.71)	0.20%	1.09	1.34
DDIT4	NM_019058	1	0.000150778	1.93 (1.37, 2.71)	1.00%	1.09	1.37
DSCR10	NR_027695	1	1.43E-05	1.44 (1.22, 1.70)	0.20%	1.09	1.34

EIF3B	NM_003751	1	0.000111832	1.82 (1.34, 2.48)	0.80%	1.09	1.38
EIF3B	NM_001037283	1	0.000111832	1.82 (1.34, 2.48)	0.80%	1.09	1.38
EIF4G2	NM_001418	1	5.03E-05	1.66 (1.30, 2.12)	0.50%	1.09	1.38
EIF4G2	NM_001172705	1	5.03E-05	1.66 (1.30, 2.12)	0.50%	1.09	1.38
EIF4G2	NM_001042559	1	5.03E-05	1.66 (1.30, 2.12)	0.50%	1.09	1.38
EPS15L1	NM_021235	-1	8.57E-05	0.53 (0.38, 0.72)	0.70%	1.09	1.38
FAM18A	NM_001079512	-1	0.000040247	0.61 (0.48, 0.77)	0.40%	1.09	1.38
FAM9C	NM_174901	1	1.14E-06	1.30 (1.17, 1.44)	<0.1%	1.09	1.27
FLJ45244	NR_015415	-1	0.000114635	0.55 (0.41, 0.75)	0.80%	1.09	1.37
FTMT	NM_177478	1	3.09E-05	1.50 (1.24, 1.81)	0.30%	1.09	1.35
GBX2	NM_001485	1	1.64E-05	1.44 (1.22, 1.70)	0.20%	1.09	1.33
GOLT1B	NM_016072	1	3.70E-05	1.57 (1.27, 1.94)	0.40%	1.09	1.37
GPR56	NM_001145774	1	0.000188458	2.06 (1.41, 3.02)	1.20%	1.09	1.36
GPR56	NM_201524	1	0.000188458	2.06 (1.41, 3.02)	1.20%	1.09	1.36
GPR56	NM_005682	1	0.000188458	2.06 (1.41, 3.02)	1.20%	1.09	1.36
GPR56	NM_001145771	1	0.000188458	2.06 (1.41, 3.02)	1.20%	1.09	1.36
GPR56	NM_001145770	1	0.000188458	2.06 (1.41, 3.02)	1.20%	1.09	1.36
GPR56	NM_001145773	1	0.000188458	2.06 (1.41, 3.02)	1.20%	1.09	1.36
GPR56	NM_001145772	1	0.000188458	2.06 (1.41, 3.02)	1.20%	1.09	1.36
GPR56	NM_201525	1	0.000188458	2.06 (1.41, 3.02)	1.20%	1.09	1.36
HEBP1	NM_015987	-1	0.000177204	0.50 (0.35, 0.72)	1.10%	1.09	1.36
HLA-DOA	NM_002119	-1	3.94E-05	0.60 (0.47, 0.77)	0.40%	1.09	1.38
HRASLS5	NM_054108	-1	0.000093912	0.54 (0.40, 0.74)	0.70%	1.09	1.38
HRASLS5	NM_001146728	-1	0.000093912	0.54 (0.40, 0.74)	0.70%	1.09	1.38
HRASLS5	NM_001146729	-1	0.000093912	0.54 (0.40, 0.74)	0.70%	1.09	1.38
JAK1	NM_002227	-1	0.000193139	0.46 (0.31, 0.69)	1.20%	1.09	1.35
KMO	NM_003679	1	0.000149756	2.05 (1.42, 2.98)	1.00%	1.09	1.37
KRT78	NM_173352	1	2.66E-05	1.48 (1.23, 1.78)	0.30%	1.09	1.35
LDLRAD3	NM_174902	-1	4.34E-05	0.64 (0.51, 0.79)	0.40%	1.09	1.36
MAP3K14	NM_003954	-1	9.19E-05	0.54 (0.40, 0.74)	0.70%	1.09	1.38
MIR196A1	NR_029582	1	2.40E-06	1.36 (1.19, 1.54)	0.10%	1.09	1.3
MIR4275	NR_036237	1	6.24E-06	1.43 (1.22, 1.66)	0.10%	1.09	1.34
NCRNA00221	NR_027457	1	5.62E-06	1.38 (1.20, 1.58)	0.10%	1.09	1.31
NGRN	NM_001033088	1	2.38E-05	1.47 (1.23, 1.76)	0.30%	1.09	1.34
NGRN	NR_028052	1	2.38E-05	1.47 (1.23, 1.76)	0.30%	1.09	1.34
NME1	NM_000269	1	7.11E-05	1.83 (1.36, 2.46)	0.60%	1.09	1.39
NME1	NM_198175	1	7.11E-05	1.83 (1.36, 2.46)	0.60%	1.09	1.39
NSUN2	NM_001193455	1	3.78E-05	1.61 (1.29, 2.03)	0.40%	1.09	1.38
NSUN2	NM_017755	1	3.78E-05	1.61 (1.29, 2.03)	0.40%	1.09	1.38
OR7G3	NM_001001958	1	6.32E-06	1.36 (1.19, 1.56)	0.10%	1.09	1.3
PIGA	NM_002641	1	0.000138341	2.13 (1.44, 3.14)	0.90%	1.09	1.36
PIGA	NM_020473	1	0.000138341	2.13 (1.44, 3.14)	0.90%	1.09	1.36
PIGA	NR_033835	1	0.000138341	2.13 (1.44, 3.14)	0.90%	1.09	1.36
PIGA	NR_033836	1	0.000138341	2.13 (1.44, 3.14)	0.90%	1.09	1.36
PRR11	NM_018304	1	0.000134896	2.14 (1.45, 3.16)	0.90%	1.09	1.36
PSMC5	NM_002805	1	3.01E-05	1.62 (1.29, 2.02)	0.30%	1.09	1.38
PSMC5	NM_001199163	1	3.01E-05	1.62 (1.29, 2.02)	0.30%	1.09	1.38
RDH10	NM_172037	1	0.000090299	1.81 (1.35, 2.44)	0.70%	1.09	1.38
RFWD3	NM_018124	1	0.000103613	1.85 (1.35, 2.51)	0.80%	1.09	1.38

RILPL2	NM_145058	-1	4.52E-05	0.61 (0.48, 0.77)	0.40%	1.09	1.38
ROBO1	NM_002941	1	6.22E-05	1.66 (1.29, 2.12)	0.50%	1.09	1.38
ROBO1	NM_001145845	1	6.22E-05	1.66 (1.29, 2.12)	0.50%	1.09	1.38
ROBO1	NM_133631	1	6.22E-05	1.66 (1.29, 2.12)	0.50%	1.09	1.38
SEPT3	NM_019106	1	0.000202646	2.23 (1.46, 3.41)	1.20%	1.09	1.35
SEPT3	NM_145733	1	0.000202646	2.23 (1.46, 3.41)	1.20%	1.09	1.35
SF3B3	NM_012426	1	8.05E-05	1.86 (1.37, 2.53)	0.60%	1.09	1.39
SKINTL	NR_026749	-1	0.000155637	0.47 (0.32, 0.70)	1.00%	1.09	1.36
SLC1A5	NM_001145145	1	0.000173422	2.23 (1.47, 3.38)	1.10%	1.09	1.35
SLC1A5	NM_005628	1	0.000173422	2.23 (1.47, 3.38)	1.10%	1.09	1.35
SLC1A5	NM_001145144	1	0.000173422	2.23 (1.47, 3.38)	1.10%	1.09	1.35
SUN1	NM_001171945	1	3.24E-05	1.56 (1.27, 1.93)	0.30%	1.09	1.37
SUN1	NM_001171946	1	3.24E-05	1.56 (1.27, 1.93)	0.30%	1.09	1.37
SUN1	NM_001171944	1	3.24E-05	1.56 (1.27, 1.93)	0.30%	1.09	1.37
SUN1	NM_025154	1	3.24E-05	1.56 (1.27, 1.93)	0.30%	1.09	1.37
SUN1	NM_001130965	1	3.24E-05	1.56 (1.27, 1.93)	0.30%	1.09	1.37
TCEA3	NM_003196	-1	1.33E-05	0.67 (0.56, 0.80)	0.20%	1.09	1.36
TIGD7	NM_033208	-1	7.22E-05	0.60 (0.46, 0.77)	0.60%	1.09	1.37
TMED3	NM_007364	1	0.000118078	1.84 (1.35, 2.50)	0.80%	1.09	1.38
UPK1A	NM_007000	1	3.33E-05	1.52 (1.25, 1.86)	0.30%	1.09	1.36
ZNF554	NM_001102651	-1	1.43E-05	0.67 (0.56, 0.80)	0.20%	1.09	1.36
ZZEF1	NM_015113	-1	0.000101352	0.51 (0.36, 0.71)	0.70%	1.09	1.38
ANKRD17	NM_198889	1	4.07E-05	1.48 (1.23, 1.79)	0.40%	1.08	1.34
ANKRD17	NM_032217	1	4.07E-05	1.48 (1.23, 1.79)	0.40%	1.08	1.34
C1orf168	NM_001004303	-1	0.000196331	0.52 (0.36, 0.73)	1.20%	1.08	1.36
CCDC103	NM_213607	-1	0.000156354	0.54 (0.39, 0.74)	1.00%	1.08	1.36
DBNDD1	NM_001042610	1	0.000265114	2.29 (1.47, 3.59)	1.40%	1.08	1.33
DBNDD1	NM_024043	1	0.000265114	2.29 (1.47, 3.59)	1.40%	1.08	1.33
EBF4	NM_001110514	-1	0.000177638	0.56 (0.42, 0.76)	1.10%	1.08	1.36
EVX1	NM_001989	1	4.40E-05	1.46 (1.22, 1.75)	0.40%	1.08	1.33
FAM120AOS	NM_198841	-1	0.000311715	0.48 (0.32, 0.71)	1.50%	1.08	1.33
FYTTD1	NM_032288	1	0.000093964	1.62 (1.27, 2.06)	0.70%	1.08	1.36
FYTTD1	NR_027840	1	0.000093964	1.62 (1.27, 2.06)	0.70%	1.08	1.36
FYTTD1	NM_001011537	1	0.000093964	1.62 (1.27, 2.06)	0.70%	1.08	1.36
GOLGA1	NM_002077	-1	0.000103896	0.62 (0.48, 0.79)	0.80%	1.08	1.36
GPI	NM_001184722	1	3.17E-05	1.46 (1.22, 1.75)	0.30%	1.08	1.34
GPI	NM_000175	1	3.17E-05	1.46 (1.22, 1.75)	0.30%	1.08	1.34
GPR157	NM_024980	1	0.000371571	2.47 (1.50, 4.07)	1.70%	1.08	1.31
GSTM3	NR_024537	-1	0.000174236	0.54 (0.39, 0.74)	1.10%	1.08	1.36
GSTM3	NM_000849	-1	0.000174236	0.54 (0.39, 0.74)	1.10%	1.08	1.36
GUK1	NM_000858	1	0.000160068	1.84 (1.34, 2.53)	1.00%	1.08	1.37
GUK1	NM_001159391	1	0.000160068	1.84 (1.34, 2.53)	1.00%	1.08	1.37
GUK1	NM_001159390	1	0.000160068	1.84 (1.34, 2.53)	1.00%	1.08	1.37
IGF2BP2	NM_001007225	1	0.000223003	1.98 (1.38, 2.85)	1.30%	1.08	1.36
IGF2BP2	NM_006548	1	0.000223003	1.98 (1.38, 2.85)	1.30%	1.08	1.36
KDM4B	NM_015015	-1	0.000289488	0.49 (0.33, 0.72)	1.50%	1.08	1.34
KIAA0226	NM_014687	1	0.00010158	1.66 (1.29, 2.15)	0.70%	1.08	1.37
KIAA0226	NM_001145642	1	0.00010158	1.66 (1.29, 2.15)	0.70%	1.08	1.37
KRT81	NM_002281	1	0.000191877	1.79 (1.32, 2.43)	1.20%	1.08	1.36

LYPD6B	NM_177964	-1	0.000135793	0.60 (0.46, 0.78)	0.90%	1.08	1.36
MAPT	NM_001123066	-1	0.000216473	0.56 (0.41, 0.76)	1.20%	1.08	1.35
MAPT	NM_001123067	-1	0.000216473	0.56 (0.41, 0.76)	1.20%	1.08	1.35
MAPT	NM_016835	-1	0.000216473	0.56 (0.41, 0.76)	1.20%	1.08	1.35
MAPT	NM_005910	-1	0.000216473	0.56 (0.41, 0.76)	1.20%	1.08	1.35
MAPT	NM_016841	-1	0.000216473	0.56 (0.41, 0.76)	1.20%	1.08	1.35
MAPT	NM_016834	-1	0.000216473	0.56 (0.41, 0.76)	1.20%	1.08	1.35
MIR3170	NR_036129	1	1.03E-05	1.38 (1.19, 1.59)	0.20%	1.08	1.31
MIR4267	NR_036225	1	7.93E-06	1.33 (1.17, 1.51)	0.10%	1.08	1.28
NDUFS6	NM_004553	1	0.000254346	1.91 (1.35, 2.70)	1.40%	1.08	1.35
NPY1R	NM_000909	-1	0.00017825	0.55 (0.41, 0.75)	1.10%	1.08	1.36
NRIP3	NM_020645	-1	0.000247739	0.50 (0.34, 0.72)	1.30%	1.08	1.35
NUDT8	NM_181843	1	7.84E-05	1.53 (1.24, 1.90)	0.60%	1.08	1.35
OPALIN	NM_033207	1	3.68E-05	1.43 (1.21, 1.69)	0.40%	1.08	1.32
OPALIN	NM_001040102	1	3.68E-05	1.43 (1.21, 1.69)	0.40%	1.08	1.32
OPALIN	NM_001040103	1	3.68E-05	1.43 (1.21, 1.69)	0.40%	1.08	1.32
PABPC1L2B	NM_001042506	1	9.64E-07	1.24 (1.14, 1.36)	<0.1%	1.08	1.23
PDE6B	NM_001145291	-1	0.000100399	0.59 (0.46, 0.77)	0.70%	1.08	1.37
PDE6B	NM_001145292	-1	0.000100399	0.59 (0.46, 0.77)	0.70%	1.08	1.37
PDE6B	NM_000283	-1	0.000100399	0.59 (0.46, 0.77)	0.70%	1.08	1.37
PRR7	NM_030567	1	0.000274525	2.20 (1.44, 3.37)	1.40%	1.08	1.34
PRR7	NM_001174101	1	0.000274525	2.20 (1.44, 3.37)	1.40%	1.08	1.34
PRR7	NM_001174102	1	0.000274525	2.20 (1.44, 3.37)	1.40%	1.08	1.34
PTP4A1	NM_003463	1	2.66E-05	1.45 (1.22, 1.73)	0.30%	1.08	1.34
RGS22	NM_015668	-1	0.000336901	0.44 (0.28, 0.69)	1.60%	1.08	1.32
SECISBP2L	NM_014701	1	0.000213295	1.98 (1.38, 2.84)	1.20%	1.08	1.36
SECISBP2L	NM_001193489	1	0.000213295	1.98 (1.38, 2.84)	1.20%	1.08	1.36
SFXN1	NM_022754	1	0.000256108	1.89 (1.34, 2.66)	1.40%	1.08	1.35
SLC27A1	NM_198580	-1	0.00014439	0.59 (0.45, 0.78)	1.00%	1.08	1.36
SLC35C1	NM_018389	1	0.000285265	1.97 (1.37, 2.84)	1.50%	1.08	1.35
SLC35C1	NM_001145265	1	0.000285265	1.97 (1.37, 2.84)	1.50%	1.08	1.35
SLC35C1	NM_001145266	1	0.000285265	1.97 (1.37, 2.84)	1.50%	1.08	1.35
SP8	NM_182700	1	6.71E-06	1.31 (1.17, 1.48)	0.10%	1.08	1.27
SP8	NM_198956	1	6.71E-06	1.31 (1.17, 1.48)	0.10%	1.08	1.27
TBRG4	NM_004749	1	8.91E-05	1.54 (1.24, 1.90)	0.70%	1.08	1.35
TBRG4	NM_199122	1	8.91E-05	1.54 (1.24, 1.90)	0.70%	1.08	1.35
TBRG4	NM_030900	1	8.91E-05	1.54 (1.24, 1.90)	0.70%	1.08	1.35
TFRC	NM_003234	1	0.000294668	2.08 (1.40, 3.09)	1.50%	1.08	1.34
TFRC	NM_001128148	1	0.000294668	2.08 (1.40, 3.09)	1.50%	1.08	1.34
USP39	NM_006590	1	0.000298617	2.18 (1.43, 3.33)	1.50%	1.08	1.34
WDR19	NM_025132	-1	0.000213805	0.53 (0.38, 0.74)	1.20%	1.08	1.35
YWHAZ	NM_001135699	1	0.000160718	1.78 (1.32, 2.41)	1.00%	1.08	1.37
YWHAZ	NM_001135701	1	0.000160718	1.78 (1.32, 2.41)	1.00%	1.08	1.37
YWHAZ	NM_001135702	1	0.000160718	1.78 (1.32, 2.41)	1.00%	1.08	1.37
YWHAZ	NM_001135700	1	0.000160718	1.78 (1.32, 2.41)	1.00%	1.08	1.37
YWHAZ	NM_145690	1	0.000160718	1.78 (1.32, 2.41)	1.00%	1.08	1.37
YWHAZ	NM_003406	1	0.000160718	1.78 (1.32, 2.41)	1.00%	1.08	1.37
ZBED4	NM_014838	1	0.000018032	1.37 (1.19, 1.59)	0.20%	1.08	1.3
ZBTB26	NM_020924	-1	0.000088049	0.65 (0.52, 0.80)	0.70%	1.08	1.35

ZNF174	NM_001032292	-1	0.00021639	0.48 (0.32, 0.71)	1.20%	1.08	1.35
ZNF174	NM_003450	-1	0.00021639	0.48 (0.32, 0.71)	1.20%	1.08	1.35
ZNF440	NM_152357	-1	0.000254996	0.53 (0.37, 0.74)	1.40%	1.08	1.35
ZNF441	NM_152355	-1	0.000204868	0.55 (0.40, 0.75)	1.20%	1.08	1.36
ZNF563	NM_145276	-1	7.39E-05	0.62 (0.49, 0.78)	0.60%	1.08	1.36
ZNF763	NM_001012753	-1	0.00014465	0.57 (0.42, 0.76)	1.00%	1.08	1.36
ZNF843	NM_001136509	-1	0.00031279	0.45 (0.29, 0.70)	1.50%	1.08	1.33
ZNF844	NM_001136501	-1	0.000119899	0.58 (0.44, 0.76)	0.80%	1.08	1.37
ANKRD30A	NM_052997	-1	0.00042874	0.52 (0.36, 0.75)	1.90%	1.07	1.33
AP1G1	NM_001128	1	0.000237846	1.75 (1.30, 2.37)	1.30%	1.07	1.35
AP1G1	NM_001030007	1	0.000237846	1.75 (1.30, 2.37)	1.30%	1.07	1.35
BRD1	NM_014577	1	4.25E-05	1.40 (1.19, 1.65)	0.40%	1.07	1.31
BUD13	NM_032725	-1	0.00033707	0.53 (0.38, 0.75)	1.60%	1.07	1.34
BUD13	NM_001159736	-1	0.00033707	0.53 (0.38, 0.75)	1.60%	1.07	1.34
BZRAP1	NM_004758	-1	0.000315545	0.54 (0.39, 0.76)	1.50%	1.07	1.34
BZRAP1	NM_024418	-1	0.000315545	0.54 (0.39, 0.76)	1.50%	1.07	1.34
C17orf91	NR_028505	-1	0.000246829	0.60 (0.46, 0.79)	1.30%	1.07	1.34
C17orf91	NR_028504	-1	0.000246829	0.60 (0.46, 0.79)	1.30%	1.07	1.34
C17orf91	NR_028502	-1	0.000246829	0.60 (0.46, 0.79)	1.30%	1.07	1.34
C17orf91	NR_028503	-1	0.000246829	0.60 (0.46, 0.79)	1.30%	1.07	1.34
C1orf220	NR_033186	-1	0.000206926	0.63 (0.50, 0.81)	1.20%	1.07	1.34
C1orf51	NM_144697	-1	0.000164444	0.60 (0.46, 0.78)	1.00%	1.07	1.35
C2orf65	NM_138804	-1	0.000242505	0.57 (0.42, 0.77)	1.30%	1.07	1.35
C9orf27	NR_024032	1	3.24E-06	1.26 (1.15, 1.40)	0.10%	1.07	1.24
C9orf64	NM_032307	-1	0.000258832	0.57 (0.42, 0.77)	1.40%	1.07	1.35
CACNA1F	NM_005183	-1	0.000196901	0.59 (0.45, 0.78)	1.20%	1.07	1.35
CBX3	NM_007276	1	0.00012881	1.53 (1.23, 1.90)	0.90%	1.07	1.34
CBX3	NM_016587	1	0.00012881	1.53 (1.23, 1.90)	0.90%	1.07	1.34
CLIC6	NM_053277	-1	0.000469076	0.47 (0.30, 0.72)	2.00%	1.07	1.32
COX6B1	NM_001863	1	7.59E-05	1.45 (1.21, 1.74)	0.60%	1.07	1.32
CWF19L2	NM_152434	-1	0.000485073	0.49 (0.33, 0.73)	2.00%	1.07	1.32
CX3CR1	NM_001171171	-1	0.000471876	0.48 (0.32, 0.72)	2.00%	1.07	1.32
CX3CR1	NM_001171172	-1	0.000471876	0.48 (0.32, 0.72)	2.00%	1.07	1.32
CX3CR1	NM_001171174	-1	0.000471876	0.48 (0.32, 0.72)	2.00%	1.07	1.32
CX3CR1	NM_001337	-1	0.000471876	0.48 (0.32, 0.72)	2.00%	1.07	1.32
DCDC1	NM_181807	-1	0.000241354	0.55 (0.40, 0.76)	1.30%	1.07	1.35
DET1	NM_017996	-1	5.20E-05	0.73 (0.63, 0.85)	0.50%	1.07	1.29
DET1	NM_001144074	-1	5.20E-05	0.73 (0.63, 0.85)	0.50%	1.07	1.29
DET1	NR_026645	-1	5.20E-05	0.73 (0.63, 0.85)	0.50%	1.07	1.29
EGLN1	NM_022051	1	0.000408781	1.87 (1.32, 2.64)	1.80%	1.07	1.34
EXO1	NM_003686	1	0.000583818	2.40 (1.46, 3.96)	2.30%	1.07	1.3
EXO1	NM_006027	1	0.000583818	2.40 (1.46, 3.96)	2.30%	1.07	1.3
EXO1	NM_130398	1	0.000583818	2.40 (1.46, 3.96)	2.30%	1.07	1.3
FAM92A1	NM_145269	1	0.000422905	1.96 (1.35, 2.84)	1.90%	1.07	1.34
FARP2	NM_014808	-1	0.000339695	0.56 (0.40, 0.77)	1.60%	1.07	1.34
FCGBP	NM_003890	-1	0.000347245	0.57 (0.42, 0.77)	1.60%	1.07	1.34
FTSJ3	NM_017647	1	0.000174103	1.54 (1.23, 1.93)	1.10%	1.07	1.34
GFPT1	NM_002056	1	0.000294139	1.66 (1.26, 2.19)	1.50%	1.07	1.34
GMCL1L	NR_003281	1	0.000277335	1.72 (1.28, 2.31)	1.40%	1.07	1.35

GPX5	NM_003996	1	0.00018895	1.58 (1.24, 2.02)	1.20%	1.07	1.34
GPX5	NM_001509	1	0.00018895	1.58 (1.24, 2.02)	1.20%	1.07	1.34
HIST1H2AJ	NM_021066	1	0.000389048	2.18 (1.42, 3.35)	1.80%	1.07	1.33
INTS1	NM_001080453	1	0.000236705	1.60 (1.25, 2.06)	1.30%	1.07	1.34
LOC284023	NR_024349	-1	6.57E-05	0.69 (0.57, 0.83)	0.50%	1.07	1.33
LOC729966	NR_036575	1	3.17E-05	1.34 (1.17, 1.54)	0.30%	1.07	1.28
MIR1208	NR_031613	1	0.000232308	1.72 (1.29, 2.30)	1.30%	1.07	1.35
MR1	NM_001194999	-1	0.000294622	0.54 (0.39, 0.75)	1.50%	1.07	1.35
MR1	NM_001531	-1	0.000294622	0.54 (0.39, 0.75)	1.50%	1.07	1.35
MR1	NM_001195035	-1	0.000294622	0.54 (0.39, 0.75)	1.50%	1.07	1.35
MR1	NM_001195000	-1	0.000294622	0.54 (0.39, 0.75)	1.50%	1.07	1.35
NEGR1	NM_173808	-1	0.000194753	0.58 (0.44, 0.77)	1.20%	1.07	1.35
NT5C2	NM_012229	1	0.000251004	1.78 (1.31, 2.43)	1.40%	1.07	1.35
NT5C2	NM_001134373	1	0.000251004	1.78 (1.31, 2.43)	1.40%	1.07	1.35
ONECUT2	NM_004852	1	0.000300598	1.90 (1.34, 2.69)	1.50%	1.07	1.35
OR52E8	NM_001005168	1	0.000183129	1.64 (1.27, 2.12)	1.10%	1.07	1.35
OR9K2	NM_001005243	1	0.000023276	1.32 (1.16, 1.49)	0.30%	1.07	1.27
PADI3	NM_016233	1	0.000184726	1.59 (1.25, 2.02)	1.10%	1.07	1.35
PION	NM_017439	-1	0.000214273	0.58 (0.44, 0.77)	1.20%	1.07	1.35
PLXNB2	NM_012401	1	0.000187459	1.55 (1.23, 1.94)	1.20%	1.07	1.34
SCARB2	NM_005506	1	9.94E-05	1.44 (1.20, 1.73)	0.70%	1.07	1.32
SERPINF2	NM_001165920	-1	0.000337351	0.56 (0.41, 0.77)	1.60%	1.07	1.34
SERPINF2	NM_000934	-1	0.000337351	0.56 (0.41, 0.77)	1.60%	1.07	1.34
SERPINF2	NM_001165921	-1	0.000337351	0.56 (0.41, 0.77)	1.60%	1.07	1.34
SHCBP1	NM_024745	1	0.000474183	2.26 (1.43, 3.58)	2.00%	1.07	1.31
SLC3A2	NM_002394	1	0.000205239	1.75 (1.30, 2.35)	1.20%	1.07	1.36
SLC3A2	NM_001012662	1	0.000205239	1.75 (1.30, 2.35)	1.20%	1.07	1.36
SLC3A2	NM_001012664	1	0.000205239	1.75 (1.30, 2.35)	1.20%	1.07	1.36
SLC3A2	NM_001012663	1	0.000205239	1.75 (1.30, 2.35)	1.20%	1.07	1.36
SLC3A2	NM_001013251	1	0.000205239	1.75 (1.30, 2.35)	1.20%	1.07	1.36
SLC3A2	NM_001012661	1	0.000205239	1.75 (1.30, 2.35)	1.20%	1.07	1.36
SLC3A2	NR_037193	1	0.000205239	1.75 (1.30, 2.35)	1.20%	1.07	1.36
SMARCC1	NM_003074	1	0.000285871	1.83 (1.32, 2.53)	1.50%	1.07	1.35
STK11IP	NM_052902	-1	0.00030755	0.58 (0.43, 0.78)	1.50%	1.07	1.34
SUSD3	NM_145006	-1	0.000203286	0.58 (0.43, 0.77)	1.20%	1.07	1.35
TBCEL	NM_152715	-1	0.000110632	0.64 (0.51, 0.80)	0.80%	1.07	1.35
TBCEL	NM_001130047	-1	0.000110632	0.64 (0.51, 0.80)	0.80%	1.07	1.35
TMEM151A	NM_153266	1	0.000109154	1.53 (1.23, 1.90)	0.80%	1.07	1.34
TMEM155	NM_152399	1	0.000285542	1.81 (1.31, 2.49)	1.50%	1.07	1.35
TMEM40	NM_018306	1	0.000431802	2.05 (1.37, 3.05)	1.90%	1.07	1.33
TMOD2	NM_014548	1	0.000120829	1.50 (1.22, 1.84)	0.80%	1.07	1.33
TMOD2	NM_001142885	1	0.000120829	1.50 (1.22, 1.84)	0.80%	1.07	1.33
TTC12	NM_017868	-1	0.000472605	0.45 (0.29, 0.70)	2.00%	1.07	1.31
ZDBF2	NM_020923	-1	0.00032201	0.55 (0.40, 0.76)	1.60%	1.07	1.34
ZNF326	NM_182976	-1	0.000367128	0.53 (0.37, 0.75)	1.70%	1.07	1.34
ZNF326	NM_182975	-1	0.000367128	0.53 (0.37, 0.75)	1.70%	1.07	1.34
ZNF484	NM_001007101	-1	0.000298688	0.52 (0.36, 0.74)	1.50%	1.07	1.34
ZNF484	NM_031486	-1	0.000298688	0.52 (0.36, 0.74)	1.50%	1.07	1.34
AARS	NM_001605	1	0.00039842	1.78 (1.29, 2.46)	1.80%	1.06	1.34

ACCN5	NM_017419	1	0.000363129	1.64 (1.25, 2.16)	1.70%	1.06	1.34
ALG3	NM_005787	1	0.000546417	1.96 (1.34, 2.87)	2.20%	1.06	1.33
ALG3	NR_024534	1	0.000546417	1.96 (1.34, 2.87)	2.20%	1.06	1.33
ALG3	NR_024533	1	0.000546417	1.96 (1.34, 2.87)	2.20%	1.06	1.33
ALG3	NM_001006941	1	0.000546417	1.96 (1.34, 2.87)	2.20%	1.06	1.33
ANLN	NM_018685	1	0.000861767	2.34 (1.42, 3.86)	2.90%	1.06	1.29
BARHL2	NM_020063	1	9.67E-05	1.33 (1.15, 1.53)	0.70%	1.06	1.27
BBC3	NM_014417	-1	0.000431133	0.58 (0.43, 0.79)	1.90%	1.06	1.33
BBC3	NM_001127240	-1	0.000431133	0.58 (0.43, 0.79)	1.90%	1.06	1.33
BBC3	NM_001127242	-1	0.000431133	0.58 (0.43, 0.79)	1.90%	1.06	1.33
BBC3	NM_001127241	-1	0.000431133	0.58 (0.43, 0.79)	1.90%	1.06	1.33
C17orf97	NM_001013672	-1	0.000476721	0.56 (0.41, 0.78)	2.00%	1.06	1.33
C7orf40	NR_003697	1	0.000244871	1.48 (1.20, 1.83)	1.30%	1.06	1.32
CCDC45	NM_138363	1	0.000315377	1.62 (1.25, 2.11)	1.50%	1.06	1.34
CCT5	NM_012073	1	0.000579782	1.92 (1.33, 2.79)	2.20%	1.06	1.33
CFL1	NM_005507	1	0.00041237	1.62 (1.24, 2.11)	1.80%	1.06	1.33
CROCC	NM_014675	-1	0.000303212	0.61 (0.46, 0.80)	1.50%	1.06	1.34
DCAF16	NM_017741	-1	0.000539706	0.51 (0.35, 0.75)	2.10%	1.06	1.32
DUS3L	NM_020175	-1	0.000318893	0.59 (0.44, 0.79)	1.50%	1.06	1.34
DUS3L	NM_001161619	-1	0.000318893	0.59 (0.44, 0.79)	1.50%	1.06	1.34
EFCAB6	NM_022785	-1	0.000411749	0.62 (0.48, 0.81)	1.80%	1.06	1.33
EFCAB6	NM_198856	-1	0.000411749	0.62 (0.48, 0.81)	1.80%	1.06	1.33
F9	NM_000133	1	4.73E-05	1.28 (1.14, 1.44)	0.40%	1.06	1.24
FAM83D	NM_030919	1	0.000660782	2.17 (1.39, 3.40)	2.50%	1.06	1.31
FANK1	NM_145235	-1	0.000363661	0.60 (0.45, 0.79)	1.70%	1.06	1.34
FSD2	NM_001007122	-1	0.000370322	0.61 (0.47, 0.80)	1.70%	1.06	1.33
GOLPH3	NM_022130	1	0.000490776	1.86 (1.31, 2.64)	2.00%	1.06	1.33
GPAA1	NM_003801	1	0.000555873	1.76 (1.28, 2.42)	2.20%	1.06	1.33
HBZ	NM_005332	1	0.000192085	1.49 (1.21, 1.83)	1.20%	1.06	1.32
HOXA13	NM_000522	1	0.000245127	1.43 (1.18, 1.74)	1.30%	1.06	1.31
HSD3B7	NM_001142778	-1	0.00023229	0.66 (0.53, 0.82)	1.30%	1.06	1.33
HSD3B7	NM_001142777	-1	0.00023229	0.66 (0.53, 0.82)	1.30%	1.06	1.33
HSD3B7	NM_025193	-1	0.00023229	0.66 (0.53, 0.82)	1.30%	1.06	1.33
IFI27L1	NM_206949	-1	0.00033531	0.61 (0.47, 0.80)	1.60%	1.06	1.34
IFI27L1	NM_145249	-1	0.00033531	0.61 (0.47, 0.80)	1.60%	1.06	1.34
IGF2BP1	NM_006546	1	0.000397318	1.75 (1.28, 2.38)	1.80%	1.06	1.34
IGF2BP1	NM_001160423	1	0.000397318	1.75 (1.28, 2.38)	1.80%	1.06	1.34
KIAA0430	NM_001184998	-1	0.000703574	0.50 (0.34, 0.75)	2.50%	1.06	1.31
KIAA0430	NM_014647	-1	0.000703574	0.50 (0.34, 0.75)	2.50%	1.06	1.31
KIAA0430	NM_001184999	-1	0.000703574	0.50 (0.34, 0.75)	2.50%	1.06	1.31
KIAA1274	NM_014431	-1	0.00041306	0.61 (0.47, 0.80)	1.80%	1.06	1.33
KIAA1407	NM_020817	-1	0.0004264	0.61 (0.47, 0.81)	1.90%	1.06	1.33
KPNA2	NM_002266	1	0.000608282	1.88 (1.31, 2.70)	2.30%	1.06	1.33
LOC100130148	NR_024560	-1	0.000334314	0.59 (0.44, 0.79)	1.60%	1.06	1.34
LOC144742	NR_024246	1	0.00015428	1.41 (1.18, 1.69)	1.00%	1.06	1.3
LOC642006	NR_030766	1	0.000338823	1.61 (1.24, 2.08)	1.60%	1.06	1.34
LRIG3	NM_001136051	1	0.000531484	1.70 (1.26, 2.30)	2.10%	1.06	1.33
LRIG3	NM_153377	1	0.000531484	1.70 (1.26, 2.30)	2.10%	1.06	1.33
LRIT2	NM_001017924	1	8.60E-05	1.34 (1.16, 1.54)	0.70%	1.06	1.27

LYRM5	NM_001001660	-1	0.00030197	0.67 (0.54, 0.83)	1.50%	1.06	1.32
MEIS3P1	NR_002211	-1	0.000277359	0.66 (0.53, 0.83)	1.40%	1.06	1.32
METTL7B	NM_152637	1	0.000534187	1.78 (1.28, 2.47)	2.10%	1.06	1.33
MIR133A1	NR_029675	1	0.000236845	1.54 (1.22, 1.93)	1.30%	1.06	1.33
MIR4256	NR_036210	1	0.000511214	1.72 (1.27, 2.33)	2.10%	1.06	1.33
MIR4258	NR_036212	1	0.000755224	2.19 (1.39, 3.46)	2.70%	1.06	1.3
NEK5	NM_199289	-1	0.000362458	0.65 (0.51, 0.82)	1.70%	1.06	1.32
NHLRC4	NM_176677	-1	0.000605306	0.55 (0.39, 0.77)	2.30%	1.06	1.32
NPM3	NM_006993	1	0.000857222	2.57 (1.47, 4.46)	2.90%	1.06	1.27
P4HB	NM_000918	1	0.000519801	1.78 (1.29, 2.47)	2.10%	1.06	1.33
PACRGL	NM_001130727	-1	0.000137922	0.70 (0.58, 0.84)	0.90%	1.06	1.31
PACRGL	NM_145048	-1	0.000137922	0.70 (0.58, 0.84)	0.90%	1.06	1.31
PAPD7	NM_006999	1	0.000569528	1.84 (1.30, 2.60)	2.20%	1.06	1.33
PAPD7	NM_001171806	1	0.000569528	1.84 (1.30, 2.60)	2.20%	1.06	1.33
PAPD7	NM_001171805	1	0.000569528	1.84 (1.30, 2.60)	2.20%	1.06	1.33
PCGF3	NM_006315	-1	0.000375263	0.57 (0.42, 0.78)	1.70%	1.06	1.34
PIM3	NM_001001852	1	0.000223066	1.45 (1.19, 1.77)	1.30%	1.06	1.31
POLK	NM_016218	-1	0.000694544	0.51 (0.34, 0.75)	2.50%	1.06	1.31
PPPDE1	NM_016076	1	0.000485656	1.95 (1.34, 2.83)	2.00%	1.06	1.33
PYGO1	NM_015617	-1	0.000513314	0.56 (0.40, 0.77)	2.10%	1.06	1.33
RASGRP4	NM_001146205	-1	0.000328822	0.60 (0.45, 0.79)	1.60%	1.06	1.34
RASGRP4	NM_170604	-1	0.000328822	0.60 (0.45, 0.79)	1.60%	1.06	1.34
RASGRP4	NM_001146203	-1	0.000328822	0.60 (0.45, 0.79)	1.60%	1.06	1.34
RASGRP4	NM_001146206	-1	0.000328822	0.60 (0.45, 0.79)	1.60%	1.06	1.34
RASGRP4	NM_001146204	-1	0.000328822	0.60 (0.45, 0.79)	1.60%	1.06	1.34
RASGRP4	NM_001146207	-1	0.000328822	0.60 (0.45, 0.79)	1.60%	1.06	1.34
RASGRP4	NM_001146202	-1	0.000328822	0.60 (0.45, 0.79)	1.60%	1.06	1.34
RHCG	NM_016321	1	0.000306566	1.62 (1.25, 2.10)	1.50%	1.06	1.34
RP1-177G6-2	NR_028345	1	0.000135136	1.36 (1.16, 1.58)	0.90%	1.06	1.28
RP1-177G6-2	NR_028344	1	0.000135136	1.36 (1.16, 1.58)	0.90%	1.06	1.28
RPP21	NM_001199120	1	0.000396352	1.66 (1.26, 2.21)	1.80%	1.06	1.34
RPP21	NM_001199121	1	0.000396352	1.66 (1.26, 2.21)	1.80%	1.06	1.34
RPP21	NM_024839	1	0.000396352	1.66 (1.26, 2.21)	1.80%	1.06	1.34
SCUBE2	NM_001170690	-1	0.000697526	0.49 (0.32, 0.74)	2.50%	1.06	1.31
SCUBE2	NM_020974	-1	0.000697526	0.49 (0.32, 0.74)	2.50%	1.06	1.31
SEC61A1	NM_013336	1	0.000689339	1.92 (1.32, 2.79)	2.50%	1.06	1.32
SENP5	NM_152699	1	0.000451373	1.64 (1.24, 2.15)	1.90%	1.06	1.33
SGOL1	NM_001012411	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SGOL1	NM_001199253	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SGOL1	NM_001199252	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SGOL1	NM_001199251	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SGOL1	NM_001012412	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SGOL1	NM_001012409	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SGOL1	NM_001199254	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SGOL1	NM_001012410	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SGOL1	NM_138484	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SGOL1	NM_001199256	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SGOL1	NM_001199257	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SGOL1	NM_001012413	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31

SGOL1	NM_001199255	1	0.000679983	2.16 (1.38, 3.36)	2.50%	1.06	1.31
SIN3B	NM_015260	-1	0.00042699	0.56 (0.41, 0.77)	1.90%	1.06	1.34
SMG6	NM_017575	-1	0.000476372	0.54 (0.38, 0.76)	2.00%	1.06	1.33
SMG6	NM_001170957	-1	0.000476372	0.54 (0.38, 0.76)	2.00%	1.06	1.33
STAT5A	NM_003152	-1	0.000296856	0.61 (0.46, 0.80)	1.50%	1.06	1.34
STX6	NM_005819	1	0.000513875	1.78 (1.29, 2.46)	2.10%	1.06	1.33
STX8	NR_033656	-1	0.000363379	0.60 (0.45, 0.80)	1.70%	1.06	1.34
STX8	NM_004853	-1	0.000363379	0.60 (0.45, 0.80)	1.70%	1.06	1.34
SYNPO2L	NM_024875	-1	0.000517753	0.50 (0.34, 0.74)	2.10%	1.06	1.32
SYNPO2L	NM_001114133	-1	0.000517753	0.50 (0.34, 0.74)	2.10%	1.06	1.32
TMEM101	NM_032376	-1	0.000487894	0.51 (0.35, 0.75)	2.00%	1.06	1.33
TNFRSF14	NM_003820	-1	0.000653957	0.49 (0.32, 0.74)	2.50%	1.06	1.31
UBE2C	NM_181799	1	0.000783989	2.51 (1.47, 4.30)	2.70%	1.06	1.28
UBE2C	NM_181800	1	0.000783989	2.51 (1.47, 4.30)	2.70%	1.06	1.28
UBE2C	NM_181803	1	0.000783989	2.51 (1.47, 4.30)	2.70%	1.06	1.28
UBE2C	NM_007019	1	0.000783989	2.51 (1.47, 4.30)	2.70%	1.06	1.28
UBE2C	NM_181802	1	0.000783989	2.51 (1.47, 4.30)	2.70%	1.06	1.28
UBE2C	NM_181801	1	0.000783989	2.51 (1.47, 4.30)	2.70%	1.06	1.28
ZNF287	NM_020653	-1	0.000326457	0.64 (0.51, 0.82)	1.60%	1.06	1.33
ZNF576	NM_024327	-1	0.000481181	0.57 (0.42, 0.78)	2.00%	1.06	1.33
ZNF576	NM_001145347	-1	0.000481181	0.57 (0.42, 0.78)	2.00%	1.06	1.33
ZNF738	NR_027130	-1	0.000598215	0.55 (0.39, 0.77)	2.30%	1.06	1.32
ABCC10	NM_033450	1	0.000517309	1.57 (1.22, 2.03)	2.10%	1.05	1.32
ABCC10	NM_001198934	1	0.000517309	1.57 (1.22, 2.03)	2.10%	1.05	1.32
ACTR3C	NM_001164458	-1	0.000635228	0.64 (0.50, 0.83)	2.40%	1.05	1.31
ACTR3C	NM_001164459	-1	0.000635228	0.64 (0.50, 0.83)	2.40%	1.05	1.31
AFM	NM_001133	1	0.000066704	1.23 (1.11, 1.36)	0.60%	1.05	1.21
AGBL2	NM_024783	-1	0.000684777	0.63 (0.48, 0.82)	2.50%	1.05	1.32
APOBEC1	NM_001644	1	5.53E-05	1.22 (1.11, 1.34)	0.50%	1.05	1.2
ARHGEF6	NM_004840	-1	0.000770839	0.54 (0.38, 0.78)	2.70%	1.05	1.32
ATAD3A	NM_018188	1	0.001027877	2.28 (1.39, 3.72)	3.20%	1.05	1.28
ATAD3A	NM_001170536	1	0.001027877	2.28 (1.39, 3.72)	3.20%	1.05	1.28
ATAD3A	NM_001170535	1	0.001027877	2.28 (1.39, 3.72)	3.20%	1.05	1.28
ATP8A2	NM_016529	-1	0.000828234	0.56 (0.40, 0.79)	2.80%	1.05	1.31
AURKA	NM_198437	1	0.001108089	2.00 (1.32, 3.02)	3.30%	1.05	1.3
AURKA	NM_198436	1	0.001108089	2.00 (1.32, 3.02)	3.30%	1.05	1.3
AURKA	NM_198435	1	0.001108089	2.00 (1.32, 3.02)	3.30%	1.05	1.3
AURKA	NM_198434	1	0.001108089	2.00 (1.32, 3.02)	3.30%	1.05	1.3
AURKA	NM_003600	1	0.001108089	2.00 (1.32, 3.02)	3.30%	1.05	1.3
AURKA	NM_198433	1	0.001108089	2.00 (1.32, 3.02)	3.30%	1.05	1.3
BAI2	NM_001703	-1	0.000813324	0.59 (0.43, 0.80)	2.80%	1.05	1.32
C10orf68	NM_024688	-1	0.000766871	0.54 (0.38, 0.77)	2.70%	1.05	1.32
C14orf33	NR_027123	-1	0.000774142	0.62 (0.47, 0.82)	2.70%	1.05	1.31
C9orf117	NM_001012502	-1	0.000748452	0.58 (0.43, 0.80)	2.60%	1.05	1.32
CDC25C	NM_022809	1	0.00105986	2.22 (1.38, 3.57)	3.30%	1.05	1.29
CDC25C	NM_001790	1	0.00105986	2.22 (1.38, 3.57)	3.30%	1.05	1.29
CENPO	NM_024322	1	0.000898127	2.08 (1.35, 3.19)	2.90%	1.05	1.3
CENPO	NM_001199803	1	0.000898127	2.08 (1.35, 3.19)	2.90%	1.05	1.3
CLCN5	NM_000084	1	0.000713564	1.83 (1.29, 2.60)	2.60%	1.05	1.32

CLCN5	NM_001127899	1	0.000713564	1.83 (1.29, 2.60)	2.60%	1.05	1.32
CLCN5	NM_001127898	1	0.000713564	1.83 (1.29, 2.60)	2.60%	1.05	1.32
CLK1	NR_027855	-1	0.000894665	0.56 (0.39, 0.79)	2.90%	1.05	1.31
CLK1	NR_027856	-1	0.000894665	0.56 (0.39, 0.79)	2.90%	1.05	1.31
CLK1	NM_004071	-1	0.000894665	0.56 (0.39, 0.79)	2.90%	1.05	1.31
CLK1	NM_001162407	-1	0.000894665	0.56 (0.39, 0.79)	2.90%	1.05	1.31
CLTC	NM_004859	1	0.000563537	1.55 (1.21, 1.98)	2.20%	1.05	1.32
COPG	NM_016128	1	0.000702768	1.78 (1.28, 2.49)	2.50%	1.05	1.32
DEFB133	NM_001166478	1	0.000294095	1.38 (1.16, 1.64)	1.50%	1.05	1.28
DGCR10	NR_026651	1	0.000654253	1.69 (1.25, 2.29)	2.50%	1.05	1.33
DHCR7	NM_001360	1	0.000806605	1.76 (1.26, 2.44)	2.80%	1.05	1.32
DHCR7	NM_001163817	1	0.000806605	1.76 (1.26, 2.44)	2.80%	1.05	1.32
DLX6-AS1	NR_015448	1	0.000705367	1.57 (1.21, 2.03)	2.50%	1.05	1.32
DMRTC2	NM_001040283	1	0.000492509	1.49 (1.19, 1.86)	2.00%	1.05	1.31
ESRP1	NM_001122827	1	0.000764406	1.86 (1.30, 2.67)	2.70%	1.05	1.32
ESRP1	NM_017697	1	0.000764406	1.86 (1.30, 2.67)	2.70%	1.05	1.32
ESRP1	NM_001122825	1	0.000764406	1.86 (1.30, 2.67)	2.70%	1.05	1.32
ESRP1	NM_001122826	1	0.000764406	1.86 (1.30, 2.67)	2.70%	1.05	1.32
ESRP1	NM_001034915	1	0.000764406	1.86 (1.30, 2.67)	2.70%	1.05	1.32
FAM184B	NM_015688	-1	0.000919699	0.50 (0.33, 0.75)	3.00%	1.05	1.3
FGD3	NM_001083536	-1	0.000878971	0.48 (0.31, 0.74)	2.90%	1.05	1.3
FGD3	NM_033086	-1	0.000878971	0.48 (0.31, 0.74)	2.90%	1.05	1.3
FRMPD2	NM_001018071	-1	0.000916891	0.50 (0.33, 0.75)	3.00%	1.05	1.3
FRMPD2	NR_033178	-1	0.000916891	0.50 (0.33, 0.75)	3.00%	1.05	1.3
GALNS	NM_000512	1	0.000779802	1.73 (1.26, 2.39)	2.70%	1.05	1.32
GPA33	NM_005814	1	0.000455791	1.51 (1.20, 1.91)	1.90%	1.05	1.32
GRIK4	NM_014619	-1	0.000983512	0.49 (0.32, 0.75)	3.10%	1.05	1.3
GRSF1	NM_002092	1	0.000455403	1.42 (1.17, 1.73)	1.90%	1.05	1.29
GRSF1	NM_001098477	1	0.000455403	1.42 (1.17, 1.73)	1.90%	1.05	1.29
GSG1	NM_031289	-1	0.000746247	0.57 (0.41, 0.79)	2.60%	1.05	1.32
GSG1	NM_153823	-1	0.000746247	0.57 (0.41, 0.79)	2.60%	1.05	1.32
GSG1	NM_001080555	-1	0.000746247	0.57 (0.41, 0.79)	2.60%	1.05	1.32
GSG1	NM_001080554	-1	0.000746247	0.57 (0.41, 0.79)	2.60%	1.05	1.32
GSTTP1	NR_003081	1	0.000281335	1.36 (1.15, 1.61)	1.50%	1.05	1.28
GZMB	NM_004131	1	0.000774473	1.64 (1.23, 2.20)	2.70%	1.05	1.32
HIVEP3	NM_024503	-1	0.000637807	0.56 (0.40, 0.78)	2.40%	1.05	1.32
HIVEP3	NM_001127714	-1	0.000637807	0.56 (0.40, 0.78)	2.40%	1.05	1.32
HRK	NM_003806	1	0.000573791	1.56 (1.21, 2.02)	2.20%	1.05	1.32
ICK	NM_016513	1	0.000708599	1.76 (1.27, 2.45)	2.50%	1.05	1.32
ICK	NM_014920	1	0.000708599	1.76 (1.27, 2.45)	2.50%	1.05	1.32
IDI1	NM_004508	1	0.000576826	1.62 (1.23, 2.12)	2.20%	1.05	1.32
INPP5K	NM_001135642	-1	0.000606796	0.61 (0.45, 0.81)	2.30%	1.05	1.32
INPP5K	NM_130766	-1	0.000606796	0.61 (0.45, 0.81)	2.30%	1.05	1.32
INPP5K	NM_016532	-1	0.000606796	0.61 (0.45, 0.81)	2.30%	1.05	1.32
KDELR2	NM_001100603	1	0.000640872	1.78 (1.28, 2.48)	2.40%	1.05	1.33
KDELR2	NM_006854	1	0.000640872	1.78 (1.28, 2.48)	2.40%	1.05	1.33
KIAA0528	NM_014802	-1	0.00067798	0.60 (0.45, 0.81)	2.50%	1.05	1.32
KIAA0664L3	NR_024034	-1	0.000538791	0.68 (0.54, 0.84)	2.10%	1.05	1.3
KIAA0753	NM_014804	-1	0.000792844	0.58 (0.43, 0.80)	2.70%	1.05	1.32

KIF14	NM_014875	1	0.000991316	2.07 (1.34, 3.20)	3.10%	1.05	1.3
KLHL5	NM_015990	-1	0.001075498	0.51 (0.34, 0.76)	3.30%	1.05	1.3
KLHL5	NM_199039	-1	0.001075498	0.51 (0.34, 0.76)	3.30%	1.05	1.3
KLHL5	NM_001007075	-1	0.001075498	0.51 (0.34, 0.76)	3.30%	1.05	1.3
KLHL5	NM_001171654	-1	0.001075498	0.51 (0.34, 0.76)	3.30%	1.05	1.3
LARP1	NM_015315	1	0.000776893	1.98 (1.33, 2.95)	2.70%	1.05	1.31
LMAN1L	NM_021819	1	0.000694431	1.58 (1.21, 2.05)	2.50%	1.05	1.32
LOC284440	NR_026956	-1	0.00064239	0.56 (0.40, 0.78)	2.40%	1.05	1.32
LOC644961	NR_033926	-1	0.000821483	0.51 (0.35, 0.76)	2.80%	1.05	1.31
MAGEA3	NM_005362	1	0.000259711	1.40 (1.17, 1.67)	1.40%	1.05	1.29
MAGEB2	NM_002364	1	0.000109866	1.28 (1.13, 1.45)	0.80%	1.05	1.24
MIR1297	NR_031628	1	0.000213996	1.30 (1.13, 1.50)	1.20%	1.05	1.25
NXNL2	NM_001161625	-1	0.000679325	0.53 (0.37, 0.77)	2.50%	1.05	1.32
NXNL2	NM_145283	-1	0.000679325	0.53 (0.37, 0.77)	2.50%	1.05	1.32
PCDH11Y	NM_032972	1	0.000256294	1.35 (1.15, 1.58)	1.40%	1.05	1.27
PCDH11Y	NM_032973	1	0.000256294	1.35 (1.15, 1.58)	1.40%	1.05	1.27
PCDH11Y	NM_032971	1	0.000256294	1.35 (1.15, 1.58)	1.40%	1.05	1.27
PGD	NM_002631	1	0.00082458	1.77 (1.27, 2.46)	2.80%	1.05	1.32
PHF2	NM_005392	-1	0.00054667	0.62 (0.47, 0.81)	2.20%	1.05	1.32
POU3F4	NM_000307	1	0.000444079	1.56 (1.22, 2.00)	1.90%	1.05	1.32
POU4F1	NM_006237	1	0.000488435	1.52 (1.20, 1.92)	2.00%	1.05	1.32
PTGER3	NM_001126044	-1	0.000851253	0.52 (0.36, 0.77)	2.80%	1.05	1.31
PTGER3	NM_198716	-1	0.000851253	0.52 (0.36, 0.77)	2.80%	1.05	1.31
PTGER3	NM_198718	-1	0.000851253	0.52 (0.36, 0.77)	2.80%	1.05	1.31
PTGER3	NM_198715	-1	0.000851253	0.52 (0.36, 0.77)	2.80%	1.05	1.31
PTGER3	NM_198719	-1	0.000851253	0.52 (0.36, 0.77)	2.80%	1.05	1.31
PTGER3	NM_198714	-1	0.000851253	0.52 (0.36, 0.77)	2.80%	1.05	1.31
PTGER3	NR_028292	-1	0.000851253	0.52 (0.36, 0.77)	2.80%	1.05	1.31
PTGER3	NR_028293	-1	0.000851253	0.52 (0.36, 0.77)	2.80%	1.05	1.31
PTGER3	NM_198717	-1	0.000851253	0.52 (0.36, 0.77)	2.80%	1.05	1.31
PTGER3	NR_028294	-1	0.000851253	0.52 (0.36, 0.77)	2.80%	1.05	1.31
RGP1	NM_001080496	-1	0.000674124	0.64 (0.49, 0.83)	2.50%	1.05	1.31
RHOV	NM_133639	1	0.000910194	1.91 (1.30, 2.81)	3.00%	1.05	1.31
RPF1	NM_025065	-1	0.000516752	0.60 (0.45, 0.80)	2.10%	1.05	1.33
SEMA4B	NM_198925	1	0.000425026	1.49 (1.19, 1.86)	1.90%	1.05	1.31
SEMA4B	NM_020210	1	0.000425026	1.49 (1.19, 1.86)	1.90%	1.05	1.31
SLC30A3	NM_003459	1	0.000459198	1.58 (1.22, 2.03)	2.00%	1.05	1.33
SLC35A2	NM_005660	1	0.000949606	2.03 (1.33, 3.08)	3.00%	1.05	1.3
SLC35A2	NM_001042498	1	0.000949606	2.03 (1.33, 3.08)	3.00%	1.05	1.3
SLC35A2	NM_001032289	1	0.000949606	2.03 (1.33, 3.08)	3.00%	1.05	1.3
SLC40A1	NM_014585	-1	0.000901525	0.50 (0.33, 0.75)	2.90%	1.05	1.3
SLC45A4	NM_001080431	1	0.000795498	1.90 (1.31, 2.76)	2.70%	1.05	1.32
SLC4A10	NM_022058	-1	0.000922314	0.50 (0.33, 0.75)	3.00%	1.05	1.3
SLC4A10	NM_001178016	-1	0.000922314	0.50 (0.33, 0.75)	3.00%	1.05	1.3
SLC4A10	NM_001178015	-1	0.000922314	0.50 (0.33, 0.75)	3.00%	1.05	1.3
SMPD2	NM_003080	-1	0.000636112	0.62 (0.47, 0.81)	2.40%	1.05	1.32
SMU1	NM_018225	-1	0.000694202	0.54 (0.37, 0.77)	2.50%	1.05	1.32
STON2	NM_033104	-1	0.000687523	0.54 (0.38, 0.77)	2.50%	1.05	1.32
TECTA	NM_005422	-1	0.000626178	0.58 (0.43, 0.79)	2.40%	1.05	1.32

TMEM8B	NM_001042590	-1	0.000970606	0.55 (0.39, 0.78)	3.10%	1.05	1.31
TMEM8B	NM_001042589	-1	0.000970606	0.55 (0.39, 0.78)	3.10%	1.05	1.31
TMEM8B	NM_016446	-1	0.000970606	0.55 (0.39, 0.78)	3.10%	1.05	1.31
TRAF3IP1	NM_015650	-1	0.000567431	0.59 (0.44, 0.80)	2.20%	1.05	1.33
TRAF3IP1	NM_001139490	-1	0.000567431	0.59 (0.44, 0.80)	2.20%	1.05	1.33
TROAP	NM_005480	1	0.000902469	1.97 (1.32, 2.94)	2.90%	1.05	1.31
TROAP	NM_001100620	1	0.000902469	1.97 (1.32, 2.94)	2.90%	1.05	1.31
TSTA3	NM_003313	1	0.000809687	1.67 (1.24, 2.25)	2.80%	1.05	1.32
TUBG2	NM_016437	-1	0.000282337	0.72 (0.60, 0.86)	1.50%	1.05	1.29
TXNDC8	NM_001003936	1	0.000444509	1.48 (1.19, 1.85)	1.90%	1.05	1.31
UGT2B10	NM_001075	1	0.000213893	1.39 (1.17, 1.65)	1.20%	1.05	1.29
UGT2B10	NM_001075	1	0.000213893	1.39 (1.17, 1.65)	1.20%	1.05	1.29
UGT2B10	NM_001144767	1	0.000213893	1.39 (1.17, 1.65)	1.20%	1.05	1.29
UGT2B10	NM_001144767	1	0.000213893	1.39 (1.17, 1.65)	1.20%	1.05	1.29
WAPAL	NM_015045	-1	0.000856095	0.55 (0.39, 0.78)	2.90%	1.05	1.31
ZNF20	NM_021143	-1	0.000772771	0.58 (0.43, 0.80)	2.70%	1.05	1.32
ZNF317	NM_020933	-1	0.000545984	0.59 (0.44, 0.80)	2.20%	1.05	1.33
ZNF317	NM_001190791	-1	0.000545984	0.59 (0.44, 0.80)	2.20%	1.05	1.33
ZNF516	NM_014643	-1	0.000706877	0.57 (0.41, 0.79)	2.50%	1.05	1.32
ZNF594	NM_032530	-1	0.000728948	0.56 (0.40, 0.78)	2.60%	1.05	1.32
ZNF625	NM_145233	-1	0.00079499	0.56 (0.40, 0.79)	2.70%	1.05	1.32
ZNF695	NM_020394	1	0.000959311	2.11 (1.35, 3.28)	3.10%	1.05	1.3
ABR	NM_001092	-1	0.00124577	0.57 (0.41, 0.80)	3.60%	1.04	1.3
ABR	NM_001159746	-1	0.00124577	0.57 (0.41, 0.80)	3.60%	1.04	1.3
ABR	NM_021962	-1	0.00124577	0.57 (0.41, 0.80)	3.60%	1.04	1.3
ACBD3	NM_022735	1	0.001654232	1.92 (1.28, 2.87)	4.10%	1.04	1.29
ACY3	NM_080658	1	0.000456993	1.33 (1.13, 1.55)	1.90%	1.04	1.26
AMY2B	NM_020978	-1	0.001380606	0.59 (0.42, 0.81)	3.80%	1.04	1.3
AP4E1	NM_007347	1	0.000480692	1.26 (1.11, 1.44)	2.00%	1.04	1.22
ASTN2	NM_001184735	-1	0.001083598	0.56 (0.40, 0.79)	3.30%	1.04	1.31
ASTN2	NM_198188	-1	0.001083598	0.56 (0.40, 0.79)	3.30%	1.04	1.31
ASTN2	NM_001184734	-1	0.001083598	0.56 (0.40, 0.79)	3.30%	1.04	1.31
ASTN2	NM_014010	-1	0.001083598	0.56 (0.40, 0.79)	3.30%	1.04	1.31
ASTN2	NM_198187	-1	0.001083598	0.56 (0.40, 0.79)	3.30%	1.04	1.31
ASTN2	NM_198186	-1	0.001083598	0.56 (0.40, 0.79)	3.30%	1.04	1.31
ATP5S	NM_001003805	-1	0.001099833	0.60 (0.44, 0.81)	3.30%	1.04	1.31
ATP5S	NR_033761	-1	0.001099833	0.60 (0.44, 0.81)	3.30%	1.04	1.31
ATP5S	NM_015684	-1	0.001099833	0.60 (0.44, 0.81)	3.30%	1.04	1.31
ATP5S	NM_001003803	-1	0.001099833	0.60 (0.44, 0.81)	3.30%	1.04	1.31
AZU1	NM_001700	1	0.001184365	1.57 (1.20, 2.06)	3.50%	1.04	1.3
BOD1L	NM_148894	-1	0.001481913	0.53 (0.36, 0.78)	3.90%	1.04	1.29
C14orf102	NM_199043	-1	0.001090373	0.57 (0.41, 0.80)	3.30%	1.04	1.31
C14orf102	NM_017970	-1	0.001090373	0.57 (0.41, 0.80)	3.30%	1.04	1.31
C15orf23	NM_001142762	1	0.001423858	1.90 (1.28, 2.82)	3.80%	1.04	1.3
C15orf23	NM_033286	1	0.001423858	1.90 (1.28, 2.82)	3.80%	1.04	1.3
C15orf23	NM_001142761	1	0.001423858	1.90 (1.28, 2.82)	3.80%	1.04	1.3
C19orf18	NM_152474	-1	0.001597281	0.52 (0.35, 0.78)	4.10%	1.04	1.29
C20orf132	NM_213631	-1	0.000972217	0.58 (0.42, 0.80)	3.10%	1.04	1.31
C20orf132	NM_152503	-1	0.000972217	0.58 (0.42, 0.80)	3.10%	1.04	1.31

C20orf132	NM_213632	-1	0.000972217	0.58 (0.42, 0.80)	3.10%	1.04	1.31
C21orf90	NR_026547	1	0.001031689	1.54 (1.19, 1.99)	3.20%	1.04	1.3
C21orf90	NR_026548	1	0.001031689	1.54 (1.19, 1.99)	3.20%	1.04	1.3
C3orf65	NR_027317	1	0.001227976	1.72 (1.24, 2.38)	3.50%	1.04	1.31
C6orf225	NM_001033564	-1	0.000824925	0.64 (0.49, 0.83)	2.80%	1.04	1.31
CDCA2	NM_152562	1	0.001763324	2.19 (1.34, 3.58)	4.30%	1.04	1.27
CLDN4	NM_001305	1	0.001451467	1.97 (1.30, 2.98)	3.90%	1.04	1.29
COL16A1	NM_001856	-1	0.00135906	0.60 (0.44, 0.82)	3.70%	1.04	1.3
COQ9	NM_020312	1	0.001364105	1.78 (1.25, 2.53)	3.70%	1.04	1.3
COX18	NM_173827	1	0.000877732	1.43 (1.16, 1.76)	2.90%	1.04	1.29
COX4NB	NM_006067	1	0.001769748	2.07 (1.31, 3.28)	4.30%	1.04	1.28
COX4NB	NM_001142288	1	0.001769748	2.07 (1.31, 3.28)	4.30%	1.04	1.28
CYCS	NM_018947	1	0.001320528	1.65 (1.22, 2.25)	3.70%	1.04	1.3
DACT2	NM_214462	1	0.001302736	1.62 (1.21, 2.17)	3.60%	1.04	1.3
DEGS1	NM_003676	1	0.001061247	1.48 (1.17, 1.87)	3.30%	1.04	1.29
DUSP9	NM_001395	1	0.001256936	1.61 (1.20, 2.14)	3.60%	1.04	1.3
DYNC2H1	NM_001080463	-1	0.001370915	0.59 (0.43, 0.82)	3.70%	1.04	1.3
DYNC2H1	NM_001377	-1	0.001370915	0.59 (0.43, 0.82)	3.70%	1.04	1.3
EIF4G1	NM_198241	1	0.001353974	1.68 (1.22, 2.31)	3.70%	1.04	1.3
EIF4G1	NM_001194947	1	0.001353974	1.68 (1.22, 2.31)	3.70%	1.04	1.3
EIF4G1	NM_198244	1	0.001353974	1.68 (1.22, 2.31)	3.70%	1.04	1.3
EIF4G1	NM_198242	1	0.001353974	1.68 (1.22, 2.31)	3.70%	1.04	1.3
EIF4G1	NM_001194946	1	0.001353974	1.68 (1.22, 2.31)	3.70%	1.04	1.3
EIF4G1	NM_182917	1	0.001353974	1.68 (1.22, 2.31)	3.70%	1.04	1.3
EIF4G1	NM_004953	1	0.001353974	1.68 (1.22, 2.31)	3.70%	1.04	1.3
ENO1	NM_001428	1	0.001364087	1.81 (1.26, 2.61)	3.70%	1.04	1.3
FAF2	NM_014613	1	0.00108376	1.88 (1.29, 2.74)	3.30%	1.04	1.31
FAM149A	NM_015398	-1	0.001194251	0.64 (0.49, 0.84)	3.50%	1.04	1.3
FAM149A	NM_001006655	-1	0.001194251	0.64 (0.49, 0.84)	3.50%	1.04	1.3
FAM154B	NM_001008226	-1	0.001023443	0.54 (0.37, 0.78)	3.20%	1.04	1.31
FGG	NM_021870	1	0.000888207	1.49 (1.18, 1.88)	2.90%	1.04	1.3
FGG	NM_000509	1	0.000888207	1.49 (1.18, 1.88)	2.90%	1.04	1.3
GET4	NM_015949	1	0.001268692	1.58 (1.20, 2.10)	3.60%	1.04	1.3
GGT1	NM_005265	1	0.00125253	1.75 (1.25, 2.46)	3.60%	1.04	1.31
GGT1	NM_013430	1	0.00125253	1.75 (1.25, 2.46)	3.60%	1.04	1.31
GGT1	NM_001032365	1	0.00125253	1.75 (1.25, 2.46)	3.60%	1.04	1.31
GGT1	NM_001032364	1	0.00125253	1.75 (1.25, 2.46)	3.60%	1.04	1.31
GPC4	NM_001448	-1	0.000911024	0.69 (0.56, 0.86)	3.00%	1.04	1.29
HNMT	NM_001024074	-1	0.001007463	0.61 (0.45, 0.82)	3.20%	1.04	1.31
HNMT	NM_006895	-1	0.001007463	0.61 (0.45, 0.82)	3.20%	1.04	1.31
HNMT	NM_001024075	-1	0.001007463	0.61 (0.45, 0.82)	3.20%	1.04	1.31
HSBP1	NM_001537	1	0.001388414	1.93 (1.29, 2.89)	3.80%	1.04	1.3
ILF2	NM_004515	1	0.001444137	1.77 (1.25, 2.51)	3.80%	1.04	1.3
INCENP	NM_001040694	1	0.001350727	1.77 (1.25, 2.52)	3.70%	1.04	1.3
INCENP	NM_020238	1	0.001350727	1.77 (1.25, 2.52)	3.70%	1.04	1.3
KIAA0802	NM_015210	-1	0.000733238	0.66 (0.52, 0.84)	2.60%	1.04	1.3
LOC100129636	NM_001195202	1	0.000568239	1.41 (1.16, 1.71)	2.20%	1.04	1.29
LRRC50	NM_178452	-1	0.001142207	0.62 (0.46, 0.83)	3.40%	1.04	1.3
LSS	NM_001145436	1	0.00102682	1.85 (1.28, 2.68)	3.20%	1.04	1.31

LSS	NM_001145437	1	0.00102682	1.85 (1.28, 2.68)	3.20%	1.04	1.31
LSS	NM_001001438	1	0.00102682	1.85 (1.28, 2.68)	3.20%	1.04	1.31
LSS	NM_002340	1	0.00102682	1.85 (1.28, 2.68)	3.20%	1.04	1.31
LYPD2	NM_205545	1	0.000432072	1.29 (1.12, 1.48)	1.90%	1.04	1.24
MARCH6	NM_005885	1	0.001493132	1.94 (1.29, 2.93)	3.90%	1.04	1.29
MDH1B	NM_001039845	-1	0.001226529	0.59 (0.43, 0.82)	3.50%	1.04	1.3
MELK	NM_014791	1	0.001334491	1.89 (1.28, 2.78)	3.70%	1.04	1.3
MEPE	NM_001184695	1	0.000345187	1.35 (1.14, 1.59)	1.60%	1.04	1.27
MEPE	NM_001184696	1	0.000345187	1.35 (1.14, 1.59)	1.60%	1.04	1.27
MEPE	NM_001184694	1	0.000345187	1.35 (1.14, 1.59)	1.60%	1.04	1.27
MEPE	NM_001184697	1	0.000345187	1.35 (1.14, 1.59)	1.60%	1.04	1.27
MEPE	NM_020203	1	0.000345187	1.35 (1.14, 1.59)	1.60%	1.04	1.27
MGAT4B	NM_014275	1	0.001660199	1.94 (1.28, 2.93)	4.10%	1.04	1.29
MGAT4B	NM_054013	1	0.001660199	1.94 (1.28, 2.93)	4.10%	1.04	1.29
MIR1266	NR_031670	1	0.000694086	1.45 (1.17, 1.79)	2.50%	1.04	1.29
MKL2	NM_014048	-1	0.001149841	0.55 (0.38, 0.79)	3.40%	1.04	1.3
MND1	NM_032117	1	0.001547106	1.80 (1.25, 2.59)	4.00%	1.04	1.3
MORC2	NM_014941	1	0.001258176	1.73 (1.24, 2.42)	3.60%	1.04	1.31
MUM1L1	NM_152423	-1	0.001393772	0.60 (0.44, 0.82)	3.80%	1.04	1.3
MUM1L1	NM_001171020	-1	0.001393772	0.60 (0.44, 0.82)	3.80%	1.04	1.3
NCRNA00094	NR_015427	-1	0.001103609	0.60 (0.44, 0.82)	3.30%	1.04	1.31
NDUFV1	NM_007103	1	0.001409686	1.72 (1.23, 2.41)	3.80%	1.04	1.3
NDUFV1	NM_001166102	1	0.001409686	1.72 (1.23, 2.41)	3.80%	1.04	1.3
NEFL	NM_006158	-1	0.001687285	0.45 (0.27, 0.74)	4.20%	1.04	1.26
NOSTRIN	NM_001171631	-1	0.001252393	0.54 (0.37, 0.78)	3.60%	1.04	1.3
NOSTRIN	NM_052946	-1	0.001252393	0.54 (0.37, 0.78)	3.60%	1.04	1.3
NOSTRIN	NM_001039724	-1	0.001252393	0.54 (0.37, 0.78)	3.60%	1.04	1.3
NOSTRIN	NM_001171632	-1	0.001252393	0.54 (0.37, 0.78)	3.60%	1.04	1.3
NPFFR1	NM_022146	1	0.000403573	1.37 (1.15, 1.63)	1.80%	1.04	1.28
NR1H4	NM_005123	1	0.000190977	1.21 (1.09, 1.34)	1.20%	1.04	1.19
OR52E6	NM_001005167	1	0.000848918	1.64 (1.23, 2.18)	2.80%	1.04	1.32
OR8S1	NM_001005203	1	0.00023101	1.27 (1.12, 1.45)	1.30%	1.04	1.23
ORM1	NM_000607	1	0.000975674	1.51 (1.18, 1.93)	3.10%	1.04	1.3
OSCP1	NM_145047	-1	0.001246562	0.64 (0.49, 0.84)	3.60%	1.04	1.3
OSCP1	NM_206837	-1	0.001246562	0.64 (0.49, 0.84)	3.60%	1.04	1.3
PAR-SN	NR_022011	-1	0.001065009	0.68 (0.54, 0.86)	3.30%	1.04	1.29
PDE4A	NM_001111308	-1	0.001540235	0.56 (0.39, 0.80)	4.00%	1.04	1.29
PDE4A	NM_001111307	-1	0.001540235	0.56 (0.39, 0.80)	4.00%	1.04	1.29
PDE4A	NM_006202	-1	0.001540235	0.56 (0.39, 0.80)	4.00%	1.04	1.29
PDE4A	NM_001111309	-1	0.001540235	0.56 (0.39, 0.80)	4.00%	1.04	1.29
PGA3	NM_001079807	1	0.000794713	1.37 (1.14, 1.65)	2.70%	1.04	1.27
PHF23	NM_024297	-1	0.00118066	0.57 (0.41, 0.80)	3.50%	1.04	1.3
PLEKHA8	NM_001197026	1	0.001145142	1.67 (1.22, 2.26)	3.40%	1.04	1.31
PLEKHA8	NM_032639	1	0.001145142	1.67 (1.22, 2.26)	3.40%	1.04	1.31
PLEKHA8	NM_001197027	1	0.001145142	1.67 (1.22, 2.26)	3.40%	1.04	1.31
POLG2	NM_007215	1	0.001113968	1.50 (1.18, 1.92)	3.30%	1.04	1.3
POTEG	NR_027480	1	0.000753813	1.52 (1.19, 1.93)	2.70%	1.04	1.31
POTEG	NM_001005356	1	0.000753813	1.52 (1.19, 1.93)	2.70%	1.04	1.31
PRDX1	NM_002574	1	0.001365139	1.96 (1.30, 2.97)	3.70%	1.04	1.29

PRDX1	NM_181697	1	0.001365139	1.96 (1.30, 2.97)	3.70%	1.04	1.29
PRDX1	NM_181696	1	0.001365139	1.96 (1.30, 2.97)	3.70%	1.04	1.29
PRKCG	NM_002739	1	0.000915815	1.43 (1.16, 1.77)	3.00%	1.04	1.29
PRRC1	NM_130809	1	0.001282446	2.02 (1.32, 3.10)	3.60%	1.04	1.29
PSMD7	NM_002811	1	0.00121422	1.76 (1.25, 2.49)	3.50%	1.04	1.31
PTPN13	NM_080683	-1	0.001238326	0.57 (0.40, 0.80)	3.60%	1.04	1.3
PTPN13	NM_080684	-1	0.001238326	0.57 (0.40, 0.80)	3.60%	1.04	1.3
PTPN13	NM_080685	-1	0.001238326	0.57 (0.40, 0.80)	3.60%	1.04	1.3
PTPN13	NM_006264	-1	0.001238326	0.57 (0.40, 0.80)	3.60%	1.04	1.3
PTPRF	NM_130440	1	0.001244621	1.71 (1.23, 2.36)	3.60%	1.04	1.31
PTPRF	NM_002840	1	0.001244621	1.71 (1.23, 2.36)	3.60%	1.04	1.31
RCBTB1	NM_018191	-1	0.001286867	0.57 (0.41, 0.80)	3.60%	1.04	1.3
RPH3A	NM_014954	1	0.00083144	1.42 (1.16, 1.75)	2.80%	1.04	1.29
RPH3A	NM_001143854	1	0.00083144	1.42 (1.16, 1.75)	2.80%	1.04	1.29
RPS19BP1	NM_194326	1	0.00131552	2.03 (1.32, 3.12)	3.70%	1.04	1.29
RRM2	NM_001034	1	0.001359597	2.12 (1.34, 3.37)	3.70%	1.04	1.28
RRM2	NM_001165931	1	0.001359597	2.12 (1.34, 3.37)	3.70%	1.04	1.28
RTKN2	NM_145307	1	0.001215644	1.79 (1.26, 2.55)	3.50%	1.04	1.31
SHMT2	NM_001166359	1	0.001409397	1.76 (1.24, 2.50)	3.80%	1.04	1.3
SHMT2	NM_001166358	1	0.001409397	1.76 (1.24, 2.50)	3.80%	1.04	1.3
SHMT2	NM_001166357	1	0.001409397	1.76 (1.24, 2.50)	3.80%	1.04	1.3
SHMT2	NM_001166356	1	0.001409397	1.76 (1.24, 2.50)	3.80%	1.04	1.3
SHMT2	NM_005412	1	0.001409397	1.76 (1.24, 2.50)	3.80%	1.04	1.3
SHMT2	NR_029416	1	0.001409397	1.76 (1.24, 2.50)	3.80%	1.04	1.3
SHMT2	NR_029417	1	0.001409397	1.76 (1.24, 2.50)	3.80%	1.04	1.3
SHMT2	NR_029415	1	0.001409397	1.76 (1.24, 2.50)	3.80%	1.04	1.3
SHPK	NM_013276	-1	0.001138133	0.50 (0.33, 0.76)	3.40%	1.04	1.29
SLC43A1	NM_001198810	-1	0.001564414	0.54 (0.37, 0.79)	4.10%	1.04	1.29
SLC43A1	NM_003627	-1	0.001564414	0.54 (0.37, 0.79)	4.10%	1.04	1.29
SMAD7	NM_001190821	-1	0.001127632	0.63 (0.48, 0.83)	3.40%	1.04	1.3
SMAD7	NM_005904	-1	0.001127632	0.63 (0.48, 0.83)	3.40%	1.04	1.3
SMAD7	NM_001190822	-1	0.001127632	0.63 (0.48, 0.83)	3.40%	1.04	1.3
SMAD7	NM_001190823	-1	0.001127632	0.63 (0.48, 0.83)	3.40%	1.04	1.3
SMG5	NM_015327	1	0.001368035	1.81 (1.26, 2.61)	3.70%	1.04	1.3
SPAG17	NM_206996	-1	0.001277464	0.54 (0.37, 0.79)	3.60%	1.04	1.3
SPRR3	NM_001097589	1	0.000735393	1.43 (1.16, 1.77)	2.60%	1.04	1.29
SPRR3	NM_005416	1	0.000735393	1.43 (1.16, 1.77)	2.60%	1.04	1.29
STARD13	NM_178007	-1	0.001355506	0.51 (0.33, 0.77)	3.70%	1.04	1.29
STARD13	NM_178006	-1	0.001355506	0.51 (0.33, 0.77)	3.70%	1.04	1.29
STARD13	NM_052851	-1	0.001355506	0.51 (0.33, 0.77)	3.70%	1.04	1.29
STH	NM_001007532	-1	0.001002598	0.61 (0.45, 0.82)	3.20%	1.04	1.31
TALDO1	NM_006755	1	0.001614891	2.06 (1.31, 3.23)	4.10%	1.04	1.28
TMC6	NM_007267	1	0.001392884	1.78 (1.25, 2.53)	3.80%	1.04	1.3
TMC6	NM_001127198	1	0.001392884	1.78 (1.25, 2.53)	3.80%	1.04	1.3
TMEM194A	NM_015257	1	0.001255127	1.78 (1.25, 2.52)	3.60%	1.04	1.31
TMEM194A	NM_001130963	1	0.001255127	1.78 (1.25, 2.52)	3.60%	1.04	1.31
TMEM229B	NM_182526	-1	0.001174425	0.60 (0.44, 0.82)	3.50%	1.04	1.3
TMPRSS11E	NM_014058	1	0.001024924	1.57 (1.20, 2.06)	3.20%	1.04	1.31
TOR1AIP2	NM_022347	1	0.001376663	1.89 (1.28, 2.80)	3.80%	1.04	1.3

TOR1AIP2	NM_145034	1	0.001376663	1.89 (1.28, 2.80)	3.80%	1.04	1.3
TOR1AIP2	NM_001199260	1	0.001376663	1.89 (1.28, 2.80)	3.80%	1.04	1.3
TPD52L2	NM_199359	1	0.001081496	1.60 (1.21, 2.12)	3.30%	1.04	1.31
TPD52L2	NM_199360	1	0.001081496	1.60 (1.21, 2.12)	3.30%	1.04	1.31
TPD52L2	NM_199361	1	0.001081496	1.60 (1.21, 2.12)	3.30%	1.04	1.31
TPD52L2	NM_199362	1	0.001081496	1.60 (1.21, 2.12)	3.30%	1.04	1.31
TPD52L2	NM_199363	1	0.001081496	1.60 (1.21, 2.12)	3.30%	1.04	1.31
TPD52L2	NM_003288	1	0.001081496	1.60 (1.21, 2.12)	3.30%	1.04	1.31
TPH2	NM_173353	1	0.001086792	1.61 (1.21, 2.14)	3.30%	1.04	1.31
TRAK1	NM_001042646	-1	0.001111813	0.57 (0.41, 0.80)	3.30%	1.04	1.31
TRAK1	NM_014965	-1	0.001111813	0.57 (0.41, 0.80)	3.30%	1.04	1.31
TTC23L	NM_144725	-1	0.00182818	0.46 (0.28, 0.75)	4.40%	1.04	1.26
UNC119B	NM_001080533	-1	0.001111663	0.56 (0.40, 0.80)	3.30%	1.04	1.31
ZNF442	NM_030824	-1	0.001384421	0.60 (0.44, 0.82)	3.80%	1.04	1.3
ZNF512	NM_032434	-1	0.001588962	0.53 (0.35, 0.78)	4.10%	1.04	1.29
ZNF528	NM_032423	-1	0.001148516	0.54 (0.38, 0.78)	3.40%	1.04	1.3
ACOX3	NM_003501	-1	0.001635988	0.59 (0.43, 0.82)	4.10%	1.03	1.29
ACOX3	NM_001101667	-1	0.001635988	0.59 (0.43, 0.82)	4.10%	1.03	1.29
ANUBL1	NM_001128324	-1	0.001585772	0.57 (0.40, 0.81)	4.10%	1.03	1.29
ANUBL1	NM_174890	-1	0.001585772	0.57 (0.40, 0.81)	4.10%	1.03	1.29
AVL9	NM_015060	1	0.001403234	1.42 (1.14, 1.75)	3.80%	1.03	1.28
BICD2	NM_001003800	-1	0.002587505	0.52 (0.34, 0.79)	5.40%	1.03	1.27
BICD2	NM_015250	-1	0.002587505	0.52 (0.34, 0.79)	5.40%	1.03	1.27
BUB1B	NM_001211	1	0.002718314	1.97 (1.27, 3.08)	5.50%	1.03	1.27
C10orf82	NM_144661	-1	0.002795215	0.48 (0.29, 0.77)	5.60%	1.03	1.25
C11orf61	NM_024631	-1	0.001104328	0.72 (0.59, 0.87)	3.30%	1.03	1.27
C12orf65	NM_001194995	-1	0.001612306	0.75 (0.62, 0.90)	4.10%	1.03	1.25
C12orf65	NM_001143905	-1	0.001612306	0.75 (0.62, 0.90)	4.10%	1.03	1.25
C12orf65	NM_152269	-1	0.001612306	0.75 (0.62, 0.90)	4.10%	1.03	1.25
C14orf147	NM_138288	1	0.001459289	1.61 (1.20, 2.15)	3.90%	1.03	1.3
C17orf85	NM_001114118	-1	0.002505604	0.55 (0.37, 0.81)	5.30%	1.03	1.28
C17orf85	NM_018553	-1	0.002505604	0.55 (0.37, 0.81)	5.30%	1.03	1.28
C19orf75	NM_173635	1	0.00067445	1.25 (1.10, 1.41)	2.50%	1.03	1.21
C1orf198	NM_032800	1	0.002616809	1.80 (1.23, 2.63)	5.50%	1.03	1.28
C1orf198	NM_001136495	1	0.002616809	1.80 (1.23, 2.63)	5.50%	1.03	1.28
C1orf198	NM_001136494	1	0.002616809	1.80 (1.23, 2.63)	5.50%	1.03	1.28
C1RL	NM_016546	-1	0.001589374	0.61 (0.45, 0.83)	4.10%	1.03	1.3
C20orf185	NM_182658	1	0.001202794	1.41 (1.15, 1.74)	3.50%	1.03	1.28
C4orf29	NM_001039717	-1	0.002120732	0.60 (0.43, 0.83)	4.90%	1.03	1.29
C5orf54	NM_022090	-1	0.000954196	0.73 (0.61, 0.88)	3.10%	1.03	1.26
C6orf155	NR_026807	-1	0.002572118	0.55 (0.37, 0.81)	5.40%	1.03	1.27
C7orf63	NM_001160138	-1	0.001543596	0.59 (0.42, 0.82)	4.00%	1.03	1.3
C7orf63	NM_001039706	-1	0.001543596	0.59 (0.42, 0.82)	4.00%	1.03	1.3
C9orf57	NM_001128618	1	0.001866683	1.51 (1.17, 1.96)	4.50%	1.03	1.29
C9orf78	NM_016520	-1	0.002244374	0.54 (0.36, 0.80)	5.00%	1.03	1.28
CASZ1	NM_017766	-1	0.002238185	0.59 (0.43, 0.83)	5.00%	1.03	1.28
CASZ1	NM_001079843	-1	0.002238185	0.59 (0.43, 0.83)	5.00%	1.03	1.28
CBLN4	NM_080617	-1	0.001922952	0.58 (0.41, 0.82)	4.60%	1.03	1.29
CCDC94	NM_018074	-1	0.002570559	0.57 (0.40, 0.82)	5.40%	1.03	1.28

CDK5RAP2	NM_001011649	-1	0.001639429	0.57 (0.40, 0.81)	4.10%	1.03	1.29
CDK5RAP2	NM_018249	-1	0.001639429	0.57 (0.40, 0.81)	4.10%	1.03	1.29
CEP55	NM_018131	1	0.002707603	2.06 (1.28, 3.30)	5.50%	1.03	1.26
CEP55	NM_001127182	1	0.002707603	2.06 (1.28, 3.30)	5.50%	1.03	1.26
CHAT	NM_020986	1	0.001696264	1.39 (1.13, 1.70)	4.20%	1.03	1.26
CHAT	NM_001142934	1	0.001696264	1.39 (1.13, 1.70)	4.20%	1.03	1.26
CHAT	NM_020985	1	0.001696264	1.39 (1.13, 1.70)	4.20%	1.03	1.26
CHAT	NM_001142933	1	0.001696264	1.39 (1.13, 1.70)	4.20%	1.03	1.26
CHAT	NM_020549	1	0.001696264	1.39 (1.13, 1.70)	4.20%	1.03	1.26
CHAT	NM_020984	1	0.001696264	1.39 (1.13, 1.70)	4.20%	1.03	1.26
CHAT	NM_001142929	1	0.001696264	1.39 (1.13, 1.70)	4.20%	1.03	1.26
COL4A5	NM_033380	-1	0.002200738	0.63 (0.47, 0.85)	5.00%	1.03	1.28
COL4A5	NM_000495	-1	0.002200738	0.63 (0.47, 0.85)	5.00%	1.03	1.28
CRELD2	NM_024324	1	0.001485273	1.40 (1.14, 1.72)	3.90%	1.03	1.27
CRELD2	NM_001135101	1	0.001485273	1.40 (1.14, 1.72)	3.90%	1.03	1.27
CYB5D1	NM_144607	-1	0.001747826	0.58 (0.41, 0.81)	4.30%	1.03	1.29
CYP19A1	NM_000103	1	0.002444512	1.73 (1.21, 2.46)	5.20%	1.03	1.28
CYP19A1	NM_031226	1	0.002444512	1.73 (1.21, 2.46)	5.20%	1.03	1.28
DDX20	NM_007204	-1	0.002289514	0.48 (0.30, 0.77)	5.10%	1.03	1.26
DDX42	NM_007372	1	0.001720318	1.44 (1.15, 1.81)	4.20%	1.03	1.28
DDX42	NM_203499	1	0.001720318	1.44 (1.15, 1.81)	4.20%	1.03	1.28
DEF8	NM_207514	1	0.002624521	2.11 (1.30, 3.43)	5.50%	1.03	1.26
DEF8	NM_017702	1	0.002624521	2.11 (1.30, 3.43)	5.50%	1.03	1.26
DGAT1	NM_012079	1	0.001720682	1.63 (1.20, 2.22)	4.20%	1.03	1.3
DNAJC28	NM_017833	-1	0.001409688	0.66 (0.51, 0.85)	3.80%	1.03	1.29
DNAJC28	NM_001040192	-1	0.001409688	0.66 (0.51, 0.85)	3.80%	1.03	1.29
DYNC1LI2	NM_006141	1	0.002089376	1.61 (1.19, 2.17)	4.80%	1.03	1.29
E2F5	NM_001951	1	0.002136056	2.12 (1.31, 3.43)	4.90%	1.03	1.27
E2F5	NM_001083588	1	0.002136056	2.12 (1.31, 3.43)	4.90%	1.03	1.27
E2F5	NM_001083589	1	0.002136056	2.12 (1.31, 3.43)	4.90%	1.03	1.27
EGOT	NR_004428	-1	0.001636301	0.65 (0.50, 0.85)	4.10%	1.03	1.29
ELOVL2	NM_017770	-1	0.002382215	0.62 (0.45, 0.84)	5.20%	1.03	1.28
ELP3	NM_018091	-1	0.002213346	0.61 (0.44, 0.84)	5.00%	1.03	1.29
EVX2	NM_001080458	1	0.001725038	1.37 (1.12, 1.66)	4.20%	1.03	1.26
FANCD2	NM_001018115	1	0.001545769	1.74 (1.23, 2.45)	4.00%	1.03	1.3
FANCD2	NM_033084	1	0.001545769	1.74 (1.23, 2.45)	4.00%	1.03	1.3
FBN3	NM_032447	1	0.001991297	1.57 (1.18, 2.10)	4.70%	1.03	1.29
FEZF1	NM_001160264	1	0.001027358	1.39 (1.14, 1.68)	3.20%	1.03	1.27
FEZF1	NM_001024613	1	0.001027358	1.39 (1.14, 1.68)	3.20%	1.03	1.27
FHL3	NM_004468	-1	0.001474563	0.70 (0.56, 0.87)	3.90%	1.03	1.27
FST	NM_013409	-1	0.001727143	0.66 (0.51, 0.85)	4.20%	1.03	1.29
FST	NM_006350	-1	0.001727143	0.66 (0.51, 0.85)	4.20%	1.03	1.29
FURIN	NM_002569	1	0.002269916	1.64 (1.19, 2.25)	5.10%	1.03	1.29
FUT2	NM_001097638	-1	0.001525692	0.72 (0.59, 0.88)	4.00%	1.03	1.27
FUT2	NM_000511	-1	0.001525692	0.72 (0.59, 0.88)	4.00%	1.03	1.27
GGCX	NM_000821	1	0.002396435	1.80 (1.23, 2.62)	5.20%	1.03	1.28
GGCX	NM_001142269	1	0.002396435	1.80 (1.23, 2.62)	5.20%	1.03	1.28
GGH	NM_003878	1	0.002274114	2.01 (1.28, 3.16)	5.10%	1.03	1.27
GLIPR1L2	NM_152436	-1	0.001862715	0.53 (0.36, 0.79)	4.50%	1.03	1.28

GNG3	NM_012202	-1	0.002062355	0.64 (0.48, 0.85)	4.80%	1.03	1.29
GRINA	NM_000837	1	0.001753597	1.62 (1.20, 2.20)	4.30%	1.03	1.3
GRINA	NM_001009184	1	0.001753597	1.62 (1.20, 2.20)	4.30%	1.03	1.3
GSTM4	NR_024538	-1	0.001336578	0.65 (0.50, 0.85)	3.70%	1.03	1.29
GSTM4	NM_147148	-1	0.001336578	0.65 (0.50, 0.85)	3.70%	1.03	1.29
GSTM4	NM_000850	-1	0.001336578	0.65 (0.50, 0.85)	3.70%	1.03	1.29
HMMR	NM_001142557	1	0.002208484	2.21 (1.33, 3.66)	5.00%	1.03	1.26
HMMR	NM_012485	1	0.002208484	2.21 (1.33, 3.66)	5.00%	1.03	1.26
HMMR	NM_012484	1	0.002208484	2.21 (1.33, 3.66)	5.00%	1.03	1.26
HMMR	NM_001142556	1	0.002208484	2.21 (1.33, 3.66)	5.00%	1.03	1.26
HMX3	NM_001105574	1	0.001618681	1.50 (1.17, 1.93)	4.10%	1.03	1.29
HTATIP2	NM_001098523	1	0.002516349	1.85 (1.24, 2.75)	5.30%	1.03	1.28
HTATIP2	NM_001098520	1	0.002516349	1.85 (1.24, 2.75)	5.30%	1.03	1.28
HTATIP2	NM_001098522	1	0.002516349	1.85 (1.24, 2.75)	5.30%	1.03	1.28
HTATIP2	NM_006410	1	0.002516349	1.85 (1.24, 2.75)	5.30%	1.03	1.28
HTATIP2	NM_001098521	1	0.002516349	1.85 (1.24, 2.75)	5.30%	1.03	1.28
IFTS7	NM_018010	-1	0.001435878	0.63 (0.47, 0.84)	3.80%	1.03	1.3
IKBKB	NR_033819	-1	0.002214905	0.58 (0.41, 0.82)	5.00%	1.03	1.28
IKBKB	NM_001190721	-1	0.002214905	0.58 (0.41, 0.82)	5.00%	1.03	1.28
IKBKB	NM_001556	-1	0.002214905	0.58 (0.41, 0.82)	5.00%	1.03	1.28
IKBKB	NM_001190722	-1	0.002214905	0.58 (0.41, 0.82)	5.00%	1.03	1.28
IKBKB	NR_033818	-1	0.002214905	0.58 (0.41, 0.82)	5.00%	1.03	1.28
IKBKB	NM_001190720	-1	0.002214905	0.58 (0.41, 0.82)	5.00%	1.03	1.28
IKBKB	NR_033820	-1	0.002214905	0.58 (0.41, 0.82)	5.00%	1.03	1.28
INTS8	NM_017864	1	0.002325883	1.59 (1.18, 2.13)	5.10%	1.03	1.29
IYD	NM_001164694	1	0.002010449	1.71 (1.22, 2.40)	4.70%	1.03	1.29
IYD	NM_001164695	1	0.002010449	1.71 (1.22, 2.40)	4.70%	1.03	1.29
IYD	NM_203395	1	0.002010449	1.71 (1.22, 2.40)	4.70%	1.03	1.29
KBTBD10	NM_006063	-1	0.001722602	0.60 (0.44, 0.83)	4.20%	1.03	1.29
KIAA1310	NM_017991	-1	0.002113999	0.54 (0.37, 0.80)	4.90%	1.03	1.28
KIAA1310	NM_001115016	-1	0.002113999	0.54 (0.37, 0.80)	4.90%	1.03	1.28
KIF25	NM_030615	1	0.002238069	1.56 (1.17, 2.08)	5.00%	1.03	1.29
KIF25	NM_005355	1	0.002238069	1.56 (1.17, 2.08)	5.00%	1.03	1.29
KIF5C	NM_004522	-1	0.002437989	0.52 (0.34, 0.79)	5.20%	1.03	1.27
KLRC1	NM_213657	1	0.002384431	1.66 (1.20, 2.31)	5.20%	1.03	1.29
KLRC1	NM_213658	1	0.002384431	1.66 (1.20, 2.31)	5.20%	1.03	1.29
KLRC1	NM_002259	1	0.002384431	1.66 (1.20, 2.31)	5.20%	1.03	1.29
KLRC1	NM_007328	1	0.002384431	1.66 (1.20, 2.31)	5.20%	1.03	1.29
KLRD1	NM_002262	1	0.002060071	1.75 (1.23, 2.50)	4.80%	1.03	1.29
KLRD1	NM_001114396	1	0.002060071	1.75 (1.23, 2.50)	4.80%	1.03	1.29
KLRD1	NM_007334	1	0.002060071	1.75 (1.23, 2.50)	4.80%	1.03	1.29
LAD1	NM_005558	1	0.001800788	1.98 (1.29, 3.04)	4.30%	1.03	1.28
LHX5	NM_022363	1	0.00111698	1.42 (1.15, 1.75)	3.30%	1.03	1.28
LHX9	NM_020204	1	0.00171801	1.41 (1.14, 1.74)	4.20%	1.03	1.27
LHX9	NM_001014434	1	0.00171801	1.41 (1.14, 1.74)	4.20%	1.03	1.27
LOC100289187	NM_001195543	-1	0.002038702	0.55 (0.37, 0.80)	4.70%	1.03	1.28
LOC100289187	NM_001195542	-1	0.002038702	0.55 (0.37, 0.80)	4.70%	1.03	1.28
LOC100289187	NM_001195541	-1	0.002038702	0.55 (0.37, 0.80)	4.70%	1.03	1.28
LOC145474	NR_027046	-1	0.001569524	0.70 (0.56, 0.87)	4.10%	1.03	1.27

LOC284276	NR_015417	-1	0.002303624	0.46 (0.28, 0.76)	5.10%	1.03	1.26
LOC648740	NR_024438	-1	0.002018901	0.63 (0.47, 0.84)	4.70%	1.03	1.29
LRP2	NM_004525	-1	0.002286764	0.61 (0.44, 0.84)	5.10%	1.03	1.28
LRRC39	NM_144620	-1	0.001617813	0.61 (0.45, 0.83)	4.10%	1.03	1.29
LRRC48	NM_031294	-1	0.002131791	0.59 (0.42, 0.83)	4.90%	1.03	1.29
LRRC48	NM_001130092	-1	0.002131791	0.59 (0.42, 0.83)	4.90%	1.03	1.29
LRRC48	NM_001130091	-1	0.002131791	0.59 (0.42, 0.83)	4.90%	1.03	1.29
LRRC48	NM_001130090	-1	0.002131791	0.59 (0.42, 0.83)	4.90%	1.03	1.29
METT10D	NM_024086	-1	0.002064663	0.55 (0.37, 0.80)	4.80%	1.03	1.28
MIR3143	NR_036096	1	0.001719228	1.51 (1.17, 1.95)	4.20%	1.03	1.29
MIR539	NR_030256	1	0.001267367	1.53 (1.18, 1.98)	3.60%	1.03	1.3
MRPL46	NM_022163	1	0.002420243	1.72 (1.21, 2.44)	5.20%	1.03	1.29
MRPS6	NM_032476	1	0.00225102	1.79 (1.23, 2.61)	5.00%	1.03	1.29
MUC21	NM_001010909	1	0.002145168	1.56 (1.18, 2.08)	4.90%	1.03	1.29
MYBL2	NM_002466	1	0.002287866	1.94 (1.27, 2.96)	5.10%	1.03	1.28
MYO15B	NR_003587	-1	0.001947645	0.61 (0.44, 0.83)	4.60%	1.03	1.29
NCAM2	NM_004540	-1	0.002198648	0.57 (0.39, 0.81)	5.00%	1.03	1.28
NEIL3	NM_018248	1	0.002666588	1.89 (1.25, 2.86)	5.50%	1.03	1.27
NEK10	NM_199347	-1	0.002329341	0.54 (0.37, 0.81)	5.10%	1.03	1.28
NEK2	NM_002497	1	0.002473048	2.01 (1.28, 3.15)	5.30%	1.03	1.27
NFXL1	NM_152995	1	0.001183142	1.45 (1.16, 1.82)	3.50%	1.03	1.29
NPPB	NM_002521	1	0.000858578	1.35 (1.13, 1.61)	2.90%	1.03	1.26
OGN	NM_014057	-1	0.002456696	0.45 (0.27, 0.75)	5.30%	1.03	1.25
OGN	NM_033014	-1	0.002456696	0.45 (0.27, 0.75)	5.30%	1.03	1.25
PARD3B	NM_205863	-1	0.001655273	0.57 (0.41, 0.81)	4.10%	1.03	1.29
PARD3B	NM_057177	-1	0.001655273	0.57 (0.41, 0.81)	4.10%	1.03	1.29
PARD3B	NM_152526	-1	0.001655273	0.57 (0.41, 0.81)	4.10%	1.03	1.29
PCM1	NM_006197	-1	0.002032488	0.50 (0.32, 0.78)	4.70%	1.03	1.27
PDE11A	NM_001077197	-1	0.001651988	0.64 (0.48, 0.84)	4.10%	1.03	1.29
PDE11A	NM_016953	-1	0.001651988	0.64 (0.48, 0.84)	4.10%	1.03	1.29
PDE11A	NM_001077196	-1	0.001651988	0.64 (0.48, 0.84)	4.10%	1.03	1.29
PDE11A	NM_001077358	-1	0.001651988	0.64 (0.48, 0.84)	4.10%	1.03	1.29
PDIA6	NM_005742	1	0.001634746	1.67 (1.21, 2.29)	4.10%	1.03	1.3
PEX1	NM_000466	-1	0.002362939	0.61 (0.44, 0.84)	5.20%	1.03	1.28
PEX13	NM_002618	1	0.001593701	1.69 (1.22, 2.34)	4.10%	1.03	1.3
PGCP	NM_016134	-1	0.001725315	0.60 (0.44, 0.83)	4.20%	1.03	1.29
PGR	NM_000926	-1	0.001909419	0.57 (0.40, 0.81)	4.50%	1.03	1.29
PHF2P1	NR_002801	1	0.001167977	1.35 (1.13, 1.62)	3.40%	1.03	1.26
PIK3C2A	NM_002645	-1	0.001585299	0.59 (0.43, 0.82)	4.10%	1.03	1.3
PMAIP1	NM_021127	-1	0.001954098	0.64 (0.49, 0.85)	4.60%	1.03	1.29
POMC	NM_001035256	1	0.001777068	1.50 (1.16, 1.93)	4.30%	1.03	1.29
POMC	NM_000939	1	0.001777068	1.50 (1.16, 1.93)	4.30%	1.03	1.29
PPP1R2P1	NR_027771	1	0.00211075	1.58 (1.18, 2.12)	4.90%	1.03	1.29
PRC1	NM_003981	1	0.0023281	1.83 (1.24, 2.70)	5.10%	1.03	1.28
PRC1	NM_199414	1	0.0023281	1.83 (1.24, 2.70)	5.10%	1.03	1.28
PRC1	NM_199413	1	0.0023281	1.83 (1.24, 2.70)	5.10%	1.03	1.28
PRSS41	NM_001135086	1	0.000819741	1.29 (1.11, 1.50)	2.80%	1.03	1.24
PVRL4	NM_030916	1	0.002436856	1.77 (1.22, 2.55)	5.20%	1.03	1.28
PVT1	NR_003367	-1	0.000985501	0.76 (0.65, 0.89)	3.10%	1.03	1.24

PYCRL	NM_023078	1	0.002594279	2.02 (1.28, 3.20)	5.40%	1.03	1.27
RAB1A	NM_004161	1	0.001769368	1.72 (1.22, 2.42)	4.30%	1.03	1.3
RAB1A	NM_015543	1	0.001769368	1.72 (1.22, 2.42)	4.30%	1.03	1.3
RAB9BP1	NR_000039	1	0.0016054	1.48 (1.16, 1.89)	4.10%	1.03	1.29
RAET1K	NR_024045	1	0.001800197	1.51 (1.16, 1.95)	4.30%	1.03	1.29
RAPGEF5	NM_012294	1	0.002154043	1.56 (1.17, 2.08)	4.90%	1.03	1.29
RBM24	NM_001143941	-1	0.002564648	0.51 (0.33, 0.79)	5.40%	1.03	1.27
RBM24	NM_153020	-1	0.002564648	0.51 (0.33, 0.79)	5.40%	1.03	1.27
RBM24	NM_001143942	-1	0.002564648	0.51 (0.33, 0.79)	5.40%	1.03	1.27
RPL6	NM_000970	-1	0.001139844	0.71 (0.57, 0.87)	3.40%	1.03	1.28
RPL6	NM_001024662	-1	0.001139844	0.71 (0.57, 0.87)	3.40%	1.03	1.28
SALL2	NM_005407	-1	0.001427511	0.66 (0.52, 0.85)	3.80%	1.03	1.29
SETBP1	NM_015559	-1	0.002219007	0.52 (0.34, 0.79)	5.00%	1.03	1.27
SETBP1	NM_001130110	-1	0.002219007	0.52 (0.34, 0.79)	5.00%	1.03	1.27
SFI1	NM_001007467	-1	0.002372759	0.62 (0.45, 0.84)	5.20%	1.03	1.28
SFI1	NM_014775	-1	0.002372759	0.62 (0.45, 0.84)	5.20%	1.03	1.28
SHC2	NM_012435	-1	0.001912735	0.57 (0.41, 0.82)	4.50%	1.03	1.29
SKA3	NM_145061	1	0.002169941	2.22 (1.33, 3.69)	4.90%	1.03	1.26
SKA3	NM_001166017	1	0.002169941	2.22 (1.33, 3.69)	4.90%	1.03	1.26
SLC25A12	NM_003705	-1	0.002428642	0.58 (0.40, 0.82)	5.20%	1.03	1.28
SNCB	NM_001001502	1	0.00093158	1.37 (1.14, 1.66)	3.00%	1.03	1.27
SNCB	NM_003085	1	0.00093158	1.37 (1.14, 1.66)	3.00%	1.03	1.27
SNORA4	NR_002588	1	0.002448167	1.75 (1.22, 2.50)	5.20%	1.03	1.28
SNX29	NM_001080530	-1	0.002032127	0.66 (0.51, 0.86)	4.70%	1.03	1.28
SPRYD5	NM_032681	1	0.001186552	1.40 (1.14, 1.72)	3.50%	1.03	1.27
SRD5A1	NM_001047	1	0.001898168	1.80 (1.24, 2.62)	4.50%	1.03	1.29
SRM	NM_003132	1	0.00241018	2.18 (1.32, 3.59)	5.20%	1.03	1.26
STK36	NM_015690	-1	0.001844542	0.61 (0.44, 0.83)	4.40%	1.03	1.29
SUCLG1	NM_003849	1	0.00282029	2.20 (1.31, 3.68)	5.60%	1.03	1.25
SYNC	NM_030786	-1	0.001703858	0.62 (0.46, 0.84)	4.20%	1.03	1.29
SYNC	NM_001161708	-1	0.001703858	0.62 (0.46, 0.84)	4.20%	1.03	1.29
TBX3	NM_005996	-1	0.001955061	0.60 (0.44, 0.83)	4.60%	1.03	1.29
TBX3	NM_016569	-1	0.001955061	0.60 (0.44, 0.83)	4.60%	1.03	1.29
TMEM165	NM_018475	1	0.00206432	1.59 (1.18, 2.13)	4.80%	1.03	1.29
TMEM214	NM_017727	1	0.001586499	1.76 (1.24, 2.50)	4.10%	1.03	1.3
TMEM214	NM_001083590	1	0.001586499	1.76 (1.24, 2.50)	4.10%	1.03	1.3
TPRG1	NM_198485	-1	0.001640284	0.56 (0.39, 0.81)	4.10%	1.03	1.29
TRIM10	NM_052828	1	0.000954844	1.38 (1.14, 1.68)	3.10%	1.03	1.27
TRIM10	NM_006778	1	0.000954844	1.38 (1.14, 1.68)	3.10%	1.03	1.27
TRIM8	NM_030912	-1	0.001839592	0.60 (0.44, 0.83)	4.40%	1.03	1.29
UBA6	NM_018227	1	0.001297805	1.52 (1.18, 1.96)	3.60%	1.03	1.3
UGT2A1	NM_006798	1	0.001411139	1.31 (1.11, 1.55)	3.80%	1.03	1.24
USP16	NM_006447	-1	0.001528441	0.58 (0.41, 0.81)	4.00%	1.03	1.3
USP16	NM_001032410	-1	0.001528441	0.58 (0.41, 0.81)	4.00%	1.03	1.3
USP16	NM_001001992	-1	0.001528441	0.58 (0.41, 0.81)	4.00%	1.03	1.3
WDR26	NM_025160	1	0.002023353	1.90 (1.26, 2.85)	4.70%	1.03	1.28
WDR26	NM_001115113	1	0.002023353	1.90 (1.26, 2.85)	4.70%	1.03	1.28
WDR81	NM_001163673	-1	0.001691753	0.60 (0.43, 0.82)	4.20%	1.03	1.29
WDR81	NM_152348	-1	0.001691753	0.60 (0.43, 0.82)	4.20%	1.03	1.29

WDR81	NM_001163811	-1	0.001691753	0.60 (0.43, 0.82)	4.20%	1.03	1.29
WDR81	NM_001163809	-1	0.001691753	0.60 (0.43, 0.82)	4.20%	1.03	1.29
YPEL3	NM_001145524	-1	0.001617231	0.58 (0.41, 0.81)	4.10%	1.03	1.29
YPEL3	NM_031477	-1	0.001617231	0.58 (0.41, 0.81)	4.10%	1.03	1.29
ZBTB1	NM_001123329	-1	0.00145875	0.67 (0.53, 0.86)	3.90%	1.03	1.29
ZBTB1	NM_014950	-1	0.00145875	0.67 (0.53, 0.86)	3.90%	1.03	1.29
ZFHX2	NM_033400	-1	0.002397291	0.58 (0.41, 0.82)	5.20%	1.03	1.28
ZMAT1	NR_036431	-1	0.002074568	0.55 (0.38, 0.81)	4.80%	1.03	1.28
ZMAT1	NM_001011657	-1	0.002074568	0.55 (0.38, 0.81)	4.80%	1.03	1.28
ZNF219	NM_016423	-1	0.001654385	0.59 (0.43, 0.82)	4.10%	1.03	1.29
ZNF219	NM_001101672	-1	0.001654385	0.59 (0.43, 0.82)	4.10%	1.03	1.29
ZNF219	NM_001102454	-1	0.001654385	0.59 (0.43, 0.82)	4.10%	1.03	1.29
ZNF682	NM_001077349	-1	0.001906028	0.61 (0.44, 0.83)	4.50%	1.03	1.29
ZNF682	NM_033196	-1	0.001906028	0.61 (0.44, 0.83)	4.50%	1.03	1.29
ZNF705D	NM_001039615	1	0.001227404	1.35 (1.13, 1.62)	3.50%	1.03	1.26
ZNF747	NM_023931	-1	0.002131843	0.64 (0.48, 0.85)	4.90%	1.03	1.28
ZNF808	NM_001039886	-1	0.002223951	0.52 (0.34, 0.79)	5.00%	1.03	1.27
ABCA11P	NR_002451	-1	0.002873693	0.67 (0.51, 0.87)	5.70%	1.02	1.27
ABCA12	NM_015657	1	0.00300345	1.71 (1.20, 2.44)	5.80%	1.02	1.28
ABCA12	NM_173076	1	0.00300345	1.71 (1.20, 2.44)	5.80%	1.02	1.28
AMT	NM_000481	-1	0.002804366	0.65 (0.50, 0.86)	5.60%	1.02	1.27
AMT	NM_001164711	-1	0.002804366	0.65 (0.50, 0.86)	5.60%	1.02	1.27
AMT	NM_001164710	-1	0.002804366	0.65 (0.50, 0.86)	5.60%	1.02	1.27
AMT	NM_001164712	-1	0.002804366	0.65 (0.50, 0.86)	5.60%	1.02	1.27
AMT	NR_028435	-1	0.002804366	0.65 (0.50, 0.86)	5.60%	1.02	1.27
ANAPC2	NM_013366	-1	0.00312125	0.66 (0.50, 0.87)	6.00%	1.02	1.27
ANKRA2	NM_023039	-1	0.002819729	0.55 (0.37, 0.81)	5.60%	1.02	1.27
AP2M1	NM_001025205	1	0.002571858	1.57 (1.17, 2.11)	5.40%	1.02	1.28
AP2M1	NM_004068	1	0.002571858	1.57 (1.17, 2.11)	5.40%	1.02	1.28
ARF1	NM_001024227	1	0.003644362	1.90 (1.23, 2.92)	6.50%	1.02	1.26
ARF1	NM_001658	1	0.003644362	1.90 (1.23, 2.92)	6.50%	1.02	1.26
ARF1	NM_001024228	1	0.003644362	1.90 (1.23, 2.92)	6.50%	1.02	1.26
ARF1	NM_001024226	1	0.003644362	1.90 (1.23, 2.92)	6.50%	1.02	1.26
ATAD1	NM_032810	-1	0.004007343	0.63 (0.45, 0.86)	6.80%	1.02	1.27
ATOH7	NM_145178	1	0.00372128	1.46 (1.13, 1.90)	6.60%	1.02	1.26
ATP9B	NM_198531	-1	0.002646669	0.58 (0.41, 0.83)	5.50%	1.02	1.28
ATXN3L	NM_001135995	1	0.002748019	1.28 (1.09, 1.50)	5.60%	1.02	1.22
BCL2L2	NM_004050	-1	0.003979713	0.49 (0.31, 0.80)	6.80%	1.02	1.24
BCL2L2	NM_001199839	-1	0.003979713	0.49 (0.31, 0.80)	6.80%	1.02	1.24
BEND5	NM_024603	-1	0.00262047	0.59 (0.42, 0.83)	5.50%	1.02	1.28
BLM	NM_000057	1	0.003237886	1.81 (1.22, 2.69)	6.10%	1.02	1.27
C10orf79	NM_025145	-1	0.003108477	0.64 (0.48, 0.86)	6.00%	1.02	1.27
C10orf91	NM_173541	1	0.002971656	1.41 (1.13, 1.78)	5.80%	1.02	1.26
C14orf34	NR_026796	1	0.0029697	1.65 (1.19, 2.29)	5.80%	1.02	1.28
C14orf34	NR_026797	1	0.0029697	1.65 (1.19, 2.29)	5.80%	1.02	1.28
C15orf39	NM_015492	1	0.002808036	1.64 (1.19, 2.28)	5.60%	1.02	1.28
C15orf42	NM_152259	1	0.004003005	1.73 (1.19, 2.51)	6.80%	1.02	1.27
C17orf48	NM_020233	-1	0.003577923	0.69 (0.54, 0.89)	6.40%	1.02	1.26
C17orf49	NM_001142798	-1	0.003771563	0.57 (0.39, 0.83)	6.60%	1.02	1.26

C17orf49	NM_174893	-1	0.003771563	0.57 (0.39, 0.83)	6.60%	1.02	1.26
C17orf49	NM_001142799	-1	0.003771563	0.57 (0.39, 0.83)	6.60%	1.02	1.26
C18orf26	NM_173629	1	0.002705318	1.52 (1.16, 1.99)	5.50%	1.02	1.28
C1orf131	NM_152379	1	0.003424964	1.93 (1.24, 2.99)	6.30%	1.02	1.26
C1orf173	NM_001002912	-1	0.003149398	0.57 (0.39, 0.83)	6.00%	1.02	1.27
C1orf63	NM_020317	-1	0.004174801	0.53 (0.34, 0.82)	7.00%	1.02	1.25
C20orf26	NM_001167816	-1	0.004008624	0.56 (0.38, 0.83)	6.80%	1.02	1.26
C20orf26	NM_015585	-1	0.004008624	0.56 (0.38, 0.83)	6.80%	1.02	1.26
C3orf25	NM_207307	-1	0.004109239	0.58 (0.39, 0.84)	6.90%	1.02	1.26
C4orf32	NM_152400	-1	0.00283046	0.60 (0.43, 0.84)	5.60%	1.02	1.28
C6orf97	NM_025059	-1	0.003169135	0.63 (0.46, 0.86)	6.00%	1.02	1.27
C7orf54	NR_027330	1	0.002867207	1.97 (1.26, 3.07)	5.70%	1.02	1.27
C9orf53	NR_024274	1	0.002759518	1.53 (1.16, 2.03)	5.60%	1.02	1.28
CAP2	NM_006366	-1	0.002320274	0.65 (0.49, 0.86)	5.10%	1.02	1.28
CASP14	NM_012114	1	0.003818253	1.57 (1.16, 2.13)	6.70%	1.02	1.27
CBX2	NM_032647	1	0.003622138	1.74 (1.20, 2.53)	6.50%	1.02	1.27
CBX2	NM_005189	1	0.003622138	1.74 (1.20, 2.53)	6.50%	1.02	1.27
CCDC104	NM_080667	-1	0.003352077	0.57 (0.39, 0.83)	6.20%	1.02	1.27
CCDC3	NM_031455	-1	0.002624067	0.58 (0.41, 0.83)	5.50%	1.02	1.28
CCDC76	NM_019083	-1	0.003763724	0.52 (0.34, 0.81)	6.60%	1.02	1.25
CCNH	NM_001239	-1	0.002673892	0.64 (0.48, 0.86)	5.50%	1.02	1.28
CCNH	NM_001199189	-1	0.002673892	0.64 (0.48, 0.86)	5.50%	1.02	1.28
CD1E	NM_001042583	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_001185112	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_001185113	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_001185114	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_001185110	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_001042584	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_001185108	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_001042585	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_001042586	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_001042587	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_001185107	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_030893	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CD1E	NM_001185115	-1	0.002526018	0.60 (0.44, 0.84)	5.40%	1.02	1.28
CDC6	NM_001254	1	0.002718983	1.76 (1.22, 2.55)	5.50%	1.02	1.28
CDRT1	NM_006382	1	0.003880336	1.65 (1.17, 2.32)	6.70%	1.02	1.27
CENPE	NM_001813	1	0.002827598	1.93 (1.25, 2.97)	5.60%	1.02	1.27
CHEK1	NM_001274	1	0.002862306	1.81 (1.23, 2.67)	5.70%	1.02	1.28
CHEK1	NM_001114122	1	0.002862306	1.81 (1.23, 2.67)	5.70%	1.02	1.28
CHEK1	NM_001114121	1	0.002862306	1.81 (1.23, 2.67)	5.70%	1.02	1.28
CHML	NM_001821	1	0.003315346	1.64 (1.18, 2.29)	6.20%	1.02	1.28
CIRBP	NM_001280	-1	0.004062264	0.61 (0.43, 0.85)	6.90%	1.02	1.27
CIRBP	NR_023313	-1	0.004062264	0.61 (0.43, 0.85)	6.90%	1.02	1.27
CIRBP	NR_023312	-1	0.004062264	0.61 (0.43, 0.85)	6.90%	1.02	1.27
CLCN1	NM_000083	1	0.003227573	1.40 (1.12, 1.75)	6.10%	1.02	1.26
CMAS	NM_018686	1	0.002866433	1.48 (1.14, 1.91)	5.70%	1.02	1.27
CNGB3	NM_019098	1	0.00409123	1.81 (1.21, 2.71)	6.90%	1.02	1.26
COL6A4P1	NR_027927	1	0.003761834	1.50 (1.14, 1.97)	6.60%	1.02	1.27

COX8C	NM_182971	1	0.003378935	1.36 (1.11, 1.68)	6.20%	1.02	1.25
CPLX1	NM_006651	-1	0.002909325	0.64 (0.47, 0.86)	5.70%	1.02	1.28
CRABP1	NM_004378	1	0.002927588	1.69 (1.20, 2.38)	5.70%	1.02	1.28
CREBBP	NM_004380	-1	0.003871914	0.54 (0.36, 0.82)	6.70%	1.02	1.26
CREBBP	NM_001079846	-1	0.003871914	0.54 (0.36, 0.82)	6.70%	1.02	1.26
CSDC2	NM_014460	-1	0.004125038	0.59 (0.41, 0.84)	6.90%	1.02	1.26
CYC1	NM_001916	1	0.003973641	1.69 (1.18, 2.42)	6.80%	1.02	1.27
DEFB135	NM_001033017	1	0.002321015	1.51 (1.16, 1.96)	5.10%	1.02	1.28
DIAPH1	NM_005219	1	0.004027699	1.70 (1.18, 2.44)	6.90%	1.02	1.27
DIAPH1	NM_001079812	1	0.004027699	1.70 (1.18, 2.44)	6.90%	1.02	1.27
DIXDC1	NM_001037954	-1	0.003336293	0.60 (0.43, 0.84)	6.20%	1.02	1.27
DIXDC1	NM_033425	-1	0.003336293	0.60 (0.43, 0.84)	6.20%	1.02	1.27
DKK3	NM_013253	-1	0.00325914	0.70 (0.55, 0.89)	6.10%	1.02	1.26
DKK3	NM_015881	-1	0.00325914	0.70 (0.55, 0.89)	6.10%	1.02	1.26
DKK3	NM_001018057	-1	0.00325914	0.70 (0.55, 0.89)	6.10%	1.02	1.26
DNAJC12	NM_021800	-1	0.003141124	0.61 (0.43, 0.84)	6.00%	1.02	1.27
DNAJC12	NM_201262	-1	0.003141124	0.61 (0.43, 0.84)	6.00%	1.02	1.27
DNMT3B	NM_175848	1	0.002642423	1.68 (1.20, 2.36)	5.50%	1.02	1.28
DNMT3B	NM_006892	1	0.002642423	1.68 (1.20, 2.36)	5.50%	1.02	1.28
DNMT3B	NM_175849	1	0.002642423	1.68 (1.20, 2.36)	5.50%	1.02	1.28
DNMT3B	NM_175850	1	0.002642423	1.68 (1.20, 2.36)	5.50%	1.02	1.28
DOC2GP	NR_033791	1	0.001636762	1.29 (1.10, 1.52)	4.10%	1.02	1.23
DOK1	NM_001381	-1	0.002983362	0.54 (0.35, 0.81)	5.80%	1.02	1.27
DOK1	NM_001197260	-1	0.002983362	0.54 (0.35, 0.81)	5.80%	1.02	1.27
DUSP13	NM_001007273	1	0.002852767	1.66 (1.19, 2.30)	5.70%	1.02	1.28
DUSP13	NM_001007271	1	0.002852767	1.66 (1.19, 2.30)	5.70%	1.02	1.28
DUSP13	NM_001007272	1	0.002852767	1.66 (1.19, 2.30)	5.70%	1.02	1.28
DUSP13	NM_016364	1	0.002852767	1.66 (1.19, 2.30)	5.70%	1.02	1.28
E2F1	NM_005225	1	0.002966928	1.81 (1.22, 2.68)	5.80%	1.02	1.27
ESRP2	NM_024939	1	0.004340825	1.90 (1.22, 2.96)	7.10%	1.02	1.25
EVL	NM_016337	-1	0.003294207	0.50 (0.31, 0.79)	6.20%	1.02	1.25
FADS1	NM_013402	1	0.003861317	1.69 (1.18, 2.41)	6.70%	1.02	1.27
FAM110B	NM_147189	-1	0.002415136	0.69 (0.54, 0.88)	5.20%	1.02	1.27
FAM161A	NM_032180	-1	0.003214575	0.68 (0.52, 0.88)	6.10%	1.02	1.27
FAM26E	NM_153711	-1	0.003603321	0.63 (0.46, 0.86)	6.40%	1.02	1.27
FBP1	NM_000507	-1	0.004003056	0.59 (0.41, 0.85)	6.80%	1.02	1.26
FBP1	NM_001127628	-1	0.004003056	0.59 (0.41, 0.85)	6.80%	1.02	1.26
FLJ37201	NR_026835	-1	0.003681387	0.62 (0.45, 0.86)	6.50%	1.02	1.27
FRY	NM_023037	-1	0.002884774	0.53 (0.35, 0.80)	5.70%	1.02	1.27
GSTA2	NM_000846	1	0.003594941	1.43 (1.12, 1.82)	6.40%	1.02	1.26
GUCA1A	NM_000409	1	0.003909224	1.58 (1.16, 2.15)	6.70%	1.02	1.27
HIST1H1C	NM_005319	1	0.003225985	1.68 (1.19, 2.38)	6.10%	1.02	1.28
HIST1H2AG	NM_021064	1	0.003513384	2.14 (1.28, 3.56)	6.40%	1.02	1.25
HIST1H2AH	NM_080596	1	0.003239424	1.96 (1.25, 3.06)	6.10%	1.02	1.26
HIST1H2AL	NM_003511	1	0.003196371	2.03 (1.27, 3.26)	6.10%	1.02	1.26
HJURP	NM_018410	1	0.003065128	1.91 (1.24, 2.93)	5.90%	1.02	1.27
HMGB3	NM_005342	1	0.003821392	1.67 (1.18, 2.35)	6.70%	1.02	1.27
HPGDS	NM_014485	-1	0.003509052	0.67 (0.51, 0.88)	6.40%	1.02	1.27
ICA1L	NM_138468	-1	0.003324089	0.60 (0.42, 0.84)	6.20%	1.02	1.27

ICA1L	NM_178231	-1	0.003324089	0.60 (0.42, 0.84)	6.20%	1.02	1.27
INCA1	NM_001167987	-1	0.003836717	0.62 (0.45, 0.86)	6.70%	1.02	1.27
INCA1	NM_001167986	-1	0.003836717	0.62 (0.45, 0.86)	6.70%	1.02	1.27
INCA1	NM_001167985	-1	0.003836717	0.62 (0.45, 0.86)	6.70%	1.02	1.27
INCA1	NM_213726	-1	0.003836717	0.62 (0.45, 0.86)	6.70%	1.02	1.27
KIAA0556	NM_015202	-1	0.00378804	0.58 (0.40, 0.84)	6.70%	1.02	1.26
KIAA0649	NM_014811	-1	0.003489552	0.60 (0.43, 0.85)	6.30%	1.02	1.27
KIAA1632	NM_020964	-1	0.004110188	0.57 (0.39, 0.84)	6.90%	1.02	1.26
KIF11	NM_004523	1	0.003849177	1.77 (1.20, 2.61)	6.70%	1.02	1.27
KIF13B	NM_015254	-1	0.003183516	0.56 (0.38, 0.82)	6.00%	1.02	1.27
KIF18B	NM_001080443	1	0.004363327	1.89 (1.22, 2.92)	7.10%	1.02	1.25
KIF2C	NM_006845	1	0.004041299	2.10 (1.27, 3.49)	6.90%	1.02	1.24
KLHDC2	NM_014315	-1	0.002795444	0.59 (0.42, 0.84)	5.60%	1.02	1.28
KLHDC4	NM_001184856	1	0.004284709	2.00 (1.24, 3.21)	7.10%	1.02	1.25
KLHDC4	NM_001184854	1	0.004284709	2.00 (1.24, 3.21)	7.10%	1.02	1.25
KLHDC4	NM_017566	1	0.004284709	2.00 (1.24, 3.21)	7.10%	1.02	1.25
LEMD1	NM_001001552	1	0.003532642	1.43 (1.12, 1.82)	6.40%	1.02	1.26
LEMD1	NM_001199051	1	0.003532642	1.43 (1.12, 1.82)	6.40%	1.02	1.26
LEMD1	NM_001199052	1	0.003532642	1.43 (1.12, 1.82)	6.40%	1.02	1.26
LEMD1	NR_037583	1	0.003532642	1.43 (1.12, 1.82)	6.40%	1.02	1.26
LEMD1	NM_001199050	1	0.003532642	1.43 (1.12, 1.82)	6.40%	1.02	1.26
LETMD1	NM_015416	-1	0.003381908	0.55 (0.37, 0.82)	6.20%	1.02	1.26
LETMD1	NM_001024668	-1	0.003381908	0.55 (0.37, 0.82)	6.20%	1.02	1.26
LOC100128338	NR_033849	1	0.003117505	1.65 (1.18, 2.29)	6.00%	1.02	1.28
LOC100190938	NR_024462	-1	0.003341277	0.64 (0.47, 0.86)	6.20%	1.02	1.27
LOC100190938	NR_024461	-1	0.003341277	0.64 (0.47, 0.86)	6.20%	1.02	1.27
LOC254559	NR_015411	1	0.003591948	1.78 (1.21, 2.63)	6.40%	1.02	1.27
LOC285577	NR_033898	1	0.002606176	1.24 (1.08, 1.43)	5.50%	1.02	1.2
LOC401177	NR_033975	1	0.001598219	1.23 (1.08, 1.40)	4.10%	1.02	1.2
LOC646960	NM_001195129	1	0.002275041	1.35 (1.11, 1.64)	5.10%	1.02	1.25
LOC728606	NR_024259	-1	0.003080953	0.56 (0.38, 0.82)	5.90%	1.02	1.27
LOC90834	NR_026993	1	0.002787462	1.49 (1.15, 1.93)	5.60%	1.02	1.27
LRP12	NM_001135703	1	0.003559777	1.69 (1.19, 2.41)	6.40%	1.02	1.27
LRP12	NM_013437	1	0.003559777	1.69 (1.19, 2.41)	6.40%	1.02	1.27
LRP8	NM_004631	1	0.003269601	1.87 (1.23, 2.84)	6.10%	1.02	1.27
LRP8	NM_017522	1	0.003269601	1.87 (1.23, 2.84)	6.10%	1.02	1.27
LRP8	NM_033300	1	0.003269601	1.87 (1.23, 2.84)	6.10%	1.02	1.27
LRP8	NM_001018054	1	0.003269601	1.87 (1.23, 2.84)	6.10%	1.02	1.27
LRRC4C	NM_020929	-1	0.003685417	0.56 (0.38, 0.83)	6.50%	1.02	1.26
LSM4	NM_012321	1	0.002719555	1.53 (1.16, 2.01)	5.50%	1.02	1.28
MACF1	NM_033044	-1	0.003907446	0.59 (0.42, 0.85)	6.70%	1.02	1.27
MACF1	NM_012090	-1	0.003907446	0.59 (0.42, 0.85)	6.70%	1.02	1.27
MBIP	NM_016586	1	0.00342382	1.87 (1.23, 2.86)	6.30%	1.02	1.26
MBIP	NM_001144891	1	0.00342382	1.87 (1.23, 2.86)	6.30%	1.02	1.26
MGC87042	NM_207342	1	0.002700608	1.46 (1.14, 1.87)	5.50%	1.02	1.27
MGC87042	NM_001164460	1	0.002700608	1.46 (1.14, 1.87)	5.50%	1.02	1.27
MIR542	NR_030399	1	0.002819598	1.53 (1.16, 2.01)	5.60%	1.02	1.28
MTHFD2	NM_006636	1	0.00387651	1.72 (1.19, 2.47)	6.70%	1.02	1.27
MTHFD2	NR_027405	1	0.00387651	1.72 (1.19, 2.47)	6.70%	1.02	1.27

NCRNA00168	NR_033387	1	0.002775618	1.39 (1.12, 1.72)	5.60%	1.02	1.26
NCRNA00242	NR_026781	-1	0.003823018	0.54 (0.36, 0.82)	6.70%	1.02	1.26
NCRNA00287	NR_026677	-1	0.002783862	0.60 (0.43, 0.84)	5.60%	1.02	1.28
NHSL1	NM_020464	1	0.003334053	1.72 (1.20, 2.48)	6.20%	1.02	1.27
NHSL1	NM_001144060	1	0.003334053	1.72 (1.20, 2.48)	6.20%	1.02	1.27
NTRK3	NM_001012338	-1	0.003070056	0.57 (0.40, 0.83)	5.90%	1.02	1.27
NTRK3	NM_002530	-1	0.003070056	0.57 (0.40, 0.83)	5.90%	1.02	1.27
NTRK3	NM_001007156	-1	0.003070056	0.57 (0.40, 0.83)	5.90%	1.02	1.27
NUDT15	NM_018283	1	0.003029893	1.74 (1.21, 2.52)	5.90%	1.02	1.28
NUDT16P1	NR_027766	-1	0.00283035	0.66 (0.51, 0.87)	5.60%	1.02	1.27
NUDT16P1	NR_002949	-1	0.00283035	0.66 (0.51, 0.87)	5.60%	1.02	1.27
NUDT21	NM_007006	1	0.002332854	1.57 (1.17, 2.10)	5.10%	1.02	1.29
NUP155	NM_004298	1	0.002877998	1.74 (1.21, 2.51)	5.70%	1.02	1.28
NUP155	NM_153485	1	0.002877998	1.74 (1.21, 2.51)	5.70%	1.02	1.28
NXPH4	NM_007224	1	0.003577666	1.74 (1.20, 2.53)	6.40%	1.02	1.27
OR2A4	NM_030908	1	0.002718898	1.46 (1.14, 1.86)	5.50%	1.02	1.27
OR2W5	NM_001004698	1	0.001067476	1.21 (1.08, 1.36)	3.30%	1.02	1.19
P2RY13	NM_176894	-1	0.002437174	0.65 (0.50, 0.86)	5.20%	1.02	1.28
PALM	NM_002579	-1	0.003697526	0.67 (0.51, 0.88)	6.50%	1.02	1.26
PALM	NM_001040134	-1	0.003697526	0.67 (0.51, 0.88)	6.50%	1.02	1.26
PCDH11X	NM_032968	1	0.002679604	1.52 (1.16, 2.01)	5.50%	1.02	1.28
PCDH11X	NM_001168360	1	0.002679604	1.52 (1.16, 2.01)	5.50%	1.02	1.28
PCDH11X	NM_032969	1	0.002679604	1.52 (1.16, 2.01)	5.50%	1.02	1.28
PCDH11X	NM_032967	1	0.002679604	1.52 (1.16, 2.01)	5.50%	1.02	1.28
PCDH11X	NM_001168363	1	0.002679604	1.52 (1.16, 2.01)	5.50%	1.02	1.28
PCDH11X	NM_001168362	1	0.002679604	1.52 (1.16, 2.01)	5.50%	1.02	1.28
PCDH11X	NM_001168361	1	0.002679604	1.52 (1.16, 2.01)	5.50%	1.02	1.28
PCDH11X	NM_014522	1	0.002679604	1.52 (1.16, 2.01)	5.50%	1.02	1.28
PCSK4	NM_017573	-1	0.002585422	0.60 (0.43, 0.84)	5.40%	1.02	1.28
PCSK5	NM_006200	-1	0.002479594	0.71 (0.56, 0.88)	5.30%	1.02	1.26
PCSK5	NM_001190482	-1	0.002479594	0.71 (0.56, 0.88)	5.30%	1.02	1.26
PCTP	NM_001102402	1	0.00297204	1.62 (1.18, 2.22)	5.80%	1.02	1.28
PCTP	NM_021213	1	0.00297204	1.62 (1.18, 2.22)	5.80%	1.02	1.28
PLTP	NM_006227	1	0.00399448	1.58 (1.16, 2.16)	6.80%	1.02	1.27
PLTP	NM_182676	1	0.00399448	1.58 (1.16, 2.16)	6.80%	1.02	1.27
PNLIP	NM_000936	1	0.00197645	1.31 (1.11, 1.56)	4.70%	1.02	1.24
PODXL2	NM_015720	1	0.003706982	1.91 (1.23, 2.96)	6.60%	1.02	1.26
PPP1R14B	NM_138689	1	0.002581467	1.64 (1.19, 2.26)	5.40%	1.02	1.28
PPP1R3C	NM_005398	-1	0.003328551	0.61 (0.44, 0.85)	6.20%	1.02	1.27
PRRC2B	NM_013318	-1	0.004341057	0.51 (0.32, 0.81)	7.10%	1.02	1.24
PSMD2	NM_002808	1	0.003173532	1.76 (1.21, 2.56)	6.00%	1.02	1.27
PUF60	NM_001136033	1	0.003952504	1.67 (1.18, 2.36)	6.80%	1.02	1.27
PUF60	NM_014281	1	0.003952504	1.67 (1.18, 2.36)	6.80%	1.02	1.27
PUF60	NM_078480	1	0.003952504	1.67 (1.18, 2.36)	6.80%	1.02	1.27
RABEP1	NM_001083585	-1	0.003501962	0.54 (0.35, 0.82)	6.40%	1.02	1.26
RABEP1	NM_004703	-1	0.003501962	0.54 (0.35, 0.82)	6.40%	1.02	1.26
RABGAP1	NM_012197	-1	0.003415188	0.54 (0.36, 0.82)	6.30%	1.02	1.26
RIPK4	NM_020639	1	0.003549519	2.23 (1.30, 3.83)	6.40%	1.02	1.24
RNF214	NM_207343	-1	0.002544607	0.63 (0.47, 0.85)	5.40%	1.02	1.28

RNF214	NM_001077239	-1	0.002544607	0.63 (0.47, 0.85)	5.40%	1.02	1.28
RPPH1	NR_002312	1	0.00400948	1.72 (1.19, 2.48)	6.80%	1.02	1.27
SCNN1D	NM_002978	-1	0.002973296	0.60 (0.42, 0.84)	5.80%	1.02	1.28
SCNN1D	NR_037668	-1	0.002973296	0.60 (0.42, 0.84)	5.80%	1.02	1.28
SCNN1D	NM_001130413	-1	0.002973296	0.60 (0.42, 0.84)	5.80%	1.02	1.28
SCRT2	NM_033129	1	0.001721059	1.23 (1.08, 1.41)	4.20%	1.02	1.2
SDCCAG3	NM_001039707	1	0.003470913	1.88 (1.23, 2.88)	6.30%	1.02	1.26
SDCCAG3	NM_001039708	1	0.003470913	1.88 (1.23, 2.88)	6.30%	1.02	1.26
SDCCAG3	NM_006643	1	0.003470913	1.88 (1.23, 2.88)	6.30%	1.02	1.26
SERINC5	NM_178276	1	0.003590438	1.51 (1.14, 2.00)	6.40%	1.02	1.27
SERINC5	NM_001174071	1	0.003590438	1.51 (1.14, 2.00)	6.40%	1.02	1.27
SERINC5	NM_001174072	1	0.003590438	1.51 (1.14, 2.00)	6.40%	1.02	1.27
SEZ6L	NM_001184776	-1	0.004348114	0.49 (0.30, 0.80)	7.10%	1.02	1.24
SEZ6L	NM_021115	-1	0.004348114	0.49 (0.30, 0.80)	7.10%	1.02	1.24
SEZ6L	NM_001184777	-1	0.004348114	0.49 (0.30, 0.80)	7.10%	1.02	1.24
SEZ6L	NM_001184775	-1	0.004348114	0.49 (0.30, 0.80)	7.10%	1.02	1.24
SEZ6L	NM_001184774	-1	0.004348114	0.49 (0.30, 0.80)	7.10%	1.02	1.24
SEZ6L	NM_001184773	-1	0.004348114	0.49 (0.30, 0.80)	7.10%	1.02	1.24
SGSM2	NM_014853	-1	0.002777129	0.55 (0.38, 0.82)	5.60%	1.02	1.27
SGSM2	NM_001098509	-1	0.002777129	0.55 (0.38, 0.82)	5.60%	1.02	1.27
SLC15A1	NM_005073	1	0.003057481	1.64 (1.18, 2.28)	5.90%	1.02	1.28
SLC26A6	NM_022911	1	0.002410675	1.55 (1.17, 2.05)	5.20%	1.02	1.28
SLC26A6	NM_134426	1	0.002410675	1.55 (1.17, 2.05)	5.20%	1.02	1.28
SLC26A6	NM_134263	1	0.002410675	1.55 (1.17, 2.05)	5.20%	1.02	1.28
SLC26A6	NM_001040454	1	0.002410675	1.55 (1.17, 2.05)	5.20%	1.02	1.28
SLC7A5	NM_003486	1	0.003613709	1.88 (1.23, 2.89)	6.50%	1.02	1.26
SLC7A8	NM_182728	-1	0.00381186	0.63 (0.46, 0.86)	6.70%	1.02	1.27
SLC7A8	NM_012244	-1	0.00381186	0.63 (0.46, 0.86)	6.70%	1.02	1.27
SMG1	NM_015092	-1	0.003487141	0.57 (0.39, 0.83)	6.30%	1.02	1.27
SNRPD3	NM_004175	1	0.003488489	1.54 (1.15, 2.07)	6.30%	1.02	1.27
SPPL2B	NM_152988	-1	0.003064537	0.64 (0.48, 0.86)	5.90%	1.02	1.27
SPPL2B	NM_001077238	-1	0.003064537	0.64 (0.48, 0.86)	5.90%	1.02	1.27
ST8SIA6	NM_001004470	-1	0.002791716	0.61 (0.44, 0.84)	5.60%	1.02	1.28
STAU2	NM_001164380	1	0.002783168	1.62 (1.18, 2.22)	5.60%	1.02	1.28
STAU2	NM_014393	1	0.002783168	1.62 (1.18, 2.22)	5.60%	1.02	1.28
STAU2	NM_001164384	1	0.002783168	1.62 (1.18, 2.22)	5.60%	1.02	1.28
STAU2	NM_001164382	1	0.002783168	1.62 (1.18, 2.22)	5.60%	1.02	1.28
STAU2	NM_001164381	1	0.002783168	1.62 (1.18, 2.22)	5.60%	1.02	1.28
STAU2	NM_001164385	1	0.002783168	1.62 (1.18, 2.22)	5.60%	1.02	1.28
STAU2	NM_001164383	1	0.002783168	1.62 (1.18, 2.22)	5.60%	1.02	1.28
STC2	NM_003714	-1	0.002916534	0.54 (0.35, 0.81)	5.70%	1.02	1.27
SYT5	NM_003180	1	0.002277553	1.32 (1.10, 1.58)	5.10%	1.02	1.24
SYT9	NM_175733	-1	0.003474054	0.65 (0.48, 0.87)	6.30%	1.02	1.27
TAAR6	NM_175067	1	0.002711741	1.45 (1.14, 1.84)	5.50%	1.02	1.27
TAF13	NM_005645	1	0.003926491	1.57 (1.16, 2.13)	6.80%	1.02	1.27
TFAP2D	NM_172238	1	0.001850588	1.38 (1.13, 1.70)	4.40%	1.02	1.26
THOC3	NM_032361	1	0.004239158	2.03 (1.25, 3.29)	7.00%	1.02	1.25
TMED9	NM_017510	1	0.002890032	1.91 (1.25, 2.92)	5.70%	1.02	1.27
TMEM30C	NR_028358	1	0.002560059	1.51 (1.15, 1.96)	5.40%	1.02	1.28

TMEM30C	NR_028357	1	0.002560059	1.51 (1.15, 1.96)	5.40%	1.02	1.28
TMOD4	NM_013353	-1	0.003403959	0.58 (0.40, 0.84)	6.30%	1.02	1.27
TMPRSS13	NM_001077263	1	0.003417183	1.79 (1.21, 2.66)	6.30%	1.02	1.27
TMSB10	NM_021103	1	0.004188438	1.78 (1.20, 2.63)	7.00%	1.02	1.26
TNRC6A	NM_014494	-1	0.003074972	0.51 (0.32, 0.79)	5.90%	1.02	1.26
TRAF3	NM_145726	-1	0.00293145	0.53 (0.35, 0.81)	5.70%	1.02	1.27
TRAF3	NM_001199427	-1	0.00293145	0.53 (0.35, 0.81)	5.70%	1.02	1.27
TRAF3	NM_003300	-1	0.00293145	0.53 (0.35, 0.81)	5.70%	1.02	1.27
TRAF3	NM_145725	-1	0.00293145	0.53 (0.35, 0.81)	5.70%	1.02	1.27
TRAM1	NM_014294	1	0.002697324	1.64 (1.19, 2.26)	5.50%	1.02	1.28
TRAM1L1	NM_152402	-1	0.003024509	0.64 (0.48, 0.86)	5.80%	1.02	1.27
TRPC7	NM_001167577	1	0.003198969	1.42 (1.12, 1.79)	6.10%	1.02	1.26
TRPC7	NM_020389	1	0.003198969	1.42 (1.12, 1.79)	6.10%	1.02	1.26
TRPC7	NM_001167576	1	0.003198969	1.42 (1.12, 1.79)	6.10%	1.02	1.26
TSC1	NM_001162427	-1	0.004320082	0.53 (0.34, 0.82)	7.10%	1.02	1.25
TSC1	NM_000368	-1	0.004320082	0.53 (0.34, 0.82)	7.10%	1.02	1.25
TSC1	NM_001162426	-1	0.004320082	0.53 (0.34, 0.82)	7.10%	1.02	1.25
TSNAX-DISC1	NR_028399	1	0.003821941	1.51 (1.14, 1.99)	6.70%	1.02	1.27
TSNAX-DISC1	NR_028400	1	0.003821941	1.51 (1.14, 1.99)	6.70%	1.02	1.27
TSNAX-DISC1	NR_028398	1	0.003821941	1.51 (1.14, 1.99)	6.70%	1.02	1.27
TSNAX-DISC1	NR_028397	1	0.003821941	1.51 (1.14, 1.99)	6.70%	1.02	1.27
TSNAX-DISC1	NR_028393	1	0.003821941	1.51 (1.14, 1.99)	6.70%	1.02	1.27
TSNAX-DISC1	NR_028396	1	0.003821941	1.51 (1.14, 1.99)	6.70%	1.02	1.27
TSNAX-DISC1	NR_028395	1	0.003821941	1.51 (1.14, 1.99)	6.70%	1.02	1.27
TSNAX-DISC1	NR_028394	1	0.003821941	1.51 (1.14, 1.99)	6.70%	1.02	1.27
TTC30A	NM_152275	-1	0.002251039	0.66 (0.51, 0.86)	5.00%	1.02	1.28
TTF1	NM_007344	-1	0.002675227	0.61 (0.44, 0.84)	5.50%	1.02	1.28
TUBA1C	NM_032704	1	0.003245041	2.12 (1.29, 3.50)	6.10%	1.02	1.25
TUSC1	NM_001004125	-1	0.003519464	0.66 (0.50, 0.87)	6.40%	1.02	1.27
UBXN10	NM_152376	-1	0.002709535	0.63 (0.46, 0.85)	5.50%	1.02	1.28
UQCRB	NM_006294	1	0.003314393	1.76 (1.21, 2.56)	6.20%	1.02	1.27
UQCRB	NM_001199975	1	0.003314393	1.76 (1.21, 2.56)	6.20%	1.02	1.27
VILL	NM_015873	-1	0.003667617	0.65 (0.49, 0.87)	6.50%	1.02	1.27
VWC2	NM_198570	1	0.002039885	1.31 (1.10, 1.56)	4.70%	1.02	1.24
WDR47	NM_001142551	-1	0.002875073	0.74 (0.61, 0.90)	5.70%	1.02	1.24
WDR47	NM_001142550	-1	0.002875073	0.74 (0.61, 0.90)	5.70%	1.02	1.24
WDR47	NM_014969	-1	0.002875073	0.74 (0.61, 0.90)	5.70%	1.02	1.24
WDR75	NM_032168	-1	0.003637692	0.53 (0.35, 0.82)	6.50%	1.02	1.26
XPOT	NM_007235	1	0.003529958	1.66 (1.18, 2.33)	6.40%	1.02	1.27
ZER1	NM_006336	-1	0.003281615	0.61 (0.44, 0.85)	6.10%	1.02	1.27
ZFP42	NM_174900	1	0.002027244	1.34 (1.11, 1.61)	4.70%	1.02	1.25
ZFYVE26	NM_015346	-1	0.003488824	0.47 (0.28, 0.78)	6.30%	1.02	1.24
ZNF487P	NR_026693	-1	0.002718434	0.62 (0.45, 0.85)	5.50%	1.02	1.28
ZNF610	NM_001161427	-1	0.00379397	0.66 (0.50, 0.88)	6.70%	1.02	1.26
ZNF610	NM_001161425	-1	0.00379397	0.66 (0.50, 0.88)	6.70%	1.02	1.26
ZNF610	NM_001161426	-1	0.00379397	0.66 (0.50, 0.88)	6.70%	1.02	1.26
ZNF610	NM_173530	-1	0.00379397	0.66 (0.50, 0.88)	6.70%	1.02	1.26
ZNF653	NM_138783	-1	0.00333192	0.58 (0.40, 0.83)	6.20%	1.02	1.27
ZNF655	NM_024061	-1	0.002999752	0.58 (0.40, 0.83)	5.80%	1.02	1.27

ZNF655	NM_001083956	-1	0.002999752	0.58 (0.40, 0.83)	5.80%	1.02	1.27
ZNF655	NM_001009958	-1	0.002999752	0.58 (0.40, 0.83)	5.80%	1.02	1.27
ZNF655	NM_001085368	-1	0.002999752	0.58 (0.40, 0.83)	5.80%	1.02	1.27
ZNF655	NM_001085366	-1	0.002999752	0.58 (0.40, 0.83)	5.80%	1.02	1.27
ZNF655	NM_138494	-1	0.002999752	0.58 (0.40, 0.83)	5.80%	1.02	1.27
ZNF655	NM_001009960	-1	0.002999752	0.58 (0.40, 0.83)	5.80%	1.02	1.27
ZNF655	NM_001085367	-1	0.002999752	0.58 (0.40, 0.83)	5.80%	1.02	1.27
ZNF701	NM_018260	-1	0.003268807	0.59 (0.41, 0.84)	6.10%	1.02	1.27
ZNF701	NM_001172655	-1	0.003268807	0.59 (0.41, 0.84)	6.10%	1.02	1.27
ZNF740	NM_001004304	-1	0.004118629	0.58 (0.40, 0.84)	6.90%	1.02	1.26
ZNF788	NR_027049	-1	0.00249849	0.60 (0.43, 0.84)	5.30%	1.02	1.28
ABCD1	NM_000033	1	0.005827069	1.69 (1.16, 2.46)	8.30%	1.01	1.25
ABCG8	NM_022437	1	0.00511131	1.41 (1.11, 1.80)	7.70%	1.01	1.25
ACAT1	NM_000019	-1	0.00445572	0.66 (0.50, 0.88)	7.20%	1.01	1.26
ACO2	NM_001098	1	0.004314322	1.70 (1.18, 2.44)	7.10%	1.01	1.27
ACTL8	NM_030812	1	0.005453351	1.59 (1.15, 2.20)	7.90%	1.01	1.26
ADRA2A	NM_000681	-1	0.004645911	0.59 (0.41, 0.85)	7.30%	1.01	1.26
AFF3	NM_001025108	-1	0.005402057	0.63 (0.45, 0.87)	7.90%	1.01	1.26
AFF3	NM_002285	-1	0.005402057	0.63 (0.45, 0.87)	7.90%	1.01	1.26
AGAP4	NM_133446	-1	0.006470733	0.61 (0.43, 0.87)	8.70%	1.01	1.25
AGAP5	NM_001144000	-1	0.005031188	0.64 (0.47, 0.87)	7.60%	1.01	1.26
AGTR1	NM_004835	-1	0.004024812	0.63 (0.46, 0.86)	6.90%	1.01	1.27
AGTR1	NM_009585	-1	0.004024812	0.63 (0.46, 0.86)	6.90%	1.01	1.27
AGTR1	NM_000685	-1	0.004024812	0.63 (0.46, 0.86)	6.90%	1.01	1.27
AGTR1	NM_032049	-1	0.004024812	0.63 (0.46, 0.86)	6.90%	1.01	1.27
AGTR1	NM_031850	-1	0.004024812	0.63 (0.46, 0.86)	6.90%	1.01	1.27
ALG10B	NM_001013620	-1	0.004720162	0.64 (0.47, 0.87)	7.40%	1.01	1.26
AMDHD1	NM_152435	-1	0.0061723	0.60 (0.41, 0.86)	8.50%	1.01	1.25
ARMC9	NM_025139	-1	0.004214321	0.63 (0.46, 0.86)	7.00%	1.01	1.26
ARPC5	NM_005717	1	0.005346223	1.71 (1.17, 2.50)	7.90%	1.01	1.26
ASPM	NM_018136	1	0.004397362	1.87 (1.22, 2.89)	7.10%	1.01	1.26
ASPN	NM_017680	-1	0.005869465	0.59 (0.40, 0.86)	8.30%	1.01	1.25
ASPN	NM_001193335	-1	0.005869465	0.59 (0.40, 0.86)	8.30%	1.01	1.25
ATP2A2	NM_001681	1	0.005992169	1.56 (1.14, 2.15)	8.40%	1.01	1.26
ATP2A2	NM_001135765	1	0.005992169	1.56 (1.14, 2.15)	8.40%	1.01	1.26
ATP2A2	NM_170665	1	0.005992169	1.56 (1.14, 2.15)	8.40%	1.01	1.26
AUP1	NM_181575	1	0.00584932	2.10 (1.24, 3.57)	8.30%	1.01	1.23
BIRC5	NM_001168	1	0.005913421	1.71 (1.17, 2.51)	8.30%	1.01	1.25
BIRC5	NM_001012270	1	0.005913421	1.71 (1.17, 2.51)	8.30%	1.01	1.25
BIRC5	NM_001012271	1	0.005913421	1.71 (1.17, 2.51)	8.30%	1.01	1.25
BTRC	NM_003939	-1	0.00443052	0.55 (0.37, 0.83)	7.10%	1.01	1.25
BTRC	NM_033637	-1	0.00443052	0.55 (0.37, 0.83)	7.10%	1.01	1.25
BUB1	NM_004336	1	0.004890814	2.22 (1.27, 3.86)	7.50%	1.01	1.23
C12orf35	NM_018169	-1	0.00533497	0.51 (0.32, 0.82)	7.90%	1.01	1.24
C12orf48	NM_017915	1	0.004706823	2.07 (1.25, 3.43)	7.40%	1.01	1.24
C14orf38	NM_001164399	-1	0.0065299	0.61 (0.43, 0.87)	8.70%	1.01	1.25
C16orf53	NM_024516	-1	0.004893843	0.58 (0.40, 0.85)	7.50%	1.01	1.26
C1orf65	NM_152610	1	0.00558459	1.52 (1.13, 2.05)	8.10%	1.01	1.26
C1orf88	NM_181643	-1	0.006237565	0.64 (0.46, 0.88)	8.50%	1.01	1.25

C22orf15	NM_182520	1	0.006327763	1.56 (1.13, 2.14)	8.60%	1.01	1.25
C2orf77	NM_001085447	-1	0.005006318	0.63 (0.46, 0.87)	7.60%	1.01	1.26
C4orf14	NM_032313	1	0.005587578	1.73 (1.17, 2.56)	8.10%	1.01	1.25
C5orf36	NM_173665	-1	0.004656591	0.61 (0.43, 0.86)	7.30%	1.01	1.26
C5orf36	NM_001145678	-1	0.004656591	0.61 (0.43, 0.86)	7.30%	1.01	1.26
C7orf70	NM_001037163	1	0.006375541	1.77 (1.17, 2.67)	8.60%	1.01	1.25
C9orf156	NM_016481	-1	0.005997679	0.68 (0.51, 0.89)	8.40%	1.01	1.25
CACNA1D	NM_001128840	-1	0.005382035	0.63 (0.46, 0.87)	7.90%	1.01	1.26
CACNA1D	NM_000720	-1	0.005382035	0.63 (0.46, 0.87)	7.90%	1.01	1.26
CACNA1D	NM_001128839	-1	0.005382035	0.63 (0.46, 0.87)	7.90%	1.01	1.26
CALCOCO1	NM_020898	-1	0.00571028	0.63 (0.45, 0.87)	8.20%	1.01	1.25
CALCOCO1	NM_001143682	-1	0.00571028	0.63 (0.45, 0.87)	8.20%	1.01	1.25
CALCOCO1	NR_026554	-1	0.00571028	0.63 (0.45, 0.87)	8.20%	1.01	1.25
CAMKV	NM_024046	1	0.004566931	1.44 (1.12, 1.85)	7.20%	1.01	1.26
CASC5	NM_170589	1	0.005135757	2.23 (1.27, 3.92)	7.70%	1.01	1.22
CASC5	NM_144508	1	0.005135757	2.23 (1.27, 3.92)	7.70%	1.01	1.22
CCDC146	NM_020879	-1	0.006404542	0.62 (0.44, 0.87)	8.60%	1.01	1.25
CCDC85A	NM_001080433	-1	0.004932883	0.64 (0.47, 0.88)	7.50%	1.01	1.26
CDK5R2	NM_003936	1	0.004167684	1.31 (1.09, 1.58)	7.00%	1.01	1.23
CENPF	NM_016343	1	0.006440669	1.86 (1.19, 2.91)	8.70%	1.01	1.24
CHMP1A	NM_002768	1	0.005284675	1.93 (1.22, 3.07)	7.80%	1.01	1.24
CHMP1A	NM_001083314	1	0.005284675	1.93 (1.22, 3.07)	7.80%	1.01	1.24
CHRNA5	NM_000745	1	0.004550155	1.82 (1.20, 2.75)	7.20%	1.01	1.26
CIB1	NM_006384	1	0.005380782	1.41 (1.11, 1.80)	7.90%	1.01	1.25
CLEC18B	NM_001011880	1	0.005051242	1.39 (1.10, 1.74)	7.60%	1.01	1.24
CLPTM1L	NM_030782	1	0.005097651	1.61 (1.15, 2.25)	7.70%	1.01	1.26
CLRN1	NM_052995	-1	0.006214457	0.54 (0.34, 0.84)	8.50%	1.01	1.24
CLRN1	NM_174878	-1	0.006214457	0.54 (0.34, 0.84)	8.50%	1.01	1.24
CLRN1	NM_001195794	-1	0.006214457	0.54 (0.34, 0.84)	8.50%	1.01	1.24
CLUAP1	NM_015041	-1	0.005214813	0.55 (0.36, 0.84)	7.70%	1.01	1.25
CLUAP1	NM_024793	-1	0.005214813	0.55 (0.36, 0.84)	7.70%	1.01	1.25
CNGB1	NM_001135639	1	0.004913341	1.44 (1.12, 1.85)	7.50%	1.01	1.25
CNGB1	NM_001297	1	0.004913341	1.44 (1.12, 1.85)	7.50%	1.01	1.25
COL6A4P2	NR_027898	-1	0.004926414	0.62 (0.45, 0.87)	7.50%	1.01	1.26
COPE	NM_199442	1	0.004505534	1.56 (1.15, 2.12)	7.20%	1.01	1.27
COPE	NM_007263	1	0.004505534	1.56 (1.15, 2.12)	7.20%	1.01	1.27
COPE	NM_199444	1	0.004505534	1.56 (1.15, 2.12)	7.20%	1.01	1.27
CPEB2	NM_001177381	-1	0.005399996	0.60 (0.42, 0.86)	7.90%	1.01	1.25
CPEB2	NM_182646	-1	0.005399996	0.60 (0.42, 0.86)	7.90%	1.01	1.25
CPEB2	NM_001177384	-1	0.005399996	0.60 (0.42, 0.86)	7.90%	1.01	1.25
CPEB2	NM_182485	-1	0.005399996	0.60 (0.42, 0.86)	7.90%	1.01	1.25
CPEB2	NM_001177382	-1	0.005399996	0.60 (0.42, 0.86)	7.90%	1.01	1.25
CPEB2	NM_001177383	-1	0.005399996	0.60 (0.42, 0.86)	7.90%	1.01	1.25
CPLX3	NM_001030005	1	0.004089055	1.54 (1.15, 2.08)	6.90%	1.01	1.27
CSPG5	NM_006574	1	0.004918683	1.64 (1.16, 2.31)	7.50%	1.01	1.26
CT62	NM_001102658	-1	0.005814335	0.61 (0.42, 0.87)	8.30%	1.01	1.25
CTCF	NM_001191022	1	0.006404212	1.78 (1.18, 2.70)	8.60%	1.01	1.25
CTCF	NM_006565	1	0.006404212	1.78 (1.18, 2.70)	8.60%	1.01	1.25
CTSA	NM_000308	1	0.006003343	1.58 (1.14, 2.20)	8.40%	1.01	1.26

CTSA	NM_001127695	1	0.006003343	1.58 (1.14, 2.20)	8.40%	1.01	1.26
CTSA	NM_001167594	1	0.006003343	1.58 (1.14, 2.20)	8.40%	1.01	1.26
CYBRD1	NM_001127383	-1	0.004229211	0.64 (0.47, 0.87)	7.00%	1.01	1.26
CYBRD1	NM_024843	-1	0.004229211	0.64 (0.47, 0.87)	7.00%	1.01	1.26
DBF4	NM_006716	1	0.004613835	1.87 (1.21, 2.88)	7.30%	1.01	1.25
DBI	NM_001178042	1	0.006179033	1.45 (1.11, 1.90)	8.50%	1.01	1.25
DBI	NM_001079863	1	0.006179033	1.45 (1.11, 1.90)	8.50%	1.01	1.25
DBI	NM_001178043	1	0.006179033	1.45 (1.11, 1.90)	8.50%	1.01	1.25
DBI	NM_001178041	1	0.006179033	1.45 (1.11, 1.90)	8.50%	1.01	1.25
DBI	NM_001178017	1	0.006179033	1.45 (1.11, 1.90)	8.50%	1.01	1.25
DBI	NM_001079862	1	0.006179033	1.45 (1.11, 1.90)	8.50%	1.01	1.25
DBI	NM_020548	1	0.006179033	1.45 (1.11, 1.90)	8.50%	1.01	1.25
DCAF7	NM_005828	1	0.005185203	1.38 (1.10, 1.73)	7.70%	1.01	1.24
DDB2	NM_000107	-1	0.005118224	0.63 (0.46, 0.87)	7.70%	1.01	1.26
DGCR2	NM_005137	1	0.006382852	1.63 (1.15, 2.31)	8.60%	1.01	1.25
DGCR2	NM_001173534	1	0.006382852	1.63 (1.15, 2.31)	8.60%	1.01	1.25
DGCR2	NM_001173533	1	0.006382852	1.63 (1.15, 2.31)	8.60%	1.01	1.25
DGCR2	NM_001184781	1	0.006382852	1.63 (1.15, 2.31)	8.60%	1.01	1.25
DGCR2	NR_033674	1	0.006382852	1.63 (1.15, 2.31)	8.60%	1.01	1.25
DGCR9	NR_024159	1	0.005993007	1.59 (1.14, 2.22)	8.40%	1.01	1.26
DHRS3	NM_004753	1	0.006567842	1.68 (1.16, 2.45)	8.80%	1.01	1.25
DHX32	NM_018180	-1	0.006433684	0.58 (0.40, 0.86)	8.70%	1.01	1.25
DKK4	NM_014420	-1	0.006648293	0.56 (0.37, 0.85)	8.80%	1.01	1.24
DLGAP5	NM_001146015	1	0.006185847	1.81 (1.18, 2.78)	8.50%	1.01	1.25
DLGAP5	NM_014750	1	0.006185847	1.81 (1.18, 2.78)	8.50%	1.01	1.25
DNA2	NM_001080449	1	0.005009309	1.65 (1.16, 2.35)	7.60%	1.01	1.26
DNAH7	NM_018897	-1	0.004588402	0.68 (0.52, 0.89)	7.30%	1.01	1.26
DNAJB11	NM_016306	1	0.005873219	1.60 (1.14, 2.23)	8.30%	1.01	1.26
DNAJC3	NM_006260	1	0.006415627	1.54 (1.13, 2.10)	8.60%	1.01	1.25
DNAJC5G	NM_173650	1	0.00515377	1.31 (1.08, 1.59)	7.70%	1.01	1.22
DPY30	NM_032574	1	0.006797135	2.07 (1.22, 3.50)	8.90%	1.01	1.22
EBP	NM_006579	1	0.006200067	1.72 (1.17, 2.53)	8.50%	1.01	1.25
EFHC1	NR_033327	-1	0.004990192	0.58 (0.40, 0.85)	7.60%	1.01	1.25
EFHC1	NM_018100	-1	0.004990192	0.58 (0.40, 0.85)	7.60%	1.01	1.25
EFHC1	NM_001172420	-1	0.004990192	0.58 (0.40, 0.85)	7.60%	1.01	1.25
EFNA3	NM_004952	1	0.006168226	1.55 (1.13, 2.12)	8.50%	1.01	1.26
EFNA5	NM_001962	1	0.005036941	1.70 (1.17, 2.46)	7.60%	1.01	1.26
EID2B	NM_152361	-1	0.00574852	0.66 (0.49, 0.89)	8.20%	1.01	1.25
ELOVL6	NM_024090	1	0.004827708	1.77 (1.19, 2.63)	7.40%	1.01	1.26
ELOVL6	NM_001130721	1	0.004827708	1.77 (1.19, 2.63)	7.40%	1.01	1.26
EMP3	NM_001425	-1	0.004017208	0.64 (0.47, 0.87)	6.90%	1.01	1.27
EPCAM	NM_002354	1	0.006251902	1.69 (1.16, 2.46)	8.50%	1.01	1.25
EPR1	NR_002219	1	0.00602072	1.80 (1.18, 2.73)	8.40%	1.01	1.25
ERBB4	NM_005235	-1	0.004724805	0.62 (0.45, 0.86)	7.40%	1.01	1.26
ERBB4	NM_001042599	-1	0.004724805	0.62 (0.45, 0.86)	7.40%	1.01	1.26
ERN2	NM_033266	1	0.00383262	1.46 (1.13, 1.88)	6.70%	1.01	1.26
F11	NM_000128	1	0.004222479	1.48 (1.13, 1.93)	7.00%	1.01	1.26
FADS2	NM_004265	1	0.00574684	1.85 (1.20, 2.86)	8.20%	1.01	1.25
FAM102A	NM_203305	-1	0.005644483	0.62 (0.44, 0.87)	8.10%	1.01	1.25

FAM102A	NM_001035254	-1	0.005644483	0.62 (0.44, 0.87)	8.10%	1.01	1.25
FAM155B	NM_015686	1	0.005996344	1.62 (1.15, 2.29)	8.40%	1.01	1.26
FAM19A1	NM_213609	1	0.006014024	1.54 (1.13, 2.09)	8.40%	1.01	1.26
FAM200A	NM_145111	-1	0.004137595	0.67 (0.51, 0.88)	6.90%	1.01	1.26
FBXL2	NM_001171713	-1	0.005598664	0.67 (0.51, 0.89)	8.10%	1.01	1.25
FBXL2	NM_012157	-1	0.005598664	0.67 (0.51, 0.89)	8.10%	1.01	1.25
FBXO45	NM_001105573	1	0.00563526	1.69 (1.17, 2.46)	8.10%	1.01	1.26
FDXACB1	NM_138378	-1	0.004699684	0.71 (0.56, 0.90)	7.40%	1.01	1.25
FGF2	NM_002006	-1	0.004723067	0.57 (0.39, 0.84)	7.40%	1.01	1.26
FLJ30403	NR_034159	-1	0.004967441	0.63 (0.46, 0.87)	7.50%	1.01	1.26
FLJ41200	NR_033863	1	0.004925314	1.75 (1.18, 2.58)	7.50%	1.01	1.26
FLJ44635	NM_207422	-1	0.006189338	0.63 (0.45, 0.88)	8.50%	1.01	1.25
FOXM1	NM_202002	1	0.004332916	1.63 (1.17, 2.28)	7.10%	1.01	1.27
FOXM1	NM_202003	1	0.004332916	1.63 (1.17, 2.28)	7.10%	1.01	1.27
FOXM1	NM_021953	1	0.004332916	1.63 (1.17, 2.28)	7.10%	1.01	1.27
FSTL3	NM_005860	-1	0.004470174	0.61 (0.44, 0.86)	7.20%	1.01	1.26
GALNT14	NM_024572	1	0.006578564	1.80 (1.18, 2.74)	8.80%	1.01	1.24
GALNTL1	NM_001168368	-1	0.004149532	0.63 (0.46, 0.86)	6.90%	1.01	1.26
GALNTL1	NM_020692	-1	0.004149532	0.63 (0.46, 0.86)	6.90%	1.01	1.26
GFRA1	NM_145793	-1	0.005973491	0.61 (0.43, 0.87)	8.40%	1.01	1.25
GFRA1	NM_001145453	-1	0.005973491	0.61 (0.43, 0.87)	8.40%	1.01	1.25
GFRA1	NM_005264	-1	0.005973491	0.61 (0.43, 0.87)	8.40%	1.01	1.25
GLRX2	NM_016066	1	0.006629201	2.04 (1.22, 3.43)	8.80%	1.01	1.23
GLRX2	NM_197962	1	0.006629201	2.04 (1.22, 3.43)	8.80%	1.01	1.23
GPR17	NM_001161415	-1	0.004359195	0.66 (0.50, 0.88)	7.10%	1.01	1.26
GPR17	NM_001161417	-1	0.004359195	0.66 (0.50, 0.88)	7.10%	1.01	1.26
GPR17	NM_001161416	-1	0.004359195	0.66 (0.50, 0.88)	7.10%	1.01	1.26
GPR17	NM_005291	-1	0.004359195	0.66 (0.50, 0.88)	7.10%	1.01	1.26
GPR33	NM_001197184	1	0.004512989	1.30 (1.08, 1.56)	7.20%	1.01	1.22
GPR33	NR_036675	1	0.004512989	1.30 (1.08, 1.56)	7.20%	1.01	1.22
GPR63	NM_001143957	1	0.006597235	1.68 (1.15, 2.44)	8.80%	1.01	1.25
GPR63	NM_030784	1	0.006597235	1.68 (1.15, 2.44)	8.80%	1.01	1.25
GREB1L	NM_001142966	-1	0.004120083	0.63 (0.46, 0.86)	6.90%	1.01	1.27
GRPEL2	NM_152407	1	0.005432863	1.99 (1.23, 3.24)	7.90%	1.01	1.24
HIF1A	NM_001530	1	0.006328987	1.64 (1.15, 2.33)	8.60%	1.01	1.25
HIF1A	NM_181054	1	0.006328987	1.64 (1.15, 2.33)	8.60%	1.01	1.25
HIST2H2AC	NM_003517	1	0.00431244	1.73 (1.19, 2.52)	7.10%	1.01	1.26
HMX1	NM_018942	1	0.003648411	1.34 (1.10, 1.63)	6.50%	1.01	1.24
HOMER1	NM_004272	1	0.004348297	1.84 (1.21, 2.79)	7.10%	1.01	1.26
HSPA12A	NM_025015	-1	0.00605439	0.62 (0.44, 0.87)	8.40%	1.01	1.25
HSPBAP1	NM_024610	-1	0.005349517	0.60 (0.42, 0.86)	7.90%	1.01	1.25
IDH1	NM_005896	1	0.004957583	1.57 (1.15, 2.15)	7.50%	1.01	1.26
IL20RB	NM_144717	1	0.004776866	1.77 (1.19, 2.64)	7.40%	1.01	1.26
IL6ST	NM_001190981	-1	0.006042753	0.55 (0.36, 0.84)	8.40%	1.01	1.24
IL6ST	NM_175767	-1	0.006042753	0.55 (0.36, 0.84)	8.40%	1.01	1.24
IL6ST	NM_002184	-1	0.006042753	0.55 (0.36, 0.84)	8.40%	1.01	1.24
IPW	NR_023915	-1	0.004512207	0.64 (0.47, 0.87)	7.20%	1.01	1.26
IRGM	NM_001145805	1	0.004422765	1.53 (1.14, 2.06)	7.10%	1.01	1.26
ITGB4	NM_001005731	1	0.004372283	1.60 (1.16, 2.21)	7.10%	1.01	1.27

ITGB4	NM_000213	1	0.004372283	1.60 (1.16, 2.21)	7.10%	1.01	1.27
ITGB4	NM_001005619	1	0.004372283	1.60 (1.16, 2.21)	7.10%	1.01	1.27
KDELR1	NM_006801	1	0.005637	1.63 (1.15, 2.31)	8.10%	1.01	1.26
KDM5A	NM_001042603	-1	0.006234911	0.58 (0.39, 0.86)	8.50%	1.01	1.25
KIAA1109	NM_015312	-1	0.004341596	0.63 (0.46, 0.87)	7.10%	1.01	1.26
KIAA1217	NM_001098500	-1	0.004307668	0.60 (0.43, 0.85)	7.10%	1.01	1.26
KIAA1217	NM_019590	-1	0.004307668	0.60 (0.43, 0.85)	7.10%	1.01	1.26
KIAA1217	NM_001098501	-1	0.004307668	0.60 (0.43, 0.85)	7.10%	1.01	1.26
KIAA1324	NM_020775	-1	0.004339938	0.68 (0.52, 0.88)	7.10%	1.01	1.26
KIF23	NM_138555	1	0.005200001	1.91 (1.21, 3.01)	7.70%	1.01	1.25
KIF23	NM_004856	1	0.005200001	1.91 (1.21, 3.01)	7.70%	1.01	1.25
KIF27	NM_017576	-1	0.005549882	0.66 (0.50, 0.89)	8.00%	1.01	1.25
KIRREL	NM_018240	-1	0.004133502	0.67 (0.51, 0.88)	6.90%	1.01	1.26
KLHL7	NR_033328	1	0.005009326	1.46 (1.12, 1.91)	7.60%	1.01	1.26
KLHL7	NM_018846	1	0.005009326	1.46 (1.12, 1.91)	7.60%	1.01	1.26
KLHL7	NR_033329	1	0.005009326	1.46 (1.12, 1.91)	7.60%	1.01	1.26
KLHL7	NM_001172428	1	0.005009326	1.46 (1.12, 1.91)	7.60%	1.01	1.26
KLHL7	NM_001031710	1	0.005009326	1.46 (1.12, 1.91)	7.60%	1.01	1.26
KRT20	NM_019010	1	0.004928084	1.36 (1.10, 1.68)	7.50%	1.01	1.24
KRT72	NM_001146225	1	0.006068111	1.44 (1.11, 1.86)	8.40%	1.01	1.25
KRT72	NM_080747	1	0.006068111	1.44 (1.11, 1.86)	8.40%	1.01	1.25
KRT72	NM_001146226	1	0.006068111	1.44 (1.11, 1.86)	8.40%	1.01	1.25
LIN54	NM_001115007	1	0.004747521	1.88 (1.21, 2.93)	7.40%	1.01	1.25
LIN54	NM_194282	1	0.004747521	1.88 (1.21, 2.93)	7.40%	1.01	1.25
LIN54	NM_001115008	1	0.004747521	1.88 (1.21, 2.93)	7.40%	1.01	1.25
LINGO1	NM_032808	1	0.004519614	1.93 (1.23, 3.03)	7.20%	1.01	1.25
LOC100129046	NR_034091	-1	0.005971508	0.58 (0.40, 0.86)	8.40%	1.01	1.25
LOC100499484	NR_036526	-1	0.004306021	0.60 (0.42, 0.85)	7.10%	1.01	1.26
LOC344595	NR_028301	-1	0.004316669	0.61 (0.43, 0.86)	7.10%	1.01	1.26
LOC344595	NR_028302	-1	0.004316669	0.61 (0.43, 0.86)	7.10%	1.01	1.26
LOC728323	NR_024437	-1	0.004035146	0.69 (0.53, 0.89)	6.90%	1.01	1.26
LRRIQ1	NM_001079910	-1	0.006050079	0.62 (0.44, 0.87)	8.40%	1.01	1.25
LRRIQ1	NM_032165	-1	0.006050079	0.62 (0.44, 0.87)	8.40%	1.01	1.25
MAD2L1	NM_002358	1	0.006190566	1.86 (1.19, 2.90)	8.50%	1.01	1.24
MAGT1	NM_032121	1	0.006485501	1.59 (1.14, 2.22)	8.70%	1.01	1.25
MAPK8IP3	NM_001040439	-1	0.0062091	0.62 (0.44, 0.87)	8.50%	1.01	1.25
MAPK8IP3	NM_015133	-1	0.0062091	0.62 (0.44, 0.87)	8.50%	1.01	1.25
MATN3	NM_002381	-1	0.004632692	0.61 (0.43, 0.86)	7.30%	1.01	1.26
METTL3	NM_019852	-1	0.005935671	0.59 (0.41, 0.86)	8.40%	1.01	1.25
MFSD7	NM_032219	-1	0.005041383	0.68 (0.52, 0.89)	7.60%	1.01	1.25
MIR501	NR_030225	1	0.004596181	1.39 (1.11, 1.74)	7.30%	1.01	1.25
MKI67	NM_002417	1	0.004838869	1.85 (1.21, 2.83)	7.40%	1.01	1.25
MKI67	NM_001145966	1	0.004838869	1.85 (1.21, 2.83)	7.40%	1.01	1.25
MOXD2P	NR_024346	1	0.00477089	1.52 (1.14, 2.02)	7.40%	1.01	1.26
MPHOSPH6	NM_005792	1	0.00484696	1.48 (1.13, 1.94)	7.40%	1.01	1.26
MTDH	NM_178812	1	0.004800288	1.55 (1.14, 2.10)	7.40%	1.01	1.26
MTMR9LP	NR_026850	-1	0.00483402	0.67 (0.51, 0.89)	7.40%	1.01	1.26
MUC12	NM_001164462	-1	0.006098226	0.59 (0.40, 0.86)	8.40%	1.01	1.25
MVD	NM_002461	1	0.005857959	2.04 (1.23, 3.39)	8.30%	1.01	1.23

NBN	NM_002485	1	0.005163332	1.63 (1.16, 2.30)	7.70%	1.01	1.26
NBPF1	NM_017940	-1	0.005126436	0.63 (0.46, 0.87)	7.70%	1.01	1.26
NOTCH1	NM_017617	1	0.004096101	1.50 (1.14, 1.99)	6.90%	1.01	1.27
NPC1L1	NM_001101648	1	0.005266683	1.44 (1.11, 1.85)	7.80%	1.01	1.25
NPC1L1	NM_013389	1	0.005266683	1.44 (1.11, 1.85)	7.80%	1.01	1.25
NUAK1	NM_014840	-1	0.00483339	0.66 (0.50, 0.88)	7.40%	1.01	1.26
NUF2	NM_145697	1	0.004332713	1.64 (1.17, 2.30)	7.10%	1.01	1.27
NUF2	NM_031423	1	0.004332713	1.64 (1.17, 2.30)	7.10%	1.01	1.27
NUP93	NM_014669	1	0.005806313	1.70 (1.17, 2.48)	8.30%	1.01	1.25
NUSAP1	NM_001129897	1	0.005759989	1.86 (1.20, 2.88)	8.20%	1.01	1.25
NUSAP1	NM_018454	1	0.005759989	1.86 (1.20, 2.88)	8.20%	1.01	1.25
NUSAP1	NM_016359	1	0.005759989	1.86 (1.20, 2.88)	8.20%	1.01	1.25
OCM	NM_001097622	1	0.004906929	1.30 (1.08, 1.56)	7.50%	1.01	1.22
ODC1	NM_002539	1	0.006073792	1.66 (1.16, 2.38)	8.40%	1.01	1.25
OGDHL	NM_001143997	1	0.005912877	1.58 (1.14, 2.18)	8.30%	1.01	1.26
OGDHL	NM_001143996	1	0.005912877	1.58 (1.14, 2.18)	8.30%	1.01	1.26
OGDHL	NM_018245	1	0.005912877	1.58 (1.14, 2.18)	8.30%	1.01	1.26
OR14J1	NM_030946	1	0.004503814	1.46 (1.12, 1.89)	7.20%	1.01	1.26
OR5T2	NM_001004746	1	0.005223593	1.71 (1.17, 2.50)	7.70%	1.01	1.26
P4HA1	NM_001017962	1	0.004247315	1.44 (1.12, 1.84)	7.00%	1.01	1.26
P4HA1	NM_001142595	1	0.004247315	1.44 (1.12, 1.84)	7.00%	1.01	1.26
P4HA1	NM_001142596	1	0.004247315	1.44 (1.12, 1.84)	7.00%	1.01	1.26
P4HA1	NM_000917	1	0.004247315	1.44 (1.12, 1.84)	7.00%	1.01	1.26
PACSIN2	NM_001184970	1	0.004070682	1.60 (1.16, 2.21)	6.90%	1.01	1.27
PACSIN2	NM_007229	1	0.004070682	1.60 (1.16, 2.21)	6.90%	1.01	1.27
PACSIN2	NM_001184971	1	0.004070682	1.60 (1.16, 2.21)	6.90%	1.01	1.27
PAPL	NM_001004318	1	0.00430893	1.48 (1.13, 1.93)	7.10%	1.01	1.26
PAR1	NR_022009	-1	0.005038754	0.64 (0.47, 0.87)	7.60%	1.01	1.26
PCDP1	NM_001029996	-1	0.00550873	0.56 (0.37, 0.84)	8.00%	1.01	1.25
PCP4L1	NM_001102566	1	0.005705339	1.77 (1.18, 2.64)	8.20%	1.01	1.25
PCYOX1L	NM_024028	-1	0.006326101	0.63 (0.45, 0.88)	8.60%	1.01	1.25
PDZRN3	NM_015009	-1	0.004230075	0.63 (0.46, 0.87)	7.00%	1.01	1.26
PGRMC1	NM_006667	1	0.005470607	1.48 (1.12, 1.95)	7.90%	1.01	1.26
PIAS2	NM_004671	-1	0.006115119	0.69 (0.53, 0.90)	8.50%	1.01	1.25
PIAS2	NM_173206	-1	0.006115119	0.69 (0.53, 0.90)	8.50%	1.01	1.25
PIH1D2	NM_001082619	-1	0.00647425	0.59 (0.40, 0.86)	8.70%	1.01	1.25
PIH1D2	NM_138789	-1	0.00647425	0.59 (0.40, 0.86)	8.70%	1.01	1.25
PINK1	NM_032409	-1	0.006364293	0.70 (0.54, 0.90)	8.60%	1.01	1.24
PLA2G2F	NM_022819	1	0.004792716	1.53 (1.14, 2.05)	7.40%	1.01	1.26
PLCD3	NM_133373	-1	0.004835269	0.68 (0.52, 0.89)	7.40%	1.01	1.25
PRKAR2A	NM_004157	1	0.004456628	1.74 (1.19, 2.56)	7.20%	1.01	1.26
PSMA4	NM_001102667	1	0.006063723	1.93 (1.21, 3.07)	8.40%	1.01	1.24
PSMA4	NM_001102668	1	0.006063723	1.93 (1.21, 3.07)	8.40%	1.01	1.24
PSMA4	NM_002789	1	0.006063723	1.93 (1.21, 3.07)	8.40%	1.01	1.24
PSMC4	NM_006503	1	0.004218907	1.38 (1.11, 1.72)	7.00%	1.01	1.25
PSMC4	NM_153001	1	0.004218907	1.38 (1.11, 1.72)	7.00%	1.01	1.25
PSMG3	NM_001134340	1	0.004706287	1.68 (1.17, 2.40)	7.40%	1.01	1.26
PSMG3	NM_032302	1	0.004706287	1.68 (1.17, 2.40)	7.40%	1.01	1.26
RALA	NM_005402	1	0.005804625	1.66 (1.16, 2.39)	8.30%	1.01	1.26

RECQL4	NM_004260	1	0.005197018	1.75 (1.18, 2.58)	7.70%	1.01	1.26
RHEB	NM_005614	1	0.005237779	1.90 (1.21, 2.98)	7.80%	1.01	1.25
RLIM	NM_183353	1	0.005064841	1.66 (1.16, 2.36)	7.60%	1.01	1.26
RLIM	NM_016120	1	0.005064841	1.66 (1.16, 2.36)	7.60%	1.01	1.26
RPL23AP53	NR_003572	-1	0.006006153	0.60 (0.42, 0.86)	8.40%	1.01	1.25
RPL8	NM_000973	1	0.005660274	1.52 (1.13, 2.05)	8.10%	1.01	1.26
RPL8	NM_033301	1	0.005660274	1.52 (1.13, 2.05)	8.10%	1.01	1.26
RSPH1	NM_080860	-1	0.004552589	0.64 (0.46, 0.87)	7.20%	1.01	1.26
RUNX1	NM_001001890	-1	0.005414839	0.53 (0.34, 0.83)	7.90%	1.01	1.24
RUNX1	NM_001754	-1	0.005414839	0.53 (0.34, 0.83)	7.90%	1.01	1.24
RUNX1	NM_001122607	-1	0.005414839	0.53 (0.34, 0.83)	7.90%	1.01	1.24
RXFP2	NM_130806	1	0.004747273	1.24 (1.07, 1.44)	7.40%	1.01	1.19
RXFP2	NM_001166058	1	0.004747273	1.24 (1.07, 1.44)	7.40%	1.01	1.19
SC4MOL	NM_006745	1	0.00570173	1.51 (1.13, 2.02)	8.20%	1.01	1.26
SC4MOL	NM_001017369	1	0.00570173	1.51 (1.13, 2.02)	8.20%	1.01	1.26
SCD	NM_005063	1	0.00542315	1.91 (1.21, 3.02)	7.90%	1.01	1.24
SEC13	NR_024273	1	0.006369561	1.64 (1.15, 2.35)	8.60%	1.01	1.25
SEC13	NM_001136232	1	0.006369561	1.64 (1.15, 2.35)	8.60%	1.01	1.25
SEC13	NR_024272	1	0.006369561	1.64 (1.15, 2.35)	8.60%	1.01	1.25
SEC13	NM_183352	1	0.006369561	1.64 (1.15, 2.35)	8.60%	1.01	1.25
SEC24A	NM_021982	1	0.006121721	1.65 (1.15, 2.37)	8.50%	1.01	1.25
SERPIND1	NM_000185	-1	0.004249699	0.57 (0.39, 0.84)	7.00%	1.01	1.26
SFXN5	NM_144579	-1	0.005790443	0.64 (0.47, 0.88)	8.20%	1.01	1.25
SKA2	NM_182620	1	0.004751619	1.58 (1.15, 2.18)	7.40%	1.01	1.26
SKA2	NM_001100595	1	0.004751619	1.58 (1.15, 2.18)	7.40%	1.01	1.26
SLC30A10	NM_018713	1	0.005198017	1.37 (1.10, 1.71)	7.70%	1.01	1.24
SLC41A2	NM_032148	1	0.005498771	1.44 (1.11, 1.87)	8.00%	1.01	1.25
SLC44A1	NM_080546	-1	0.004388528	0.62 (0.45, 0.86)	7.10%	1.01	1.26
SLC9A5	NM_004594	1	0.006146031	1.70 (1.16, 2.47)	8.50%	1.01	1.25
SMG7	NM_173156	1	0.005723927	1.47 (1.12, 1.93)	8.20%	1.01	1.25
SMG7	NM_201569	1	0.005723927	1.47 (1.12, 1.93)	8.20%	1.01	1.25
SMG7	NM_201568	1	0.005723927	1.47 (1.12, 1.93)	8.20%	1.01	1.25
SMG7	NM_001174061	1	0.005723927	1.47 (1.12, 1.93)	8.20%	1.01	1.25
SND1	NM_014390	1	0.004484231	1.70 (1.18, 2.45)	7.20%	1.01	1.26
SNORD116-12	NR_003327	1	0.006075002	1.32 (1.08, 1.60)	8.40%	1.01	1.22
SNRNP70	NM_003089	-1	0.004606328	0.54 (0.36, 0.83)	7.30%	1.01	1.25
SQSTM1	NM_003900	1	0.004571164	1.83 (1.20, 2.78)	7.20%	1.01	1.26
SQSTM1	NM_001142299	1	0.004571164	1.83 (1.20, 2.78)	7.20%	1.01	1.26
SQSTM1	NM_001142298	1	0.004571164	1.83 (1.20, 2.78)	7.20%	1.01	1.26
SREBF2	NM_004599	1	0.004241128	1.61 (1.16, 2.22)	7.00%	1.01	1.27
SRSF5	NM_006925	-1	0.005863942	0.54 (0.35, 0.84)	8.30%	1.01	1.24
SRSF5	NM_001039465	-1	0.005863942	0.54 (0.35, 0.84)	8.30%	1.01	1.24
SSR1	NM_003144	1	0.005569398	1.63 (1.15, 2.31)	8.10%	1.01	1.26
STATH	NM_001009181	1	0.003857366	1.36 (1.11, 1.68)	6.70%	1.01	1.24
STATH	NM_003154	1	0.003857366	1.36 (1.11, 1.68)	6.70%	1.01	1.24
STIP1	NM_006819	1	0.006434469	1.58 (1.14, 2.19)	8.70%	1.01	1.25
STX1A	NM_004603	1	0.006602765	1.71 (1.16, 2.52)	8.80%	1.01	1.25
STX1A	NM_001165903	1	0.006602765	1.71 (1.16, 2.52)	8.80%	1.01	1.25
STX1B	NM_052874	-1	0.004730101	0.61 (0.44, 0.86)	7.40%	1.01	1.26

SUMO3	NM_006936	1	0.005665759	1.83 (1.19, 2.80)	8.10%	1.01	1.25
TADA1	NM_053053	1	0.00455637	1.54 (1.14, 2.08)	7.20%	1.01	1.26
TARS	NM_152295	1	0.005460832	1.63 (1.15, 2.30)	7.90%	1.01	1.26
TBC1D19	NM_018317	-1	0.004309516	0.66 (0.50, 0.88)	7.10%	1.01	1.26
TCTN2	NM_024809	-1	0.00482289	0.58 (0.40, 0.85)	7.40%	1.01	1.26
TCTN2	NM_001143850	-1	0.00482289	0.58 (0.40, 0.85)	7.40%	1.01	1.26
TMEM132A	NM_178031	1	0.005666749	1.66 (1.16, 2.38)	8.10%	1.01	1.26
TMEM132A	NM_017870	1	0.005666749	1.66 (1.16, 2.38)	8.10%	1.01	1.26
TMEM150A	NR_033179	1	0.004738486	1.78 (1.19, 2.67)	7.40%	1.01	1.26
TMEM150A	NM_001031738	1	0.004738486	1.78 (1.19, 2.67)	7.40%	1.01	1.26
TMEM200C	NM_001080209	-1	0.006303527	0.59 (0.41, 0.86)	8.60%	1.01	1.25
TOMM70A	NM_014820	1	0.005119582	1.65 (1.16, 2.34)	7.70%	1.01	1.26
TPD52L1	NM_003287	1	0.00467689	1.74 (1.18, 2.55)	7.30%	1.01	1.26
TPD52L1	NM_001003397	1	0.00467689	1.74 (1.18, 2.55)	7.30%	1.01	1.26
TPD52L1	NM_001003396	1	0.00467689	1.74 (1.18, 2.55)	7.30%	1.01	1.26
TPD52L1	NM_001003395	1	0.00467689	1.74 (1.18, 2.55)	7.30%	1.01	1.26
TPTE	NM_199259	1	0.003424575	1.34 (1.10, 1.63)	6.30%	1.01	1.24
TPTE	NM_199261	1	0.003424575	1.34 (1.10, 1.63)	6.30%	1.01	1.24
TPTE	NM_199260	1	0.003424575	1.34 (1.10, 1.63)	6.30%	1.01	1.24
TRIM66	NM_014818	-1	0.006607717	0.60 (0.41, 0.87)	8.80%	1.01	1.25
TRIP13	NM_004237	1	0.006392425	2.19 (1.25, 3.86)	8.60%	1.01	1.22
TRIP13	NM_001166260	1	0.006392425	2.19 (1.25, 3.86)	8.60%	1.01	1.22
TRPC6	NM_004621	-1	0.004611756	0.63 (0.46, 0.87)	7.30%	1.01	1.26
TRPM1	NM_002420	1	0.003408407	1.31 (1.09, 1.56)	6.30%	1.01	1.23
TRYX3	NM_001001317	1	0.005404072	1.62 (1.15, 2.28)	7.90%	1.01	1.26
TSPAN19	NM_001100917	1	0.005213327	1.31 (1.08, 1.59)	7.70%	1.01	1.22
TTC4	NM_004623	-1	0.005824634	0.53 (0.34, 0.83)	8.30%	1.01	1.24
UNC5B	NM_170744	-1	0.005298662	0.63 (0.46, 0.87)	7.80%	1.01	1.26
VTA1	NM_016485	1	0.006405376	1.46 (1.11, 1.92)	8.60%	1.01	1.25
WDR60	NM_018051	-1	0.005425427	0.64 (0.47, 0.88)	7.90%	1.01	1.26
WDR65	NM_001195831	-1	0.005313098	0.62 (0.45, 0.87)	7.80%	1.01	1.26
WDR65	NM_001167965	-1	0.005313098	0.62 (0.45, 0.87)	7.80%	1.01	1.26
WDR65	NM_152498	-1	0.005313098	0.62 (0.45, 0.87)	7.80%	1.01	1.26
WDR65	NM_001167966	-1	0.005313098	0.62 (0.45, 0.87)	7.80%	1.01	1.26
WDR65	NR_030778	-1	0.005313098	0.62 (0.45, 0.87)	7.80%	1.01	1.26
WDTC1	NM_015023	-1	0.006462542	0.69 (0.53, 0.90)	8.70%	1.01	1.24
YIF1A	NM_020470	1	0.004460223	1.70 (1.18, 2.46)	7.20%	1.01	1.26
ZBTB4	NM_001128833	-1	0.004317842	0.63 (0.46, 0.86)	7.10%	1.01	1.26
ZBTB4	NM_020899	-1	0.004317842	0.63 (0.46, 0.86)	7.10%	1.01	1.26
ZCCHC7	NM_032226	-1	0.00624057	0.51 (0.31, 0.83)	8.50%	1.01	1.23
ZNF43	NM_003423	-1	0.005996525	0.64 (0.47, 0.88)	8.40%	1.01	1.25
ZNF438	NM_001143771	-1	0.005439166	0.62 (0.44, 0.87)	7.90%	1.01	1.26
ZNF438	NM_001143767	-1	0.005439166	0.62 (0.44, 0.87)	7.90%	1.01	1.26
ZNF438	NM_001143766	-1	0.005439166	0.62 (0.44, 0.87)	7.90%	1.01	1.26
ZNF438	NM_001143770	-1	0.005439166	0.62 (0.44, 0.87)	7.90%	1.01	1.26
ZNF438	NM_182755	-1	0.005439166	0.62 (0.44, 0.87)	7.90%	1.01	1.26
ZNF438	NR_026560	-1	0.005439166	0.62 (0.44, 0.87)	7.90%	1.01	1.26
ZNF438	NM_001143768	-1	0.005439166	0.62 (0.44, 0.87)	7.90%	1.01	1.26
ZNF438	NM_001143769	-1	0.005439166	0.62 (0.44, 0.87)	7.90%	1.01	1.26

ZNF564	NM_144976	-1	0.004988278	0.59 (0.41, 0.85)	7.60%	1.01	1.26
ZNF668	NM_024706	-1	0.004456171	0.66 (0.50, 0.88)	7.20%	1.01	1.26
ZNF668	NM_001172670	-1	0.004456171	0.66 (0.50, 0.88)	7.20%	1.01	1.26
ZNF668	NM_001172669	-1	0.004456171	0.66 (0.50, 0.88)	7.20%	1.01	1.26
ZNF668	NM_001172668	-1	0.004456171	0.66 (0.50, 0.88)	7.20%	1.01	1.26
ZNF839	NM_018335	-1	0.005746311	0.56 (0.37, 0.85)	8.20%	1.01	1.25
ADAM22	NM_004194	-1	0.008205802	0.65 (0.47, 0.89)	9.80%	1	1.24
ADAM22	NM_021722	-1	0.008205802	0.65 (0.47, 0.89)	9.80%	1	1.24
ADAM22	NM_021721	-1	0.008205802	0.65 (0.47, 0.89)	9.80%	1	1.24
ADAM22	NM_021723	-1	0.008205802	0.65 (0.47, 0.89)	9.80%	1	1.24
ADAM22	NM_016351	-1	0.008205802	0.65 (0.47, 0.89)	9.80%	1	1.24
ADM	NM_001124	1	0.007902715	1.60 (1.13, 2.27)	9.70%	1	1.25
ALG9	NM_001077691	-1	0.006987624	0.69 (0.52, 0.90)	9.10%	1	1.24
ALG9	NM_024740	-1	0.006987624	0.69 (0.52, 0.90)	9.10%	1	1.24
ALG9	NM_001077690	-1	0.006987624	0.69 (0.52, 0.90)	9.10%	1	1.24
ALG9	NM_001077692	-1	0.006987624	0.69 (0.52, 0.90)	9.10%	1	1.24
APCS	NM_001639	1	0.00751427	1.21 (1.05, 1.40)	9.40%	1	1.18
ARMCX4	NR_028407	-1	0.007606047	0.59 (0.40, 0.87)	9.50%	1	1.24
ATL2	NM_022374	1	0.006753427	1.47 (1.11, 1.94)	8.90%	1	1.25
ATL2	NM_001135673	1	0.006753427	1.47 (1.11, 1.94)	8.90%	1	1.25
ATL2	NR_024191	1	0.006753427	1.47 (1.11, 1.94)	8.90%	1	1.25
BAZ2B	NM_013450	-1	0.007896861	0.63 (0.44, 0.88)	9.70%	1	1.24
BNIP3	NM_004052	1	0.008214484	1.55 (1.12, 2.13)	9.90%	1	1.25
BRDT	NM_001726	-1	0.00773667	0.53 (0.33, 0.85)	9.60%	1	1.23
BRDT	NM_207189	-1	0.00773667	0.53 (0.33, 0.85)	9.60%	1	1.23
BUB3	NM_004725	1	0.007105129	1.48 (1.11, 1.98)	9.10%	1	1.25
BUB3	NM_001007793	1	0.007105129	1.48 (1.11, 1.98)	9.10%	1	1.25
C15orf2	NM_018958	1	0.007451532	1.51 (1.12, 2.04)	9.30%	1	1.25
C6orf123	NR_026773	1	0.007331897	1.64 (1.14, 2.34)	9.30%	1	1.25
C9orf116	NM_144654	-1	0.007781927	0.62 (0.44, 0.88)	9.60%	1	1.24
C9orf116	NM_001048265	-1	0.007781927	0.62 (0.44, 0.88)	9.60%	1	1.24
CA5A	NM_001739	1	0.007743248	1.74 (1.16, 2.62)	9.60%	1	1.24
CASK	NM_001126055	1	0.008238136	1.60 (1.13, 2.26)	9.90%	1	1.24
CASK	NM_001126054	1	0.008238136	1.60 (1.13, 2.26)	9.90%	1	1.24
CASK	NM_003688	1	0.008238136	1.60 (1.13, 2.26)	9.90%	1	1.24
CAV3	NM_033337	1	0.007209523	1.56 (1.13, 2.15)	9.20%	1	1.25
CAV3	NM_001234	1	0.007209523	1.56 (1.13, 2.15)	9.20%	1	1.25
CCDC41	NM_016122	-1	0.008020691	0.60 (0.41, 0.88)	9.70%	1	1.24
CCDC41	NM_001042399	-1	0.008020691	0.60 (0.41, 0.88)	9.70%	1	1.24
CCNB2	NM_004701	1	0.007331535	2.05 (1.21, 3.47)	9.30%	1	1.22
CCR10	NM_016602	-1	0.007757267	0.60 (0.41, 0.87)	9.60%	1	1.24
CDHR3	NM_152750	-1	0.008293294	0.63 (0.44, 0.89)	9.90%	1	1.24
CHCHD2	NM_016139	1	0.006949779	1.76 (1.17, 2.65)	9.10%	1	1.24
CHP	NM_007236	1	0.007990476	1.61 (1.13, 2.30)	9.70%	1	1.25
CHRNA6	NM_004198	-1	0.00809738	0.64 (0.47, 0.89)	9.80%	1	1.24
CHRNA6	NM_001199279	-1	0.00809738	0.64 (0.47, 0.89)	9.80%	1	1.24
CHRNE	NM_000080	-1	0.007041906	0.68 (0.51, 0.90)	9.10%	1	1.24
CMYA5	NM_153610	-1	0.006763751	0.61 (0.42, 0.87)	8.90%	1	1.25
COL8A2	NM_005202	-1	0.007593958	0.64 (0.46, 0.89)	9.50%	1	1.24

COLEC12	NM_130386	-1	0.007113712	0.67 (0.50, 0.90)	9.20%	1	1.25
COQ4	NM_016035	-1	0.008371696	0.66 (0.48, 0.90)	10.00%	1	1.24
COX5A	NM_004255	1	0.008188332	1.79 (1.16, 2.76)	9.80%	1	1.23
CREB3L2	NM_194071	1	0.007316954	1.72 (1.16, 2.55)	9.30%	1	1.24
CSNK2A2	NM_001896	1	0.007911319	1.76 (1.16, 2.67)	9.70%	1	1.24
CST5	NM_001900	-1	0.007660357	0.41 (0.21, 0.79)	9.50%	1	1.19
CTDSP1	NM_021198	-1	0.006755543	0.63 (0.45, 0.88)	8.90%	1	1.25
CTDSP1	NM_182642	-1	0.006755543	0.63 (0.45, 0.88)	8.90%	1	1.25
DCDC2	NM_001195610	-1	0.007215502	0.61 (0.43, 0.88)	9.20%	1	1.24
DCDC2	NM_016356	-1	0.007215502	0.61 (0.43, 0.88)	9.20%	1	1.24
DSCR4	NM_005867	1	0.006963957	1.35 (1.09, 1.68)	9.10%	1	1.23
ECT2	NM_018098	1	0.007045075	1.62 (1.14, 2.30)	9.10%	1	1.25
EPRS	NM_004446	1	0.007248665	1.70 (1.15, 2.50)	9.20%	1	1.25
ESRRA	NM_004451	1	0.008289243	1.77 (1.16, 2.71)	9.90%	1	1.24
F5	NM_000130	1	0.007141726	1.45 (1.11, 1.90)	9.20%	1	1.25
FAM169B	NM_182562	1	0.006944878	1.33 (1.08, 1.63)	9.10%	1	1.22
FAM38B	NM_022068	-1	0.007143819	0.50 (0.30, 0.83)	9.20%	1	1.22
FBXO15	NM_152676	-1	0.008149201	0.63 (0.44, 0.89)	9.80%	1	1.24
FBXO15	NM_001142958	-1	0.008149201	0.63 (0.44, 0.89)	9.80%	1	1.24
FCAR	NM_133279	-1	0.00758047	0.60 (0.42, 0.87)	9.50%	1	1.24
FCAR	NM_133274	-1	0.00758047	0.60 (0.42, 0.87)	9.50%	1	1.24
FCAR	NM_133273	-1	0.00758047	0.60 (0.42, 0.87)	9.50%	1	1.24
FCAR	NM_002000	-1	0.00758047	0.60 (0.42, 0.87)	9.50%	1	1.24
FCAR	NM_133277	-1	0.00758047	0.60 (0.42, 0.87)	9.50%	1	1.24
FCAR	NM_133278	-1	0.00758047	0.60 (0.42, 0.87)	9.50%	1	1.24
FCAR	NM_133271	-1	0.00758047	0.60 (0.42, 0.87)	9.50%	1	1.24
FCAR	NM_133269	-1	0.00758047	0.60 (0.42, 0.87)	9.50%	1	1.24
FCAR	NM_133272	-1	0.00758047	0.60 (0.42, 0.87)	9.50%	1	1.24
FCGR2C	NM_201563	-1	0.007000324	0.62 (0.44, 0.88)	9.10%	1	1.25
FMNL3	NM_175736	-1	0.007177176	0.64 (0.47, 0.89)	9.20%	1	1.25
FMNL3	NM_198900	-1	0.007177176	0.64 (0.47, 0.89)	9.20%	1	1.25
FOXD4L5	NM_001126334	1	0.00836323	1.43 (1.10, 1.87)	10.00%	1	1.24
FOXJ2	NM_018416	-1	0.006621301	0.65 (0.48, 0.89)	8.80%	1	1.25
GALNT5	NM_014568	-1	0.007050223	0.61 (0.43, 0.87)	9.10%	1	1.25
GATA3	NM_001002295	-1	0.007666942	0.66 (0.48, 0.89)	9.50%	1	1.24
GATA3	NM_002051	-1	0.007666942	0.66 (0.48, 0.89)	9.50%	1	1.24
GATAD2A	NM_017660	1	0.006855234	1.35 (1.09, 1.68)	9.00%	1	1.23
GGT3P	NR_003267	1	0.00774438	1.41 (1.10, 1.83)	9.60%	1	1.24
GOT1	NM_002079	1	0.007928124	1.68 (1.14, 2.45)	9.70%	1	1.24
GPR12	NM_005288	1	0.006922215	1.38 (1.09, 1.75)	9.10%	1	1.24
GPR156	NM_153002	1	0.007917594	1.57 (1.13, 2.20)	9.70%	1	1.25
GPR156	NM_001168271	1	0.007917594	1.57 (1.13, 2.20)	9.70%	1	1.25
HCRTR2	NM_001526	1	0.007044644	1.27 (1.07, 1.52)	9.10%	1	1.21
HDC	NM_002112	-1	0.006715858	0.61 (0.43, 0.87)	8.90%	1	1.25
HNRNPA2B1	NM_002137	1	0.006950753	1.38 (1.09, 1.75)	9.10%	1	1.24
HNRNPA2B1	NM_031243	1	0.006950753	1.38 (1.09, 1.75)	9.10%	1	1.24
HOXB13	NM_006361	1	0.00679441	1.59 (1.14, 2.21)	8.90%	1	1.25
INSIG1	NM_005542	1	0.007908076	1.75 (1.16, 2.64)	9.70%	1	1.24
INSIG1	NM_198337	1	0.007908076	1.75 (1.16, 2.64)	9.70%	1	1.24

INSIG1	NM_198336	1	0.007908076	1.75 (1.16, 2.64)	9.70%	1	1.24
ITIH3	NM_002217	-1	0.008089965	0.58 (0.39, 0.87)	9.80%	1	1.24
KCNK5	NM_003740	1	0.006644671	1.52 (1.12, 2.05)	8.80%	1	1.25
KIAA1609	NM_020947	1	0.006816877	1.56 (1.13, 2.15)	9.00%	1	1.25
KLF6	NR_027653	1	0.007216712	1.54 (1.12, 2.10)	9.20%	1	1.25
KLF6	NM_001160124	1	0.007216712	1.54 (1.12, 2.10)	9.20%	1	1.25
KLF6	NM_001300	1	0.007216712	1.54 (1.12, 2.10)	9.20%	1	1.25
KLF6	NM_001160125	1	0.007216712	1.54 (1.12, 2.10)	9.20%	1	1.25
LIX1	NM_153234	1	0.007284268	1.70 (1.15, 2.50)	9.30%	1	1.25
LOC145845	NR_024264	1	0.007192082	1.42 (1.10, 1.83)	9.20%	1	1.24
LPCAT1	NM_024830	1	0.006993251	1.67 (1.15, 2.42)	9.10%	1	1.25
MAGI2	NM_012301	-1	0.008130755	0.57 (0.38, 0.86)	9.80%	1	1.23
MAP3K12	NM_006301	-1	0.007048049	0.62 (0.44, 0.88)	9.10%	1	1.25
MAP3K12	NM_001193511	-1	0.007048049	0.62 (0.44, 0.88)	9.10%	1	1.25
MFGE8	NM_001114614	1	0.006919473	1.56 (1.13, 2.16)	9.10%	1	1.25
MFGE8	NM_005928	1	0.006919473	1.56 (1.13, 2.16)	9.10%	1	1.25
MINK1	NM_015716	-1	0.007173123	0.54 (0.35, 0.85)	9.20%	1	1.23
MINK1	NM_153827	-1	0.007173123	0.54 (0.35, 0.85)	9.20%	1	1.23
MINK1	NM_170663	-1	0.007173123	0.54 (0.35, 0.85)	9.20%	1	1.23
MINK1	NM_001024937	-1	0.007173123	0.54 (0.35, 0.85)	9.20%	1	1.23
MIR195	NR_029712	1	0.00787247	1.37 (1.09, 1.74)	9.70%	1	1.23
MIR3183	NR_036148	1	0.006747778	1.68 (1.15, 2.44)	8.90%	1	1.25
MIR4318	NR_036202	1	0.007957654	1.61 (1.13, 2.29)	9.70%	1	1.25
MTA1	NM_004689	-1	0.007359437	0.59 (0.40, 0.87)	9.30%	1	1.24
NOL11	NM_015462	1	0.006772141	1.56 (1.13, 2.14)	8.90%	1	1.25
NR1I2	NM_022002	-1	0.007225406	0.55 (0.36, 0.85)	9.20%	1	1.23
NR1I2	NM_003889	-1	0.007225406	0.55 (0.36, 0.85)	9.20%	1	1.23
NR1I2	NM_033013	-1	0.007225406	0.55 (0.36, 0.85)	9.20%	1	1.23
NXF1	NM_001081491	-1	0.00708175	0.60 (0.41, 0.87)	9.10%	1	1.24
NXF1	NM_006362	-1	0.00708175	0.60 (0.41, 0.87)	9.10%	1	1.24
OGDH	NM_002541	1	0.007291529	1.46 (1.11, 1.93)	9.30%	1	1.25
OGDH	NM_001003941	1	0.007291529	1.46 (1.11, 1.93)	9.30%	1	1.25
OGDH	NM_001165036	1	0.007291529	1.46 (1.11, 1.93)	9.30%	1	1.25
OPLAH	NM_017570	1	0.007363069	1.73 (1.16, 2.59)	9.30%	1	1.24
OR52E4	NM_001005165	1	0.007563025	1.58 (1.13, 2.22)	9.40%	1	1.25
PA2G4P4	NR_003284	-1	0.007765185	0.66 (0.48, 0.90)	9.60%	1	1.24
PALLD	NM_001166108	-1	0.007412269	0.62 (0.44, 0.88)	9.30%	1	1.24
PALLD	NM_001166109	-1	0.007412269	0.62 (0.44, 0.88)	9.30%	1	1.24
PALLD	NM_001166110	-1	0.007412269	0.62 (0.44, 0.88)	9.30%	1	1.24
PALLD	NM_016081	-1	0.007412269	0.62 (0.44, 0.88)	9.30%	1	1.24
PARP11	NM_020367	-1	0.006969466	0.62 (0.44, 0.88)	9.10%	1	1.25
PFN4	NM_199346	-1	0.007867198	0.63 (0.44, 0.88)	9.70%	1	1.24
PGK1	NM_000291	1	0.007371341	1.70 (1.15, 2.50)	9.30%	1	1.24
PIK3C3	NM_002647	-1	0.007928522	0.63 (0.45, 0.89)	9.70%	1	1.24
PLA2G16	NM_001128203	-1	0.007338932	0.59 (0.40, 0.87)	9.30%	1	1.24
PLA2G16	NM_007069	-1	0.007338932	0.59 (0.40, 0.87)	9.30%	1	1.24
POM121L10P	NR_024593	1	0.008015909	1.47 (1.11, 1.96)	9.70%	1	1.24
PPIB	NM_000942	1	0.008136977	1.60 (1.13, 2.27)	9.80%	1	1.25
PPIG	NM_004792	-1	0.007743418	0.67 (0.50, 0.90)	9.60%	1	1.24

PRAME	NM_206954	1	0.00807234	1.60 (1.13, 2.28)	9.80%	1	1.25
PRAME	NM_206953	1	0.00807234	1.60 (1.13, 2.28)	9.80%	1	1.25
PRAME	NM_006115	1	0.00807234	1.60 (1.13, 2.28)	9.80%	1	1.25
PRAME	NM_206956	1	0.00807234	1.60 (1.13, 2.28)	9.80%	1	1.25
PRAME	NM_206955	1	0.00807234	1.60 (1.13, 2.28)	9.80%	1	1.25
PTPRT	NM_007050	-1	0.007844377	0.64 (0.46, 0.89)	9.70%	1	1.24
PTPRT	NM_133170	-1	0.007844377	0.64 (0.46, 0.89)	9.70%	1	1.24
PVR	NM_006505	1	0.007178986	1.73 (1.16, 2.57)	9.20%	1	1.24
PVR	NM_001135768	1	0.007178986	1.73 (1.16, 2.57)	9.20%	1	1.24
PVR	NM_001135769	1	0.007178986	1.73 (1.16, 2.57)	9.20%	1	1.24
PVR	NM_001135770	1	0.007178986	1.73 (1.16, 2.57)	9.20%	1	1.24
RBBP6	NM_006910	-1	0.008045393	0.59 (0.40, 0.87)	9.80%	1	1.24
RBBP6	NM_032626	-1	0.008045393	0.59 (0.40, 0.87)	9.80%	1	1.24
RBBP6	NM_018703	-1	0.008045393	0.59 (0.40, 0.87)	9.80%	1	1.24
RBM38	NM_017495	1	0.007553277	1.79 (1.17, 2.73)	9.40%	1	1.24
RBM38	NM_183425	1	0.007553277	1.79 (1.17, 2.73)	9.40%	1	1.24
RILPL1	NM_178314	-1	0.007013837	0.61 (0.43, 0.88)	9.10%	1	1.25
RNFT1	NM_016125	1	0.007629214	1.78 (1.17, 2.73)	9.50%	1	1.24
RPAP2	NM_024813	-1	0.007531085	0.57 (0.38, 0.86)	9.40%	1	1.24
RPS6KB1	NM_003161	1	0.008065183	1.43 (1.10, 1.87)	9.80%	1	1.24
SAMD15	NM_001010860	-1	0.007388814	0.67 (0.50, 0.90)	9.30%	1	1.24
SCARNA23	NR_003007	1	0.007993669	1.51 (1.11, 2.04)	9.70%	1	1.25
SERPINB10	NM_005024	1	0.006313415	1.26 (1.07, 1.49)	8.60%	1	1.2
SERPINB8	NM_002640	-1	0.007336561	0.64 (0.46, 0.89)	9.30%	1	1.25
SERPINB8	NM_001031848	-1	0.007336561	0.64 (0.46, 0.89)	9.30%	1	1.25
SERPINB8	NM_198833	-1	0.007336561	0.64 (0.46, 0.89)	9.30%	1	1.25
SHISA3	NM_001080505	1	0.007387467	1.38 (1.09, 1.75)	9.30%	1	1.24
SLC25A13	NR_027662	1	0.007684969	1.69 (1.15, 2.49)	9.50%	1	1.24
SLC25A13	NM_014251	1	0.007684969	1.69 (1.15, 2.49)	9.50%	1	1.24
SLC25A13	NM_001160210	1	0.007684969	1.69 (1.15, 2.49)	9.50%	1	1.24
SLC35C2	NM_173073	1	0.006914089	1.48 (1.11, 1.97)	9.10%	1	1.25
SLC35C2	NM_015945	1	0.006914089	1.48 (1.11, 1.97)	9.10%	1	1.25
SLC35C2	NM_173179	1	0.006914089	1.48 (1.11, 1.97)	9.10%	1	1.25
SLC37A2	NM_001145290	-1	0.007397611	0.61 (0.42, 0.88)	9.30%	1	1.24
SLC37A2	NM_198277	-1	0.007397611	0.61 (0.42, 0.88)	9.30%	1	1.24
SPAG7	NM_004890	-1	0.007433804	0.66 (0.49, 0.89)	9.30%	1	1.24
SQLE	NM_003129	1	0.008169599	1.61 (1.13, 2.29)	9.80%	1	1.24
SRR	NM_021947	-1	0.007802797	0.68 (0.51, 0.90)	9.60%	1	1.24
STAU1	NM_004602	1	0.007966457	1.46 (1.10, 1.93)	9.70%	1	1.24
STAU1	NM_017454	1	0.007966457	1.46 (1.10, 1.93)	9.70%	1	1.24
STAU1	NM_001037328	1	0.007966457	1.46 (1.10, 1.93)	9.70%	1	1.24
STAU1	NM_017452	1	0.007966457	1.46 (1.10, 1.93)	9.70%	1	1.24
STAU1	NM_017453	1	0.007966457	1.46 (1.10, 1.93)	9.70%	1	1.24
SURF4	NM_033161	1	0.00710138	1.61 (1.14, 2.28)	9.10%	1	1.25
TBC1D16	NM_019020	-1	0.007903348	0.57 (0.38, 0.86)	9.70%	1	1.23
TCP11L2	NM_152772	-1	0.006709472	0.63 (0.46, 0.88)	8.90%	1	1.25
THEG	NM_016585	1	0.007652171	1.50 (1.11, 2.03)	9.50%	1	1.25
THEG	NM_199202	1	0.007652171	1.50 (1.11, 2.03)	9.50%	1	1.25
TMED11P	NR_033768	-1	0.008112229	0.60 (0.41, 0.88)	9.80%	1	1.24

TMEM189	NM_001162505	1	0.007119372	1.79 (1.17, 2.74)	9.20%	1	1.24
TMEM189	NR_027889	1	0.007119372	1.79 (1.17, 2.74)	9.20%	1	1.24
TMEM189	NM_199129	1	0.007119372	1.79 (1.17, 2.74)	9.20%	1	1.24
TNFSF12	NR_037146	-1	0.006806283	0.65 (0.48, 0.89)	8.90%	1	1.25
TNFSF12	NM_003809	-1	0.006806283	0.65 (0.48, 0.89)	8.90%	1	1.25
TNK1	NM_003985	-1	0.007866596	0.63 (0.45, 0.89)	9.70%	1	1.24
TNS1	NM_022648	-1	0.008198294	0.60 (0.41, 0.88)	9.80%	1	1.24
TRIM39	NM_021253	-1	0.006654211	0.67 (0.50, 0.89)	8.80%	1	1.25
TRIM39	NM_172016	-1	0.006654211	0.67 (0.50, 0.89)	8.80%	1	1.25
TUBA1B	NM_006082	1	0.006986711	1.56 (1.13, 2.15)	9.10%	1	1.25
USP51	NM_201286	-1	0.007929716	0.66 (0.49, 0.90)	9.70%	1	1.24
WDR52	NM_001164496	-1	0.007394432	0.61 (0.42, 0.87)	9.30%	1	1.24
WDR52	NM_018338	-1	0.007394432	0.61 (0.42, 0.87)	9.30%	1	1.24
WWP2	NM_199424	1	0.006541054	1.34 (1.09, 1.66)	8.70%	1	1.23
WWP2	NM_007014	1	0.006541054	1.34 (1.09, 1.66)	8.70%	1	1.23
WWP2	NM_199423	1	0.006541054	1.34 (1.09, 1.66)	8.70%	1	1.23
XPO1	NM_003400	1	0.006983767	1.63 (1.14, 2.34)	9.10%	1	1.25
YES1	NM_005433	1	0.007385459	1.78 (1.17, 2.70)	9.30%	1	1.24
ZFAND1	NM_001170797	1	0.007371855	1.59 (1.13, 2.23)	9.30%	1	1.25
ZFAND1	NM_001170796	1	0.007371855	1.59 (1.13, 2.23)	9.30%	1	1.25
ZFAND1	NR_033193	1	0.007371855	1.59 (1.13, 2.23)	9.30%	1	1.25
ZFAND1	NR_033194	1	0.007371855	1.59 (1.13, 2.23)	9.30%	1	1.25
ZFAND1	NM_024699	1	0.007371855	1.59 (1.13, 2.23)	9.30%	1	1.25
ZFAND1	NR_033195	1	0.007371855	1.59 (1.13, 2.23)	9.30%	1	1.25
ZFAND1	NR_033196	1	0.007371855	1.59 (1.13, 2.23)	9.30%	1	1.25
ZMYND10	NM_015896	-1	0.008232538	0.61 (0.42, 0.88)	9.90%	1	1.24
ZNF160	NM_001102603	-1	0.008143054	0.58 (0.39, 0.87)	9.80%	1	1.24
ZNF160	NM_198893	-1	0.008143054	0.58 (0.39, 0.87)	9.80%	1	1.24
ZNF160	NM_033288	-1	0.008143054	0.58 (0.39, 0.87)	9.80%	1	1.24
ZNF175	NM_007147	-1	0.007576003	0.63 (0.44, 0.88)	9.50%	1	1.24
ZNF187	NM_001023560	-1	0.006949723	0.67 (0.50, 0.90)	9.10%	1	1.25
ZNF187	NM_001111039	-1	0.006949723	0.67 (0.50, 0.90)	9.10%	1	1.25
ZNF187	NM_152736	-1	0.006949723	0.67 (0.50, 0.90)	9.10%	1	1.25
ZNF486	NM_052852	-1	0.008185949	0.50 (0.30, 0.84)	9.80%	1	1.21
ZNF782	NM_001001662	-1	0.007410404	0.50 (0.30, 0.83)	9.30%	1	1.22

Table 2. List of Assembled RefSeq RNAs Associated with Risk of Breast Cancer Recurrence in 111 Patients Designated as ESR1 Positive

Gene	Accession no.	Direction of Association (1=Higher Expression Means Higher Risk)	p-value	Standardized Hazard Ratio Estimate (95% Confidence Interval)	q-value (FDR)	Maximum Lower Bound Std HR @ 10% FDR	Regression-to-the-Mean-Corrected Std HR
C17orf97	NM_001013672	-1	1.28E-08	0.38 (0.27, 0.53)	<0.1%	1.24	1.58
ZFP3	NM_153018	-1	6.18E-08	0.31 (0.21, 0.48)	<0.1%	1.24	1.52
ULBP3	NM_024518	1	1.95E-08	2.51 (1.82, 3.46)	<0.1%	1.23	1.6
GUCY2F	NM_001522	1	3.37E-11	1.68 (1.44, 1.96)	<0.1%	1.2	1.53
IFT74	NM_001099222	-1	2.40E-08	0.49 (0.38, 0.63)	<0.1%	1.2	1.55

IFT74	NM_025103	-1	2.40E-08	0.49 (0.38, 0.63)	<0.1%	1.2	1.55
IFT74	NM_001099224	-1	2.40E-08	0.49 (0.38, 0.63)	<0.1%	1.2	1.55
IFT74	NM_001099223	-1	2.40E-08	0.49 (0.38, 0.63)	<0.1%	1.2	1.55
MIR1208	NR_031613	1	1.43E-08	1.95 (1.55, 2.46)	<0.1%	1.2	1.56
PADI3	NM_016233	1	9.99E-09	1.93 (1.54, 2.42)	<0.1%	1.2	1.56
RPP21	NM_001199120	1	3.14E-08	2.02 (1.58, 2.59)	<0.1%	1.2	1.56
RPP21	NM_001199121	1	3.14E-08	2.02 (1.58, 2.59)	<0.1%	1.2	1.56
RPP21	NM_024839	1	3.14E-08	2.02 (1.58, 2.59)	<0.1%	1.2	1.56
CWF19L2	NM_152434	-1	1.30E-06	0.37 (0.24, 0.55)	0.10%	1.17	1.46
ZNF141	NM_003441	-1	6.43E-07	0.41 (0.29, 0.58)	<0.1%	1.17	1.49
RP1-177G6-2	NR_028345	1	1.05E-09	1.55 (1.35, 1.79)	<0.1%	1.16	1.45
RP1-177G6-2	NR_028344	1	1.05E-09	1.55 (1.35, 1.79)	<0.1%	1.16	1.45
APOL3	NR_027834	-1	5.44E-07	0.50 (0.38, 0.66)	<0.1%	1.15	1.49
APOL3	NR_027833	-1	5.44E-07	0.50 (0.38, 0.66)	<0.1%	1.15	1.49
APOL3	NR_027835	-1	5.44E-07	0.50 (0.38, 0.66)	<0.1%	1.15	1.49
APOL3	NM_145642	-1	5.44E-07	0.50 (0.38, 0.66)	<0.1%	1.15	1.49
APOL3	NM_145641	-1	5.44E-07	0.50 (0.38, 0.66)	<0.1%	1.15	1.49
APOL3	NM_145640	-1	5.44E-07	0.50 (0.38, 0.66)	<0.1%	1.15	1.49
CYB5B	NM_030579	1	6.41E-06	3.17 (1.92, 5.22)	0.20%	1.15	1.42
DEGS1	NM_003676	1	2.21E-07	1.76 (1.42, 2.18)	<0.1%	1.15	1.49
FLJ14186	NR_037596	-1	1.79E-06	0.46 (0.34, 0.63)	0.10%	1.15	1.47
HMX1	NM_018942	1	2.17E-09	1.53 (1.33, 1.75)	<0.1%	1.15	1.43
KIAA0664L3	NR_024034	-1	2.18E-07	0.56 (0.45, 0.70)	<0.1%	1.15	1.48
KRT83	NM_002282	1	2.64E-08	1.60 (1.35, 1.88)	<0.1%	1.15	1.45
ZNF326	NM_182976	-1	4.30E-06	0.41 (0.28, 0.60)	0.20%	1.15	1.44
ZNF326	NM_182975	-1	4.30E-06	0.41 (0.28, 0.60)	0.20%	1.15	1.44
ZNF486	NM_052852	-1	3.31E-06	0.35 (0.23, 0.55)	0.10%	1.15	1.43
NAA35	NM_024635	-1	5.42E-06	0.43 (0.30, 0.62)	0.20%	1.14	1.44
RBMXL1	NM_001162536	-1	3.46E-06	0.45 (0.32, 0.63)	0.10%	1.14	1.45
RBMXL1	NM_019610	-1	3.46E-06	0.45 (0.32, 0.63)	0.10%	1.14	1.45
TMEM81	NM_203376	1	1.08E-05	3.15 (1.89, 5.26)	0.30%	1.14	1.4
CENPN	NM_001100625	1	1.82E-05	3.08 (1.84, 5.15)	0.40%	1.13	1.39
CENPN	NM_018455	1	1.82E-05	3.08 (1.84, 5.15)	0.40%	1.13	1.39
CENPN	NM_001100624	1	1.82E-05	3.08 (1.84, 5.15)	0.40%	1.13	1.39
FUBP1	NM_003902	-1	1.31E-05	0.36 (0.22, 0.57)	0.30%	1.13	1.38
LOC642345	NR_033829	1	2.97E-07	1.62 (1.35, 1.95)	<0.1%	1.13	1.44
ZZZ3	NM_015534	-1	1.63E-05	0.34 (0.21, 0.56)	0.40%	1.13	1.37
CDK20	NM_001170639	-1	1.0423E-05	0.46 (0.33, 0.65)	0.30%	1.12	1.42
CDK20	NM_178432	-1	1.0423E-05	0.46 (0.33, 0.65)	0.30%	1.12	1.42
CDK20	NM_001170640	-1	1.0423E-05	0.46 (0.33, 0.65)	0.30%	1.12	1.42
CDK20	NM_001039803	-1	1.0423E-05	0.46 (0.33, 0.65)	0.30%	1.12	1.42
CDK20	NM_012119	-1	1.0423E-05	0.46 (0.33, 0.65)	0.30%	1.12	1.42
DEFB133	NM_001166478	1	1.74E-07	1.50 (1.29, 1.75)	<0.1%	1.12	1.4
GLMN	NM_053274	-1	2.57E-05	0.36 (0.22, 0.58)	0.60%	1.12	1.36
LOC100129636	NM_001195202	1	2.82E-06	1.83 (1.42, 2.36)	0.10%	1.12	1.46
LPO	NM_001160102	1	6.17E-07	1.60 (1.33, 1.92)	<0.1%	1.12	1.43
LPO	NM_006151	1	6.17E-07	1.60 (1.33, 1.92)	<0.1%	1.12	1.43
LPO	NR_027647	1	6.17E-07	1.60 (1.33, 1.92)	<0.1%	1.12	1.43
OMA1	NM_145243	-1	4.89E-06	0.53 (0.40, 0.70)	0.20%	1.12	1.44
PCDH11Y	NM_032972	1	1.89E-07	1.48 (1.28, 1.72)	<0.1%	1.12	1.39

PCDH11Y	NM_032973	1	1.89E-07	1.48 (1.28, 1.72)	<0.1%	1.12	1.39
PCDH11Y	NM_032971	1	1.89E-07	1.48 (1.28, 1.72)	<0.1%	1.12	1.39
PPP3CB	NM_021132	1	1.02E-06	1.70 (1.37, 2.10)	0.10%	1.12	1.45
PPP3CB	NM_001142354	1	1.02E-06	1.70 (1.37, 2.10)	0.10%	1.12	1.45
PPP3CB	NM_001142353	1	1.02E-06	1.70 (1.37, 2.10)	0.10%	1.12	1.45
ATXN3L	NM_001135995	1	2.23E-07	1.40 (1.23, 1.60)	<0.1%	1.11	1.34
C3orf15	NM_033364	-1	2.52E-05	0.42 (0.28, 0.63)	0.60%	1.11	1.39
C9orf27	NR_024032	1	6.75E-09	1.34 (1.21, 1.47)	<0.1%	1.11	1.31
CCDC105	NM_173482	1	1.01E-06	1.55 (1.30, 1.84)	0.10%	1.11	1.41
FANK1	NM_145235	-1	1.13E-05	0.49 (0.35, 0.67)	0.30%	1.11	1.42
GGCT	NR_037669	1	1.21E-05	1.86 (1.41, 2.45)	0.30%	1.11	1.44
GGCT	NM_001199815	1	1.21E-05	1.86 (1.41, 2.45)	0.30%	1.11	1.44
GGCT	NM_001199817	1	1.21E-05	1.86 (1.41, 2.45)	0.30%	1.11	1.44
GGCT	NM_001199816	1	1.21E-05	1.86 (1.41, 2.45)	0.30%	1.11	1.44
GGCT	NM_024051	1	1.21E-05	1.86 (1.41, 2.45)	0.30%	1.11	1.44
GPAA1	NM_003801	1	2.95E-05	2.28 (1.55, 3.35)	0.60%	1.11	1.41
HCRTR2	NM_001526	1	2.02E-07	1.41 (1.24, 1.60)	<0.1%	1.11	1.35
KLHDC8A	NM_018203	-1	4.87E-05	0.36 (0.22, 0.59)	0.80%	1.11	1.35
LOC339290	NR_015389	-1	4.68E-05	0.35 (0.21, 0.58)	0.80%	1.11	1.34
LOC729966	NR_036575	1	8.19E-08	1.40 (1.24, 1.59)	<0.1%	1.11	1.35
MARCH6	NM_005885	1	2.93E-05	2.22 (1.53, 3.23)	0.60%	1.11	1.42
MEX3B	NM_032246	1	2.55E-05	2.66 (1.69, 4.20)	0.60%	1.11	1.4
NQO1	NM_001025434	1	3.17E-05	2.58 (1.65, 4.04)	0.60%	1.11	1.4
NQO1	NM_000903	1	3.17E-05	2.58 (1.65, 4.04)	0.60%	1.11	1.4
NQO1	NM_001025433	1	3.17E-05	2.58 (1.65, 4.04)	0.60%	1.11	1.4
ORM1	NM_000607	1	1.22E-06	1.55 (1.30, 1.85)	0.10%	1.11	1.4
RAET1L	NM_130900	1	2.80E-06	1.66 (1.34, 2.05)	0.10%	1.11	1.43
SERPINB10	NM_005024	1	1.11E-07	1.43 (1.25, 1.63)	<0.1%	1.11	1.36
TMOD3	NM_014547	1	2.08E-08	1.39 (1.24, 1.55)	<0.1%	1.11	1.34
TSKU	NM_015516	1	6.77E-06	1.84 (1.41, 2.41)	0.20%	1.11	1.45
CG030	NR_026928	-1	2.93E-05	0.49 (0.35, 0.68)	0.60%	1.1	1.4
GAN	NM_022041	1	7.87E-05	3.09 (1.76, 5.40)	1.10%	1.1	1.34
LRGUK	NM_144648	-1	3.71E-05	0.45 (0.31, 0.66)	0.70%	1.1	1.39
MAGEA10	NM_021048	1	7.05E-07	1.45 (1.25, 1.67)	<0.1%	1.1	1.36
MAGEA10	NM_001011543	1	7.05E-07	1.45 (1.25, 1.67)	<0.1%	1.1	1.36
NCRNA00200	NR_015376	1	9.14E-07	1.44 (1.24, 1.66)	0.10%	1.1	1.36
NCRNA00221	NR_027457	1	1.13E-06	1.45 (1.25, 1.68)	0.10%	1.1	1.36
PGA3	NM_001079807	1	2.24E-06	1.47 (1.25, 1.73)	0.10%	1.1	1.37
PYCRL	NM_023078	1	7.01E-05	2.88 (1.71, 4.86)	1.10%	1.1	1.35
AZU1	NM_001700	1	4.61E-05	1.90 (1.40, 2.60)	0.80%	1.09	1.41
C21orf63	NM_058187	-1	4.43E-05	0.48 (0.34, 0.68)	0.80%	1.09	1.39
C7orf30	NM_138446	1	3.48E-05	1.94 (1.42, 2.64)	0.70%	1.09	1.41
CHAT	NM_020986	1	5.09E-06	1.50 (1.26, 1.78)	0.20%	1.09	1.37
CHAT	NM_001142934	1	5.09E-06	1.50 (1.26, 1.78)	0.20%	1.09	1.37
CHAT	NM_020985	1	5.09E-06	1.50 (1.26, 1.78)	0.20%	1.09	1.37
CHAT	NM_001142933	1	5.09E-06	1.50 (1.26, 1.78)	0.20%	1.09	1.37
CHAT	NM_020549	1	5.09E-06	1.50 (1.26, 1.78)	0.20%	1.09	1.37
CHAT	NM_020984	1	5.09E-06	1.50 (1.26, 1.78)	0.20%	1.09	1.37
CHAT	NM_001142929	1	5.09E-06	1.50 (1.26, 1.78)	0.20%	1.09	1.37
COX8C	NM_182971	1	8.22E-06	1.55 (1.28, 1.88)	0.30%	1.09	1.39

GOLPH3	NM_022130	1	9.17E-05	2.38 (1.54, 3.67)	1.30%	1.09	1.37
GSTA2	NM_000846	1	5.09E-06	1.50 (1.26, 1.78)	0.20%	1.09	1.37
JAK1	NM_002227	-1	9.2776E-05	0.38 (0.23, 0.62)	1.30%	1.09	1.33
LOC647107	NR_033945	1	1.27E-05	1.64 (1.31, 2.04)	0.30%	1.09	1.4
LRIT2	NM_001017924	1	6.98E-07	1.38 (1.21, 1.56)	<0.1%	1.09	1.32
LRP12	NM_001135703	1	6.92E-05	2.17 (1.48, 3.18)	1.10%	1.09	1.39
LRP12	NM_013437	1	6.92E-05	2.17 (1.48, 3.18)	1.10%	1.09	1.39
MAPK6	NM_002748	1	4.24E-07	1.37 (1.21, 1.55)	<0.1%	1.09	1.32
MIR1266	NR_031670	1	1.70E-05	1.68 (1.33, 2.12)	0.40%	1.09	1.41
MIR3117	NR_036060	1	4.01E-05	2.00 (1.44, 2.78)	0.70%	1.09	1.41
PAR-SN	NR_022011	-1	1.63E-05	0.61 (0.48, 0.76)	0.40%	1.09	1.39
SF3B3	NM_012426	1	4.66E-05	2.11 (1.47, 3.02)	0.80%	1.09	1.41
SLC35D2	NM_007001	-1	4.11E-05	0.54 (0.41, 0.73)	0.70%	1.09	1.39
TFF2	NM_005423	1	3.48E-06	1.42 (1.22, 1.65)	0.10%	1.09	1.34
USO1	NM_003715	1	1.60E-06	1.40 (1.22, 1.60)	0.10%	1.09	1.33
WFDC9	NM_147198	1	7.58E-05	2.21 (1.49, 3.28)	1.10%	1.09	1.39
ACAP2	NM_012287	1	6.50E-05	1.92 (1.39, 2.64)	1.00%	1.08	1.4
ACSL5	NM_016234	-1	0.00011296	0.45 (0.30, 0.67)	1.50%	1.08	1.35
ACSL5	NM_203380	-1	0.00011296	0.45 (0.30, 0.67)	1.50%	1.08	1.35
ACSL5	NM_203379	-1	0.00011296	0.45 (0.30, 0.67)	1.50%	1.08	1.35
APOBEC1	NM_001644	1	1.27E-07	1.27 (1.16, 1.39)	<0.1%	1.08	1.25
CCNA2	NM_001237	1	0.00013361	2.46 (1.55, 3.91)	1.70%	1.08	1.36
DBNDD1	NM_001042610	1	0.00014445	2.73 (1.63, 4.58)	1.80%	1.08	1.34
DBNDD1	NM_024043	1	0.00014445	2.73 (1.63, 4.58)	1.80%	1.08	1.34
EVX2	NM_001080458	1	1.16E-05	1.51 (1.25, 1.81)	0.30%	1.08	1.37
FAM18A	NM_001079512	-1	3.73E-05	0.59 (0.46, 0.76)	0.70%	1.08	1.38
GRSF1	NM_002092	1	1.87E-05	1.51 (1.25, 1.83)	0.50%	1.08	1.36
GRSF1	NM_001098477	1	1.87E-05	1.51 (1.25, 1.83)	0.50%	1.08	1.36
LOC145845	NR_024264	1	5.07E-05	1.79 (1.35, 2.37)	0.80%	1.08	1.4
LOC645971	NM_001195256	1	1.00E-04	2.15 (1.46, 3.16)	1.40%	1.08	1.38
LRRC37A4	NR_002940	-1	2.18E-05	0.66 (0.54, 0.80)	0.50%	1.08	1.35
MIR542	NR_030399	1	3.03E-05	1.65 (1.31, 2.10)	0.60%	1.08	1.39
OR14J1	NM_030946	1	2.85E-05	1.65 (1.30, 2.08)	0.60%	1.08	1.39
PKN2	NM_006256	-1	0.00014097	0.33 (0.18, 0.58)	1.80%	1.08	1.29
PRPF38B	NR_037185	-1	0.00016322	0.36 (0.22, 0.62)	2.00%	1.08	1.3
PRPF38B	NM_018061	-1	0.00016322	0.36 (0.22, 0.62)	2.00%	1.08	1.3
RAB9BP1	NR_000039	1	2.04E-05	1.59 (1.29, 1.97)	0.50%	1.08	1.39
SERINC5	NM_178276	1	3.54E-05	1.72 (1.33, 2.23)	0.70%	1.08	1.4
SERINC5	NM_001174071	1	3.54E-05	1.72 (1.33, 2.23)	0.70%	1.08	1.4
SERINC5	NM_001174072	1	3.54E-05	1.72 (1.33, 2.23)	0.70%	1.08	1.4
TRPM8	NM_024080	1	2.78E-05	1.56 (1.27, 1.92)	0.60%	1.08	1.37
USPL1	NM_005800	-1	0.00016305	0.38 (0.23, 0.63)	2.00%	1.08	1.31
ZNF227	NM_182490	-1	0.00013956	0.41 (0.26, 0.65)	1.80%	1.08	1.33
ZNF512	NM_032434	-1	7.91E-05	0.46 (0.32, 0.68)	1.10%	1.08	1.36
ZNF595	NM_182524	-1	3.08E-05	0.64 (0.51, 0.79)	0.60%	1.08	1.36
AP1G1	NM_001128	1	0.00015448	2.04 (1.41, 2.96)	1.90%	1.07	1.37
AP1G1	NM_001030007	1	0.00015448	2.04 (1.41, 2.96)	1.90%	1.07	1.37
AP4E1	NM_007347	1	1.22E-05	1.35 (1.18, 1.55)	0.30%	1.07	1.3
C15orf34	NR_027262	-1	7.82E-05	0.59 (0.45, 0.76)	1.10%	1.07	1.37
COL20A1	NM_020882	1	2.83E-05	1.44 (1.21, 1.71)	0.60%	1.07	1.33

COX7B2	NM_130902	1	1.35E-06	1.25 (1.14, 1.38)	0.10%	1.07	1.23
EVX1	NM_001989	1	3.66E-05	1.58 (1.27, 1.95)	0.70%	1.07	1.37
HLA-DOA	NM_002119	-1	7.86E-05	0.55 (0.41, 0.74)	1.10%	1.07	1.37
MMP15	NM_002428	1	0.0001989	2.48 (1.54, 4.00)	2.30%	1.07	1.34
PIBF1	NM_006346	-1	0.00012808	0.50 (0.35, 0.71)	1.70%	1.07	1.36
SNCB	NM_001001502	1	2.13E-05	1.43 (1.21, 1.68)	0.50%	1.07	1.33
SNCB	NM_003085	1	2.13E-05	1.43 (1.21, 1.68)	0.50%	1.07	1.33
STX8	NR_033656	-1	0.00012845	0.52 (0.37, 0.73)	1.70%	1.07	1.36
STX8	NM_004853	-1	0.00012845	0.52 (0.37, 0.73)	1.70%	1.07	1.36
TMEM91	NM_001098823	-1	0.00013958	0.51 (0.36, 0.72)	1.80%	1.07	1.36
TMEM91	NM_001042595	-1	0.00013958	0.51 (0.36, 0.72)	1.80%	1.07	1.36
TMEM91	NM_001098821	-1	0.00013958	0.51 (0.36, 0.72)	1.80%	1.07	1.36
TMEM91	NM_001098822	-1	0.00013958	0.51 (0.36, 0.72)	1.80%	1.07	1.36
TMEM91	NM_001098825	-1	0.00013958	0.51 (0.36, 0.72)	1.80%	1.07	1.36
TMEM91	NM_001098824	-1	0.00013958	0.51 (0.36, 0.72)	1.80%	1.07	1.36
ZNF738	NR_027130	-1	0.00018472	0.44 (0.28, 0.67)	2.20%	1.07	1.33
ANKZF1	NM_018089	-1	0.00013353	0.54 (0.39, 0.74)	1.70%	1.06	1.36
ANKZF1	NM_001042410	-1	0.00013353	0.54 (0.39, 0.74)	1.70%	1.06	1.36
APCS	NM_001639	1	6.64E-06	1.27 (1.15, 1.41)	0.20%	1.06	1.24
BAGE	NM_001187	1	4.69E-05	1.44 (1.21, 1.72)	0.80%	1.06	1.33
FAM21C	NM_015262	-1	0.00021151	0.49 (0.33, 0.71)	2.30%	1.06	1.34
FAM21C	NM_001169107	-1	0.00021151	0.49 (0.33, 0.71)	2.30%	1.06	1.34
FAM21C	NM_001169106	-1	0.00021151	0.49 (0.33, 0.71)	2.30%	1.06	1.34
GFOD2	NM_030819	1	0.0002683	2.24 (1.45, 3.45)	2.70%	1.06	1.34
GFOD2	NR_027398	1	0.0002683	2.24 (1.45, 3.45)	2.70%	1.06	1.34
GFOD2	NR_027399	1	0.0002683	2.24 (1.45, 3.45)	2.70%	1.06	1.34
GPX5	NM_003996	1	7.14E-05	1.58 (1.26, 1.98)	1.10%	1.06	1.36
GPX5	NM_001509	1	7.14E-05	1.58 (1.26, 1.98)	1.10%	1.06	1.36
IRAK4	NM_001145256	-1	0.00018709	0.47 (0.32, 0.70)	2.20%	1.06	1.34
IRAK4	NM_001114182	-1	0.00018709	0.47 (0.32, 0.70)	2.20%	1.06	1.34
IRAK4	NM_001145258	-1	0.00018709	0.47 (0.32, 0.70)	2.20%	1.06	1.34
IRAK4	NM_001145257	-1	0.00018709	0.47 (0.32, 0.70)	2.20%	1.06	1.34
IRAK4	NM_016123	-1	0.00018709	0.47 (0.32, 0.70)	2.20%	1.06	1.34
KIAA1324	NM_020775	-1	0.00020766	0.46 (0.31, 0.69)	2.30%	1.06	1.33
LOC286186	NR_033893	1	6.18E-05	1.50 (1.23, 1.83)	1.00%	1.06	1.35
LOC401177	NR_033975	1	9.63E-06	1.29 (1.15, 1.45)	0.30%	1.06	1.26
LRRC46	NM_033413	-1	0.00020068	0.48 (0.33, 0.71)	2.30%	1.06	1.34
MIR1251	NR_031653	1	0.00019134	1.89 (1.35, 2.65)	2.20%	1.06	1.37
MIR195	NR_029712	1	9.96E-05	1.56 (1.25, 1.96)	1.40%	1.06	1.36
MIR4275	NR_036237	1	6.85E-05	1.53 (1.24, 1.89)	1.10%	1.06	1.35
NKX1-2	NM_001146340	1	9.19E-05	1.58 (1.26, 1.99)	1.30%	1.06	1.36
OR2W5	NM_001004698	1	3.95E-06	1.25 (1.14, 1.38)	0.10%	1.06	1.23
SCARB2	NM_005506	1	0.00010943	1.71 (1.30, 2.24)	1.50%	1.06	1.38
SNAR-G1	NR_004383	1	7.37E-05	1.47 (1.21, 1.77)	1.10%	1.06	1.33
TKT	NM_001135055	1	0.00011508	1.77 (1.32, 2.37)	1.60%	1.06	1.38
TKT	NM_001064	1	0.00011508	1.77 (1.32, 2.37)	1.60%	1.06	1.38
TMOD2	NM_014548	1	6.75E-05	1.50 (1.23, 1.82)	1.10%	1.06	1.34
TMOD2	NM_001142885	1	6.75E-05	1.50 (1.23, 1.82)	1.10%	1.06	1.34
USP33	NM_201626	-1	0.00030132	0.36 (0.21, 0.63)	3.00%	1.06	1.28
USP33	NM_015017	-1	0.00030132	0.36 (0.21, 0.63)	3.00%	1.06	1.28

USP33	NM_201624	-1	0.00030132	0.36 (0.21, 0.63)	3.00%	1.06	1.28
VDAC1	NM_003374	1	0.00026933	2.74 (1.59, 4.72)	2.70%	1.06	1.31
VDAC1	NR_036625	1	0.00026933	2.74 (1.59, 4.72)	2.70%	1.06	1.31
VDAC1	NR_036624	1	0.00026933	2.74 (1.59, 4.72)	2.70%	1.06	1.31
C12orf35	NM_018169	-1	0.00036212	0.34 (0.19, 0.62)	3.40%	1.05	1.27
GALNS	NM_000512	1	0.00030441	2.31 (1.47, 3.65)	3.00%	1.05	1.34
KRT78	NM_173352	1	5.86E-05	1.41 (1.19, 1.66)	1.00%	1.05	1.31
LSM4	NM_012321	1	0.00018189	1.79 (1.32, 2.43)	2.20%	1.05	1.37
MIR4318	NR_036202	1	0.00020629	1.76 (1.30, 2.37)	2.30%	1.05	1.36
OR5T2	NM_001004746	1	0.00020529	1.85 (1.34, 2.57)	2.30%	1.05	1.37
PNPLA4	NM_004650	-1	0.00020112	0.57 (0.43, 0.77)	2.30%	1.05	1.35
PNPLA4	NM_001142389	-1	0.00020112	0.57 (0.43, 0.77)	2.30%	1.05	1.35
PNPLA4	NM_001172672	-1	0.00020112	0.57 (0.43, 0.77)	2.30%	1.05	1.35
SNORD116-12	NR_003327	1	0.00013681	1.49 (1.21, 1.82)	1.80%	1.05	1.33
TFAP2A	NM_003220	-1	0.00019691	0.60 (0.45, 0.78)	2.30%	1.05	1.34
TFAP2A	NM_001032280	-1	0.00019691	0.60 (0.45, 0.78)	2.30%	1.05	1.34
TFAP2A	NM_001042425	-1	0.00019691	0.60 (0.45, 0.78)	2.30%	1.05	1.34
TTC9	NM_015351	1	0.00025891	1.89 (1.34, 2.67)	2.60%	1.05	1.36
C17orf88	NR_026770	1	0.00022622	1.66 (1.27, 2.17)	2.40%	1.04	1.36
C19orf75	NM_173635	1	3.05E-05	1.26 (1.13, 1.40)	0.60%	1.04	1.23
DUSP13	NM_001007273	1	0.00031933	1.95 (1.35, 2.80)	3.10%	1.04	1.35
DUSP13	NM_001007271	1	0.00031933	1.95 (1.35, 2.80)	3.10%	1.04	1.35
DUSP13	NM_001007272	1	0.00031933	1.95 (1.35, 2.80)	3.10%	1.04	1.35
DUSP13	NM_016364	1	0.00031933	1.95 (1.35, 2.80)	3.10%	1.04	1.35
G3BP2	NM_203504	1	0.00018881	1.58 (1.24, 2.02)	2.20%	1.04	1.35
G3BP2	NM_203505	1	0.00018881	1.58 (1.24, 2.02)	2.20%	1.04	1.35
G3BP2	NM_012297	1	0.00018881	1.58 (1.24, 2.02)	2.20%	1.04	1.35
HSPBAP1	NM_024610	-1	0.00032784	0.48 (0.32, 0.72)	3.10%	1.04	1.32
LRRIQ1	NM_001079910	-1	0.00037432	0.50 (0.34, 0.73)	3.50%	1.04	1.32
LRRIQ1	NM_032165	-1	0.00037432	0.50 (0.34, 0.73)	3.50%	1.04	1.32
LYPD2	NM_205545	1	4.58E-05	1.27 (1.13, 1.43)	0.80%	1.04	1.24
MAGEB10	NM_182506	1	0.00022296	1.50 (1.21, 1.86)	2.40%	1.04	1.33
MGC87042	NM_207342	1	0.00026627	1.56 (1.23, 1.99)	2.70%	1.04	1.34
MGC87042	NM_001164460	1	0.00026627	1.56 (1.23, 1.99)	2.70%	1.04	1.34
MOBKL1A	NM_173468	1	0.00023167	1.52 (1.22, 1.91)	2.40%	1.04	1.33
PILRA	NM_013439	-1	0.00022195	0.63 (0.50, 0.81)	2.40%	1.04	1.33
PILRA	NM_178273	-1	0.00022195	0.63 (0.50, 0.81)	2.40%	1.04	1.33
PILRA	NM_178272	-1	0.00022195	0.63 (0.50, 0.81)	2.40%	1.04	1.33
POGK	NM_017542	1	0.00029434	1.82 (1.32, 2.51)	2.90%	1.04	1.36
PRSS41	NM_001135086	1	3.53E-05	1.25 (1.12, 1.39)	0.70%	1.04	1.23
SOST	NM_025237	1	0.00021545	1.59 (1.24, 2.03)	2.30%	1.04	1.35
ZNF140	NM_003440	-1	0.00023704	0.64 (0.51, 0.81)	2.50%	1.04	1.33
ZNF682	NM_001077349	-1	0.00029535	0.53 (0.37, 0.75)	2.90%	1.04	1.33
ZNF682	NM_033196	-1	0.00029535	0.53 (0.37, 0.75)	2.90%	1.04	1.33
AAGAB	NM_024666	1	0.0003973	1.50 (1.20, 1.89)	3.70%	1.03	1.32
AARS	NM_001605	1	0.00051635	2.05 (1.37, 3.08)	4.40%	1.03	1.33
ADHFE1	NM_144650	-1	0.00059544	0.53 (0.37, 0.76)	4.80%	1.03	1.31
ARPP19	NM_006628	1	0.00025921	1.32 (1.14, 1.53)	2.60%	1.03	1.26
BZRAP1	NM_004758	-1	0.00068405	0.50 (0.34, 0.75)	5.30%	1.03	1.3
BZRAP1	NM_024418	-1	0.00068405	0.50 (0.34, 0.75)	5.30%	1.03	1.3

C14orf102	NM_199043	-1	0.00056259	0.50 (0.34, 0.74)	4.70%	1.03	1.31
C14orf102	NM_017970	-1	0.00056259	0.50 (0.34, 0.74)	4.70%	1.03	1.31
C17orf68	NM_025099	-1	0.00057208	0.38 (0.22, 0.66)	4.70%	1.03	1.27
CLUL1	NM_014410	-1	0.00044779	0.57 (0.42, 0.78)	4.00%	1.03	1.32
CLUL1	NM_199167	-1	0.00044779	0.57 (0.42, 0.78)	4.00%	1.03	1.32
DEF8	NM_207514	1	0.00060461	3.04 (1.61, 5.73)	4.90%	1.03	1.27
DEF8	NM_017702	1	0.00060461	3.04 (1.61, 5.73)	4.90%	1.03	1.27
DKFZp779M0652	NR_027134	1	0.00043937	1.53 (1.21, 1.95)	4.00%	1.03	1.32
DKK4	NM_014420	-1	0.00068191	0.43 (0.27, 0.70)	5.30%	1.03	1.28
DSCR10	NR_027695	1	0.00037115	1.40 (1.16, 1.68)	3.50%	1.03	1.29
FAM169B	NM_182562	1	0.00023936	1.46 (1.19, 1.78)	2.50%	1.03	1.32
GARS	NM_002047	1	0.0002165	1.39 (1.17, 1.65)	2.30%	1.03	1.29
HIST2H2AC	NM_003517	1	0.00055643	2.72 (1.54, 4.79)	4.70%	1.03	1.29
HMX3	NM_001105574	1	0.00032223	1.63 (1.25, 2.13)	3.10%	1.03	1.34
HOXA13	NM_000522	1	0.00047312	1.47 (1.18, 1.82)	4.20%	1.03	1.31
IDI1	NM_004508	1	0.00059295	2.54 (1.49, 4.33)	4.80%	1.03	1.3
JUND	NM_005354	1	0.00044453	1.44 (1.18, 1.77)	4.00%	1.03	1.3
LOC285577	NR_033898	1	0.00019503	1.30 (1.13, 1.50)	2.20%	1.03	1.25
LOC648740	NR_024438	-1	0.00063182	0.54 (0.38, 0.77)	5.00%	1.03	1.31
MCMBP	NM_024834	1	0.00056948	1.77 (1.28, 2.46)	4.70%	1.03	1.34
MIR133A1	NR_029675	1	0.00035238	1.67 (1.26, 2.22)	3.30%	1.03	1.35
MMP25	NM_022468	-1	0.00050839	0.45 (0.28, 0.70)	4.40%	1.03	1.3
NPPB	NM_002521	1	0.00015182	1.29 (1.13, 1.47)	1.90%	1.03	1.25
NTRK3	NM_001012338	-1	0.00048234	0.50 (0.34, 0.74)	4.20%	1.03	1.31
NTRK3	NM_002530	-1	0.00048234	0.50 (0.34, 0.74)	4.20%	1.03	1.31
NTRK3	NM_001007156	-1	0.00048234	0.50 (0.34, 0.74)	4.20%	1.03	1.31
ODF2L	NM_001007022	-1	0.00054085	0.50 (0.34, 0.74)	4.60%	1.03	1.31
ODF2L	NM_020729	-1	0.00054085	0.50 (0.34, 0.74)	4.60%	1.03	1.31
ODF2L	NM_001184765	-1	0.00054085	0.50 (0.34, 0.74)	4.60%	1.03	1.31
ODF2L	NM_001184766	-1	0.00054085	0.50 (0.34, 0.74)	4.60%	1.03	1.31
OR2B3	NM_001005226	1	0.00055355	1.60 (1.23, 2.09)	4.70%	1.03	1.33
OR8S1	NM_001005203	1	0.00014925	1.33 (1.15, 1.54)	1.90%	1.03	1.27
PGM5P2	NR_002836	-1	0.00047907	0.48 (0.32, 0.72)	4.20%	1.03	1.31
RAD51L3	NM_133629	1	0.00053965	1.68 (1.25, 2.25)	4.60%	1.03	1.34
RAD51L3	NM_001142571	1	0.00053965	1.68 (1.25, 2.25)	4.60%	1.03	1.34
RAD51L3	NM_002878	1	0.00053965	1.68 (1.25, 2.25)	4.60%	1.03	1.34
RBM27	NM_018989	1	0.00056605	1.93 (1.33, 2.80)	4.70%	1.03	1.33
RILPL2	NM_145058	-1	0.00047818	0.61 (0.46, 0.80)	4.20%	1.03	1.32
RNASE9	NM_001001673	1	0.00047969	2.10 (1.39, 3.20)	4.20%	1.03	1.33
RNASE9	NM_001110358	1	0.00047969	2.10 (1.39, 3.20)	4.20%	1.03	1.33
RNASE9	NM_001110359	1	0.00047969	2.10 (1.39, 3.20)	4.20%	1.03	1.33
RNASE9	NM_001110360	1	0.00047969	2.10 (1.39, 3.20)	4.20%	1.03	1.33
RNASE9	NM_001110361	1	0.00047969	2.10 (1.39, 3.20)	4.20%	1.03	1.33
RNASE9	NM_001110356	1	0.00047969	2.10 (1.39, 3.20)	4.20%	1.03	1.33
RNASE9	NM_001110357	1	0.00047969	2.10 (1.39, 3.20)	4.20%	1.03	1.33
SCRT2	NM_033129	1	0.00019487	1.27 (1.12, 1.44)	2.20%	1.03	1.23
SENP5	NM_152699	1	0.00049234	1.68 (1.26, 2.26)	4.30%	1.03	1.34
SPRR3	NM_001097589	1	0.00034206	1.40 (1.16, 1.68)	3.30%	1.03	1.29
SPRR3	NM_005416	1	0.00034206	1.40 (1.16, 1.68)	3.30%	1.03	1.29

TPTE	NM_199259	1	0.00025602	1.34 (1.15, 1.58)	2.60%	1.03	1.27
TPTE	NM_199261	1	0.00025602	1.34 (1.15, 1.58)	2.60%	1.03	1.27
TPTE	NM_199260	1	0.00025602	1.34 (1.15, 1.58)	2.60%	1.03	1.27
TSC22D3	NM_198057	1	0.00043616	1.96 (1.35, 2.85)	4.00%	1.03	1.34
TSC22D3	NM_004089	1	0.00043616	1.96 (1.35, 2.85)	4.00%	1.03	1.34
TSC22D3	NM_001015881	1	0.00043616	1.96 (1.35, 2.85)	4.00%	1.03	1.34
USP40	NM_018218	-1	0.00058533	0.52 (0.36, 0.75)	4.80%	1.03	1.31
ZCWPW1	NM_017984	-1	0.00057031	0.59 (0.43, 0.80)	4.70%	1.03	1.32
AMY2B	NM_020978	-1	0.00080037	0.46 (0.29, 0.72)	5.90%	1.02	1.28
ATG5	NM_004849	1	0.00080307	1.39 (1.15, 1.68)	5.90%	1.02	1.28
C18orf26	NM_173629	1	0.00074956	1.66 (1.24, 2.23)	5.70%	1.02	1.33
C2orf70	NM_001105519	1	0.00075733	1.87 (1.30, 2.69)	5.70%	1.02	1.33
CCDC66	NM_001141947	-1	0.0008218	0.54 (0.37, 0.77)	6.00%	1.02	1.3
CCDC66	NR_024460	-1	0.0008218	0.54 (0.37, 0.77)	6.00%	1.02	1.3
CCDC66	NM_001012506	-1	0.0008218	0.54 (0.37, 0.77)	6.00%	1.02	1.3
CCDC93	NM_019044	-1	0.00078652	0.49 (0.32, 0.74)	5.90%	1.02	1.29
COQ6	NM_182480	-1	0.00096649	0.60 (0.45, 0.81)	6.50%	1.02	1.3
COQ6	NM_182476	-1	0.00096649	0.60 (0.45, 0.81)	6.50%	1.02	1.3
CRNDE	NR_034106	1	0.00080709	2.12 (1.37, 3.29)	5.90%	1.02	1.31
CRNDE	NR_034105	1	0.00080709	2.12 (1.37, 3.29)	5.90%	1.02	1.31
CRY1	NM_004075	-1	0.00115448	0.45 (0.28, 0.73)	7.10%	1.02	1.27
CSF2RB	NM_000395	-1	0.00105596	0.47 (0.30, 0.74)	6.80%	1.02	1.28
CYP20A1	NM_177538	-1	0.00090837	0.40 (0.23, 0.69)	6.30%	1.02	1.26
DAG1	NM_001177644	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_001177643	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_001177642	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_001177641	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_001177640	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_001177634	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_004393	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_001165928	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_001177637	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_001177639	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_001177638	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_001177635	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAG1	NM_001177636	1	0.00099617	2.35 (1.41, 3.92)	6.60%	1.02	1.29
DAP	NM_004394	1	0.00098142	2.05 (1.34, 3.15)	6.60%	1.02	1.31
DDX56	NM_019082	1	0.00044191	1.38 (1.15, 1.64)	4.00%	1.02	1.28
DNAH6	NM_001370	-1	0.00084767	0.53 (0.36, 0.77)	6.10%	1.02	1.3
DUSP9	NM_001395	1	0.00099293	1.67 (1.23, 2.27)	6.60%	1.02	1.32
EBP	NM_006579	1	0.0008591	2.33 (1.42, 3.82)	6.10%	1.02	1.3
FEZF1	NM_001160264	1	0.00066372	1.53 (1.20, 1.95)	5.20%	1.02	1.32
FEZF1	NM_001024613	1	0.00066372	1.53 (1.20, 1.95)	5.20%	1.02	1.32
FRMPD2	NM_001018071	-1	0.00102321	0.51 (0.34, 0.76)	6.70%	1.02	1.29
FRMPD2	NR_033178	-1	0.00102321	0.51 (0.34, 0.76)	6.70%	1.02	1.29
G6PD	NM_000402	1	0.00095547	2.06 (1.34, 3.16)	6.50%	1.02	1.31
G6PD	NM_001042351	1	0.00095547	2.06 (1.34, 3.16)	6.50%	1.02	1.31
GABPB1	NM_016654	1	0.0007582	1.44 (1.16, 1.78)	5.70%	1.02	1.29
GABPB1	NM_181427	1	0.0007582	1.44 (1.16, 1.78)	5.70%	1.02	1.29
GABPB1	NM_005254	1	0.0007582	1.44 (1.16, 1.78)	5.70%	1.02	1.29

GABPB1	NM_002041	1	0.0007582	1.44 (1.16, 1.78)	5.70%	1.02	1.29
GABPB1	NM_016655	1	0.0007582	1.44 (1.16, 1.78)	5.70%	1.02	1.29
GALNT1	NM_020474	1	0.00088364	1.87 (1.29, 2.71)	6.20%	1.02	1.32
GPR50	NM_004224	1	0.00059725	1.26 (1.11, 1.45)	4.80%	1.02	1.22
HKR1	NM_181786	-1	0.00088702	0.48 (0.32, 0.74)	6.20%	1.02	1.29
HSPA14	NM_016299	1	0.00115563	2.11 (1.34, 3.30)	7.10%	1.02	1.3
IGF2BP2	NM_001007225	1	0.00095786	2.69 (1.49, 4.83)	6.50%	1.02	1.27
IGF2BP2	NM_006548	1	0.00095786	2.69 (1.49, 4.83)	6.50%	1.02	1.27
IPW	NR_023915	-1	0.00102737	0.62 (0.46, 0.82)	6.70%	1.02	1.3
KIAA0467	NM_015284	-1	0.00107902	0.39 (0.22, 0.69)	6.80%	1.02	1.25
KIF20A	NM_005733	1	0.00106069	2.64 (1.48, 4.72)	6.80%	1.02	1.27
LOC144742	NR_024246	1	0.00076829	1.38 (1.14, 1.66)	5.80%	1.02	1.28
LRRC39	NM_144620	-1	0.00099003	0.54 (0.38, 0.78)	6.60%	1.02	1.3
MIR24-2	NR_029497	1	0.00095954	1.64 (1.22, 2.19)	6.50%	1.02	1.32
MTHFR	NM_005957	-1	0.00117686	0.46 (0.29, 0.74)	7.20%	1.02	1.27
MTHFSD	NR_027490	1	0.00078921	1.89 (1.30, 2.73)	5.90%	1.02	1.32
MTHFSD	NR_027489	1	0.00078921	1.89 (1.30, 2.73)	5.90%	1.02	1.32
MTHFSD	NM_022764	1	0.00078921	1.89 (1.30, 2.73)	5.90%	1.02	1.32
MTHFSD	NM_001159379	1	0.00078921	1.89 (1.30, 2.73)	5.90%	1.02	1.32
MTHFSD	NM_001159378	1	0.00078921	1.89 (1.30, 2.73)	5.90%	1.02	1.32
MTHFSD	NM_001159377	1	0.00078921	1.89 (1.30, 2.73)	5.90%	1.02	1.32
MTHFSD	NM_001159380	1	0.00078921	1.89 (1.30, 2.73)	5.90%	1.02	1.32
MYSM1	NM_001085487	-1	0.00086284	0.38 (0.21, 0.67)	6.10%	1.02	1.25
N4BP2L2	NM_033111	-1	0.00082672	0.54 (0.38, 0.78)	6.00%	1.02	1.3
N4BP2L2	NM_014887	-1	0.00082672	0.54 (0.38, 0.78)	6.00%	1.02	1.3
NENF	NM_013349	1	0.00111716	2.06 (1.33, 3.19)	7.00%	1.02	1.3
NENF	NR_026598	1	0.00111716	2.06 (1.33, 3.19)	7.00%	1.02	1.3
NPY1R	NM_000909	-1	0.00069841	0.53 (0.37, 0.77)	5.40%	1.02	1.31
OR2J2	NM_030905	1	0.0006695	1.55 (1.20, 1.99)	5.20%	1.02	1.32
PLA2G2F	NM_022819	1	0.00106176	1.72 (1.24, 2.38)	6.80%	1.02	1.32
POTEG	NR_027480	1	0.0008735	1.50 (1.18, 1.90)	6.20%	1.02	1.31
POTEG	NM_001005356	1	0.0008735	1.50 (1.18, 1.90)	6.20%	1.02	1.31
PRDM9	NM_020227	1	0.00109686	1.80 (1.26, 2.56)	6.90%	1.02	1.32
PRPF38A	NM_032864	-1	0.00092473	0.45 (0.28, 0.72)	6.40%	1.02	1.28
RPAP2	NM_024813	-1	0.0010711	0.35 (0.19, 0.66)	6.80%	1.02	1.23
SERPINF2	NM_001165920	-1	0.00083318	0.51 (0.34, 0.76)	6.00%	1.02	1.3
SERPINF2	NM_000934	-1	0.00083318	0.51 (0.34, 0.76)	6.00%	1.02	1.3
SERPINF2	NM_001165921	-1	0.00083318	0.51 (0.34, 0.76)	6.00%	1.02	1.3
SLC17A6	NM_020346	1	0.00061603	1.59 (1.22, 2.07)	4.90%	1.02	1.33
SMC5	NM_015110	-1	0.00090526	0.52 (0.35, 0.76)	6.30%	1.02	1.3
SNORD115-40	NR_003355	1	0.00100408	1.58 (1.20, 2.08)	6.60%	1.02	1.31
SRSF11	NM_001190987	-1	0.00107233	0.52 (0.35, 0.77)	6.80%	1.02	1.29
SRSF11	NM_004768	-1	0.00107233	0.52 (0.35, 0.77)	6.80%	1.02	1.29
THEG	NM_016585	1	0.00063156	1.70 (1.25, 2.30)	5.00%	1.02	1.33
THEG	NM_199202	1	0.00063156	1.70 (1.25, 2.30)	5.00%	1.02	1.33
TMEM30C	NR_028358	1	0.00083733	1.66 (1.23, 2.23)	6.00%	1.02	1.32
TMEM30C	NR_028357	1	0.00083733	1.66 (1.23, 2.23)	6.00%	1.02	1.32
TRAF3IP1	NM_015650	-1	0.00080751	0.47 (0.30, 0.73)	5.90%	1.02	1.29
TRAF3IP1	NM_001139490	-1	0.00080751	0.47 (0.30, 0.73)	5.90%	1.02	1.29
TTC12	NM_017868	-1	0.00111797	0.40 (0.23, 0.69)	7.00%	1.02	1.25

USP24	NM_015306	-1	0.00099068	0.46 (0.29, 0.73)	6.60%	1.02	1.28
WBP4	NM_007187	-1	0.00083437	0.48 (0.32, 0.74)	6.00%	1.02	1.29
ZNF440	NM_152357	-1	0.00113941	0.50 (0.33, 0.76)	7.10%	1.02	1.28
ZNF644	NM_032186	-1	0.001187	0.44 (0.27, 0.72)	7.20%	1.02	1.26
ZNF644	NM_016620	-1	0.001187	0.44 (0.27, 0.72)	7.20%	1.02	1.26
ZNF644	NM_201269	-1	0.001187	0.44 (0.27, 0.72)	7.20%	1.02	1.26
ZNF701	NM_018260	-1	0.00075297	0.47 (0.31, 0.73)	5.70%	1.02	1.29
ZNF701	NM_001172655	-1	0.00075297	0.47 (0.31, 0.73)	5.70%	1.02	1.29
AGBL2	NM_024783	-1	0.00142443	0.61 (0.45, 0.82)	7.80%	1.01	1.29
BRP44	NM_001143674	1	0.00172654	1.99 (1.30, 3.07)	8.70%	1.01	1.29
BRP44	NM_015415	1	0.00172654	1.99 (1.30, 3.07)	8.70%	1.01	1.29
BRP44	NR_026550	1	0.00172654	1.99 (1.30, 3.07)	8.70%	1.01	1.29
BUB3	NM_004725	1	0.00114919	1.73 (1.24, 2.40)	7.10%	1.01	1.32
BUB3	NM_001007793	1	0.00114919	1.73 (1.24, 2.40)	7.10%	1.01	1.32
C10orf68	NM_024688	-1	0.00138334	0.52 (0.34, 0.77)	7.70%	1.01	1.28
C1orf168	NM_001004303	-1	0.00118419	0.53 (0.36, 0.78)	7.20%	1.01	1.29
CA5A	NM_001739	1	0.00164802	1.82 (1.25, 2.64)	8.50%	1.01	1.3
CCDC39	NM_181426	-1	0.00165504	0.69 (0.55, 0.87)	8.50%	1.01	1.27
CDC25B	NM_004358	1	0.00150067	1.93 (1.28, 2.88)	8.10%	1.01	1.3
CDC25B	NM_021873	1	0.00150067	1.93 (1.28, 2.88)	8.10%	1.01	1.3
CDC25B	NM_021872	1	0.00150067	1.93 (1.28, 2.88)	8.10%	1.01	1.3
CDK5RAP2	NM_001011649	-1	0.00157691	0.49 (0.32, 0.76)	8.30%	1.01	1.27
CDK5RAP2	NM_018249	-1	0.00157691	0.49 (0.32, 0.76)	8.30%	1.01	1.27
CEP110	NM_007018	-1	0.00153006	0.40 (0.23, 0.71)	8.20%	1.01	1.24
CEP72	NM_018140	1	0.00125053	2.10 (1.34, 3.28)	7.30%	1.01	1.3
CRABP1	NM_004378	1	0.00130325	1.86 (1.27, 2.71)	7.50%	1.01	1.31
CROCC	NM_014675	-1	0.00134738	0.58 (0.42, 0.81)	7.50%	1.01	1.29
DBT	NM_001918	-1	0.00183357	0.36 (0.19, 0.68)	9.00%	1.01	1.21
DGCR10	NR_026651	1	0.00120541	1.77 (1.25, 2.51)	7.20%	1.01	1.31
DMRTC2	NM_001040283	1	0.0016167	1.43 (1.14, 1.78)	8.40%	1.01	1.28
EIF4EBP1	NM_004095	1	0.00155936	1.58 (1.19, 2.09)	8.30%	1.01	1.3
FAM120AOS	NM_198841	-1	0.00179665	0.45 (0.27, 0.74)	8.90%	1.01	1.25
FAM184B	NM_015688	-1	0.00132516	0.41 (0.24, 0.71)	7.50%	1.01	1.25
FANCD2	NM_001018115	1	0.00173006	1.97 (1.29, 3.00)	8.70%	1.01	1.29
FANCD2	NM_033084	1	0.00173006	1.97 (1.29, 3.00)	8.70%	1.01	1.29
FANCL	NM_001114636	-1	0.00127386	0.61 (0.45, 0.82)	7.40%	1.01	1.29
FANCL	NM_018062	-1	0.00127386	0.61 (0.45, 0.82)	7.40%	1.01	1.29
FRY	NM_023037	-1	0.00162735	0.48 (0.30, 0.76)	8.40%	1.01	1.26
GAB4	NM_001037814	1	0.0010639	1.31 (1.12, 1.55)	6.80%	1.01	1.25
GATS	NR_028040	-1	0.00180899	0.45 (0.27, 0.74)	9.00%	1.01	1.25
GATS	NR_028038	-1	0.00180899	0.45 (0.27, 0.74)	9.00%	1.01	1.25
GATS	NR_028039	-1	0.00180899	0.45 (0.27, 0.74)	9.00%	1.01	1.25
GATS	NM_178831	-1	0.00180899	0.45 (0.27, 0.74)	9.00%	1.01	1.25
GDF15	NM_004864	1	0.00152308	1.91 (1.28, 2.86)	8.20%	1.01	1.3
GDF7	NM_182828	1	0.00091412	1.28 (1.10, 1.47)	6.30%	1.01	1.23
GMCL1L	NR_003281	1	0.00162165	1.74 (1.23, 2.45)	8.40%	1.01	1.3
GPRIN1	NM_052899	1	0.00164633	2.21 (1.35, 3.63)	8.50%	1.01	1.28
HAX1	NM_006118	1	0.00171232	2.26 (1.36, 3.76)	8.70%	1.01	1.27
HAX1	NM_001018837	1	0.00171232	2.26 (1.36, 3.76)	8.70%	1.01	1.27
HYDIN	NM_032821	-1	0.0013742	0.55 (0.38, 0.79)	7.60%	1.01	1.29

HYDIN	NM_017558	-1	0.0013742	0.55 (0.38, 0.79)	7.60%	1.01	1.29
HYDIN	NM_001198542	-1	0.0013742	0.55 (0.38, 0.79)	7.60%	1.01	1.29
HYDIN	NM_001198543	-1	0.0013742	0.55 (0.38, 0.79)	7.60%	1.01	1.29
KDELR1	NM_006801	1	0.00120971	1.94 (1.30, 2.90)	7.20%	1.01	1.31
LAMP1	NM_005561	1	0.00113874	1.89 (1.29, 2.77)	7.10%	1.01	1.31
LOC646862	NM_001195135	1	0.00178119	1.81 (1.25, 2.62)	8.90%	1.01	1.3
MAP3K14	NM_003954	-1	0.00125057	0.51 (0.34, 0.77)	7.30%	1.01	1.28
MEGF9	NM_001080497	-1	0.00183087	0.37 (0.20, 0.69)	9.00%	1.01	1.22
MIR548I2	NR_031688	1	0.00172026	1.48 (1.16, 1.90)	8.70%	1.01	1.29
MITD1	NM_138798	-1	0.00149032	0.58 (0.42, 0.81)	8.10%	1.01	1.29
MRPL45P2	NR_033934	-1	0.00136399	0.49 (0.31, 0.76)	7.60%	1.01	1.27
MST4	NM_001042452	1	0.00185523	2.47 (1.40, 4.35)	9.00%	1.01	1.26
MST4	NM_016542	1	0.00185523	2.47 (1.40, 4.35)	9.00%	1.01	1.26
MST4	NM_001042453	1	0.00185523	2.47 (1.40, 4.35)	9.00%	1.01	1.26
MVD	NM_002461	1	0.001646	2.33 (1.38, 3.94)	8.50%	1.01	1.27
NCRNA00115	NR_024321	-1	0.00141638	0.49 (0.32, 0.76)	7.80%	1.01	1.27
NCRNA00287	NR_026677	-1	0.00120549	0.50 (0.32, 0.76)	7.20%	1.01	1.28
NFAM1	NM_145912	-1	0.00171875	0.55 (0.38, 0.80)	8.70%	1.01	1.28
NME1	NM_000269	1	0.00140178	1.88 (1.28, 2.77)	7.70%	1.01	1.31
NME1	NM_198175	1	0.00140178	1.88 (1.28, 2.77)	7.70%	1.01	1.31
NUDT21	NM_007006	1	0.0017855	1.91 (1.27, 2.86)	8.90%	1.01	1.3
PARD3B	NM_205863	-1	0.00120268	0.61 (0.46, 0.82)	7.20%	1.01	1.29
PARD3B	NM_057177	-1	0.00120268	0.61 (0.46, 0.82)	7.20%	1.01	1.29
PARD3B	NM_152526	-1	0.00120268	0.61 (0.46, 0.82)	7.20%	1.01	1.29
PBX1	NM_002585	1	0.00147845	1.64 (1.21, 2.23)	8.00%	1.01	1.31
RFWD3	NM_018124	1	0.00121663	1.83 (1.27, 2.64)	7.20%	1.01	1.31
RFX7	NM_022841	-1	0.00158617	0.46 (0.28, 0.74)	8.30%	1.01	1.26
RGS4	NM_005613	1	0.00159894	2.17 (1.34, 3.51)	8.40%	1.01	1.28
RGS4	NM_001113381	1	0.00159894	2.17 (1.34, 3.51)	8.40%	1.01	1.28
RGS4	NM_001102445	1	0.00159894	2.17 (1.34, 3.51)	8.40%	1.01	1.28
RGS4	NM_001113380	1	0.00159894	2.17 (1.34, 3.51)	8.40%	1.01	1.28
RHCG	NM_016321	1	0.0015871	1.72 (1.23, 2.40)	8.30%	1.01	1.31
RNPC3	NM_017619	-1	0.0015841	0.45 (0.28, 0.74)	8.30%	1.01	1.26
SEC61A1	NM_013336	1	0.00127515	1.92 (1.29, 2.85)	7.40%	1.01	1.31
SFXN1	NM_022754	1	0.00126021	1.97 (1.30, 2.97)	7.40%	1.01	1.3
SGIP1	NM_032291	1	0.00131363	2.33 (1.39, 3.90)	7.50%	1.01	1.28
SH3GLB2	NM_020145	-1	0.00133594	0.57 (0.40, 0.80)	7.50%	1.01	1.29
SIN3B	NM_015260	-1	0.001324	0.47 (0.30, 0.75)	7.50%	1.01	1.27
SLC1A5	NM_001145145	1	0.00133504	2.79 (1.49, 5.23)	7.50%	1.01	1.25
SLC1A5	NM_005628	1	0.00133504	2.79 (1.49, 5.23)	7.50%	1.01	1.25
SLC1A5	NM_001145144	1	0.00133504	2.79 (1.49, 5.23)	7.50%	1.01	1.25
SMU1	NM_018225	-1	0.00176915	0.51 (0.34, 0.78)	8.90%	1.01	1.27
SNORD18C	NR_002443	1	0.00106266	1.56 (1.20, 2.04)	6.80%	1.01	1.31
SPCS1	NM_014041	1	0.00124058	2.15 (1.35, 3.42)	7.30%	1.01	1.29
TBRG4	NM_004749	1	0.0009404	1.46 (1.17, 1.83)	6.40%	1.01	1.3
TBRG4	NM_199122	1	0.0009404	1.46 (1.17, 1.83)	6.40%	1.01	1.3
TBRG4	NM_030900	1	0.0009404	1.46 (1.17, 1.83)	6.40%	1.01	1.3
TEX2	NM_018469	1	0.00126006	1.64 (1.22, 2.22)	7.40%	1.01	1.31
TNFSF4	NM_003326	1	0.00129531	2.33 (1.39, 3.90)	7.50%	1.01	1.28
UPK1A	NM_007000	1	0.00147695	1.46 (1.16, 1.84)	8.00%	1.01	1.29

ZIC2	NM_007129	1	0.00133972	2.12 (1.34, 3.36)	7.50%	1.01	1.29
ZNF317	NM_020933	-1	0.00145044	0.58 (0.41, 0.81)	7.90%	1.01	1.29
ZNF317	NM_001190791	-1	0.00145044	0.58 (0.41, 0.81)	7.90%	1.01	1.29
ZNF626	NM_145297	-1	0.0015675	0.53 (0.36, 0.79)	8.30%	1.01	1.28
ZNF626	NM_001076675	-1	0.0015675	0.53 (0.36, 0.79)	8.30%	1.01	1.28
ZNF829	NM_001171979	-1	0.00120516	0.56 (0.39, 0.79)	7.20%	1.01	1.29
ZNF829	NM_001037232	-1	0.00120516	0.56 (0.39, 0.79)	7.20%	1.01	1.29
ZRANB2	NM_005455	-1	0.00127193	0.47 (0.30, 0.75)	7.40%	1.01	1.27
ZRANB2	NM_203350	-1	0.00127193	0.47 (0.30, 0.75)	7.40%	1.01	1.27
APOBEC2	NM_006789	-1	0.00205447	0.50 (0.33, 0.78)	9.60%	1	1.26
BICD2	NM_001003800	-1	0.00208035	0.43 (0.25, 0.73)	9.60%	1	1.24
BICD2	NM_015250	-1	0.00208035	0.43 (0.25, 0.73)	9.60%	1	1.24
BUD13	NM_032725	-1	0.0020833	0.47 (0.29, 0.76)	9.60%	1	1.25
BUD13	NM_001159736	-1	0.0020833	0.47 (0.29, 0.76)	9.60%	1	1.25
CCDC103	NM_213607	-1	0.00214716	0.55 (0.38, 0.81)	9.80%	1	1.27
CHCHD1	NM_203298	1	0.00187362	1.95 (1.28, 2.97)	9.10%	1	1.29
CLDN4	NM_001305	1	0.00214986	1.92 (1.27, 2.91)	9.80%	1	1.29
CLK1	NR_027855	-1	0.00214838	0.54 (0.36, 0.80)	9.80%	1	1.27
CLK1	NR_027856	-1	0.00214838	0.54 (0.36, 0.80)	9.80%	1	1.27
CLK1	NM_004071	-1	0.00214838	0.54 (0.36, 0.80)	9.80%	1	1.27
CLK1	NM_001162407	-1	0.00214838	0.54 (0.36, 0.80)	9.80%	1	1.27
DCK	NM_000788	1	0.00205322	1.78 (1.23, 2.57)	9.60%	1	1.3
EGLN1	NM_022051	1	0.00196644	1.82 (1.25, 2.66)	9.40%	1	1.3
ESRP2	NM_024939	1	0.00213417	2.28 (1.35, 3.86)	9.80%	1	1.26
FNBP4	NM_015308	-1	0.0020334	0.53 (0.35, 0.79)	9.60%	1	1.27
FUT11	NM_173540	1	0.00189847	1.98 (1.29, 3.06)	9.20%	1	1.29
FYTTD1	NM_032288	1	0.00192913	1.54 (1.17, 2.03)	9.20%	1	1.29
FYTTD1	NR_027840	1	0.00192913	1.54 (1.17, 2.03)	9.20%	1	1.29
FYTTD1	NM_001011537	1	0.00192913	1.54 (1.17, 2.03)	9.20%	1	1.29
GALNTL1	NM_001168368	-1	0.00217436	0.48 (0.30, 0.77)	9.90%	1	1.25
GALNTL1	NM_020692	-1	0.00217436	0.48 (0.30, 0.77)	9.90%	1	1.25
GSTM3	NR_024537	-1	0.00185428	0.50 (0.32, 0.77)	9.00%	1	1.26
GSTM3	NM_000849	-1	0.00185428	0.50 (0.32, 0.77)	9.00%	1	1.26
HECW2	NM_020760	-1	0.0021151	0.55 (0.38, 0.81)	9.70%	1	1.27
KIF27	NM_017576	-1	0.00181164	0.58 (0.41, 0.81)	9.00%	1	1.28
KRTCAP2	NM_173852	1	0.00192061	1.92 (1.27, 2.90)	9.20%	1	1.29
LAMA1	NM_005559	1	0.00202571	2.18 (1.33, 3.56)	9.60%	1	1.27
MIR603	NR_030334	1	0.00201767	1.78 (1.24, 2.57)	9.60%	1	1.3
MYO5A	NM_000259	1	0.00177654	1.36 (1.12, 1.65)	8.90%	1	1.26
MYO5A	NM_001142495	1	0.00177654	1.36 (1.12, 1.65)	8.90%	1	1.26
PCGF3	NM_006315	-1	0.00202742	0.54 (0.36, 0.80)	9.60%	1	1.27
RAB11B	NM_004218	-1	0.00191529	0.48 (0.30, 0.76)	9.20%	1	1.26
SCD	NM_005063	1	0.00208616	2.39 (1.37, 4.16)	9.60%	1	1.26
SMG5	NM_015327	1	0.0020908	1.80 (1.24, 2.62)	9.60%	1	1.29
SYNPO	NM_001109974	-1	0.00206694	0.51 (0.33, 0.78)	9.60%	1	1.26
SYNPO	NM_007286	-1	0.00206694	0.51 (0.33, 0.78)	9.60%	1	1.26
SYNPO	NM_001166209	-1	0.00206694	0.51 (0.33, 0.78)	9.60%	1	1.26
SYNPO	NM_001166208	-1	0.00206694	0.51 (0.33, 0.78)	9.60%	1	1.26
TAF5L	NM_014409	1	0.00200753	1.92 (1.27, 2.90)	9.50%	1	1.29
TAF5L	NM_001025247	1	0.00200753	1.92 (1.27, 2.90)	9.50%	1	1.29

USP16	NM_006447	-1	0.00184893	0.56 (0.39, 0.81)	9.00%	1	1.28
USP16	NM_001032410	-1	0.00184893	0.56 (0.39, 0.81)	9.00%	1	1.28
USP16	NM_001001992	-1	0.00184893	0.56 (0.39, 0.81)	9.00%	1	1.28
ZNF44	NM_016264	-1	0.00189847	0.36 (0.19, 0.68)	9.20%	1	1.21
ZNF44	NM_001164276	-1	0.00189847	0.36 (0.19, 0.68)	9.20%	1	1.21

Table 3. Assembled Intronic RNAs Identified as Associated with Risk of Breast Cancer Recurrence in 136 Breast Cancer Patients

Intron	Direction of Association (1=Higher Expression Means Higher Risk)	p-value	Standardized Hazard Ratio Estimate (95% Confidence Interval)	q-value (FDR)	Maximum Lower Bound Std HR @ 10% FDR	Regression-to-the-Mean-Corrected Std HR
NUDT19	1	2.99E-13	2.22 (1.79, 2.75)	<0.1%	1.35	1.77
CLINT1	1	1.74E-11	2.17 (1.73, 2.72)	<0.1%	1.31	1.71
CLINT1	1	1.74E-11	2.17 (1.73, 2.72)	<0.1%	1.31	1.71
CLINT1	1	1.74E-11	2.17 (1.73, 2.72)	<0.1%	1.31	1.71
KIF1B	1	8.27E-09	2.85 (2.00, 4.07)	<0.1%	1.3	1.65
KIF1B	1	8.27E-09	2.85 (2.00, 4.07)	<0.1%	1.3	1.65
ANKRD27	1	5.11E-16	1.66 (1.47, 1.88)	<0.1%	1.28	1.57
NOL8	-1	3.80E-09	0.43 (0.32, 0.57)	<0.1%	1.28	1.67
NOL8	-1	3.80E-09	0.43 (0.32, 0.57)	<0.1%	1.28	1.67
TTLL3	-1	4.56E-09	0.41 (0.30, 0.55)	<0.1%	1.28	1.68
TTLL3	-1	4.56E-09	0.41 (0.30, 0.55)	<0.1%	1.28	1.68
SECISBP2L	1	3.74E-10	1.93 (1.57, 2.37)	<0.1%	1.25	1.62
SECISBP2L	1	3.74E-10	1.93 (1.57, 2.37)	<0.1%	1.25	1.62
FOXJ2	-1	5.35E-08	0.48 (0.37, 0.62)	<0.1%	1.21	1.6
SEC24A	1	7.26E-09	1.90 (1.53, 2.37)	<0.1%	1.21	1.58
FRS3	-1	2.70E-08	0.52 (0.41, 0.65)	<0.1%	1.2	1.58
LOC100129518	1	1.04E-09	1.73 (1.45, 2.07)	<0.1%	1.2	1.54
MEGF9	-1	3.53E-07	0.42 (0.30, 0.59)	<0.1%	1.2	1.58
CANX	1	6.36E-08	1.94 (1.52, 2.46)	<0.1%	1.19	1.55
CANX	1	6.36E-08	1.94 (1.52, 2.46)	<0.1%	1.19	1.55
LRCH3	1	5.43E-09	1.71 (1.43, 2.04)	<0.1%	1.19	1.52
MPP6	1	6.89E-09	1.74 (1.44, 2.10)	<0.1%	1.19	1.53
TOMM20L	-1	3.52E-08	0.56 (0.45, 0.68)	<0.1%	1.19	1.54
ZNF484	-1	7.30E-07	0.43 (0.31, 0.60)	<0.1%	1.19	1.56
ZNF484	-1	7.30E-07	0.43 (0.31, 0.60)	<0.1%	1.19	1.56
AACSP1	1	1.95E-08	1.71 (1.42, 2.06)	<0.1%	1.18	1.51
CDHR2	1	2.94E-07	1.83 (1.45, 2.31)	<0.1%	1.17	1.51

CDHR2	1	2.94E-07	1.83 (1.45, 2.31)	<0.1%	1.17	1.51
CEP152	1	6.13E-07	1.87 (1.46, 2.39)	<0.1%	1.17	1.51
CEP152	1	6.13E-07	1.87 (1.46, 2.39)	<0.1%	1.17	1.51
FAM83A	1	3.27E-06	2.24 (1.59, 3.14)	0.10%	1.17	1.5
FAM83A	1	3.27E-06	2.24 (1.59, 3.14)	0.10%	1.17	1.5
GALNT12	1	7.50E-08	1.70 (1.40, 2.06)	<0.1%	1.17	1.49
HIVEP2	1	1.01E-06	2.17 (1.59, 2.96)	<0.1%	1.17	1.52
HOMEZ	-1	1.87E-08	0.61 (0.52, 0.73)	<0.1%	1.17	1.49
NCCRP1	1	1.69E-07	1.72 (1.41, 2.12)	<0.1%	1.17	1.49
NPRL2	-1	1.39E-10	0.69 (0.62, 0.77)	<0.1%	1.17	1.4
POLG2	1	8.71E-08	1.68 (1.39, 2.03)	<0.1%	1.17	1.48
PRAM1	-1	1.56E-07	0.54 (0.43, 0.68)	<0.1%	1.17	1.53
SPATA21	-1	1.74E-07	0.55 (0.44, 0.69)	<0.1%	1.17	1.53
SUN1	1	2.45E-08	1.60 (1.36, 1.89)	<0.1%	1.17	1.46
SUN1	1	2.45E-08	1.60 (1.36, 1.89)	<0.1%	1.17	1.46
SUN1	1	2.45E-08	1.60 (1.36, 1.89)	<0.1%	1.17	1.46
SUN1	1	2.45E-08	1.60 (1.36, 1.89)	<0.1%	1.17	1.46
SUN1	1	2.45E-08	1.60 (1.36, 1.89)	<0.1%	1.17	1.46
TCTN2	-1	7.74E-07	0.52 (0.40, 0.68)	<0.1%	1.17	1.52
TCTN2	-1	7.74E-07	0.52 (0.40, 0.68)	<0.1%	1.17	1.52
TMEM101	-1	1.18E-06	0.51 (0.39, 0.67)	<0.1%	1.17	1.52
ZMAT1	-1	1.22E-06	0.46 (0.34, 0.63)	<0.1%	1.17	1.54
ZMAT1	-1	1.22E-06	0.46 (0.34, 0.63)	<0.1%	1.17	1.54
C14orf50	-1	9.54E-08	0.61 (0.51, 0.73)	<0.1%	1.16	1.47
C2orf73	-1	2.94E-07	0.57 (0.46, 0.71)	<0.1%	1.16	1.5
C9orf64	-1	2.45E-06	0.49 (0.37, 0.66)	<0.1%	1.16	1.52
KCMF1	1	3.74E-07	1.73 (1.40, 2.13)	<0.1%	1.16	1.48
PDE6B	-1	5.88E-06	0.45 (0.32, 0.64)	0.10%	1.16	1.5
PDE6B	-1	5.88E-06	0.45 (0.32, 0.64)	0.10%	1.16	1.5
PDE6B	-1	5.88E-06	0.45 (0.32, 0.64)	0.10%	1.16	1.5
SF3B3	1	4.06E-06	2.03 (1.50, 2.75)	0.10%	1.16	1.49
SIRT6	-1	2.10E-08	0.64 (0.55, 0.75)	<0.1%	1.16	1.45
SIRT6	-1	2.10E-08	0.64 (0.55, 0.75)	<0.1%	1.16	1.45
SLC35D1	-1	4.54E-06	0.45 (0.32, 0.63)	0.10%	1.16	1.51
SMURF2	1	3.34E-07	1.75 (1.41, 2.16)	<0.1%	1.16	1.49
SPIN1	-1	5.97E-06	0.43 (0.30, 0.62)	0.10%	1.16	1.5
TEX2	1	1.23E-07	1.62 (1.35, 1.94)	<0.1%	1.16	1.46
ZNF44	-1	1.16E-06	0.53 (0.40, 0.68)	<0.1%	1.16	1.52
ZNF44	-1	1.16E-06	0.53 (0.40, 0.68)	<0.1%	1.16	1.52
ACAP2	1	2.30E-06	1.82 (1.42, 2.33)	<0.1%	1.15	1.48
CCDC47	1	2.83E-07	1.61 (1.34, 1.92)	<0.1%	1.15	1.45
CIC	-1	3.57E-06	0.52 (0.40, 0.69)	0.10%	1.15	1.5

GPR126	1	5.67E-06	2.00 (1.48, 2.69)	0.10%	1.15	1.48
GPR126	1	5.67E-06	2.00 (1.48, 2.69)	0.10%	1.15	1.48
GPR126	1	5.67E-06	2.00 (1.48, 2.69)	0.10%	1.15	1.48
GPR126	1	5.67E-06	2.00 (1.48, 2.69)	0.10%	1.15	1.48
IDH2	1	1.20E-07	1.60 (1.34, 1.90)	<0.1%	1.15	1.45
KIAA0649	-1	2.15E-06	0.54 (0.42, 0.70)	<0.1%	1.15	1.5
LOC100128977	-1	7.62E-06	0.50 (0.37, 0.68)	0.10%	1.15	1.49
MAGEA10	1	7.79E-08	1.55 (1.32, 1.82)	<0.1%	1.15	1.43
MAGEA10	1	7.79E-08	1.55 (1.32, 1.82)	<0.1%	1.15	1.43
MARCH6	1	8.72E-06	2.14 (1.53, 2.99)	0.10%	1.15	1.47
MCART6	-1	1.04E-05	0.48 (0.35, 0.67)	0.10%	1.15	1.48
PAPD7	1	1.08E-05	2.13 (1.52, 2.99)	0.10%	1.15	1.46
PAPD7	1	1.08E-05	2.13 (1.52, 2.99)	0.10%	1.15	1.46
PAPD7	1	1.08E-05	2.13 (1.52, 2.99)	0.10%	1.15	1.46
PLD1	1	3.54E-08	1.53 (1.32, 1.78)	<0.1%	1.15	1.43
PLD1	1	3.54E-08	1.53 (1.32, 1.78)	<0.1%	1.15	1.43
RAD9B	-1	1.83E-06	0.57 (0.45, 0.72)	<0.1%	1.15	1.48
SMARCD2	1	7.24E-07	1.63 (1.34, 1.98)	<0.1%	1.15	1.45
TRPM8	1	1.83E-06	1.82 (1.42, 2.33)	<0.1%	1.15	1.48
TTF1	-1	1.08E-05	0.47 (0.33, 0.66)	0.10%	1.15	1.48
UGT2B7	1	4.60E-08	1.50 (1.29, 1.73)	<0.1%	1.15	1.41
WARS2	-1	2.69E-05	0.40 (0.26, 0.61)	0.20%	1.15	1.45
WARS2	-1	2.69E-05	0.40 (0.26, 0.61)	0.20%	1.15	1.45
ZDHHC19	1	1.05E-05	2.22 (1.56, 3.17)	0.10%	1.15	1.46
ZFR	1	1.11E-05	2.08 (1.50, 2.88)	0.10%	1.15	1.46
ANKRD17	1	2.20E-07	1.49 (1.28, 1.74)	<0.1%	1.14	1.4
ANKRD17	1	2.20E-07	1.49 (1.28, 1.74)	<0.1%	1.14	1.4
C10orf93	-1	2.49E-05	0.44 (0.30, 0.65)	0.20%	1.14	1.46
DAP	1	1.93E-05	2.05 (1.47, 2.85)	0.20%	1.14	1.45
G3BP2	1	1.38E-07	1.50 (1.29, 1.75)	<0.1%	1.14	1.4
G3BP2	1	1.38E-07	1.50 (1.29, 1.75)	<0.1%	1.14	1.4
G3BP2	1	1.38E-07	1.50 (1.29, 1.75)	<0.1%	1.14	1.4
GAN	1	2.40E-05	2.16 (1.51, 3.09)	0.20%	1.14	1.44
GSTM2	-1	1.12E-05	0.53 (0.40, 0.70)	0.10%	1.14	1.47
GSTM2	-1	1.12E-05	0.53 (0.40, 0.70)	0.10%	1.14	1.47
IGF2BP2	1	6.05E-06	1.84 (1.41, 2.40)	0.10%	1.14	1.46
IGF2BP2	1	6.05E-06	1.84 (1.41, 2.40)	0.10%	1.14	1.46
INPP5K	-1	1.47E-05	0.48 (0.35, 0.67)	0.10%	1.14	1.47
INPP5K	-1	1.47E-05	0.48 (0.35, 0.67)	0.10%	1.14	1.47
INPP5K	-1	1.47E-05	0.48 (0.35, 0.67)	0.10%	1.14	1.47
LANCL1	-1	2.01E-05	0.48 (0.34, 0.67)	0.20%	1.14	1.47
LANCL1	-1	2.01E-05	0.48 (0.34, 0.67)	0.20%	1.14	1.47

LANCL1	-1	2.01E-05	0.48 (0.34, 0.67)	0.20%	1.14	1.47
MT4	1	8.97E-10	1.35 (1.22, 1.48)	<0.1%	1.14	1.32
SCN1B	-1	1.11E-05	0.52 (0.39, 0.70)	0.10%	1.14	1.47
SCN1B	-1	1.11E-05	0.52 (0.39, 0.70)	0.10%	1.14	1.47
TXNRD1	1	9.57E-06	1.93 (1.44, 2.58)	0.10%	1.14	1.46
TXNRD1	1	9.57E-06	1.93 (1.44, 2.58)	0.10%	1.14	1.46
TXNRD1	1	9.57E-06	1.93 (1.44, 2.58)	0.10%	1.14	1.46
TXNRD1	1	9.57E-06	1.93 (1.44, 2.58)	0.10%	1.14	1.46
TXNRD1	1	9.57E-06	1.93 (1.44, 2.58)	0.10%	1.14	1.46
USO1	1	1.96E-07	1.49 (1.28, 1.74)	<0.1%	1.14	1.4
ZBED4	1	1.01E-07	1.47 (1.27, 1.69)	<0.1%	1.14	1.39
ZFP42	1	1.85E-07	1.50 (1.29, 1.75)	<0.1%	1.14	1.4
ZNF415	-1	5.33E-06	0.57 (0.44, 0.72)	0.10%	1.14	1.47
ZNF415	-1	5.33E-06	0.57 (0.44, 0.72)	0.10%	1.14	1.47
ZNF415	-1	5.33E-06	0.57 (0.44, 0.72)	0.10%	1.14	1.47
ZNF415	-1	5.33E-06	0.57 (0.44, 0.72)	0.10%	1.14	1.47
ZNF625	-1	6.20E-06	0.53 (0.40, 0.69)	0.10%	1.14	1.48
ACBD4	-1	4.09E-06	0.62 (0.51, 0.76)	0.10%	1.13	1.43
ACBD4	-1	4.09E-06	0.62 (0.51, 0.76)	0.10%	1.13	1.43
ACBD4	-1	4.09E-06	0.62 (0.51, 0.76)	0.10%	1.13	1.43
ACBD4	-1	4.09E-06	0.62 (0.51, 0.76)	0.10%	1.13	1.43
ACBD4	-1	4.09E-06	0.62 (0.51, 0.76)	0.10%	1.13	1.43
ANKRD19	-1	7.74E-06	0.56 (0.44, 0.72)	0.10%	1.13	1.46
BPTF	1	2.42E-06	1.61 (1.32, 1.96)	<0.1%	1.13	1.43
BPTF	1	2.42E-06	1.61 (1.32, 1.96)	<0.1%	1.13	1.43
C17orf49	-1	5.27E-07	0.69 (0.59, 0.79)	<0.1%	1.13	1.38
C17orf49	-1	5.27E-07	0.69 (0.59, 0.79)	<0.1%	1.13	1.38
C17orf49	-1	5.27E-07	0.69 (0.59, 0.79)	<0.1%	1.13	1.38
C2orf84	-1	3.24E-06	0.62 (0.51, 0.76)	0.10%	1.13	1.43
C3orf15	-1	5.65E-05	0.45 (0.30, 0.66)	0.40%	1.13	1.43
C6orf225	-1	3.63E-06	0.60 (0.49, 0.75)	0.10%	1.13	1.45
CCDC45	1	3.36E-06	1.62 (1.32, 1.99)	0.10%	1.13	1.43
CDK20	-1	0.000014394	0.52 (0.38, 0.70)	0.10%	1.13	1.47
CDK20	-1	0.000014394	0.52 (0.38, 0.70)	0.10%	1.13	1.47
CDK20	-1	0.000014394	0.52 (0.38, 0.70)	0.10%	1.13	1.47
CDK20	-1	0.000014394	0.52 (0.38, 0.70)	0.10%	1.13	1.47
CDK20	-1	0.000014394	0.52 (0.38, 0.70)	0.10%	1.13	1.47
COG4	1	2.32E-05	1.94 (1.43, 2.64)	0.20%	1.13	1.44
COG4	1	2.32E-05	1.94 (1.43, 2.64)	0.20%	1.13	1.44
CXCL13	1	1.08E-05	1.84 (1.40, 2.41)	0.10%	1.13	1.45
FBP1	-1	2.23E-05	0.53 (0.40, 0.71)	0.20%	1.13	1.45
FBP1	-1	2.23E-05	0.53 (0.40, 0.71)	0.20%	1.13	1.45

FRMPD2	-1	7.60E-06	0.57 (0.45, 0.73)	0.10%	1.13	1.46
FRMPD2	-1	7.60E-06	0.57 (0.45, 0.73)	0.10%	1.13	1.46
GUCA2B	1	4.56E-06	1.63 (1.32, 2.00)	0.10%	1.13	1.42
LALBA	1	1.41E-05	1.76 (1.36, 2.28)	0.10%	1.13	1.43
LOC100131366	1	7.36E-06	1.70 (1.35, 2.14)	0.10%	1.13	1.43
LRIG3	1	7.68E-06	1.70 (1.35, 2.15)	0.10%	1.13	1.43
LRIG3	1	7.68E-06	1.70 (1.35, 2.15)	0.10%	1.13	1.43
OLIG2	1	2.36E-05	2.09 (1.48, 2.94)	0.20%	1.13	1.44
PADI3	1	1.40E-05	1.80 (1.38, 2.35)	0.10%	1.13	1.44
PRICKLE4	-1	1.17E-07	0.69 (0.60, 0.79)	<0.1%	1.13	1.38
RNF145	1	1.10E-05	1.80 (1.38, 2.33)	0.10%	1.13	1.44
RNF145	1	1.10E-05	1.80 (1.38, 2.33)	0.10%	1.13	1.44
RNF145	1	1.10E-05	1.80 (1.38, 2.33)	0.10%	1.13	1.44
RNF145	1	1.10E-05	1.80 (1.38, 2.33)	0.10%	1.13	1.44
RNF145	1	1.10E-05	1.80 (1.38, 2.33)	0.10%	1.13	1.44
SNRPN	-1	7.19E-06	0.57 (0.45, 0.73)	0.10%	1.13	1.46
SNRPN	-1	7.19E-06	0.57 (0.45, 0.73)	0.10%	1.13	1.46
SNRPN	-1	7.19E-06	0.57 (0.45, 0.73)	0.10%	1.13	1.46
SNRPN	-1	7.19E-06	0.57 (0.45, 0.73)	0.10%	1.13	1.46
SNRPN	-1	7.19E-06	0.57 (0.45, 0.73)	0.10%	1.13	1.46
SUSD3	-1	1.88E-05	0.50 (0.37, 0.69)	0.20%	1.13	1.46
TBX10	1	3.65E-06	1.61 (1.32, 1.98)	0.10%	1.13	1.42
TRAIP	1	4.20E-05	2.16 (1.49, 3.12)	0.30%	1.13	1.42
UGT2B10	1	1.95E-07	1.47 (1.27, 1.70)	<0.1%	1.13	1.38
UGT2B10	1	1.95E-07	1.47 (1.27, 1.70)	<0.1%	1.13	1.38
UGT2B10	1	1.95E-07	1.47 (1.27, 1.70)	<0.1%	1.13	1.38
UGT2B10	1	1.95E-07	1.47 (1.27, 1.70)	<0.1%	1.13	1.38
ZNF214	-1	6.93E-06	0.57 (0.44, 0.73)	0.10%	1.13	1.46
ZNF835	-1	4.54E-05	0.45 (0.31, 0.66)	0.30%	1.13	1.44
ATAD2B	1	0.000010614	1.61 (1.30, 1.99)	0.10%	1.12	1.41
C10orf18	1	1.23E-05	1.61 (1.30, 2.00)	0.10%	1.12	1.41
C14orf79	-1	5.74E-05	0.51 (0.37, 0.71)	0.40%	1.12	1.43
C9orf27	1	3.70E-06	1.51 (1.27, 1.79)	0.10%	1.12	1.38
CALU	1	1.63E-05	1.75 (1.35, 2.25)	0.20%	1.12	1.43
CALU	1	1.63E-05	1.75 (1.35, 2.25)	0.20%	1.12	1.43
CALU	1	1.63E-05	1.75 (1.35, 2.25)	0.20%	1.12	1.43
CALU	1	1.63E-05	1.75 (1.35, 2.25)	0.20%	1.12	1.43
CALU	1	1.63E-05	1.75 (1.35, 2.25)	0.20%	1.12	1.43
CALU	1	1.63E-05	1.75 (1.35, 2.25)	0.20%	1.12	1.43
CARD18	1	4.65E-06	1.54 (1.28, 1.86)	0.10%	1.12	1.39
CCL2	-1	3.89E-05	0.53 (0.39, 0.72)	0.30%	1.12	1.44
CELF6	-1	7.61E-05	0.50 (0.35, 0.70)	0.50%	1.12	1.43

CELF6	-1	7.61E-05	0.50 (0.35, 0.70)	0.50%	1.12	1.43
CELF6	-1	7.61E-05	0.50 (0.35, 0.70)	0.50%	1.12	1.43
CREBL2	-1	2.02E-05	0.61 (0.48, 0.76)	0.20%	1.12	1.42
CSHL1	1	1.03E-06	1.42 (1.23, 1.63)	<0.1%	1.12	1.35
CSHL1	1	1.03E-06	1.42 (1.23, 1.63)	<0.1%	1.12	1.35
CSHL1	1	1.03E-06	1.42 (1.23, 1.63)	<0.1%	1.12	1.35
CSHL1	1	1.03E-06	1.42 (1.23, 1.63)	<0.1%	1.12	1.35
CXorf64	1	1.85E-06	1.49 (1.26, 1.75)	<0.1%	1.12	1.38
DCDC5	-1	0.000050342	0.49 (0.35, 0.69)	0.30%	1.12	1.44
DDX42	1	3.64E-06	1.54 (1.28, 1.85)	0.10%	1.12	1.4
DDX42	1	3.64E-06	1.54 (1.28, 1.85)	0.10%	1.12	1.4
DLG1	1	1.70E-05	1.74 (1.35, 2.24)	0.20%	1.12	1.43
DLG1	1	1.70E-05	1.74 (1.35, 2.24)	0.20%	1.12	1.43
DSCR10	1	9.45E-07	1.48 (1.26, 1.73)	<0.1%	1.12	1.38
HIST1H2BK	1	6.59E-05	2.00 (1.42, 2.82)	0.40%	1.12	1.41
HRASLS5	-1	2.85E-05	0.53 (0.39, 0.71)	0.20%	1.12	1.45
HRASLS5	-1	2.85E-05	0.53 (0.39, 0.71)	0.20%	1.12	1.45
HRASLS5	-1	2.85E-05	0.53 (0.39, 0.71)	0.20%	1.12	1.45
INSIG1	1	6.08E-05	1.98 (1.42, 2.76)	0.40%	1.12	1.41
INSIG1	1	6.08E-05	1.98 (1.42, 2.76)	0.40%	1.12	1.41
INSIG1	1	6.08E-05	1.98 (1.42, 2.76)	0.40%	1.12	1.41
IRF2BP2	1	4.85E-05	2.06 (1.45, 2.92)	0.30%	1.12	1.42
IRF2BP2	1	4.85E-05	2.06 (1.45, 2.92)	0.30%	1.12	1.42
ITLN2	1	5.74E-05	1.91 (1.40, 2.63)	0.40%	1.12	1.41
KLHL23	-1	3.95E-05	0.51 (0.37, 0.70)	0.30%	1.12	1.44
KLHL23	-1	3.95E-05	0.51 (0.37, 0.70)	0.30%	1.12	1.44
LCE1C	1	3.13E-06	1.48 (1.26, 1.74)	0.10%	1.12	1.37
MTCH1	1	1.38E-06	1.45 (1.24, 1.68)	<0.1%	1.12	1.36
MYOF	-1	1.35E-05	0.62 (0.50, 0.77)	0.10%	1.12	1.42
MYOF	-1	1.35E-05	0.62 (0.50, 0.77)	0.10%	1.12	1.42
NHSL1	1	3.34E-05	1.87 (1.39, 2.51)	0.30%	1.12	1.43
NHSL1	1	3.34E-05	1.87 (1.39, 2.51)	0.30%	1.12	1.43
NRM	-1	5.27E-05	0.52 (0.38, 0.71)	0.40%	1.12	1.43
NSD1	1	1.13E-06	1.49 (1.27, 1.74)	<0.1%	1.12	1.38
NSD1	1	1.13E-06	1.49 (1.27, 1.74)	<0.1%	1.12	1.38
NUP54	1	1.51E-06	1.47 (1.26, 1.73)	<0.1%	1.12	1.37
PDXDC2P	1	6.41E-05	1.94 (1.40, 2.69)	0.40%	1.12	1.41
PIR	1	4.31E-05	1.96 (1.42, 2.70)	0.30%	1.12	1.42
PIR	1	4.31E-05	1.96 (1.42, 2.70)	0.30%	1.12	1.42
PLEKHM1P	1	7.39E-06	1.54 (1.28, 1.86)	0.10%	1.12	1.39
PRRC1	1	6.79E-05	2.10 (1.46, 3.02)	0.40%	1.12	1.41
PSMG3	1	0.000078564	2.30 (1.52, 3.48)	0.50%	1.12	1.4

PSMG3	1	0.000078564	2.30 (1.52, 3.48)	0.50%	1.12	1.4
PYY	-1	5.43E-05	0.49 (0.34, 0.69)	0.40%	1.12	1.44
RAX	1	3.33E-05	1.75 (1.35, 2.29)	0.30%	1.12	1.42
RTN1	-1	5.29E-05	0.47 (0.33, 0.68)	0.40%	1.12	1.44
RTN1	-1	5.29E-05	0.47 (0.33, 0.68)	0.40%	1.12	1.44
RTN1	-1	5.29E-05	0.47 (0.33, 0.68)	0.40%	1.12	1.44
SLC35D2	-1	6.31E-06	0.62 (0.51, 0.77)	0.10%	1.12	1.42
SLC7A5	1	3.32E-05	1.88 (1.40, 2.53)	0.30%	1.12	1.43
SQSTM1	1	2.49E-05	1.78 (1.36, 2.33)	0.20%	1.12	1.43
SQSTM1	1	2.49E-05	1.78 (1.36, 2.33)	0.20%	1.12	1.43
SQSTM1	1	2.49E-05	1.78 (1.36, 2.33)	0.20%	1.12	1.43
TBX4	1	3.19E-05	1.81 (1.37, 2.39)	0.30%	1.12	1.42
TKT	1	4.20E-05	1.81 (1.36, 2.41)	0.30%	1.12	1.42
TKT	1	4.20E-05	1.81 (1.36, 2.41)	0.30%	1.12	1.42
TMEM26	-1	2.62E-05	0.55 (0.41, 0.73)	0.20%	1.12	1.44
TMEM88	-1	0.000067009	0.50 (0.36, 0.70)	0.40%	1.12	1.43
TMEM88	-1	0.000067009	0.50 (0.36, 0.70)	0.40%	1.12	1.43
TMEM88	-1	0.000067009	0.50 (0.36, 0.70)	0.40%	1.12	1.43
USP8	1	3.60E-09	1.29 (1.18, 1.40)	<0.1%	1.12	1.27
USP8	1	3.60E-09	1.29 (1.18, 1.40)	<0.1%	1.12	1.27
USP8	1	3.60E-09	1.29 (1.18, 1.40)	<0.1%	1.12	1.27
WDR70	1	4.01E-05	1.98 (1.43, 2.73)	0.30%	1.12	1.42
WDR78	-1	1.82E-05	0.58 (0.45, 0.74)	0.20%	1.12	1.44
WDR78	-1	1.82E-05	0.58 (0.45, 0.74)	0.20%	1.12	1.44
ZNF433	-1	4.82E-06	0.63 (0.52, 0.77)	0.10%	1.12	1.42
ZNF563	-1	1.21E-05	0.59 (0.47, 0.75)	0.10%	1.12	1.44
ZNF788	-1	2.72E-05	0.59 (0.46, 0.75)	0.20%	1.12	1.43
ZNF836	-1	4.08E-05	0.51 (0.37, 0.71)	0.30%	1.12	1.44
AK8	-1	5.55E-05	0.54 (0.40, 0.73)	0.40%	1.11	1.43
C11orf70	-1	0.000056385	0.59 (0.46, 0.76)	0.40%	1.11	1.41
C11orf70	-1	0.000056385	0.59 (0.46, 0.76)	0.40%	1.11	1.41
C15orf23	1	0.000143369	2.27 (1.49, 3.46)	0.70%	1.11	1.38
C15orf23	1	0.000143369	2.27 (1.49, 3.46)	0.70%	1.11	1.38
C15orf23	1	0.000143369	2.27 (1.49, 3.46)	0.70%	1.11	1.38
C16orf52	-1	8.04E-05	0.54 (0.40, 0.73)	0.50%	1.11	1.42
C1orf168	-1	0.000132664	0.50 (0.35, 0.71)	0.70%	1.11	1.41
C20orf26	-1	0.000125264	0.46 (0.31, 0.69)	0.60%	1.11	1.41
C20orf26	-1	0.000125264	0.46 (0.31, 0.69)	0.60%	1.11	1.41
CX3CR1	-1	6.03E-05	0.54 (0.40, 0.73)	0.40%	1.11	1.43
CX3CR1	-1	6.03E-05	0.54 (0.40, 0.73)	0.40%	1.11	1.43
CX3CR1	-1	6.03E-05	0.54 (0.40, 0.73)	0.40%	1.11	1.43
CX3CR1	-1	6.03E-05	0.54 (0.40, 0.73)	0.40%	1.11	1.43

DAB1	-1	0.000102041	0.52 (0.38, 0.73)	0.60%	1.11	1.42
DMRTC2	1	5.88E-05	1.70 (1.31, 2.20)	0.40%	1.11	1.4
FAM98A	1	0.000152723	2.15 (1.45, 3.20)	0.70%	1.11	1.38
FAM9C	1	7.08E-07	1.39 (1.22, 1.58)	<0.1%	1.11	1.33
FBXO15	-1	0.00014207	0.49 (0.34, 0.71)	0.70%	1.11	1.41
FBXO15	-1	0.00014207	0.49 (0.34, 0.71)	0.70%	1.11	1.41
GABPB1	1	3.07E-07	1.32 (1.19, 1.47)	<0.1%	1.11	1.29
GABPB1	1	3.07E-07	1.32 (1.19, 1.47)	<0.1%	1.11	1.29
GABPB1	1	3.07E-07	1.32 (1.19, 1.47)	<0.1%	1.11	1.29
GABPB1	1	3.07E-07	1.32 (1.19, 1.47)	<0.1%	1.11	1.29
GABPB1	1	3.07E-07	1.32 (1.19, 1.47)	<0.1%	1.11	1.29
GARS	1	0.000025817	1.62 (1.29, 2.03)	0.20%	1.11	1.4
GLRA1	1	4.64E-05	1.66 (1.30, 2.12)	0.30%	1.11	1.4
GLRA1	1	4.64E-05	1.66 (1.30, 2.12)	0.30%	1.11	1.4
GOLPH3	1	0.000116993	1.95 (1.39, 2.74)	0.60%	1.11	1.39
GP9	1	1.93E-07	1.34 (1.20, 1.49)	<0.1%	1.11	1.3
GPRIN1	1	9.56E-05	2.00 (1.41, 2.84)	0.50%	1.11	1.4
IGFBP3	1	0.000195883	2.33 (1.49, 3.64)	0.90%	1.11	1.36
IGFBP3	1	0.000195883	2.33 (1.49, 3.64)	0.90%	1.11	1.36
KCNJ5	-1	9.79E-05	0.50 (0.35, 0.71)	0.50%	1.11	1.42
KLHL5	-1	0.000134571	0.49 (0.34, 0.71)	0.70%	1.11	1.41
KLHL5	-1	0.000134571	0.49 (0.34, 0.71)	0.70%	1.11	1.41
KLHL5	-1	0.000134571	0.49 (0.34, 0.71)	0.70%	1.11	1.41
KLHL5	-1	0.000134571	0.49 (0.34, 0.71)	0.70%	1.11	1.41
KRT27	1	1.79E-05	1.54 (1.27, 1.88)	0.20%	1.11	1.38
LMAN1L	1	0.000147619	2.05 (1.41, 2.96)	0.70%	1.11	1.38
LOC100271722	-1	2.89E-05	0.64 (0.52, 0.79)	0.20%	1.11	1.39
LYL1	-1	4.58E-05	0.58 (0.45, 0.75)	0.30%	1.11	1.42
MAD1L1	1	0.000102969	1.87 (1.36, 2.56)	0.60%	1.11	1.4
MAD1L1	1	0.000102969	1.87 (1.36, 2.56)	0.60%	1.11	1.4
MAD1L1	1	0.000102969	1.87 (1.36, 2.56)	0.60%	1.11	1.4
MAPK6	1	1.97E-07	1.33 (1.20, 1.48)	<0.1%	1.11	1.3
MRPS26	-1	6.20E-06	0.70 (0.60, 0.82)	0.10%	1.11	1.35
NAGS	-1	0.00010598	0.50 (0.36, 0.71)	0.60%	1.11	1.42
OTP	1	3.84E-05	1.62 (1.29, 2.05)	0.30%	1.11	1.39
PINK1	-1	7.63E-05	0.53 (0.39, 0.73)	0.50%	1.11	1.42
RESP18	1	6.15E-06	1.46 (1.24, 1.72)	0.10%	1.11	1.36
SLC22A6	1	5.02E-05	1.82 (1.36, 2.42)	0.30%	1.11	1.41
SLC22A6	1	5.02E-05	1.82 (1.36, 2.42)	0.30%	1.11	1.41
SLC22A6	1	5.02E-05	1.82 (1.36, 2.42)	0.30%	1.11	1.41
SLC22A6	1	5.02E-05	1.82 (1.36, 2.42)	0.30%	1.11	1.41
SPATC1	1	0.000142376	2.22 (1.47, 3.36)	0.70%	1.11	1.38

SPATC1	1	0.000142376	2.22 (1.47, 3.36)	0.70%	1.11	1.38
TBX19	1	5.35E-05	1.76 (1.34, 2.32)	0.40%	1.11	1.41
TNFRSF14	-1	0.000166546	0.47 (0.31, 0.69)	0.80%	1.11	1.4
TRPM7	1	7.91E-09	1.27 (1.17, 1.38)	<0.1%	1.11	1.25
TSC22D1	1	0.000124731	2.10 (1.44, 3.07)	0.60%	1.11	1.39
TSC22D1	1	0.000124731	2.10 (1.44, 3.07)	0.60%	1.11	1.39
WWP2	1	2.60E-05	1.60 (1.29, 2.00)	0.20%	1.11	1.39
WWP2	1	2.60E-05	1.60 (1.29, 2.00)	0.20%	1.11	1.39
WWP2	1	2.60E-05	1.60 (1.29, 2.00)	0.20%	1.11	1.39
ZNF136	-1	0.000105463	0.49 (0.35, 0.71)	0.60%	1.11	1.42
ZNF175	-1	5.57E-05	0.56 (0.42, 0.74)	0.40%	1.11	1.42
ZNF396	-1	2.46E-05	0.61 (0.48, 0.76)	0.20%	1.11	1.42
ZNF429	-1	0.000110212	0.51 (0.36, 0.72)	0.60%	1.11	1.41
ZNF491	-1	1.25E-05	0.66 (0.55, 0.80)	0.10%	1.11	1.38
ZNF721	-1	6.35E-05	0.57 (0.43, 0.75)	0.40%	1.11	1.42
ZNF79	-1	1.31E-05	0.64 (0.53, 0.78)	0.10%	1.11	1.4
ACSBG2	-1	0.000112734	0.58 (0.44, 0.76)	0.60%	1.1	1.4
ADCK5	1	0.000108958	1.77 (1.33, 2.37)	0.60%	1.1	1.39
ANKS6	1	0.000189078	1.98 (1.38, 2.83)	0.90%	1.1	1.38
ARMC9	-1	4.50E-05	0.62 (0.49, 0.78)	0.30%	1.1	1.4
ATP1A3	1	0.000078271	1.65 (1.29, 2.12)	0.50%	1.1	1.38
ATP7B	-1	8.98E-05	0.59 (0.45, 0.77)	0.50%	1.1	1.4
ATP7B	-1	8.98E-05	0.59 (0.45, 0.77)	0.50%	1.1	1.4
BGN	-1	4.71E-05	0.65 (0.53, 0.80)	0.30%	1.1	1.38
C1orf146	-1	7.80E-05	0.59 (0.45, 0.76)	0.50%	1.1	1.41
CFHR5	1	0.000144896	1.85 (1.35, 2.54)	0.70%	1.1	1.39
CREB3	-1	4.27E-05	0.64 (0.52, 0.79)	0.30%	1.1	1.38
CROCC	-1	0.000170204	0.52 (0.37, 0.73)	0.80%	1.1	1.4
DNAH7	-1	9.52E-05	0.56 (0.41, 0.75)	0.50%	1.1	1.41
DSCR4	1	5.00E-05	1.64 (1.29, 2.09)	0.30%	1.1	1.39
EGLN1	1	9.70E-05	1.80 (1.34, 2.41)	0.50%	1.1	1.39
GGCT	1	0.000050126	1.56 (1.26, 1.94)	0.30%	1.1	1.37
GGCT	1	0.000050126	1.56 (1.26, 1.94)	0.30%	1.1	1.37
GGCT	1	0.000050126	1.56 (1.26, 1.94)	0.30%	1.1	1.37
GGCT	1	0.000050126	1.56 (1.26, 1.94)	0.30%	1.1	1.37
GGCT	1	0.000050126	1.56 (1.26, 1.94)	0.30%	1.1	1.37
GRHL2	1	0.000165793	2.03 (1.40, 2.93)	0.80%	1.1	1.38
GRIK4	-1	0.000250003	0.43 (0.27, 0.67)	1.00%	1.1	1.38
HIP1	-1	4.88E-05	0.63 (0.50, 0.79)	0.30%	1.1	1.39
INCENP	1	0.000223059	2.03 (1.39, 2.96)	0.90%	1.1	1.37
INCENP	1	0.000223059	2.03 (1.39, 2.96)	0.90%	1.1	1.37
KCNH7	1	1.43E-05	1.45 (1.23, 1.72)	0.10%	1.1	1.35

KCNH7	1	1.43E-05	1.45 (1.23, 1.72)	0.10%	1.1	1.35
KMO	1	0.000124999	1.75 (1.32, 2.33)	0.60%	1.1	1.39
LCE3E	1	1.98E-06	1.35 (1.19, 1.53)	<0.1%	1.1	1.3
LOC100130950	-1	0.000224114	0.48 (0.33, 0.71)	1.00%	1.1	1.39
LYPD6B	-1	0.000130737	0.56 (0.41, 0.75)	0.70%	1.1	1.4
MAGEA5	1	2.64E-05	1.50 (1.24, 1.81)	0.20%	1.1	1.36
MYO1C	-1	0.000148018	0.52 (0.37, 0.73)	0.70%	1.1	1.41
MYO1C	-1	0.000148018	0.52 (0.37, 0.73)	0.70%	1.1	1.41
MYO1C	-1	0.000148018	0.52 (0.37, 0.73)	0.70%	1.1	1.41
NDRG1	1	0.00006342	1.60 (1.27, 2.02)	0.40%	1.1	1.38
NDRG1	1	0.00006342	1.60 (1.27, 2.02)	0.40%	1.1	1.38
ONECUT2	1	0.000116006	1.87 (1.36, 2.57)	0.60%	1.1	1.39
PAIP1	1	3.95E-05	1.61 (1.28, 2.02)	0.30%	1.1	1.39
PAIP1	1	3.95E-05	1.61 (1.28, 2.02)	0.30%	1.1	1.39
PAIP1	1	3.95E-05	1.61 (1.28, 2.02)	0.30%	1.1	1.39
RAPGEF5	1	7.22E-05	1.71 (1.31, 2.22)	0.40%	1.1	1.39
RNASE2	1	1.62E-05	1.48 (1.24, 1.76)	0.20%	1.1	1.36
SCARB2	1	2.26E-05	1.47 (1.23, 1.77)	0.20%	1.1	1.35
SEC14L3	1	1.41E-05	1.47 (1.23, 1.74)	0.10%	1.1	1.35
SELO	1	3.85E-06	1.37 (1.20, 1.57)	0.10%	1.1	1.31
SLC15A1	1	0.000192161	2.05 (1.41, 2.99)	0.90%	1.1	1.38
SLITRK5	1	0.000119475	1.86 (1.35, 2.55)	0.60%	1.1	1.39
SPINK5	1	0.00014485	1.79 (1.33, 2.42)	0.70%	1.1	1.38
SPINK5	1	0.00014485	1.79 (1.33, 2.42)	0.70%	1.1	1.38
SPINK5	1	0.00014485	1.79 (1.33, 2.42)	0.70%	1.1	1.38
TMEM164	-1	0.000184554	0.51 (0.36, 0.72)	0.80%	1.1	1.4
TMEM164	-1	0.000184554	0.51 (0.36, 0.72)	0.80%	1.1	1.4
TMOD3	1	4.02E-08	1.27 (1.17, 1.38)	<0.1%	1.1	1.25
TRIM32	-1	0.000162106	0.53 (0.38, 0.74)	0.80%	1.1	1.4
TRIM32	-1	0.000162106	0.53 (0.38, 0.74)	0.80%	1.1	1.4
TRIP13	1	0.00024036	2.25 (1.46, 3.47)	1.00%	1.1	1.36
TRIP13	1	0.00024036	2.25 (1.46, 3.47)	1.00%	1.1	1.36
ZNF347	-1	0.000123774	0.55 (0.40, 0.74)	0.60%	1.1	1.41
ZNF347	-1	0.000123774	0.55 (0.40, 0.74)	0.60%	1.1	1.41
ZNF347	-1	0.000123774	0.55 (0.40, 0.74)	0.60%	1.1	1.41
BCAR3	-1	0.000312727	0.49 (0.33, 0.72)	1.20%	1.09	1.38
BCL2	-1	0.000271683	0.53 (0.38, 0.75)	1.10%	1.09	1.39
BCL2	-1	0.000271683	0.53 (0.38, 0.75)	1.10%	1.09	1.39
BCL7C	-1	0.00023086	0.53 (0.38, 0.74)	1.00%	1.09	1.39
BICD2	-1	0.000133159	0.57 (0.43, 0.76)	0.70%	1.09	1.4
BICD2	-1	0.000133159	0.57 (0.43, 0.76)	0.70%	1.09	1.4
C18orf54	1	0.000202177	1.74 (1.30, 2.34)	0.90%	1.09	1.37

CA10	1	1.34E-05	1.37 (1.19, 1.57)	0.10%	1.09	1.3
CA10	1	1.34E-05	1.37 (1.19, 1.57)	0.10%	1.09	1.3
CA10	1	1.34E-05	1.37 (1.19, 1.57)	0.10%	1.09	1.3
CLIC6	-1	0.000542023	0.38 (0.22, 0.66)	1.70%	1.09	1.33
EFCAB6	-1	0.000168016	0.59 (0.44, 0.77)	0.80%	1.09	1.39
EFCAB6	-1	0.000168016	0.59 (0.44, 0.77)	0.80%	1.09	1.39
EIF2B2	-1	0.000117388	0.59 (0.45, 0.77)	0.60%	1.09	1.4
ENO2	-1	0.000134221	0.58 (0.44, 0.77)	0.70%	1.09	1.4
FAM66C	-1	0.000163471	0.59 (0.45, 0.78)	0.80%	1.09	1.39
FANK1	-1	0.000257189	0.54 (0.39, 0.75)	1.00%	1.09	1.39
FGFRL1	-1	0.000111716	0.60 (0.46, 0.78)	0.60%	1.09	1.39
FGFRL1	-1	0.000111716	0.60 (0.46, 0.78)	0.60%	1.09	1.39
FGFRL1	-1	0.000111716	0.60 (0.46, 0.78)	0.60%	1.09	1.39
FOXH1	1	2.16E-05	1.39 (1.20, 1.62)	0.20%	1.09	1.32
HIF1A	1	0.000181495	1.79 (1.32, 2.43)	0.80%	1.09	1.38
HIF1A	1	0.000181495	1.79 (1.32, 2.43)	0.80%	1.09	1.38
HJURP	1	0.000352551	2.12 (1.40, 3.20)	1.30%	1.09	1.35
LOC642345	1	0.000195592	1.75 (1.30, 2.35)	0.90%	1.09	1.37
LOX	1	0.000192189	1.82 (1.33, 2.50)	0.90%	1.09	1.38
LOX	1	0.000192189	1.82 (1.33, 2.50)	0.90%	1.09	1.38
LRIT2	1	2.01E-06	1.31 (1.17, 1.46)	<0.1%	1.09	1.27
MYF5	1	7.41E-06	1.34 (1.18, 1.52)	0.10%	1.09	1.29
MYH2	-1	7.14E-05	0.63 (0.51, 0.79)	0.40%	1.09	1.38
MYH2	-1	7.14E-05	0.63 (0.51, 0.79)	0.40%	1.09	1.38
NAA35	-1	0.000347317	0.48 (0.32, 0.72)	1.30%	1.09	1.38
NCRNA00221	1	3.23E-05	1.42 (1.20, 1.67)	0.30%	1.09	1.33
NINJ1	-1	0.000222676	0.54 (0.38, 0.75)	0.90%	1.09	1.39
NPY1R	-1	0.000241391	0.51 (0.35, 0.73)	1.00%	1.09	1.39
NR1I2	-1	0.000242263	0.55 (0.40, 0.75)	1.00%	1.09	1.39
NR1I2	-1	0.000242263	0.55 (0.40, 0.75)	1.00%	1.09	1.39
NR1I2	-1	0.000242263	0.55 (0.40, 0.75)	1.00%	1.09	1.39
NUP205	1	0.000108468	1.57 (1.25, 1.96)	0.60%	1.09	1.36
RAI2	-1	0.000402941	0.44 (0.28, 0.70)	1.40%	1.09	1.36
RAI2	-1	0.000402941	0.44 (0.28, 0.70)	1.40%	1.09	1.36
RAI2	-1	0.000402941	0.44 (0.28, 0.70)	1.40%	1.09	1.36
RAI2	-1	0.000402941	0.44 (0.28, 0.70)	1.40%	1.09	1.36
RAI2	-1	0.000402941	0.44 (0.28, 0.70)	1.40%	1.09	1.36
RAI2	-1	0.000402941	0.44 (0.28, 0.70)	1.40%	1.09	1.36
RDH10	1	0.000149274	1.79 (1.33, 2.42)	0.70%	1.09	1.38
RP1-177G6-2	1	2.00E-06	1.29 (1.16, 1.43)	<0.1%	1.09	1.26
RP1-177G6-2	1	2.00E-06	1.29 (1.16, 1.43)	<0.1%	1.09	1.26
SCD	1	0.000258891	2.04 (1.39, 2.99)	1.00%	1.09	1.37

SREBF2	1	0.000116715	1.66 (1.28, 2.15)	0.60%	1.09	1.38
TCEA3	-1	0.000146171	0.60 (0.46, 0.78)	0.70%	1.09	1.39
TROAP	1	0.000469135	2.65 (1.53, 4.57)	1.60%	1.09	1.31
TROAP	1	0.000469135	2.65 (1.53, 4.57)	1.60%	1.09	1.31
UIMC1	1	4.35E-05	1.47 (1.22, 1.77)	0.30%	1.09	1.34
UIMC1	1	4.35E-05	1.47 (1.22, 1.77)	0.30%	1.09	1.34
UIMC1	1	4.35E-05	1.47 (1.22, 1.77)	0.30%	1.09	1.34
XPA	-1	0.000185424	0.57 (0.43, 0.77)	0.80%	1.09	1.39
XPA	-1	0.000185424	0.57 (0.43, 0.77)	0.80%	1.09	1.39
YWHAZ	1	0.000084608	1.54 (1.24, 1.91)	0.50%	1.09	1.36
YWHAZ	1	0.000084608	1.54 (1.24, 1.91)	0.50%	1.09	1.36
YWHAZ	1	0.000084608	1.54 (1.24, 1.91)	0.50%	1.09	1.36
YWHAZ	1	0.000084608	1.54 (1.24, 1.91)	0.50%	1.09	1.36
YWHAZ	1	0.000084608	1.54 (1.24, 1.91)	0.50%	1.09	1.36
YWHAZ	1	0.000084608	1.54 (1.24, 1.91)	0.50%	1.09	1.36
ZNF626	-1	0.000106466	0.61 (0.48, 0.78)	0.60%	1.09	1.39
ZNF626	-1	0.000106466	0.61 (0.48, 0.78)	0.60%	1.09	1.39
ZNF709	-1	0.000178037	0.56 (0.41, 0.76)	0.80%	1.09	1.4
ADHFE1	-1	0.000429195	0.51 (0.35, 0.74)	1.50%	1.08	1.37
AP1G1	1	0.000239608	1.74 (1.29, 2.33)	1.00%	1.08	1.37
AP1G1	1	0.000239608	1.74 (1.29, 2.33)	1.00%	1.08	1.37
AP4E1	1	6.06E-06	1.28 (1.15, 1.42)	0.10%	1.08	1.25
BRD7	1	0.000271783	1.72 (1.29, 2.31)	1.10%	1.08	1.36
BRD7	1	0.000271783	1.72 (1.29, 2.31)	1.10%	1.08	1.36
C11orf24	1	0.000366903	1.84 (1.32, 2.57)	1.30%	1.08	1.36
C11orf40	1	0.00012651	1.53 (1.23, 1.91)	0.60%	1.08	1.35
C15orf42	1	0.000366951	1.89 (1.33, 2.68)	1.30%	1.08	1.36
C17orf68	-1	0.000267187	0.55 (0.40, 0.76)	1.10%	1.08	1.39
C17orf85	-1	0.000408898	0.49 (0.33, 0.73)	1.40%	1.08	1.37
C17orf85	-1	0.000408898	0.49 (0.33, 0.73)	1.40%	1.08	1.37
C18orf26	1	0.000269333	1.73 (1.29, 2.33)	1.10%	1.08	1.36
C2orf34	1	0.000480591	2.01 (1.36, 2.96)	1.60%	1.08	1.35
CALHM2	-1	0.000105504	0.65 (0.53, 0.81)	0.60%	1.08	1.36
CALHM2	-1	0.000105504	0.65 (0.53, 0.81)	0.60%	1.08	1.36
CNGB3	1	0.000314415	1.85 (1.32, 2.58)	1.20%	1.08	1.36
FLJ21408	-1	0.00017901	0.61 (0.47, 0.79)	0.80%	1.08	1.38
GALK2	1	0.000248814	1.80 (1.31, 2.47)	1.00%	1.08	1.37
GALK2	1	0.000248814	1.80 (1.31, 2.47)	1.00%	1.08	1.37
GNB2L1	1	0.000244751	1.77 (1.30, 2.40)	1.00%	1.08	1.37
HAUS1	-1	0.000455791	0.46 (0.30, 0.71)	1.50%	1.08	1.36
HAUS1	-1	0.000455791	0.46 (0.30, 0.71)	1.50%	1.08	1.36
IL17F	1	7.09E-05	1.42 (1.19, 1.69)	0.40%	1.08	1.32

KIAA0174	1	0.000369657	1.91 (1.34, 2.73)	1.30%	1.08	1.36
KLF3	1	0.000371138	1.81 (1.31, 2.52)	1.30%	1.08	1.36
LDLRAD3	-1	0.00028695	0.55 (0.39, 0.76)	1.10%	1.08	1.38
LOC100302640	-1	0.000386012	0.50 (0.35, 0.74)	1.40%	1.08	1.38
MAP3K14	-1	0.000279615	0.55 (0.40, 0.76)	1.10%	1.08	1.38
MVP	-1	0.000337882	0.55 (0.40, 0.76)	1.20%	1.08	1.38
MVP	-1	0.000337882	0.55 (0.40, 0.76)	1.20%	1.08	1.38
NEUROD2	1	8.72E-05	1.49 (1.22, 1.82)	0.50%	1.08	1.34
NFXL1	1	9.20E-05	1.51 (1.23, 1.86)	0.50%	1.08	1.35
NXF5	-1	0.000312889	0.54 (0.39, 0.76)	1.20%	1.08	1.38
NXF5	-1	0.000312889	0.54 (0.39, 0.76)	1.20%	1.08	1.38
PABPN1L	1	7.99E-05	1.46 (1.21, 1.76)	0.50%	1.08	1.33
PACSIN2	1	0.000313177	1.80 (1.31, 2.48)	1.20%	1.08	1.36
PACSIN2	1	0.000313177	1.80 (1.31, 2.48)	1.20%	1.08	1.36
PACSIN2	1	0.000313177	1.80 (1.31, 2.48)	1.20%	1.08	1.36
PLCD3	-1	0.00020193	0.63 (0.49, 0.80)	0.90%	1.08	1.37
PRSS41	1	5.10E-05	1.45 (1.21, 1.73)	0.30%	1.08	1.33
RGPD2	1	0.000329641	1.83 (1.32, 2.55)	1.20%	1.08	1.36
RGPD2	1	0.000329641	1.83 (1.32, 2.55)	1.20%	1.08	1.36
RIPK4	1	0.000629791	2.40 (1.45, 3.96)	1.80%	1.08	1.31
RPF1	-1	0.000340725	0.52 (0.36, 0.74)	1.20%	1.08	1.38
SLCO6A1	1	0.000282574	1.72 (1.28, 2.31)	1.10%	1.08	1.36
SPTAN1	-1	0.000302919	0.55 (0.40, 0.76)	1.20%	1.08	1.38
SPTAN1	-1	0.000302919	0.55 (0.40, 0.76)	1.20%	1.08	1.38
SPTAN1	-1	0.000302919	0.55 (0.40, 0.76)	1.20%	1.08	1.38
ST8SIA3	1	3.00E-07	1.24 (1.14, 1.34)	<0.1%	1.08	1.22
TMEM106A	-1	0.000264069	0.57 (0.42, 0.77)	1.10%	1.08	1.38
VCX3B	1	3.69E-05	1.41 (1.20, 1.66)	0.30%	1.08	1.32
ADAMTSL2	-1	0.000193672	0.65 (0.52, 0.82)	0.90%	1.07	1.35
ADAMTSL2	-1	0.000193672	0.65 (0.52, 0.82)	0.90%	1.07	1.35
ALG14	-1	0.000562384	0.52 (0.36, 0.75)	1.70%	1.07	1.36
ANLN	1	0.000800701	2.41 (1.44, 4.02)	2.10%	1.07	1.3
ANUBL1	-1	0.000562446	0.50 (0.34, 0.74)	1.70%	1.07	1.36
ANUBL1	-1	0.000562446	0.50 (0.34, 0.74)	1.70%	1.07	1.36
ARRDC3	1	0.000609525	1.87 (1.31, 2.67)	1.80%	1.07	1.34
ATG5	1	6.58E-05	1.31 (1.15, 1.49)	0.40%	1.07	1.26
ATP1A1OS	-1	0.00067514	0.44 (0.27, 0.70)	1.90%	1.07	1.34
ATP1A1OS	-1	0.00067514	0.44 (0.27, 0.70)	1.90%	1.07	1.34
ATP1A1OS	-1	0.00067514	0.44 (0.27, 0.70)	1.90%	1.07	1.34
ATP1A1OS	-1	0.00067514	0.44 (0.27, 0.70)	1.90%	1.07	1.34
ATP1A1OS	-1	0.00067514	0.44 (0.27, 0.70)	1.90%	1.07	1.34
AURKA	1	0.000564508	1.96 (1.34, 2.86)	1.70%	1.07	1.34

AURKA	1	0.000564508	1.96 (1.34, 2.86)	1.70%	1.07	1.34
AURKA	1	0.000564508	1.96 (1.34, 2.86)	1.70%	1.07	1.34
AURKA	1	0.000564508	1.96 (1.34, 2.86)	1.70%	1.07	1.34
AURKA	1	0.000564508	1.96 (1.34, 2.86)	1.70%	1.07	1.34
AURKA	1	0.000564508	1.96 (1.34, 2.86)	1.70%	1.07	1.34
BRD1	1	0.000134308	1.37 (1.17, 1.62)	0.70%	1.07	1.29
C20orf191	1	0.00028668	1.50 (1.20, 1.86)	1.10%	1.07	1.33
C2orf77	-1	0.000330919	0.58 (0.43, 0.78)	1.20%	1.07	1.37
C5	-1	0.000477055	0.56 (0.41, 0.78)	1.60%	1.07	1.37
C6orf103	-1	0.00075103	0.49 (0.32, 0.74)	2.10%	1.07	1.35
CAMTA2	-1	0.000585964	0.54 (0.38, 0.77)	1.80%	1.07	1.36
CAMTA2	-1	0.000585964	0.54 (0.38, 0.77)	1.80%	1.07	1.36
CAMTA2	-1	0.000585964	0.54 (0.38, 0.77)	1.80%	1.07	1.36
CAMTA2	-1	0.000585964	0.54 (0.38, 0.77)	1.80%	1.07	1.36
CCDC40	-1	0.000595988	0.55 (0.39, 0.77)	1.80%	1.07	1.36
CENPP	-1	0.00100693	0.39 (0.22, 0.68)	2.50%	1.07	1.31
CHRNA6	-1	0.000417968	0.60 (0.45, 0.80)	1.40%	1.07	1.36
CHRNA6	-1	0.000417968	0.60 (0.45, 0.80)	1.40%	1.07	1.36
DCTN3	-1	0.000423018	0.59 (0.44, 0.79)	1.50%	1.07	1.37
DCTN3	-1	0.000423018	0.59 (0.44, 0.79)	1.50%	1.07	1.37
DDX5	1	0.000330009	1.53 (1.21, 1.92)	1.20%	1.07	1.33
DNAJC24	-1	0.000858705	0.38 (0.21, 0.67)	2.20%	1.07	1.31
EBF4	-1	0.000723231	0.52 (0.36, 0.76)	2.00%	1.07	1.35
ENO1	1	0.000286748	1.61 (1.25, 2.09)	1.10%	1.07	1.35
ESRP1	1	0.000526689	1.83 (1.30, 2.58)	1.70%	1.07	1.35
ESRP1	1	0.000526689	1.83 (1.30, 2.58)	1.70%	1.07	1.35
ESRP1	1	0.000526689	1.83 (1.30, 2.58)	1.70%	1.07	1.35
ESRP1	1	0.000526689	1.83 (1.30, 2.58)	1.70%	1.07	1.35
ESRP1	1	0.000526689	1.83 (1.30, 2.58)	1.70%	1.07	1.35
EVX1	1	0.000155183	1.47 (1.21, 1.80)	0.70%	1.07	1.33
EXO1	1	0.000815942	2.21 (1.39, 3.52)	2.10%	1.07	1.31
EXO1	1	0.000815942	2.21 (1.39, 3.52)	2.10%	1.07	1.31
EXO1	1	0.000815942	2.21 (1.39, 3.52)	2.10%	1.07	1.31
FAHD1	-1	0.000285382	0.63 (0.49, 0.81)	1.10%	1.07	1.36
FAHD1	-1	0.000285382	0.63 (0.49, 0.81)	1.10%	1.07	1.36
FTSJ3	1	0.000250886	1.56 (1.23, 1.98)	1.00%	1.07	1.35
GJB6	1	0.000361532	1.59 (1.23, 2.05)	1.30%	1.07	1.34
GJB6	1	0.000361532	1.59 (1.23, 2.05)	1.30%	1.07	1.34
GJB6	1	0.000361532	1.59 (1.23, 2.05)	1.30%	1.07	1.34
GJB6	1	0.000361532	1.59 (1.23, 2.05)	1.30%	1.07	1.34
GTF2IRD2B	-1	0.000489747	0.53 (0.37, 0.76)	1.60%	1.07	1.37
HIBADH	1	7.51E-05	1.41 (1.19, 1.67)	0.50%	1.07	1.31

HIVEP3	-1	0.000580798	0.50 (0.34, 0.74)	1.80%	1.07	1.36
HIVEP3	-1	0.000580798	0.50 (0.34, 0.74)	1.80%	1.07	1.36
HMGCL	-1	0.00045336	0.56 (0.41, 0.78)	1.50%	1.07	1.37
HMGCL	-1	0.00045336	0.56 (0.41, 0.78)	1.50%	1.07	1.37
HSBP1	1	0.000764687	2.07 (1.36, 3.17)	2.10%	1.07	1.32
INTS1	1	0.000425057	1.59 (1.23, 2.06)	1.50%	1.07	1.34
KIAA1274	-1	0.000322419	0.62 (0.48, 0.80)	1.20%	1.07	1.36
KIF4A	1	0.000565152	2.01 (1.35, 2.99)	1.70%	1.07	1.34
KLHL28	-1	0.000499515	0.52 (0.36, 0.75)	1.60%	1.07	1.37
KPNA2	1	0.000366643	1.80 (1.30, 2.49)	1.30%	1.07	1.36
KRT81	1	0.000377924	1.69 (1.27, 2.26)	1.30%	1.07	1.35
LOC100128881	1	0.000625392	2.08 (1.37, 3.16)	1.80%	1.07	1.33
LOC100129636	1	0.000323962	1.68 (1.27, 2.23)	1.20%	1.07	1.36
LOC284276	-1	0.000423828	0.57 (0.42, 0.78)	1.50%	1.07	1.37
LOXL1	-1	0.000510308	0.59 (0.44, 0.79)	1.60%	1.07	1.36
LRP8	1	0.000675065	2.00 (1.34, 2.98)	1.90%	1.07	1.33
LRP8	1	0.000675065	2.00 (1.34, 2.98)	1.90%	1.07	1.33
LRP8	1	0.000675065	2.00 (1.34, 2.98)	1.90%	1.07	1.33
LRP8	1	0.000675065	2.00 (1.34, 2.98)	1.90%	1.07	1.33
LRRC8A	-1	0.00053552	0.51 (0.35, 0.75)	1.70%	1.07	1.36
LRRC8A	-1	0.00053552	0.51 (0.35, 0.75)	1.70%	1.07	1.36
LRRC8A	-1	0.00053552	0.51 (0.35, 0.75)	1.70%	1.07	1.36
MAP7	1	0.000510806	1.69 (1.26, 2.26)	1.60%	1.07	1.34
MAP7	1	0.000510806	1.69 (1.26, 2.26)	1.60%	1.07	1.34
MAP7	1	0.000510806	1.69 (1.26, 2.26)	1.60%	1.07	1.34
MAP7	1	0.000510806	1.69 (1.26, 2.26)	1.60%	1.07	1.34
MAP7	1	0.000510806	1.69 (1.26, 2.26)	1.60%	1.07	1.34
MAP7	1	0.000510806	1.69 (1.26, 2.26)	1.60%	1.07	1.34
MAP7	1	0.000510806	1.69 (1.26, 2.26)	1.60%	1.07	1.34
MAP7	1	0.000510806	1.69 (1.26, 2.26)	1.60%	1.07	1.34
MAP7	1	0.000510806	1.69 (1.26, 2.26)	1.60%	1.07	1.34
MGC3771	-1	0.000568687	0.55 (0.39, 0.77)	1.70%	1.07	1.36
MGC3771	-1	0.000568687	0.55 (0.39, 0.77)	1.70%	1.07	1.36
MT1G	1	0.000312285	1.56 (1.22, 1.98)	1.20%	1.07	1.34
NGRN	1	0.000282469	1.57 (1.23, 2.01)	1.10%	1.07	1.35
NGRN	1	0.000282469	1.57 (1.23, 2.01)	1.10%	1.07	1.35
NLRP8	-1	0.000622004	0.50 (0.34, 0.74)	1.80%	1.07	1.36
NPHP1	-1	0.000473665	0.54 (0.38, 0.76)	1.60%	1.07	1.37
NPHP1	-1	0.000473665	0.54 (0.38, 0.76)	1.60%	1.07	1.37
NPHP1	-1	0.000473665	0.54 (0.38, 0.76)	1.60%	1.07	1.37
NPHP1	-1	0.000473665	0.54 (0.38, 0.76)	1.60%	1.07	1.37

NPY	1	0.00011211	1.35 (1.16, 1.57)	0.60%	1.07	1.28
PGK1	1	0.000239238	1.59 (1.24, 2.04)	1.00%	1.07	1.35
PGR	-1	0.000509769	0.53 (0.37, 0.76)	1.60%	1.07	1.37
PIH1D2	-1	0.000210904	0.65 (0.52, 0.82)	0.90%	1.07	1.35
PIH1D2	-1	0.000210904	0.65 (0.52, 0.82)	0.90%	1.07	1.35
PLA2G2E	1	0.000289748	1.57 (1.23, 2.00)	1.10%	1.07	1.34
PLD2	-1	0.000493619	0.57 (0.42, 0.78)	1.60%	1.07	1.37
PLEKHA8	1	0.000432361	1.63 (1.24, 2.13)	1.50%	1.07	1.34
PLEKHA8	1	0.000432361	1.63 (1.24, 2.13)	1.50%	1.07	1.34
PLEKHA8	1	0.000432361	1.63 (1.24, 2.13)	1.50%	1.07	1.34
PMAIP1	-1	0.000483779	0.54 (0.39, 0.77)	1.60%	1.07	1.37
PRC1	1	0.000661503	1.87 (1.30, 2.67)	1.90%	1.07	1.34
PRC1	1	0.000661503	1.87 (1.30, 2.67)	1.90%	1.07	1.34
PRC1	1	0.000661503	1.87 (1.30, 2.67)	1.90%	1.07	1.34
PRKAG2	-1	0.000805839	0.48 (0.31, 0.74)	2.10%	1.07	1.35
PRKAG2	-1	0.000805839	0.48 (0.31, 0.74)	2.10%	1.07	1.35
PRKAG2	-1	0.000805839	0.48 (0.31, 0.74)	2.10%	1.07	1.35
PRR7	1	0.000736074	2.09 (1.36, 3.21)	2.00%	1.07	1.33
PRR7	1	0.000736074	2.09 (1.36, 3.21)	2.00%	1.07	1.33
PRR7	1	0.000736074	2.09 (1.36, 3.21)	2.00%	1.07	1.33
SARNP	1	0.000200909	1.48 (1.20, 1.83)	0.90%	1.07	1.33
SARNP	1	0.000200909	1.48 (1.20, 1.83)	0.90%	1.07	1.33
SARNP	1	0.000200909	1.48 (1.20, 1.83)	0.90%	1.07	1.33
SCUBE2	-1	0.000658247	0.48 (0.32, 0.73)	1.90%	1.07	1.35
SCUBE2	-1	0.000658247	0.48 (0.32, 0.73)	1.90%	1.07	1.35
SEC31A	1	0.000358109	1.68 (1.26, 2.23)	1.30%	1.07	1.35
SEC31A	1	0.000358109	1.68 (1.26, 2.23)	1.30%	1.07	1.35
SEC31A	1	0.000358109	1.68 (1.26, 2.23)	1.30%	1.07	1.35
SEC31A	1	0.000358109	1.68 (1.26, 2.23)	1.30%	1.07	1.35
SEC31A	1	0.000358109	1.68 (1.26, 2.23)	1.30%	1.07	1.35
SEC31A	1	0.000358109	1.68 (1.26, 2.23)	1.30%	1.07	1.35
SEMA4B	1	0.000291864	1.53 (1.21, 1.92)	1.10%	1.07	1.34
SEMA4B	1	0.000291864	1.53 (1.21, 1.92)	1.10%	1.07	1.34
SERPINB3	1	4.56E-05	1.34 (1.17, 1.55)	0.30%	1.07	1.28
SEZ6L	-1	0.00098828	0.42 (0.25, 0.70)	2.40%	1.07	1.32
SEZ6L	-1	0.00098828	0.42 (0.25, 0.70)	2.40%	1.07	1.32
SEZ6L	-1	0.00098828	0.42 (0.25, 0.70)	2.40%	1.07	1.32
SEZ6L	-1	0.00098828	0.42 (0.25, 0.70)	2.40%	1.07	1.32
SEZ6L	-1	0.00098828	0.42 (0.25, 0.70)	2.40%	1.07	1.32
SEZ6L	-1	0.00098828	0.42 (0.25, 0.70)	2.40%	1.07	1.32
SH3GLB2	-1	0.000498384	0.57 (0.41, 0.78)	1.60%	1.07	1.37
SLC10A7	1	0.000332852	1.59 (1.23, 2.05)	1.20%	1.07	1.34

SLC10A7	1	0.000332852	1.59 (1.23, 2.05)	1.20%	1.07	1.34
SLC12A1	1	0.000204056	1.49 (1.21, 1.83)	0.90%	1.07	1.33
SLC12A1	1	0.000204056	1.49 (1.21, 1.83)	0.90%	1.07	1.33
SLC6A17	1	0.000424003	1.66 (1.25, 2.19)	1.50%	1.07	1.35
SND1	1	0.000527599	1.82 (1.30, 2.55)	1.70%	1.07	1.35
SPATA4	-1	0.000630371	0.51 (0.35, 0.75)	1.80%	1.07	1.36
SPPL2A	1	5.23E-06	1.25 (1.14, 1.38)	0.10%	1.07	1.23
SURF1	-1	0.000200776	0.64 (0.51, 0.81)	0.90%	1.07	1.36
SYT9	-1	0.000684006	0.54 (0.38, 0.77)	1.90%	1.07	1.36
TBRG4	1	0.000200243	1.49 (1.21, 1.85)	0.90%	1.07	1.33
TBRG4	1	0.000200243	1.49 (1.21, 1.85)	0.90%	1.07	1.33
TBRG4	1	0.000200243	1.49 (1.21, 1.85)	0.90%	1.07	1.33
TFRC	1	0.000315917	1.71 (1.28, 2.29)	1.20%	1.07	1.36
TFRC	1	0.000315917	1.71 (1.28, 2.29)	1.20%	1.07	1.36
TRABD	1	0.000122576	1.47 (1.21, 1.79)	0.60%	1.07	1.33
TSTD2	-1	0.000818708	0.48 (0.31, 0.74)	2.10%	1.07	1.34
TUG1	1	0.000491525	1.91 (1.33, 2.76)	1.60%	1.07	1.35
UCA1	-1	0.000575028	0.54 (0.38, 0.76)	1.80%	1.07	1.36
UGT2A1	1	0.000173025	1.43 (1.19, 1.73)	0.80%	1.07	1.32
ULBP3	1	0.000274042	1.57 (1.23, 2.00)	1.10%	1.07	1.35
USP39	1	0.000493416	1.78 (1.29, 2.47)	1.60%	1.07	1.35
VPS41	1	0.000370817	1.62 (1.24, 2.12)	1.30%	1.07	1.35
VPS41	1	0.000370817	1.62 (1.24, 2.12)	1.30%	1.07	1.35
WDR19	-1	0.000547998	0.54 (0.38, 0.77)	1.70%	1.07	1.36
XAB2	-1	0.000225163	0.68 (0.55, 0.83)	1.00%	1.07	1.34
ZNF516	-1	0.000417543	0.53 (0.38, 0.76)	1.40%	1.07	1.37
ZNF665	-1	0.000397142	0.57 (0.42, 0.78)	1.40%	1.07	1.37
ZNF768	-1	0.00038939	0.60 (0.46, 0.80)	1.40%	1.07	1.36
ZNF782	-1	0.000573696	0.57 (0.41, 0.78)	1.80%	1.07	1.36
ZSCAN30	-1	0.000437804	0.55 (0.39, 0.77)	1.50%	1.07	1.37
ZSCAN30	-1	0.000437804	0.55 (0.39, 0.77)	1.50%	1.07	1.37
ADC	-1	0.00054168	0.63 (0.48, 0.82)	1.70%	1.06	1.35
ANKRD30A	-1	0.000861337	0.55 (0.39, 0.78)	2.20%	1.06	1.35
ANKRD5	-1	0.000461483	0.63 (0.48, 0.81)	1.50%	1.06	1.35
ANKRD5	-1	0.000461483	0.63 (0.48, 0.81)	1.50%	1.06	1.35
ARMCX4	-1	0.000894017	0.53 (0.36, 0.77)	2.30%	1.06	1.35
ATP5S	-1	0.000805348	0.52 (0.35, 0.76)	2.10%	1.06	1.35
ATP5S	-1	0.000805348	0.52 (0.35, 0.76)	2.10%	1.06	1.35
ATP5S	-1	0.000805348	0.52 (0.35, 0.76)	2.10%	1.06	1.35
ATP5S	-1	0.000805348	0.52 (0.35, 0.76)	2.10%	1.06	1.35
AZI2	1	0.000790058	1.85 (1.29, 2.65)	2.10%	1.06	1.33
AZI2	1	0.000790058	1.85 (1.29, 2.65)	2.10%	1.06	1.33

AZI2	1	0.000790058	1.85 (1.29, 2.65)	2.10%	1.06	1.33
BCAS3	1	0.000602033	1.60 (1.22, 2.10)	1.80%	1.06	1.33
BCAS3	1	0.000602033	1.60 (1.22, 2.10)	1.80%	1.06	1.33
C16orf71	-1	0.000979549	0.51 (0.34, 0.76)	2.40%	1.06	1.34
C1orf173	-1	0.000725234	0.54 (0.37, 0.77)	2.00%	1.06	1.36
C1orf198	1	0.000803782	1.80 (1.28, 2.54)	2.10%	1.06	1.33
C1orf198	1	0.000803782	1.80 (1.28, 2.54)	2.10%	1.06	1.33
C1orf198	1	0.000803782	1.80 (1.28, 2.54)	2.10%	1.06	1.33
C2orf78	1	0.000483098	1.58 (1.22, 2.04)	1.60%	1.06	1.33
C4orf45	1	0.000764755	1.79 (1.28, 2.51)	2.10%	1.06	1.34
CALCOCO2	1	0.00019697	1.33 (1.15, 1.55)	0.90%	1.06	1.27
CDCA8	1	0.001355782	2.59 (1.45, 4.65)	2.90%	1.06	1.27
CEP110	-1	0.00077961	0.52 (0.36, 0.76)	2.10%	1.06	1.35
CGRRF1	-1	0.000645901	0.60 (0.45, 0.81)	1.90%	1.06	1.35
CNTNAP1	-1	0.000689153	0.60 (0.45, 0.81)	2.00%	1.06	1.35
COL11A2	1	0.00025518	1.37 (1.16, 1.62)	1.00%	1.06	1.29
COL11A2	1	0.00025518	1.37 (1.16, 1.62)	1.00%	1.06	1.29
COL11A2	1	0.00025518	1.37 (1.16, 1.62)	1.00%	1.06	1.29
COL11A2	1	0.00025518	1.37 (1.16, 1.62)	1.00%	1.06	1.29
COPB1	1	0.000543696	1.69 (1.26, 2.28)	1.70%	1.06	1.34
COPB1	1	0.000543696	1.69 (1.26, 2.28)	1.70%	1.06	1.34
COPB1	1	0.000543696	1.69 (1.26, 2.28)	1.70%	1.06	1.34
CREB3L2	1	0.00060177	1.72 (1.26, 2.35)	1.80%	1.06	1.34
DCDC1	-1	0.000539347	0.59 (0.44, 0.80)	1.70%	1.06	1.36
EFNA5	1	0.000714322	1.71 (1.25, 2.34)	2.00%	1.06	1.34
EIF3B	1	0.000597068	1.67 (1.25, 2.24)	1.80%	1.06	1.34
EIF3B	1	0.000597068	1.67 (1.25, 2.24)	1.80%	1.06	1.34
ELOVL2	-1	0.000664075	0.56 (0.40, 0.78)	1.90%	1.06	1.36
FBXO8	-1	0.000806276	0.56 (0.40, 0.79)	2.10%	1.06	1.35
FGD3	-1	0.000941348	0.49 (0.32, 0.75)	2.40%	1.06	1.34
FGD3	-1	0.000941348	0.49 (0.32, 0.75)	2.40%	1.06	1.34
GALNT5	-1	0.000684822	0.55 (0.39, 0.78)	1.90%	1.06	1.36
GTSE1	1	0.000929866	2.10 (1.35, 3.26)	2.40%	1.06	1.32
INHBE	1	0.000208267	1.37 (1.16, 1.61)	0.90%	1.06	1.29
IPMK	1	0.00077886	1.67 (1.24, 2.24)	2.10%	1.06	1.33
KRT4	1	0.00047149	1.55 (1.21, 1.98)	1.60%	1.06	1.33
LDLR	1	0.000708045	1.70 (1.25, 2.31)	2.00%	1.06	1.34
LDLR	1	0.000708045	1.70 (1.25, 2.31)	2.00%	1.06	1.34
LDLR	1	0.000708045	1.70 (1.25, 2.31)	2.00%	1.06	1.34
LDLR	1	0.000708045	1.70 (1.25, 2.31)	2.00%	1.06	1.34
LDLR	1	0.000708045	1.70 (1.25, 2.31)	2.00%	1.06	1.34
LDLR	1	0.000708045	1.70 (1.25, 2.31)	2.00%	1.06	1.34

LIN28A	1	0.000535605	1.50 (1.19, 1.88)	1.70%	1.06	1.32
LOC100128788	-1	0.001181148	0.48 (0.31, 0.75)	2.70%	1.06	1.33
LOC100128788	-1	0.001181148	0.48 (0.31, 0.75)	2.70%	1.06	1.33
LOC283038	-1	0.000583488	0.60 (0.45, 0.80)	1.80%	1.06	1.36
MAPT	-1	0.000668769	0.59 (0.43, 0.80)	1.90%	1.06	1.35
MAPT	-1	0.000668769	0.59 (0.43, 0.80)	1.90%	1.06	1.35
MAPT	-1	0.000668769	0.59 (0.43, 0.80)	1.90%	1.06	1.35
MAPT	-1	0.000668769	0.59 (0.43, 0.80)	1.90%	1.06	1.35
MAPT	-1	0.000668769	0.59 (0.43, 0.80)	1.90%	1.06	1.35
MAPT	-1	0.000668769	0.59 (0.43, 0.80)	1.90%	1.06	1.35
MATN3	-1	0.000797381	0.59 (0.43, 0.80)	2.10%	1.06	1.35
MKI67	1	0.001246003	2.15 (1.35, 3.41)	2.80%	1.06	1.3
MKI67	1	0.001246003	2.15 (1.35, 3.41)	2.80%	1.06	1.3
MORC2	1	0.000833522	1.86 (1.29, 2.68)	2.20%	1.06	1.33
NLGN2	-1	0.000244843	0.71 (0.59, 0.85)	1.00%	1.06	1.31
NT5C2	1	0.000631267	1.73 (1.26, 2.37)	1.80%	1.06	1.34
NT5C2	1	0.000631267	1.73 (1.26, 2.37)	1.80%	1.06	1.34
OSBP2	1	0.000812952	1.71 (1.25, 2.33)	2.10%	1.06	1.33
PDE11A	-1	0.000734955	0.57 (0.42, 0.79)	2.00%	1.06	1.35
PDE11A	-1	0.000734955	0.57 (0.42, 0.79)	2.00%	1.06	1.35
PDE11A	-1	0.000734955	0.57 (0.42, 0.79)	2.00%	1.06	1.35
PDE11A	-1	0.000734955	0.57 (0.42, 0.79)	2.00%	1.06	1.35
PI3	1	0.000476303	1.49 (1.19, 1.86)	1.60%	1.06	1.32
PIGG	-1	0.000571553	0.60 (0.45, 0.80)	1.70%	1.06	1.36
PIGG	-1	0.000571553	0.60 (0.45, 0.80)	1.70%	1.06	1.36
POLDIP3	1	0.000528218	1.55 (1.21, 1.98)	1.70%	1.06	1.33
POLDIP3	1	0.000528218	1.55 (1.21, 1.98)	1.70%	1.06	1.33
POU4F3	1	0.000229501	1.40 (1.17, 1.67)	1.00%	1.06	1.3
PRDX6	1	0.000780619	1.70 (1.25, 2.32)	2.10%	1.06	1.33
PRKD1	1	0.000548992	1.50 (1.19, 1.89)	1.70%	1.06	1.32
PSMD7	1	0.000563721	1.68 (1.25, 2.25)	1.70%	1.06	1.34
RILPL2	-1	0.000768058	0.57 (0.41, 0.79)	2.10%	1.06	1.35
RORB	-1	0.000604719	0.59 (0.44, 0.80)	1.80%	1.06	1.36
RPS3	1	0.000337452	1.44 (1.18, 1.75)	1.20%	1.06	1.31
RTN4RL1	-1	0.000608443	0.63 (0.49, 0.82)	1.80%	1.06	1.34
SC4MOL	1	0.000437147	1.51 (1.20, 1.89)	1.50%	1.06	1.32
SC4MOL	1	0.000437147	1.51 (1.20, 1.89)	1.50%	1.06	1.32
SLC40A1	-1	0.001006056	0.51 (0.34, 0.76)	2.50%	1.06	1.34
SLC9A6	1	0.00076266	1.81 (1.28, 2.56)	2.10%	1.06	1.34
SLC9A6	1	0.00076266	1.81 (1.28, 2.56)	2.10%	1.06	1.34
SLC9A6	1	0.00076266	1.81 (1.28, 2.56)	2.10%	1.06	1.34
TAX1BP1	1	0.000335077	1.39 (1.16, 1.66)	1.20%	1.06	1.29

TAX1BP1	1	0.000335077	1.39 (1.16, 1.66)	1.20%	1.06	1.29
TMEM39A	1	0.000692396	1.77 (1.27, 2.47)	2.00%	1.06	1.34
TMEM5	-1	0.000852491	0.56 (0.40, 0.79)	2.20%	1.06	1.35
TMOD2	1	0.000221131	1.43 (1.18, 1.72)	0.90%	1.06	1.31
TMOD2	1	0.000221131	1.43 (1.18, 1.72)	0.90%	1.06	1.31
TMPRSS11E	1	0.000771096	1.72 (1.25, 2.36)	2.10%	1.06	1.33
TNFAIP8L2	-1	0.000648477	0.57 (0.41, 0.79)	1.90%	1.06	1.36
TNFSF12-TNFSF13	-1	0.000593768	0.58 (0.43, 0.79)	1.80%	1.06	1.36
TRAF3IP1	-1	0.000786338	0.56 (0.40, 0.79)	2.10%	1.06	1.35
TRAF3IP1	-1	0.000786338	0.56 (0.40, 0.79)	2.10%	1.06	1.35
TRIM10	1	0.000210243	1.33 (1.14, 1.55)	0.90%	1.06	1.27
TRIM10	1	0.000210243	1.33 (1.14, 1.55)	0.90%	1.06	1.27
VILL	-1	0.000741792	0.60 (0.44, 0.81)	2.10%	1.06	1.35
ZFHX2	-1	0.000723459	0.55 (0.39, 0.78)	2.00%	1.06	1.36
ZNF652	1	0.000337669	1.51 (1.20, 1.89)	1.20%	1.06	1.33
ZNF652	1	0.000337669	1.51 (1.20, 1.89)	1.20%	1.06	1.33
ACCN5	1	0.001052716	1.88 (1.29, 2.74)	2.50%	1.05	1.32
ACTL8	1	0.000978531	1.78 (1.26, 2.52)	2.40%	1.05	1.33
AGTR1	-1	0.001529539	0.50 (0.32, 0.77)	3.10%	1.05	1.32
AGTR1	-1	0.001529539	0.50 (0.32, 0.77)	3.10%	1.05	1.32
AGTR1	-1	0.001529539	0.50 (0.32, 0.77)	3.10%	1.05	1.32
AGTR1	-1	0.001529539	0.50 (0.32, 0.77)	3.10%	1.05	1.32
AGTR1	-1	0.001529539	0.50 (0.32, 0.77)	3.10%	1.05	1.32
APOF	1	0.000357244	1.36 (1.15, 1.61)	1.30%	1.05	1.28
ARPP19	1	0.000140299	1.23 (1.11, 1.37)	0.70%	1.05	1.21
ATN1	-1	0.00113338	0.57 (0.41, 0.80)	2.60%	1.05	1.34
ATN1	-1	0.00113338	0.57 (0.41, 0.80)	2.60%	1.05	1.34
BIRC6	1	0.001242408	1.68 (1.23, 2.30)	2.80%	1.05	1.32
BTG3	1	0.00134171	1.79 (1.25, 2.55)	2.90%	1.05	1.32
BTG3	1	0.00134171	1.79 (1.25, 2.55)	2.90%	1.05	1.32
C10orf79	-1	0.001408252	0.59 (0.42, 0.81)	3.00%	1.05	1.33
C14orf105	1	0.001588324	1.90 (1.27, 2.82)	3.20%	1.05	1.31
C14orf135	-1	0.001008184	0.60 (0.44, 0.81)	2.50%	1.05	1.34
C16orf61	1	0.001288809	1.78 (1.25, 2.53)	2.90%	1.05	1.32
C17orf102	1	0.000181996	1.24 (1.11, 1.39)	0.80%	1.05	1.21
C17orf64	1	0.00063311	1.48 (1.18, 1.86)	1.80%	1.05	1.31
C20orf132	-1	0.00106845	0.53 (0.36, 0.77)	2.60%	1.05	1.34
C20orf132	-1	0.00106845	0.53 (0.36, 0.77)	2.60%	1.05	1.34
C20orf132	-1	0.00106845	0.53 (0.36, 0.77)	2.60%	1.05	1.34
C21orf29	1	0.001264027	1.74 (1.24, 2.44)	2.80%	1.05	1.32
C6orf155	-1	0.001092707	0.53 (0.36, 0.78)	2.60%	1.05	1.34
C9orf102	-1	0.001523324	0.50 (0.33, 0.77)	3.10%	1.05	1.32

C9orf156	-1	0.001347547	0.52 (0.34, 0.77)	2.90%	1.05	1.33
C9orf43	-1	0.001198516	0.60 (0.44, 0.82)	2.70%	1.05	1.34
CASC1	-1	0.000936736	0.59 (0.43, 0.81)	2.40%	1.05	1.34
CASC1	-1	0.000936736	0.59 (0.43, 0.81)	2.40%	1.05	1.34
CASC1	-1	0.000936736	0.59 (0.43, 0.81)	2.40%	1.05	1.34
CASK	1	0.001007193	1.81 (1.27, 2.57)	2.50%	1.05	1.33
CASK	1	0.001007193	1.81 (1.27, 2.57)	2.50%	1.05	1.33
CASK	1	0.001007193	1.81 (1.27, 2.57)	2.50%	1.05	1.33
CBFB	1	0.001037169	1.65 (1.22, 2.23)	2.50%	1.05	1.32
CBFB	1	0.001037169	1.65 (1.22, 2.23)	2.50%	1.05	1.32
CCNB2	1	0.001408285	1.72 (1.23, 2.40)	3.00%	1.05	1.32
CDK13	1	7.62E-05	1.22 (1.11, 1.35)	0.50%	1.05	1.2
CDK13	1	7.62E-05	1.22 (1.11, 1.35)	0.50%	1.05	1.2
CEP72	1	0.001459446	1.82 (1.26, 2.63)	3.10%	1.05	1.31
CKAP2L	1	0.001319145	2.12 (1.34, 3.35)	2.90%	1.05	1.3
CLTC	1	0.000745682	1.49 (1.18, 1.88)	2.10%	1.05	1.31
COX5A	1	0.000669975	1.51 (1.19, 1.91)	1.90%	1.05	1.32
CRNN	1	0.000789381	1.45 (1.17, 1.80)	2.10%	1.05	1.3
CYP19A1	1	0.001318685	1.75 (1.24, 2.47)	2.90%	1.05	1.32
CYP19A1	1	0.001318685	1.75 (1.24, 2.47)	2.90%	1.05	1.32
DCHS1	-1	0.001479235	0.56 (0.39, 0.80)	3.10%	1.05	1.33
DET1	-1	0.000618527	0.72 (0.59, 0.87)	1.80%	1.05	1.29
DET1	-1	0.000618527	0.72 (0.59, 0.87)	1.80%	1.05	1.29
DET1	-1	0.000618527	0.72 (0.59, 0.87)	1.80%	1.05	1.29
DNAJA1	-1	0.001074517	0.64 (0.49, 0.84)	2.60%	1.05	1.33
EPGN	1	0.001109057	1.71 (1.24, 2.36)	2.60%	1.05	1.32
ERBB4	-1	0.001313858	0.59 (0.42, 0.81)	2.90%	1.05	1.33
ERBB4	-1	0.001313858	0.59 (0.42, 0.81)	2.90%	1.05	1.33
EXOC3L	1	0.001576091	2.03 (1.31, 3.14)	3.20%	1.05	1.3
FBN3	1	0.000998771	1.55 (1.19, 2.02)	2.50%	1.05	1.31
FBXO22	1	0.000970814	1.79 (1.27, 2.53)	2.40%	1.05	1.33
FBXO22	1	0.000970814	1.79 (1.27, 2.53)	2.40%	1.05	1.33
FBXO22	1	0.000970814	1.79 (1.27, 2.53)	2.40%	1.05	1.33
FBXO36	-1	0.000983445	0.56 (0.40, 0.79)	2.40%	1.05	1.35
FLJ26245	1	0.000549548	1.46 (1.18, 1.81)	1.70%	1.05	1.31
FLJ46361	1	0.000467876	1.42 (1.17, 1.73)	1.60%	1.05	1.3
GALNT13	1	0.001008619	1.66 (1.23, 2.24)	2.50%	1.05	1.32
GALNTL1	-1	0.001388679	0.54 (0.37, 0.79)	3.00%	1.05	1.33
GALNTL1	-1	0.001388679	0.54 (0.37, 0.79)	3.00%	1.05	1.33
GPR107	-1	0.001371972	0.46 (0.29, 0.74)	2.90%	1.05	1.32
GPR107	-1	0.001371972	0.46 (0.29, 0.74)	2.90%	1.05	1.32
GPR107	-1	0.001371972	0.46 (0.29, 0.74)	2.90%	1.05	1.32

GSTA5	1	0.000405719	1.37 (1.15, 1.62)	1.40%	1.05	1.28
HHLA3	-1	0.001094742	0.58 (0.42, 0.80)	2.60%	1.05	1.34
HHLA3	-1	0.001094742	0.58 (0.42, 0.80)	2.60%	1.05	1.34
HHLA3	-1	0.001094742	0.58 (0.42, 0.80)	2.60%	1.05	1.34
HHLA3	-1	0.001094742	0.58 (0.42, 0.80)	2.60%	1.05	1.34
HINFP	-1	0.000768103	0.65 (0.50, 0.84)	2.10%	1.05	1.33
HINFP	-1	0.000768103	0.65 (0.50, 0.84)	2.10%	1.05	1.33
HMGCR	1	0.000609854	1.48 (1.18, 1.85)	1.80%	1.05	1.31
HMGCR	1	0.000609854	1.48 (1.18, 1.85)	1.80%	1.05	1.31
HYDIN	-1	0.001297953	0.58 (0.42, 0.81)	2.90%	1.05	1.34
HYDIN	-1	0.001297953	0.58 (0.42, 0.81)	2.90%	1.05	1.34
HYDIN	-1	0.001297953	0.58 (0.42, 0.81)	2.90%	1.05	1.34
HYDIN	-1	0.001297953	0.58 (0.42, 0.81)	2.90%	1.05	1.34
IARS2	1	0.001187981	1.68 (1.23, 2.30)	2.70%	1.05	1.32
IFT88	-1	0.001402791	0.57 (0.40, 0.80)	3.00%	1.05	1.33
IFT88	-1	0.001402791	0.57 (0.40, 0.80)	3.00%	1.05	1.33
IGF2BP1	1	0.000806815	1.61 (1.22, 2.13)	2.10%	1.05	1.33
IGF2BP1	1	0.000806815	1.61 (1.22, 2.13)	2.10%	1.05	1.33
IL1F10	1	0.000806465	1.47 (1.17, 1.84)	2.10%	1.05	1.3
IL1F10	1	0.000806465	1.47 (1.17, 1.84)	2.10%	1.05	1.3
INTU	-1	0.000791038	0.64 (0.49, 0.83)	2.10%	1.05	1.34
IQGAP3	1	0.001269109	2.03 (1.32, 3.13)	2.80%	1.05	1.31
KYNU	1	0.000833126	1.48 (1.18, 1.87)	2.20%	1.05	1.31
KYNU	1	0.000833126	1.48 (1.18, 1.87)	2.20%	1.05	1.31
KYNU	1	0.000833126	1.48 (1.18, 1.87)	2.20%	1.05	1.31
LEKR1	-1	0.001095433	0.55 (0.39, 0.79)	2.60%	1.05	1.34
LEKR1	-1	0.001095433	0.55 (0.39, 0.79)	2.60%	1.05	1.34
LOC100129046	-1	0.001505992	0.56 (0.40, 0.80)	3.10%	1.05	1.33
LOC100130015	1	0.000973928	1.60 (1.21, 2.11)	2.40%	1.05	1.32
LOC100130015	1	0.000973928	1.60 (1.21, 2.11)	2.40%	1.05	1.32
LOC386758	-1	0.001056927	0.60 (0.44, 0.82)	2.50%	1.05	1.34
LOC386758	-1	0.001056927	0.60 (0.44, 0.82)	2.50%	1.05	1.34
LOC386758	-1	0.001056927	0.60 (0.44, 0.82)	2.50%	1.05	1.34
LOC389765	-1	0.001342509	0.56 (0.39, 0.80)	2.90%	1.05	1.34
LOC401242	1	0.000156056	1.27 (1.12, 1.43)	0.70%	1.05	1.23
LRRC48	-1	0.001316854	0.54 (0.38, 0.79)	2.90%	1.05	1.34
LRRC48	-1	0.001316854	0.54 (0.38, 0.79)	2.90%	1.05	1.34
LRRC48	-1	0.001316854	0.54 (0.38, 0.79)	2.90%	1.05	1.34
LRRC48	-1	0.001316854	0.54 (0.38, 0.79)	2.90%	1.05	1.34
MAGEA12	1	0.000281529	1.29 (1.12, 1.48)	1.10%	1.05	1.24
MAGEA12	1	0.000281529	1.29 (1.12, 1.48)	1.10%	1.05	1.24
MAGEA12	1	0.000281529	1.29 (1.12, 1.48)	1.10%	1.05	1.24

MLF1IP	1	0.00175043	1.95 (1.28, 2.97)	3.40%	1.05	1.3
MRPL54	-1	0.001508008	0.52 (0.35, 0.78)	3.10%	1.05	1.33
MTNR1A	1	0.001122268	1.71 (1.24, 2.36)	2.60%	1.05	1.32
MYBL2	1	0.001307241	1.82 (1.26, 2.63)	2.90%	1.05	1.32
NBPF1	-1	0.001260206	0.58 (0.41, 0.81)	2.80%	1.05	1.34
NCBP1	-1	0.001356126	0.57 (0.41, 0.80)	2.90%	1.05	1.33
NCOA5	-1	0.001192077	0.55 (0.39, 0.79)	2.70%	1.05	1.34
NUBP1	-1	0.000937501	0.59 (0.43, 0.81)	2.40%	1.05	1.34
NUP155	1	0.00100456	1.82 (1.27, 2.59)	2.50%	1.05	1.33
NUP155	1	0.00100456	1.82 (1.27, 2.59)	2.50%	1.05	1.33
OPN3	1	0.001078316	1.89 (1.29, 2.78)	2.60%	1.05	1.32
PABPC1	1	0.001122107	1.62 (1.21, 2.17)	2.60%	1.05	1.32
PACRGL	-1	0.000964235	0.59 (0.43, 0.81)	2.40%	1.05	1.34
PACRGL	-1	0.000964235	0.59 (0.43, 0.81)	2.40%	1.05	1.34
PALM	-1	0.000885604	0.59 (0.43, 0.80)	2.30%	1.05	1.35
PALM	-1	0.000885604	0.59 (0.43, 0.80)	2.30%	1.05	1.35
PHF2	-1	0.001491851	0.58 (0.41, 0.81)	3.10%	1.05	1.33
PIF1	1	0.001559389	2.22 (1.35, 3.64)	3.20%	1.05	1.29
PLA2G16	-1	0.001171353	0.52 (0.35, 0.77)	2.70%	1.05	1.34
PLA2G16	-1	0.001171353	0.52 (0.35, 0.77)	2.70%	1.05	1.34
PNPLA4	-1	0.001295225	0.55 (0.38, 0.79)	2.90%	1.05	1.34
PNPLA4	-1	0.001295225	0.55 (0.38, 0.79)	2.90%	1.05	1.34
PNPLA4	-1	0.001295225	0.55 (0.38, 0.79)	2.90%	1.05	1.34
PPIA	1	0.000543774	1.42 (1.16, 1.73)	1.70%	1.05	1.3
PPM1M	-1	0.000929062	0.67 (0.52, 0.85)	2.40%	1.05	1.32
PPM1M	-1	0.000929062	0.67 (0.52, 0.85)	2.40%	1.05	1.32
PPP1CB	1	0.001307362	1.75 (1.24, 2.45)	2.90%	1.05	1.32
PPP1CB	1	0.001307362	1.75 (1.24, 2.45)	2.90%	1.05	1.32
PRRG1	1	0.001335665	2.05 (1.32, 3.17)	2.90%	1.05	1.3
PRRG1	1	0.001335665	2.05 (1.32, 3.17)	2.90%	1.05	1.3
PRRG1	1	0.001335665	2.05 (1.32, 3.17)	2.90%	1.05	1.3
PRRG1	1	0.001335665	2.05 (1.32, 3.17)	2.90%	1.05	1.3
PRRG1	1	0.001335665	2.05 (1.32, 3.17)	2.90%	1.05	1.3
PYGO1	-1	0.000933796	0.59 (0.43, 0.80)	2.40%	1.05	1.35
RASGEF1C	1	0.000782881	1.63 (1.23, 2.17)	2.10%	1.05	1.33
RBBP6	-1	0.001298068	0.53 (0.36, 0.78)	2.90%	1.05	1.33
RBBP6	-1	0.001298068	0.53 (0.36, 0.78)	2.90%	1.05	1.33
RBBP6	-1	0.001298068	0.53 (0.36, 0.78)	2.90%	1.05	1.33
RBM24	-1	0.00141751	0.54 (0.37, 0.79)	3.00%	1.05	1.33
RBM24	-1	0.00141751	0.54 (0.37, 0.79)	3.00%	1.05	1.33
RBM24	-1	0.00141751	0.54 (0.37, 0.79)	3.00%	1.05	1.33
REM2	-1	0.000882487	0.63 (0.48, 0.83)	2.30%	1.05	1.34

SEPSECS	-1	0.001221472	0.59 (0.43, 0.81)	2.80%	1.05	1.34
SHCBP1	1	0.001555367	1.94 (1.29, 2.93)	3.20%	1.05	1.3
SLC25A12	-1	0.001161342	0.53 (0.36, 0.78)	2.70%	1.05	1.34
SRP9	1	0.001180657	1.64 (1.22, 2.22)	2.70%	1.05	1.32
SRP9	1	0.001180657	1.64 (1.22, 2.22)	2.70%	1.05	1.32
SYT6	-1	0.00123582	0.51 (0.34, 0.77)	2.80%	1.05	1.33
TARBP2	-1	0.000916321	0.62 (0.47, 0.82)	2.30%	1.05	1.34
TARBP2	-1	0.000916321	0.62 (0.47, 0.82)	2.30%	1.05	1.34
TARBP2	-1	0.000916321	0.62 (0.47, 0.82)	2.30%	1.05	1.34
TCAM1P	1	0.000940114	1.64 (1.22, 2.20)	2.40%	1.05	1.32
THAP4	-1	0.001221209	0.55 (0.38, 0.79)	2.80%	1.05	1.34
THAP4	-1	0.001221209	0.55 (0.38, 0.79)	2.80%	1.05	1.34
TLR3	-1	0.001127044	0.59 (0.43, 0.81)	2.60%	1.05	1.34
TMEM127	-1	0.000890354	0.59 (0.43, 0.81)	2.30%	1.05	1.35
TMEM127	-1	0.000890354	0.59 (0.43, 0.81)	2.30%	1.05	1.35
TPTE	1	0.000758552	1.57 (1.21, 2.04)	2.10%	1.05	1.32
TPTE	1	0.000758552	1.57 (1.21, 2.04)	2.10%	1.05	1.32
TPTE	1	0.000758552	1.57 (1.21, 2.04)	2.10%	1.05	1.32
TRNP1	-1	0.001093981	0.62 (0.46, 0.83)	2.60%	1.05	1.33
TRPV1	-1	0.001166172	0.51 (0.34, 0.77)	2.70%	1.05	1.34
TRPV1	-1	0.001166172	0.51 (0.34, 0.77)	2.70%	1.05	1.34
TRPV1	-1	0.001166172	0.51 (0.34, 0.77)	2.70%	1.05	1.34
TRPV1	-1	0.001166172	0.51 (0.34, 0.77)	2.70%	1.05	1.34
TTC23L	-1	0.001233032	0.57 (0.41, 0.80)	2.80%	1.05	1.34
TTC26	-1	0.000762816	0.66 (0.52, 0.84)	2.10%	1.05	1.33
TTC26	-1	0.000762816	0.66 (0.52, 0.84)	2.10%	1.05	1.33
TTC26	-1	0.000762816	0.66 (0.52, 0.84)	2.10%	1.05	1.33
UNC5B	-1	0.001174314	0.61 (0.46, 0.82)	2.70%	1.05	1.33
USP9X	1	0.001402489	1.73 (1.24, 2.43)	3.00%	1.05	1.32
USP9X	1	0.001402489	1.73 (1.24, 2.43)	3.00%	1.05	1.32
WDR16	-1	0.001158488	0.53 (0.36, 0.78)	2.70%	1.05	1.34
WDR16	-1	0.001158488	0.53 (0.36, 0.78)	2.70%	1.05	1.34
YWHAE	-1	0.001115707	0.52 (0.35, 0.77)	2.60%	1.05	1.34
YWHAE	-1	0.001115707	0.52 (0.35, 0.77)	2.60%	1.05	1.34
ZBTB26	-1	0.001225918	0.59 (0.43, 0.81)	2.80%	1.05	1.34
ZFP112	-1	0.00123204	0.54 (0.37, 0.78)	2.80%	1.05	1.34
ZFP112	-1	0.00123204	0.54 (0.37, 0.78)	2.80%	1.05	1.34
ZFP28	-1	0.000981399	0.58 (0.42, 0.80)	2.40%	1.05	1.34
ZFP3	-1	0.001069592	0.56 (0.40, 0.79)	2.60%	1.05	1.34
ZNF358	-1	0.000693963	0.66 (0.52, 0.84)	2.00%	1.05	1.33
ZNF420	-1	0.001324154	0.57 (0.40, 0.80)	2.90%	1.05	1.34
ZNF597	-1	0.000903345	0.59 (0.44, 0.81)	2.30%	1.05	1.34

ZNF610	-1	0.001280906	0.60 (0.44, 0.82)	2.80%	1.05	1.33
ZNF610	-1	0.001280906	0.60 (0.44, 0.82)	2.80%	1.05	1.33
ZNF610	-1	0.001280906	0.60 (0.44, 0.82)	2.80%	1.05	1.33
ZNF610	-1	0.001280906	0.60 (0.44, 0.82)	2.80%	1.05	1.33
ZNF862	-1	0.00105257	0.55 (0.39, 0.79)	2.50%	1.05	1.34
ABCA12	1	0.002161248	1.74 (1.22, 2.47)	3.90%	1.04	1.3
ABCA12	1	0.002161248	1.74 (1.22, 2.47)	3.90%	1.04	1.3
ACSM5	-1	0.002054386	0.56 (0.39, 0.81)	3.80%	1.04	1.32
ADM2	1	0.001274536	1.46 (1.16, 1.84)	2.80%	1.04	1.29
AMDHD1	-1	0.001536666	0.61 (0.45, 0.83)	3.10%	1.04	1.33
AMN1	-1	0.002178846	0.52 (0.35, 0.79)	3.90%	1.04	1.31
AMN1	-1	0.002178846	0.52 (0.35, 0.79)	3.90%	1.04	1.31
ANKAR	-1	0.002007581	0.62 (0.46, 0.84)	3.70%	1.04	1.32
B3GNT8	-1	0.001926614	0.55 (0.38, 0.80)	3.60%	1.04	1.32
BBS5	-1	0.001546773	0.60 (0.44, 0.82)	3.20%	1.04	1.33
BDNF-AS1	-1	0.001646972	0.64 (0.48, 0.84)	3.30%	1.04	1.32
BDNF-AS1	-1	0.001646972	0.64 (0.48, 0.84)	3.30%	1.04	1.32
BDNF-AS1	-1	0.001646972	0.64 (0.48, 0.84)	3.30%	1.04	1.32
BDNF-AS1	-1	0.001646972	0.64 (0.48, 0.84)	3.30%	1.04	1.32
BDNF-AS1	-1	0.001646972	0.64 (0.48, 0.84)	3.30%	1.04	1.32
BZRAP1	-1	0.001603336	0.58 (0.41, 0.81)	3.20%	1.04	1.33
BZRAP1	-1	0.001603336	0.58 (0.41, 0.81)	3.20%	1.04	1.33
C22orf9	-1	0.001457169	0.59 (0.42, 0.81)	3.10%	1.04	1.33
C22orf9	-1	0.001457169	0.59 (0.42, 0.81)	3.10%	1.04	1.33
C5orf22	1	0.00164001	1.82 (1.25, 2.64)	3.30%	1.04	1.31
C7orf30	1	0.001468584	1.43 (1.15, 1.79)	3.10%	1.04	1.28
C7orf53	1	0.00256683	1.97 (1.27, 3.06)	4.30%	1.04	1.28
C7orf53	1	0.00256683	1.97 (1.27, 3.06)	4.30%	1.04	1.28
C8orf75	1	0.001454158	1.62 (1.20, 2.19)	3.10%	1.04	1.31
C9orf89	-1	0.001984738	0.52 (0.34, 0.78)	3.70%	1.04	1.32
CBX3	1	0.001431883	1.40 (1.14, 1.72)	3.00%	1.04	1.27
CBX3	1	0.001431883	1.40 (1.14, 1.72)	3.00%	1.04	1.27
CELA2B	-1	0.001884979	0.56 (0.39, 0.81)	3.60%	1.04	1.32
CENPF	1	0.002672209	2.01 (1.28, 3.18)	4.40%	1.04	1.28
CENPI	1	0.00200314	1.76 (1.23, 2.52)	3.70%	1.04	1.3
CLRN1	-1	0.001811077	0.59 (0.42, 0.82)	3.50%	1.04	1.32
CLRN1	-1	0.001811077	0.59 (0.42, 0.82)	3.50%	1.04	1.32
CLRN1	-1	0.001811077	0.59 (0.42, 0.82)	3.50%	1.04	1.32
CNOT1	1	0.002044545	1.67 (1.20, 2.31)	3.80%	1.04	1.3
CNOT1	1	0.002044545	1.67 (1.20, 2.31)	3.80%	1.04	1.3
COX4I1	1	0.001837639	1.78 (1.24, 2.56)	3.50%	1.04	1.31
CREBBP	-1	0.002076809	0.56 (0.39, 0.81)	3.80%	1.04	1.32

CREBBP	-1	0.002076809	0.56 (0.39, 0.81)	3.80%	1.04	1.32
DCP1B	-1	0.002232642	0.55 (0.37, 0.81)	4.00%	1.04	1.32
DEGS2	-1	0.002313022	0.58 (0.41, 0.83)	4.10%	1.04	1.32
DNAH6	-1	0.001467242	0.62 (0.46, 0.83)	3.10%	1.04	1.33
DYNLRB2	-1	0.001832614	0.62 (0.46, 0.84)	3.50%	1.04	1.32
EIF3E	1	0.001989926	1.72 (1.22, 2.42)	3.70%	1.04	1.3
EPRS	1	0.002365345	1.81 (1.24, 2.67)	4.10%	1.04	1.29
ETFDH	-1	0.00230326	0.58 (0.41, 0.82)	4.10%	1.04	1.32
FAM131C	1	0.002298543	1.77 (1.23, 2.55)	4.10%	1.04	1.3
GALC	-1	0.001803912	0.61 (0.44, 0.83)	3.50%	1.04	1.32
GALC	-1	0.001803912	0.61 (0.44, 0.83)	3.50%	1.04	1.32
GALNT14	1	0.001837704	1.76 (1.23, 2.52)	3.50%	1.04	1.31
HEATR2	1	0.001823293	1.54 (1.18, 2.03)	3.50%	1.04	1.3
HEATR3	1	0.001554545	1.73 (1.23, 2.42)	3.20%	1.04	1.31
HEATR7A	1	0.001790133	1.61 (1.19, 2.18)	3.50%	1.04	1.3
HEATR7A	1	0.001790133	1.61 (1.19, 2.18)	3.50%	1.04	1.3
HEATR7A	1	0.001790133	1.61 (1.19, 2.18)	3.50%	1.04	1.3
HMGCS1	1	0.001069341	1.47 (1.17, 1.85)	2.60%	1.04	1.3
HMGCS1	1	0.001069341	1.47 (1.17, 1.85)	2.60%	1.04	1.3
HOXB9	1	0.001509092	1.61 (1.20, 2.17)	3.10%	1.04	1.31
IFT74	-1	0.001765925	0.58 (0.42, 0.82)	3.40%	1.04	1.33
IFT74	-1	0.001765925	0.58 (0.42, 0.82)	3.40%	1.04	1.33
IFT74	-1	0.001765925	0.58 (0.42, 0.82)	3.40%	1.04	1.33
IFT74	-1	0.001765925	0.58 (0.42, 0.82)	3.40%	1.04	1.33
KCNK5	1	0.001161172	1.52 (1.18, 1.97)	2.70%	1.04	1.31
KDELR2	1	0.001508021	1.70 (1.22, 2.35)	3.10%	1.04	1.31
KDELR2	1	0.001508021	1.70 (1.22, 2.35)	3.10%	1.04	1.31
KDM4B	-1	0.001823372	0.53 (0.35, 0.79)	3.50%	1.04	1.32
KIAA0226	1	0.001751246	1.55 (1.18, 2.04)	3.40%	1.04	1.3
KIAA0226	1	0.001751246	1.55 (1.18, 2.04)	3.40%	1.04	1.3
KIAA1737	-1	0.002117405	0.59 (0.42, 0.83)	3.90%	1.04	1.32
LOC100130581	-1	0.00105557	0.72 (0.59, 0.88)	2.50%	1.04	1.29
LOC100130581	-1	0.00105557	0.72 (0.59, 0.88)	2.50%	1.04	1.29
LOC100288730	-1	0.002074681	0.55 (0.37, 0.80)	3.80%	1.04	1.32
LOC285629	1	0.001639129	1.47 (1.16, 1.87)	3.30%	1.04	1.29
LOC348021	1	0.000629483	1.26 (1.10, 1.44)	1.80%	1.04	1.22
LOC389033	-1	0.001863566	0.56 (0.38, 0.81)	3.50%	1.04	1.32
LOC494141	1	0.001552204	1.50 (1.17, 1.92)	3.20%	1.04	1.3
LOC494141	1	0.001552204	1.50 (1.17, 1.92)	3.20%	1.04	1.3
LOC494141	1	0.001552204	1.50 (1.17, 1.92)	3.20%	1.04	1.3
LPPR2	-1	0.001724289	0.62 (0.45, 0.83)	3.40%	1.04	1.32
LPPR2	-1	0.001724289	0.62 (0.45, 0.83)	3.40%	1.04	1.32

LRP12	1	0.001577381	1.60 (1.20, 2.15)	3.20%	1.04	1.31
LRP12	1	0.001577381	1.60 (1.20, 2.15)	3.20%	1.04	1.31
LRP2	-1	0.001813236	0.55 (0.38, 0.80)	3.50%	1.04	1.32
LYPD2	1	0.001349535	1.39 (1.14, 1.70)	2.90%	1.04	1.27
MAP7D1	-1	0.001687535	0.57 (0.40, 0.81)	3.30%	1.04	1.33
MED16	-1	0.001899319	0.59 (0.42, 0.82)	3.60%	1.04	1.32
MEMO1	1	0.002174585	2.05 (1.29, 3.24)	3.90%	1.04	1.28
MEMO1	1	0.002174585	2.05 (1.29, 3.24)	3.90%	1.04	1.28
MICAL3	1	0.001535676	1.71 (1.23, 2.38)	3.10%	1.04	1.31
MICAL3	1	0.001535676	1.71 (1.23, 2.38)	3.10%	1.04	1.31
MICAL3	1	0.001535676	1.71 (1.23, 2.38)	3.10%	1.04	1.31
MIP	1	0.000829718	1.39 (1.15, 1.70)	2.20%	1.04	1.28
MKL2	-1	0.001781182	0.53 (0.36, 0.79)	3.50%	1.04	1.32
MPHOSPH6	1	0.001626864	1.51 (1.17, 1.96)	3.30%	1.04	1.3
MSRA	-1	0.001531353	0.61 (0.44, 0.83)	3.10%	1.04	1.33
MSRA	-1	0.001531353	0.61 (0.44, 0.83)	3.10%	1.04	1.33
MSRA	-1	0.001531353	0.61 (0.44, 0.83)	3.10%	1.04	1.33
MSRA	-1	0.001531353	0.61 (0.44, 0.83)	3.10%	1.04	1.33
MTIF3	-1	0.002132573	0.58 (0.41, 0.82)	3.90%	1.04	1.32
MTIF3	-1	0.002132573	0.58 (0.41, 0.82)	3.90%	1.04	1.32
MTIF3	-1	0.002132573	0.58 (0.41, 0.82)	3.90%	1.04	1.32
MTIF3	-1	0.002132573	0.58 (0.41, 0.82)	3.90%	1.04	1.32
MUM1L1	-1	0.001404473	0.61 (0.45, 0.82)	3.00%	1.04	1.33
MUM1L1	-1	0.001404473	0.61 (0.45, 0.82)	3.00%	1.04	1.33
NCALD	1	0.00188018	1.65 (1.20, 2.25)	3.60%	1.04	1.3
NCALD	1	0.00188018	1.65 (1.20, 2.25)	3.60%	1.04	1.3
NCALD	1	0.00188018	1.65 (1.20, 2.25)	3.60%	1.04	1.3
NCALD	1	0.00188018	1.65 (1.20, 2.25)	3.60%	1.04	1.3
NCALD	1	0.00188018	1.65 (1.20, 2.25)	3.60%	1.04	1.3
NCALD	1	0.00188018	1.65 (1.20, 2.25)	3.60%	1.04	1.3
NCALD	1	0.00188018	1.65 (1.20, 2.25)	3.60%	1.04	1.3
NCALD	1	0.00188018	1.65 (1.20, 2.25)	3.60%	1.04	1.3
NCRNA00094	1	0.001484442	1.64 (1.21, 2.22)	3.10%	1.04	1.31
NDUFA12	-1	0.001796493	0.67 (0.52, 0.86)	3.50%	1.04	1.3
NME1-NME2	1	0.001608921	1.59 (1.19, 2.12)	3.20%	1.04	1.31
NME1-NME2	1	0.001608921	1.59 (1.19, 2.12)	3.20%	1.04	1.31
NUP93	1	0.001568961	1.63 (1.20, 2.20)	3.20%	1.04	1.31
NUTF2	1	0.002638761	2.03 (1.28, 3.21)	4.40%	1.04	1.28
PARP11	-1	0.001639941	0.56 (0.39, 0.80)	3.30%	1.04	1.33
PCDH12	-1	0.002217348	0.54 (0.36, 0.80)	4.00%	1.04	1.32
PCOLCE	-1	0.001169185	0.69 (0.55, 0.86)	2.70%	1.04	1.3
PIGA	1	0.001611291	1.71 (1.23, 2.39)	3.20%	1.04	1.31

PIGA	1	0.001611291	1.71 (1.23, 2.39)	3.20%	1.04	1.31
PIGA	1	0.001611291	1.71 (1.23, 2.39)	3.20%	1.04	1.31
PIGA	1	0.001611291	1.71 (1.23, 2.39)	3.20%	1.04	1.31
PRAMEF11	1	0.001218956	1.49 (1.17, 1.89)	2.80%	1.04	1.3
PRDM4	-1	0.002295022	0.57 (0.39, 0.82)	4.10%	1.04	1.32
PRR11	1	0.001592327	1.68 (1.22, 2.31)	3.20%	1.04	1.31
PRR25	-1	0.00181547	0.61 (0.45, 0.83)	3.50%	1.04	1.32
PVRL4	1	0.002362673	1.76 (1.22, 2.54)	4.10%	1.04	1.3
RAD52	-1	0.001826287	0.58 (0.42, 0.82)	3.50%	1.04	1.32
RBM19	-1	0.001710729	0.58 (0.41, 0.81)	3.40%	1.04	1.33
RBM19	-1	0.001710729	0.58 (0.41, 0.81)	3.40%	1.04	1.33
RBM19	-1	0.001710729	0.58 (0.41, 0.81)	3.40%	1.04	1.33
RCHY1	1	0.001382457	1.40 (1.14, 1.71)	3.00%	1.04	1.28
RCHY1	1	0.001382457	1.40 (1.14, 1.71)	3.00%	1.04	1.28
RCHY1	1	0.001382457	1.40 (1.14, 1.71)	3.00%	1.04	1.28
RGS12	-1	0.00204249	0.62 (0.46, 0.84)	3.80%	1.04	1.32
RGS12	-1	0.00204249	0.62 (0.46, 0.84)	3.80%	1.04	1.32
RGS12	-1	0.00204249	0.62 (0.46, 0.84)	3.80%	1.04	1.32
RHOV	1	0.002052837	1.61 (1.19, 2.17)	3.80%	1.04	1.3
RPL17-C18ORF32	1	0.002254262	1.78 (1.23, 2.58)	4.00%	1.04	1.3
RPL17-C18ORF32	1	0.002254262	1.78 (1.23, 2.58)	4.00%	1.04	1.3
SCFD1	1	0.001110852	1.39 (1.14, 1.69)	2.60%	1.04	1.28
SCFD1	1	0.001110852	1.39 (1.14, 1.69)	2.60%	1.04	1.28
SENP5	1	0.001328803	1.44 (1.15, 1.80)	2.90%	1.04	1.29
SERPINF1	-1	0.001927763	0.58 (0.41, 0.82)	3.60%	1.04	1.32
SGOL2	1	0.001766454	1.62 (1.20, 2.20)	3.40%	1.04	1.31
SGOL2	1	0.001766454	1.62 (1.20, 2.20)	3.40%	1.04	1.31
SGOL2	1	0.001766454	1.62 (1.20, 2.20)	3.40%	1.04	1.31
SLC43A1	-1	0.002668902	0.51 (0.33, 0.79)	4.40%	1.04	1.3
SLC43A1	-1	0.002668902	0.51 (0.33, 0.79)	4.40%	1.04	1.3
SMPDL3A	1	0.00123104	1.52 (1.18, 1.95)	2.80%	1.04	1.3
SOX8	1	0.000931789	1.46 (1.17, 1.82)	2.40%	1.04	1.3
SPRR1B	1	0.000777744	1.29 (1.11, 1.50)	2.10%	1.04	1.24
STX1B	-1	0.002150231	0.58 (0.41, 0.82)	3.90%	1.04	1.32
SYNPO2L	-1	0.001652246	0.62 (0.45, 0.83)	3.30%	1.04	1.32
SYNPO2L	-1	0.001652246	0.62 (0.45, 0.83)	3.30%	1.04	1.32
TBCEL	-1	0.001739503	0.67 (0.52, 0.86)	3.40%	1.04	1.31
TBCEL	-1	0.001739503	0.67 (0.52, 0.86)	3.40%	1.04	1.31
TECTA	-1	0.00137001	0.68 (0.54, 0.86)	2.90%	1.04	1.31
TMEM229B	-1	0.001467076	0.59 (0.43, 0.82)	3.10%	1.04	1.33
TOR1A	-1	0.001857485	0.51 (0.33, 0.78)	3.50%	1.04	1.32
TRIM15	1	0.001090987	1.36 (1.13, 1.64)	2.60%	1.04	1.27

TYW3	-1	0.001970278	0.62 (0.46, 0.84)	3.70%	1.04	1.32
TYW3	-1	0.001970278	0.62 (0.46, 0.84)	3.70%	1.04	1.32
TYW3	-1	0.001970278	0.62 (0.46, 0.84)	3.70%	1.04	1.32
UBA6	1	0.001190224	1.54 (1.19, 2.00)	2.70%	1.04	1.31
UBXN11	-1	0.002331967	0.58 (0.41, 0.82)	4.10%	1.04	1.32
UBXN11	-1	0.002331967	0.58 (0.41, 0.82)	4.10%	1.04	1.32
UBXN11	-1	0.002331967	0.58 (0.41, 0.82)	4.10%	1.04	1.32
USP28	-1	0.001429182	0.60 (0.44, 0.82)	3.00%	1.04	1.33
VSTM2B	1	0.001630655	1.53 (1.18, 2.00)	3.30%	1.04	1.3
WDR62	1	0.002082929	1.75 (1.22, 2.49)	3.80%	1.04	1.3
WDR62	1	0.002082929	1.75 (1.22, 2.49)	3.80%	1.04	1.3
WFDC12	1	0.001028037	1.38 (1.14, 1.67)	2.50%	1.04	1.27
WFS1	-1	0.001502849	0.62 (0.47, 0.84)	3.10%	1.04	1.32
WFS1	-1	0.001502849	0.62 (0.47, 0.84)	3.10%	1.04	1.32
ZNF564	-1	0.001983109	0.56 (0.39, 0.81)	3.70%	1.04	1.32
ZNF627	-1	0.001961641	0.59 (0.42, 0.82)	3.70%	1.04	1.32
ZNF799	-1	0.001796488	0.54 (0.37, 0.80)	3.50%	1.04	1.32
ACBD3	1	0.003108527	1.67 (1.19, 2.34)	4.80%	1.03	1.29
ACRBP	-1	0.002527232	0.59 (0.42, 0.83)	4.30%	1.03	1.31
ADAM17	1	0.002756749	1.73 (1.21, 2.47)	4.50%	1.03	1.29
AHCTF1	1	0.002833846	1.82 (1.23, 2.68)	4.60%	1.03	1.29
AIDA	1	0.002305105	1.42 (1.13, 1.77)	4.10%	1.03	1.27
AK7	-1	0.002397849	0.60 (0.43, 0.84)	4.20%	1.03	1.31
AKD1	-1	0.003540384	0.55 (0.37, 0.82)	5.20%	1.03	1.3
AKD1	-1	0.003540384	0.55 (0.37, 0.82)	5.20%	1.03	1.3
ALB	1	0.002271626	1.60 (1.18, 2.16)	4.10%	1.03	1.3
ANKMY1	-1	0.003302577	0.59 (0.42, 0.84)	4.90%	1.03	1.3
ANKMY1	-1	0.003302577	0.59 (0.42, 0.84)	4.90%	1.03	1.3
ANKRD24	-1	0.002274319	0.62 (0.46, 0.84)	4.10%	1.03	1.31
ANKRD37	1	0.003334199	2.07 (1.27, 3.38)	5.00%	1.03	1.26
ARHGEF6	-1	0.003627718	0.60 (0.43, 0.85)	5.30%	1.03	1.3
ASB18	1	0.002578858	1.74 (1.21, 2.48)	4.40%	1.03	1.29
ATP2A2	1	0.003253492	1.60 (1.17, 2.18)	4.90%	1.03	1.29
ATP2A2	1	0.003253492	1.60 (1.17, 2.18)	4.90%	1.03	1.29
ATP2A2	1	0.003253492	1.60 (1.17, 2.18)	4.90%	1.03	1.29
BAI2	-1	0.003578065	0.60 (0.43, 0.85)	5.20%	1.03	1.3
BANP	1	0.003069281	1.50 (1.15, 1.96)	4.80%	1.03	1.28
BANP	1	0.003069281	1.50 (1.15, 1.96)	4.80%	1.03	1.28
BANP	1	0.003069281	1.50 (1.15, 1.96)	4.80%	1.03	1.28
BANP	1	0.003069281	1.50 (1.15, 1.96)	4.80%	1.03	1.28
BANP	1	0.003069281	1.50 (1.15, 1.96)	4.80%	1.03	1.28
BANP	1	0.003069281	1.50 (1.15, 1.96)	4.80%	1.03	1.28

BANP	1	0.003069281	1.50 (1.15, 1.96)	4.80%	1.03	1.28
BLM	1	0.003819008	1.79 (1.21, 2.65)	5.40%	1.03	1.28
C10orf82	-1	0.00290893	0.53 (0.35, 0.81)	4.60%	1.03	1.3
C11orf34	-1	0.003273096	0.60 (0.43, 0.84)	4.90%	1.03	1.3
C12orf35	-1	0.003559999	0.52 (0.33, 0.81)	5.20%	1.03	1.29
C19orf76	1	0.002020895	1.50 (1.16, 1.94)	3.70%	1.03	1.29
C1orf106	1	0.003304843	1.94 (1.25, 3.01)	4.90%	1.03	1.27
C1orf106	1	0.003304843	1.94 (1.25, 3.01)	4.90%	1.03	1.27
C20orf185	1	0.003007008	1.45 (1.13, 1.85)	4.70%	1.03	1.27
C2orf65	-1	0.002411185	0.61 (0.44, 0.84)	4.20%	1.03	1.31
C4orf32	-1	0.003456897	0.56 (0.38, 0.82)	5.10%	1.03	1.3
C6orf124	1	0.002597838	1.72 (1.21, 2.46)	4.40%	1.03	1.29
C9orf130	-1	0.003706858	0.57 (0.39, 0.83)	5.30%	1.03	1.3
C9orf130	-1	0.003706858	0.57 (0.39, 0.83)	5.30%	1.03	1.3
CADM4	-1	0.002653642	0.63 (0.47, 0.85)	4.40%	1.03	1.31
CALCOCO1	-1	0.003000491	0.63 (0.46, 0.85)	4.70%	1.03	1.3
CALCOCO1	-1	0.003000491	0.63 (0.46, 0.85)	4.70%	1.03	1.3
CALCOCO1	-1	0.003000491	0.63 (0.46, 0.85)	4.70%	1.03	1.3
CCDC144NL	1	0.002348542	1.56 (1.17, 2.08)	4.10%	1.03	1.29
CCDC76	-1	0.004138708	0.53 (0.34, 0.82)	5.60%	1.03	1.29
CCDC92	-1	0.002468024	0.57 (0.40, 0.82)	4.20%	1.03	1.31
CD300C	-1	0.002609931	0.60 (0.43, 0.84)	4.40%	1.03	1.31
CD33	-1	0.003435908	0.59 (0.42, 0.84)	5.10%	1.03	1.3
CD33	-1	0.003435908	0.59 (0.42, 0.84)	5.10%	1.03	1.3
CD33	-1	0.003435908	0.59 (0.42, 0.84)	5.10%	1.03	1.3
CDC45	1	0.002832865	1.82 (1.23, 2.70)	4.60%	1.03	1.29
CDC45	1	0.002832865	1.82 (1.23, 2.70)	4.60%	1.03	1.29
CDC45	1	0.002832865	1.82 (1.23, 2.70)	4.60%	1.03	1.29
CENPN	1	0.003679416	1.73 (1.19, 2.50)	5.30%	1.03	1.28
CENPN	1	0.003679416	1.73 (1.19, 2.50)	5.30%	1.03	1.28
CENPN	1	0.003679416	1.73 (1.19, 2.50)	5.30%	1.03	1.28
CENPV	-1	0.002354532	0.64 (0.49, 0.86)	4.10%	1.03	1.31
CFHR1	1	0.001445939	1.29 (1.10, 1.51)	3.10%	1.03	1.23
CHKA	1	0.003263824	1.71 (1.20, 2.46)	4.90%	1.03	1.29
CHKA	1	0.003263824	1.71 (1.20, 2.46)	4.90%	1.03	1.29
CLEC4A	-1	0.003825871	0.58 (0.40, 0.84)	5.40%	1.03	1.3
CLEC4A	-1	0.003825871	0.58 (0.40, 0.84)	5.40%	1.03	1.3
CLEC4A	-1	0.003825871	0.58 (0.40, 0.84)	5.40%	1.03	1.3
CLEC4A	-1	0.003825871	0.58 (0.40, 0.84)	5.40%	1.03	1.3
CLPTM1	-1	0.00357314	0.60 (0.42, 0.85)	5.20%	1.03	1.3
CLPTM1	-1	0.00357314	0.60 (0.42, 0.85)	5.20%	1.03	1.3
COL20A1	1	0.002174665	1.59 (1.18, 2.13)	3.90%	1.03	1.3

COQ9	1	0.003239597	2.01 (1.26, 3.20)	4.90%	1.03	1.27
CRYZ	-1	0.002899901	0.59 (0.42, 0.84)	4.60%	1.03	1.31
CRYZ	-1	0.002899901	0.59 (0.42, 0.84)	4.60%	1.03	1.31
CRYZ	-1	0.002899901	0.59 (0.42, 0.84)	4.60%	1.03	1.31
CRYZ	-1	0.002899901	0.59 (0.42, 0.84)	4.60%	1.03	1.31
CYB5D1	-1	0.003353239	0.67 (0.51, 0.87)	5.00%	1.03	1.29
DCDC2	-1	0.00250085	0.59 (0.42, 0.83)	4.30%	1.03	1.31
DCDC2	-1	0.00250085	0.59 (0.42, 0.83)	4.30%	1.03	1.31
DEFB112	1	0.00201406	1.43 (1.14, 1.79)	3.70%	1.03	1.28
DFNA5	1	0.002721206	1.53 (1.16, 2.02)	4.50%	1.03	1.29
DFNA5	1	0.002721206	1.53 (1.16, 2.02)	4.50%	1.03	1.29
DFNA5	1	0.002721206	1.53 (1.16, 2.02)	4.50%	1.03	1.29
DIO1	-1	0.002787562	0.63 (0.46, 0.85)	4.50%	1.03	1.31
DIO1	-1	0.002787562	0.63 (0.46, 0.85)	4.50%	1.03	1.31
DIO1	-1	0.002787562	0.63 (0.46, 0.85)	4.50%	1.03	1.31
DIO1	-1	0.002787562	0.63 (0.46, 0.85)	4.50%	1.03	1.31
DIS3L	-1	0.003001161	0.56 (0.38, 0.82)	4.70%	1.03	1.31
DIS3L	-1	0.003001161	0.56 (0.38, 0.82)	4.70%	1.03	1.31
DLGAP5	1	0.00278647	1.94 (1.26, 2.99)	4.50%	1.03	1.28
DLGAP5	1	0.00278647	1.94 (1.26, 2.99)	4.50%	1.03	1.28
DLX4	1	0.00416168	1.88 (1.22, 2.89)	5.60%	1.03	1.27
DLX4	1	0.00416168	1.88 (1.22, 2.89)	5.60%	1.03	1.27
DNMT3B	1	0.002143803	1.59 (1.18, 2.13)	3.90%	1.03	1.3
DNMT3B	1	0.002143803	1.59 (1.18, 2.13)	3.90%	1.03	1.3
DNMT3B	1	0.002143803	1.59 (1.18, 2.13)	3.90%	1.03	1.3
DNMT3B	1	0.002143803	1.59 (1.18, 2.13)	3.90%	1.03	1.3
DPM3	1	0.003717491	1.78 (1.21, 2.63)	5.30%	1.03	1.28
DROSHA	1	0.002278248	1.67 (1.20, 2.33)	4.10%	1.03	1.3
DROSHA	1	0.002278248	1.67 (1.20, 2.33)	4.10%	1.03	1.3
DYNC1LI2	1	0.002945366	1.68 (1.19, 2.36)	4.70%	1.03	1.29
DYX1C1	-1	0.003170085	0.66 (0.50, 0.87)	4.90%	1.03	1.3
DYX1C1	-1	0.003170085	0.66 (0.50, 0.87)	4.90%	1.03	1.3
DYX1C1	-1	0.003170085	0.66 (0.50, 0.87)	4.90%	1.03	1.3
ECEL1	1	0.001529034	1.25 (1.09, 1.44)	3.10%	1.03	1.21
ENDOG	-1	0.002977538	0.60 (0.43, 0.84)	4.70%	1.03	1.31
EPOR	-1	0.002953308	0.65 (0.49, 0.86)	4.70%	1.03	1.3
EPOR	-1	0.002953308	0.65 (0.49, 0.86)	4.70%	1.03	1.3
ESRP2	1	0.00358533	1.74 (1.20, 2.53)	5.20%	1.03	1.28
FAM149A	-1	0.003077443	0.60 (0.43, 0.84)	4.80%	1.03	1.31
FAM149A	-1	0.003077443	0.60 (0.43, 0.84)	4.80%	1.03	1.31
FAM35A	-1	0.003261698	0.62 (0.45, 0.85)	4.90%	1.03	1.3
FAM38B	-1	0.003890881	0.43 (0.24, 0.76)	5.40%	1.03	1.26

FAM73A	-1	0.003419709	0.47 (0.29, 0.78)	5.10%	1.03	1.28
FBXO5	1	0.002655563	1.89 (1.25, 2.86)	4.40%	1.03	1.29
FBXO5	1	0.002655563	1.89 (1.25, 2.86)	4.40%	1.03	1.29
FGG	1	0.002203049	1.41 (1.13, 1.76)	4.00%	1.03	1.27
FGG	1	0.002203049	1.41 (1.13, 1.76)	4.00%	1.03	1.27
FLJ14186	1	0.002707068	1.37 (1.12, 1.68)	4.50%	1.03	1.26
FLJ42969	1	0.002377951	1.52 (1.16, 2.00)	4.10%	1.03	1.29
FSTL3	-1	0.003015843	0.60 (0.43, 0.84)	4.70%	1.03	1.31
GFOD2	1	0.00388773	1.92 (1.23, 2.98)	5.40%	1.03	1.27
GFOD2	1	0.00388773	1.92 (1.23, 2.98)	5.40%	1.03	1.27
GFOD2	1	0.00388773	1.92 (1.23, 2.98)	5.40%	1.03	1.27
GJC3	-1	0.002130385	0.66 (0.51, 0.86)	3.90%	1.03	1.31
GLG1	1	0.00232853	1.60 (1.18, 2.15)	4.10%	1.03	1.3
GLG1	1	0.00232853	1.60 (1.18, 2.15)	4.10%	1.03	1.3
GLG1	1	0.00232853	1.60 (1.18, 2.15)	4.10%	1.03	1.3
GLG1	1	0.00232853	1.60 (1.18, 2.15)	4.10%	1.03	1.3
GLG1	1	0.00232853	1.60 (1.18, 2.15)	4.10%	1.03	1.3
GMPR2	-1	0.002889811	0.61 (0.44, 0.84)	4.60%	1.03	1.31
GMPR2	-1	0.002889811	0.61 (0.44, 0.84)	4.60%	1.03	1.31
GMPR2	-1	0.002889811	0.61 (0.44, 0.84)	4.60%	1.03	1.31
GMPR2	-1	0.002889811	0.61 (0.44, 0.84)	4.60%	1.03	1.31
GNPDA2	-1	0.003200059	0.57 (0.39, 0.83)	4.90%	1.03	1.3
GPR78	1	0.001899031	1.30 (1.10, 1.54)	3.60%	1.03	1.23
HDGFRP2	-1	0.002470922	0.58 (0.41, 0.82)	4.20%	1.03	1.31
HDGFRP2	-1	0.002470922	0.58 (0.41, 0.82)	4.20%	1.03	1.31
HDGFRP3	-1	0.002866543	0.58 (0.41, 0.83)	4.60%	1.03	1.31
HLA-DQB2	-1	0.002601447	0.61 (0.44, 0.84)	4.40%	1.03	1.31
HMX2	1	0.001633074	1.36 (1.12, 1.66)	3.30%	1.03	1.26
IVNS1ABP	1	0.003215304	1.62 (1.17, 2.22)	4.90%	1.03	1.29
JKAMP	-1	0.002816042	0.58 (0.40, 0.83)	4.60%	1.03	1.31
JKAMP	-1	0.002816042	0.58 (0.40, 0.83)	4.60%	1.03	1.31
KCNMB2	1	0.002365787	1.55 (1.17, 2.05)	4.10%	1.03	1.29
KCNMB2	1	0.002365787	1.55 (1.17, 2.05)	4.10%	1.03	1.29
KIAA0182	1	0.00400237	1.79 (1.21, 2.67)	5.50%	1.03	1.27
KIAA0182	1	0.00400237	1.79 (1.21, 2.67)	5.50%	1.03	1.27
KIAA1524	1	0.002658234	1.76 (1.22, 2.56)	4.40%	1.03	1.29
KIAA1609	1	0.003411463	1.72 (1.20, 2.47)	5.10%	1.03	1.28
KIF14	1	0.002967379	1.90 (1.24, 2.91)	4.70%	1.03	1.28
KIF15	1	0.002847341	1.91 (1.25, 2.92)	4.60%	1.03	1.28
KIR3DL1	1	0.002292839	1.39 (1.12, 1.72)	4.10%	1.03	1.27
LILRA2	-1	0.003038167	0.62 (0.46, 0.85)	4.70%	1.03	1.3
LILRA2	-1	0.003038167	0.62 (0.46, 0.85)	4.70%	1.03	1.3

LMO2	-1	0.002944661	0.65 (0.48, 0.86)	4.70%	1.03	1.3
LMO2	-1	0.002944661	0.65 (0.48, 0.86)	4.70%	1.03	1.3
LMO2	-1	0.002944661	0.65 (0.48, 0.86)	4.70%	1.03	1.3
LOC100132707	-1	0.002472978	0.62 (0.45, 0.84)	4.20%	1.03	1.31
LOC100132707	-1	0.002472978	0.62 (0.45, 0.84)	4.20%	1.03	1.31
LOC100289187	-1	0.002804418	0.66 (0.50, 0.87)	4.60%	1.03	1.3
LOC100289187	-1	0.002804418	0.66 (0.50, 0.87)	4.60%	1.03	1.3
LOC100289187	-1	0.002804418	0.66 (0.50, 0.87)	4.60%	1.03	1.3
LOC146880	1	0.002469876	1.45 (1.14, 1.85)	4.20%	1.03	1.28
LOC146880	1	0.002469876	1.45 (1.14, 1.85)	4.20%	1.03	1.28
LOC283033	-1	0.002659531	0.60 (0.43, 0.84)	4.40%	1.03	1.31
LOC375190	-1	0.002118296	0.64 (0.48, 0.85)	3.90%	1.03	1.31
LOC401431	-1	0.002536678	0.65 (0.50, 0.86)	4.30%	1.03	1.3
LOC728606	-1	0.003271325	0.60 (0.42, 0.84)	4.90%	1.03	1.3
LOC730441	1	0.00284141	1.55 (1.16, 2.06)	4.60%	1.03	1.29
LRP11	1	0.002676431	1.85 (1.24, 2.77)	4.40%	1.03	1.29
LRRC49	-1	0.004003969	0.52 (0.33, 0.81)	5.50%	1.03	1.29
LRRC49	-1	0.004003969	0.52 (0.33, 0.81)	5.50%	1.03	1.29
LRRC49	-1	0.004003969	0.52 (0.33, 0.81)	5.50%	1.03	1.29
LRRC50	-1	0.003723262	0.57 (0.39, 0.83)	5.30%	1.03	1.3
LRRC69	1	0.00326634	1.64 (1.18, 2.28)	4.90%	1.03	1.29
LYPD1	-1	0.003495354	0.57 (0.39, 0.83)	5.10%	1.03	1.3
LYPD1	-1	0.003495354	0.57 (0.39, 0.83)	5.10%	1.03	1.3
MDGA2	1	0.002999416	1.51 (1.15, 1.98)	4.70%	1.03	1.28
MDGA2	1	0.002999416	1.51 (1.15, 1.98)	4.70%	1.03	1.28
MED13	1	0.001791043	1.40 (1.13, 1.73)	3.50%	1.03	1.27
MED23	1	0.002771728	1.43 (1.13, 1.80)	4.50%	1.03	1.27
MED23	1	0.002771728	1.43 (1.13, 1.80)	4.50%	1.03	1.27
MRPL33	-1	0.002810203	0.56 (0.39, 0.82)	4.60%	1.03	1.31
MRPL33	-1	0.002810203	0.56 (0.39, 0.82)	4.60%	1.03	1.31
MRPS25	1	0.00232796	1.57 (1.18, 2.11)	4.10%	1.03	1.29
NAALADL1	-1	0.003229161	0.59 (0.42, 0.84)	4.90%	1.03	1.3
NCOA2	1	0.0028789	1.57 (1.17, 2.11)	4.60%	1.03	1.29
NDC80	1	0.004332624	2.09 (1.26, 3.47)	5.70%	1.03	1.25
NEGR1	-1	0.003356882	0.60 (0.43, 0.84)	5.00%	1.03	1.3
NEK2	1	0.004390513	2.20 (1.28, 3.77)	5.80%	1.03	1.24
NEURL4	-1	0.002512267	0.61 (0.45, 0.84)	4.30%	1.03	1.31
NEURL4	-1	0.002512267	0.61 (0.45, 0.84)	4.30%	1.03	1.31
NIPBL	1	0.003678237	1.81 (1.21, 2.69)	5.30%	1.03	1.28
NIPBL	1	0.003678237	1.81 (1.21, 2.69)	5.30%	1.03	1.28
NKX2-3	1	0.00288716	1.51 (1.15, 1.98)	4.60%	1.03	1.28
NRIP3	-1	0.003165915	0.55 (0.37, 0.82)	4.90%	1.03	1.3

NSMCE1	-1	0.00397664	0.52 (0.33, 0.81)	5.50%	1.03	1.29
OGDHL	1	0.00273305	1.84 (1.24, 2.75)	4.50%	1.03	1.29
OGDHL	1	0.00273305	1.84 (1.24, 2.75)	4.50%	1.03	1.29
OGDHL	1	0.00273305	1.84 (1.24, 2.75)	4.50%	1.03	1.29
OMA1	-1	0.003329284	0.61 (0.44, 0.85)	5.00%	1.03	1.3
ORC6	1	0.002725216	1.84 (1.24, 2.75)	4.50%	1.03	1.29
OSCP1	-1	0.002803854	0.65 (0.48, 0.86)	4.60%	1.03	1.3
OSCP1	-1	0.002803854	0.65 (0.48, 0.86)	4.60%	1.03	1.3
P2RX4	-1	0.003773817	0.54 (0.35, 0.82)	5.40%	1.03	1.29
P4HA1	1	0.002479967	1.46 (1.14, 1.86)	4.20%	1.03	1.28
P4HA1	1	0.002479967	1.46 (1.14, 1.86)	4.20%	1.03	1.28
P4HA1	1	0.002479967	1.46 (1.14, 1.86)	4.20%	1.03	1.28
P4HA1	1	0.002479967	1.46 (1.14, 1.86)	4.20%	1.03	1.28
PCGF3	-1	0.002417253	0.66 (0.50, 0.86)	4.20%	1.03	1.3
PDE8A	1	0.002954651	1.58 (1.17, 2.13)	4.70%	1.03	1.29
PDE8A	1	0.002954651	1.58 (1.17, 2.13)	4.70%	1.03	1.29
PDIA5	1	0.003793083	1.64 (1.17, 2.28)	5.40%	1.03	1.28
PDIA5	1	0.003793083	1.64 (1.17, 2.28)	5.40%	1.03	1.28
PDSS2	1	0.002270205	1.30 (1.10, 1.53)	4.10%	1.03	1.23
PHACTR2	1	0.003548548	1.77 (1.20, 2.59)	5.20%	1.03	1.28
PHACTR2	1	0.003548548	1.77 (1.20, 2.59)	5.20%	1.03	1.28
PHACTR2	1	0.003548548	1.77 (1.20, 2.59)	5.20%	1.03	1.28
PHACTR2	1	0.003548548	1.77 (1.20, 2.59)	5.20%	1.03	1.28
PHYHD1	-1	0.002869757	0.57 (0.39, 0.82)	4.60%	1.03	1.31
PHYHD1	-1	0.002869757	0.57 (0.39, 0.82)	4.60%	1.03	1.31
PHYHD1	-1	0.002869757	0.57 (0.39, 0.82)	4.60%	1.03	1.31
PNKP	-1	0.002981421	0.55 (0.37, 0.81)	4.70%	1.03	1.31
PNMA2	-1	0.00372139	0.61 (0.44, 0.85)	5.30%	1.03	1.3
PODXL2	1	0.003649098	1.84 (1.22, 2.77)	5.30%	1.03	1.28
POLQ	1	0.002981188	1.84 (1.23, 2.76)	4.70%	1.03	1.28
POLR2D	-1	0.002769807	0.69 (0.55, 0.88)	4.50%	1.03	1.29
PRPF31	-1	0.003398135	0.50 (0.31, 0.79)	5.00%	1.03	1.29
PRSS23	-1	0.003988776	0.54 (0.35, 0.82)	5.50%	1.03	1.29
PSMA1	1	0.003851406	1.70 (1.19, 2.43)	5.40%	1.03	1.28
PSMA1	1	0.003851406	1.70 (1.19, 2.43)	5.40%	1.03	1.28
PSMA1	1	0.003851406	1.70 (1.19, 2.43)	5.40%	1.03	1.28
PTCD3	1	0.002483485	1.72 (1.21, 2.43)	4.20%	1.03	1.3
PTPRK	1	0.003767173	1.70 (1.19, 2.44)	5.40%	1.03	1.28
PTPRK	1	0.003767173	1.70 (1.19, 2.44)	5.40%	1.03	1.28
RAB11B	-1	0.003087506	0.59 (0.41, 0.83)	4.80%	1.03	1.31
RAB14	-1	0.002933672	0.60 (0.42, 0.84)	4.70%	1.03	1.31
RAB3GAP2	1	0.002212459	1.62 (1.19, 2.20)	4.00%	1.03	1.3

RAD51	1	0.003473055	1.82 (1.22, 2.71)	5.10%	1.03	1.28
RAD51	1	0.003473055	1.82 (1.22, 2.71)	5.10%	1.03	1.28
RAD51	1	0.003473055	1.82 (1.22, 2.71)	5.10%	1.03	1.28
RAD51	1	0.003473055	1.82 (1.22, 2.71)	5.10%	1.03	1.28
RALGPS1	-1	0.003164278	0.62 (0.45, 0.85)	4.90%	1.03	1.3
RALGPS1	-1	0.003164278	0.62 (0.45, 0.85)	4.90%	1.03	1.3
RALGPS1	-1	0.003164278	0.62 (0.45, 0.85)	4.90%	1.03	1.3
RALGPS1	-1	0.003164278	0.62 (0.45, 0.85)	4.90%	1.03	1.3
RASAL1	1	0.002891275	1.81 (1.22, 2.67)	4.60%	1.03	1.29
RASAL1	1	0.002891275	1.81 (1.22, 2.67)	4.60%	1.03	1.29
RASAL1	1	0.002891275	1.81 (1.22, 2.67)	4.60%	1.03	1.29
RBKS	-1	0.002599049	0.58 (0.41, 0.83)	4.40%	1.03	1.31
RETNLB	1	0.00184757	1.34 (1.11, 1.61)	3.50%	1.03	1.25
RG9MTD3	-1	0.003210008	0.60 (0.43, 0.84)	4.90%	1.03	1.3
RHCG	1	0.003916067	1.97 (1.24, 3.13)	5.40%	1.03	1.26
RIPK3	-1	0.003278775	0.65 (0.48, 0.86)	4.90%	1.03	1.3
RNF168	1	0.002917142	1.56 (1.16, 2.09)	4.60%	1.03	1.29
RNF19A	1	0.00310618	1.56 (1.16, 2.08)	4.80%	1.03	1.28
RNF19A	1	0.00310618	1.56 (1.16, 2.08)	4.80%	1.03	1.28
ROBO1	1	0.002242507	1.48 (1.15, 1.90)	4.00%	1.03	1.29
ROBO1	1	0.002242507	1.48 (1.15, 1.90)	4.00%	1.03	1.29
ROBO1	1	0.002242507	1.48 (1.15, 1.90)	4.00%	1.03	1.29
RPGR	-1	0.003675682	0.56 (0.38, 0.83)	5.30%	1.03	1.3
RPGR	-1	0.003675682	0.56 (0.38, 0.83)	5.30%	1.03	1.3
RPGRIP1	-1	0.002745549	0.58 (0.40, 0.83)	4.50%	1.03	1.31
SETBP1	-1	0.003662366	0.54 (0.35, 0.82)	5.30%	1.03	1.3
SETBP1	-1	0.003662366	0.54 (0.35, 0.82)	5.30%	1.03	1.3
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SGOL1	1	0.003377474	1.92 (1.24, 2.96)	5.00%	1.03	1.27
SIX5	-1	0.002411377	0.60 (0.43, 0.84)	4.20%	1.03	1.31
SLC25A32	1	0.002217418	1.60 (1.18, 2.16)	4.00%	1.03	1.3

SLC26A6	1	0.002285648	1.55 (1.17, 2.04)	4.10%	1.03	1.29
SLC26A6	1	0.002285648	1.55 (1.17, 2.04)	4.10%	1.03	1.29
SLC26A6	1	0.002285648	1.55 (1.17, 2.04)	4.10%	1.03	1.29
SLC26A6	1	0.002285648	1.55 (1.17, 2.04)	4.10%	1.03	1.29
SLC34A1	1	0.002879478	1.64 (1.18, 2.27)	4.60%	1.03	1.29
SLC34A1	1	0.002879478	1.64 (1.18, 2.27)	4.60%	1.03	1.29
SLC3A2	1	0.003758233	1.76 (1.20, 2.58)	5.40%	1.03	1.28
SLC3A2	1	0.003758233	1.76 (1.20, 2.58)	5.40%	1.03	1.28
SLC3A2	1	0.003758233	1.76 (1.20, 2.58)	5.40%	1.03	1.28
SLC3A2	1	0.003758233	1.76 (1.20, 2.58)	5.40%	1.03	1.28
SLC3A2	1	0.003758233	1.76 (1.20, 2.58)	5.40%	1.03	1.28
SLC3A2	1	0.003758233	1.76 (1.20, 2.58)	5.40%	1.03	1.28
SLC3A2	1	0.003758233	1.76 (1.20, 2.58)	5.40%	1.03	1.28
SNHG9	1	0.002692923	1.60 (1.18, 2.18)	4.50%	1.03	1.29
SORBS3	-1	0.002232728	0.62 (0.46, 0.84)	4.00%	1.03	1.31
SORBS3	-1	0.002232728	0.62 (0.46, 0.84)	4.00%	1.03	1.31
SOST	1	0.002828316	1.57 (1.17, 2.10)	4.60%	1.03	1.29
SREK1IP1	-1	0.00381954	0.56 (0.38, 0.83)	5.40%	1.03	1.3
SRP72	1	0.001984343	1.47 (1.15, 1.87)	3.70%	1.03	1.29
STRADA	1	0.001851162	1.44 (1.15, 1.82)	3.50%	1.03	1.28
STRADA	1	0.001851162	1.44 (1.15, 1.82)	3.50%	1.03	1.28
STRADA	1	0.001851162	1.44 (1.15, 1.82)	3.50%	1.03	1.28
STRADA	1	0.001851162	1.44 (1.15, 1.82)	3.50%	1.03	1.28
STRADA	1	0.001851162	1.44 (1.15, 1.82)	3.50%	1.03	1.28
STRADA	1	0.001851162	1.44 (1.15, 1.82)	3.50%	1.03	1.28
SVIP	-1	0.00233855	0.67 (0.52, 0.87)	4.10%	1.03	1.3
TAF9B	1	0.003841595	1.82 (1.21, 2.74)	5.40%	1.03	1.27
TALDO1	1	0.002598718	1.82 (1.23, 2.68)	4.40%	1.03	1.29
TARS	1	0.003276379	1.71 (1.20, 2.44)	4.90%	1.03	1.29
TBC1D19	-1	0.003039839	0.59 (0.41, 0.83)	4.70%	1.03	1.31
TEKT3	-1	0.003310535	0.57 (0.39, 0.83)	4.90%	1.03	1.3
TIGD7	-1	0.003861327	0.54 (0.35, 0.82)	5.40%	1.03	1.29
TJP1	1	0.003251585	1.62 (1.17, 2.23)	4.90%	1.03	1.29
TJP1	1	0.003251585	1.62 (1.17, 2.23)	4.90%	1.03	1.29
TLE1	1	0.00347973	1.85 (1.22, 2.80)	5.10%	1.03	1.28
TMEM221	-1	0.003086562	0.60 (0.43, 0.84)	4.80%	1.03	1.31
TNFAIP8L3	1	0.003178113	1.67 (1.19, 2.35)	4.90%	1.03	1.29
TOMM7	1	0.002338876	1.53 (1.16, 2.02)	4.10%	1.03	1.29
TPPP2	1	0.003263204	1.53 (1.15, 2.03)	4.90%	1.03	1.28
TPX2	1	0.003467271	2.06 (1.27, 3.35)	5.10%	1.03	1.26
TRIM8	-1	0.002552093	0.58 (0.40, 0.82)	4.30%	1.03	1.31
TTK	1	0.003825485	1.94 (1.24, 3.05)	5.40%	1.03	1.27

TTK	1	0.003825485	1.94 (1.24, 3.05)	5.40%	1.03	1.27
UBE2E2	1	0.003261146	1.77 (1.21, 2.59)	4.90%	1.03	1.28
UQCRB	1	0.003918973	2.01 (1.25, 3.24)	5.40%	1.03	1.26
UQCRB	1	0.003918973	2.01 (1.25, 3.24)	5.40%	1.03	1.26
USH1G	1	0.002435828	1.52 (1.16, 1.99)	4.20%	1.03	1.29
VAMP1	-1	0.003323775	0.55 (0.36, 0.82)	5.00%	1.03	1.3
VAMP1	-1	0.003323775	0.55 (0.36, 0.82)	5.00%	1.03	1.3
VAMP1	-1	0.003323775	0.55 (0.36, 0.82)	5.00%	1.03	1.3
VNN3	1	0.002945726	1.57 (1.17, 2.11)	4.70%	1.03	1.29
VNN3	1	0.002945726	1.57 (1.17, 2.11)	4.70%	1.03	1.29
WBSCR17	1	0.002745076	1.51 (1.15, 1.97)	4.50%	1.03	1.28
ZBTB34	-1	0.002143612	0.63 (0.47, 0.85)	3.90%	1.03	1.31
ZMYND10	-1	0.003201542	0.62 (0.45, 0.85)	4.90%	1.03	1.3
ZNF132	-1	0.002418386	0.70 (0.56, 0.88)	4.20%	1.03	1.28
ZNF137P	-1	0.002738324	0.66 (0.51, 0.87)	4.50%	1.03	1.3
ZNF142	-1	0.002752334	0.52 (0.34, 0.80)	4.50%	1.03	1.31
ZNF143	1	0.003902798	1.78 (1.20, 2.62)	5.40%	1.03	1.28
ZNF284	-1	0.001742621	0.72 (0.58, 0.88)	3.40%	1.03	1.28
ZNF343	-1	0.002492691	0.67 (0.52, 0.87)	4.30%	1.03	1.3
ZNF510	-1	0.003447286	0.63 (0.46, 0.86)	5.10%	1.03	1.3
ZNF85	-1	0.00269138	0.59 (0.42, 0.83)	4.50%	1.03	1.31
ZNF85	-1	0.00269138	0.59 (0.42, 0.83)	4.50%	1.03	1.31
ACER2	-1	0.005258002	0.59 (0.41, 0.86)	6.30%	1.02	1.29
AFF3	-1	0.006224386	0.61 (0.43, 0.87)	6.90%	1.02	1.28
AFF3	-1	0.006224386	0.61 (0.43, 0.87)	6.90%	1.02	1.28
AGBL4	-1	0.004756402	0.59 (0.41, 0.85)	6.10%	1.02	1.29
AGTR2	1	0.004593311	1.31 (1.09, 1.58)	5.90%	1.02	1.23
ALDH3A1	1	0.005741471	1.47 (1.12, 1.93)	6.60%	1.02	1.26
ALDH3A1	1	0.005741471	1.47 (1.12, 1.93)	6.60%	1.02	1.26
ALDH3A1	1	0.005741471	1.47 (1.12, 1.93)	6.60%	1.02	1.26
ALG1L	1	0.005751645	1.64 (1.15, 2.32)	6.60%	1.02	1.27
ALG1L	1	0.005751645	1.64 (1.15, 2.32)	6.60%	1.02	1.27
ALKBH5	-1	0.005864328	0.54 (0.35, 0.84)	6.70%	1.02	1.28
ANKK1	-1	0.004982445	0.56 (0.37, 0.84)	6.20%	1.02	1.29
ANKRD11	1	0.00420042	1.58 (1.16, 2.16)	5.60%	1.02	1.28
ANKZF1	-1	0.003835427	0.62 (0.45, 0.86)	5.40%	1.02	1.3
ANKZF1	-1	0.003835427	0.62 (0.45, 0.86)	5.40%	1.02	1.3
ANO10	1	0.005187033	1.81 (1.19, 2.74)	6.30%	1.02	1.26
ATP6V0C	-1	0.004151532	0.59 (0.42, 0.85)	5.60%	1.02	1.3
ATP6V0C	-1	0.004151532	0.59 (0.42, 0.85)	5.60%	1.02	1.3
B3GALNT2	1	0.004947216	1.81 (1.20, 2.75)	6.20%	1.02	1.26
B9D2	-1	0.004413471	0.64 (0.47, 0.87)	5.80%	1.02	1.29

BAGE	1	0.003883658	1.52 (1.14, 2.03)	5.40%	1.02	1.28
BBS12	-1	0.004913742	0.61 (0.43, 0.86)	6.20%	1.02	1.29
BBS12	-1	0.004913742	0.61 (0.43, 0.86)	6.20%	1.02	1.29
BUB1	1	0.004514942	1.93 (1.23, 3.03)	5.90%	1.02	1.26
C12orf26	-1	0.006126167	0.54 (0.35, 0.84)	6.90%	1.02	1.28
C12orf47	-1	0.005171331	0.67 (0.50, 0.89)	6.30%	1.02	1.28
C12orf48	1	0.004544654	1.76 (1.19, 2.60)	5.90%	1.02	1.27
C12orf5	-1	0.004934346	0.61 (0.44, 0.86)	6.20%	1.02	1.29
C12orf57	-1	0.00493224	0.70 (0.54, 0.90)	6.20%	1.02	1.27
C16orf58	-1	0.005936891	0.61 (0.43, 0.87)	6.80%	1.02	1.28
C18orf62	1	0.004064416	1.63 (1.17, 2.28)	5.60%	1.02	1.28
C19orf20	-1	0.005286341	0.65 (0.48, 0.88)	6.30%	1.02	1.28
C5orf30	-1	0.005136301	0.60 (0.42, 0.86)	6.20%	1.02	1.29
C6orf58	1	0.004731205	1.47 (1.13, 1.92)	6.00%	1.02	1.27
C9orf80	-1	0.004122841	0.61 (0.43, 0.85)	5.60%	1.02	1.3
C9orf9	-1	0.00449506	0.68 (0.52, 0.89)	5.90%	1.02	1.28
CASC5	1	0.005050283	2.06 (1.24, 3.41)	6.20%	1.02	1.25
CASC5	1	0.005050283	2.06 (1.24, 3.41)	6.20%	1.02	1.25
CBLN4	-1	0.005236558	0.55 (0.37, 0.84)	6.30%	1.02	1.28
CDKN3	1	0.00470614	1.56 (1.15, 2.11)	6.00%	1.02	1.27
CDKN3	1	0.00470614	1.56 (1.15, 2.11)	6.00%	1.02	1.27
CENPE	1	0.005043144	1.82 (1.20, 2.76)	6.20%	1.02	1.26
CHP	1	0.00474853	1.71 (1.18, 2.47)	6.10%	1.02	1.27
CHRM3	1	0.004463794	1.55 (1.14, 2.09)	5.80%	1.02	1.27
CLDN6	1	0.003130215	1.42 (1.13, 1.80)	4.80%	1.02	1.27
CLEC10A	-1	0.005671891	0.56 (0.37, 0.85)	6.60%	1.02	1.28
CLEC10A	-1	0.005671891	0.56 (0.37, 0.85)	6.60%	1.02	1.28
COL4A5	-1	0.005952194	0.63 (0.45, 0.88)	6.80%	1.02	1.28
COL4A5	-1	0.005952194	0.63 (0.45, 0.88)	6.80%	1.02	1.28
COMP	-1	0.005307774	0.65 (0.48, 0.88)	6.30%	1.02	1.28
CPA3	-1	0.004401849	0.64 (0.47, 0.87)	5.80%	1.02	1.29
CPLX3	1	0.003893832	1.47 (1.13, 1.90)	5.40%	1.02	1.27
CT62	-1	0.004298148	0.60 (0.43, 0.85)	5.70%	1.02	1.29
CTDSP1	-1	0.004831508	0.65 (0.48, 0.88)	6.10%	1.02	1.29
CTDSP1	-1	0.004831508	0.65 (0.48, 0.88)	6.10%	1.02	1.29
CTXN2	1	0.004461247	1.53 (1.14, 2.06)	5.80%	1.02	1.27
CYB5R1	-1	0.005236004	0.67 (0.50, 0.89)	6.30%	1.02	1.28
CYBRD1	-1	0.00448011	0.61 (0.44, 0.86)	5.80%	1.02	1.29
CYBRD1	-1	0.00448011	0.61 (0.44, 0.86)	5.80%	1.02	1.29
CYP4B1	-1	0.006117908	0.62 (0.44, 0.87)	6.90%	1.02	1.28
CYP4B1	-1	0.006117908	0.62 (0.44, 0.87)	6.90%	1.02	1.28
DARS2	-1	0.004193228	0.61 (0.43, 0.86)	5.60%	1.02	1.3

DCTD	-1	0.004336513	0.65 (0.48, 0.87)	5.70%	1.02	1.29
DCTD	-1	0.004336513	0.65 (0.48, 0.87)	5.70%	1.02	1.29
DDIT4	1	0.006657073	2.06 (1.22, 3.46)	7.10%	1.02	1.23
DDX12	1	0.005232168	1.71 (1.17, 2.50)	6.30%	1.02	1.27
DDX19A	1	0.005506264	1.72 (1.17, 2.51)	6.40%	1.02	1.27
DEPDC1B	1	0.005895254	1.80 (1.18, 2.73)	6.70%	1.02	1.26
DEPDC1B	1	0.005895254	1.80 (1.18, 2.73)	6.70%	1.02	1.26
DHCR7	1	0.004895545	1.61 (1.16, 2.25)	6.10%	1.02	1.27
DHCR7	1	0.004895545	1.61 (1.16, 2.25)	6.10%	1.02	1.27
DMWD	-1	0.004951827	0.70 (0.54, 0.90)	6.20%	1.02	1.27
DNAJC16	-1	0.005555333	0.61 (0.43, 0.87)	6.50%	1.02	1.29
DNAJC5	1	0.004961512	1.58 (1.15, 2.17)	6.20%	1.02	1.27
DNAL1	-1	0.005480966	0.62 (0.45, 0.87)	6.40%	1.02	1.29
DSG4	1	0.005276336	1.58 (1.15, 2.19)	6.30%	1.02	1.27
DSG4	1	0.005276336	1.58 (1.15, 2.19)	6.30%	1.02	1.27
DYNLL1	-1	0.005877927	0.58 (0.40, 0.86)	6.70%	1.02	1.28
DYNLL1	-1	0.005877927	0.58 (0.40, 0.86)	6.70%	1.02	1.28
DYNLL1	-1	0.005877927	0.58 (0.40, 0.86)	6.70%	1.02	1.28
E2F8	1	0.006071337	2.36 (1.28, 4.36)	6.90%	1.02	1.22
EFNA2	1	0.004879866	1.55 (1.14, 2.11)	6.10%	1.02	1.27
EGFEM1P	-1	0.006582566	0.53 (0.33, 0.84)	7.10%	1.02	1.27
ELL3	1	0.005132124	2.00 (1.23, 3.26)	6.20%	1.02	1.25
ERRFI1	1	0.004022383	1.57 (1.15, 2.13)	5.50%	1.02	1.28
EXD2	-1	0.004992909	0.62 (0.44, 0.87)	6.20%	1.02	1.29
EXD2	-1	0.004992909	0.62 (0.44, 0.87)	6.20%	1.02	1.29
EXD2	-1	0.004992909	0.62 (0.44, 0.87)	6.20%	1.02	1.29
EXD2	-1	0.004992909	0.62 (0.44, 0.87)	6.20%	1.02	1.29
EXD2	-1	0.004992909	0.62 (0.44, 0.87)	6.20%	1.02	1.29
EXD2	-1	0.004992909	0.62 (0.44, 0.87)	6.20%	1.02	1.29
EXD2	-1	0.004992909	0.62 (0.44, 0.87)	6.20%	1.02	1.29
FADS2	1	0.00451137	1.85 (1.21, 2.82)	5.90%	1.02	1.27
FAM19A1	1	0.004486786	1.72 (1.18, 2.51)	5.80%	1.02	1.27
FAM24A	1	0.003464128	1.48 (1.14, 1.93)	5.10%	1.02	1.28
FAM75C1	1	0.003067161	1.29 (1.09, 1.52)	4.80%	1.02	1.22
FAM83D	1	0.005258982	2.10 (1.25, 3.55)	6.30%	1.02	1.24
FANCA	1	0.006453602	1.74 (1.17, 2.60)	7.10%	1.02	1.26
FANCA	1	0.006453602	1.74 (1.17, 2.60)	7.10%	1.02	1.26
FARP2	-1	0.00480468	0.61 (0.43, 0.86)	6.10%	1.02	1.29
FCGBP	-1	0.005135347	0.61 (0.43, 0.86)	6.20%	1.02	1.29
FGF12	1	0.00508741	1.49 (1.13, 1.97)	6.20%	1.02	1.27
FGF12	1	0.00508741	1.49 (1.13, 1.97)	6.20%	1.02	1.27
FLJ31306	-1	0.005207343	0.56 (0.38, 0.84)	6.30%	1.02	1.29

FLJ31306	-1	0.005207343	0.56 (0.38, 0.84)	6.30%	1.02	1.29
FLYWCH2	-1	0.00602473	0.63 (0.45, 0.88)	6.80%	1.02	1.28
FLYWCH2	-1	0.00602473	0.63 (0.45, 0.88)	6.80%	1.02	1.28
FLYWCH2	-1	0.00602473	0.63 (0.45, 0.88)	6.80%	1.02	1.28
FRMD8	1	0.005100953	1.53 (1.14, 2.07)	6.20%	1.02	1.27
GDAP1L1	-1	0.004064739	0.64 (0.48, 0.87)	5.60%	1.02	1.29
GLIPR1L2	-1	0.004844215	0.67 (0.51, 0.88)	6.10%	1.02	1.28
GNAI1	1	0.004921212	1.52 (1.14, 2.03)	6.20%	1.02	1.27
GNN	-1	0.00547683	0.55 (0.36, 0.84)	6.40%	1.02	1.28
GOT1L1	1	0.005030656	1.50 (1.13, 2.00)	6.20%	1.02	1.27
GPR56	1	0.005127944	1.67 (1.17, 2.39)	6.20%	1.02	1.27
GPR56	1	0.005127944	1.67 (1.17, 2.39)	6.20%	1.02	1.27
GPR56	1	0.005127944	1.67 (1.17, 2.39)	6.20%	1.02	1.27
GPR56	1	0.005127944	1.67 (1.17, 2.39)	6.20%	1.02	1.27
GPR56	1	0.005127944	1.67 (1.17, 2.39)	6.20%	1.02	1.27
GPR56	1	0.005127944	1.67 (1.17, 2.39)	6.20%	1.02	1.27
GPR56	1	0.005127944	1.67 (1.17, 2.39)	6.20%	1.02	1.27
GPR56	1	0.005127944	1.67 (1.17, 2.39)	6.20%	1.02	1.27
GTF2F1	-1	0.004162542	0.65 (0.49, 0.87)	5.60%	1.02	1.29
HDAC7	-1	0.004641148	0.64 (0.46, 0.87)	6.00%	1.02	1.29
HDAC7	-1	0.004641148	0.64 (0.46, 0.87)	6.00%	1.02	1.29
HERV-V2	1	0.003227481	1.41 (1.12, 1.76)	4.90%	1.02	1.26
HHEX	-1	0.005145369	0.65 (0.48, 0.88)	6.20%	1.02	1.28
HMMR	1	0.005103266	1.91 (1.22, 3.02)	6.20%	1.02	1.26
HMMR	1	0.005103266	1.91 (1.22, 3.02)	6.20%	1.02	1.26
HMMR	1	0.005103266	1.91 (1.22, 3.02)	6.20%	1.02	1.26
HMMR	1	0.005103266	1.91 (1.22, 3.02)	6.20%	1.02	1.26
HN1	1	0.005386748	1.69 (1.17, 2.46)	6.40%	1.02	1.27
HN1	1	0.005386748	1.69 (1.17, 2.46)	6.40%	1.02	1.27
HN1	1	0.005386748	1.69 (1.17, 2.46)	6.40%	1.02	1.27
HRNR	-1	0.005968075	0.65 (0.48, 0.88)	6.80%	1.02	1.28
HS3ST1	1	0.005320771	1.50 (1.13, 2.00)	6.30%	1.02	1.27
HSPA9	1	0.005701331	1.64 (1.15, 2.32)	6.60%	1.02	1.27
IBSP	1	0.004575031	1.59 (1.15, 2.18)	5.90%	1.02	1.27
ICA1L	-1	0.005336018	0.59 (0.41, 0.85)	6.30%	1.02	1.29
ICA1L	-1	0.005336018	0.59 (0.41, 0.85)	6.30%	1.02	1.29
IFRD1	1	0.005335466	1.56 (1.14, 2.14)	6.30%	1.02	1.27
IFRD1	1	0.005335466	1.56 (1.14, 2.14)	6.30%	1.02	1.27
IFRD1	1	0.005335466	1.56 (1.14, 2.14)	6.30%	1.02	1.27
IFRD1	1	0.005335466	1.56 (1.14, 2.14)	6.30%	1.02	1.27
IFRD2	-1	0.004620541	0.68 (0.52, 0.89)	6.00%	1.02	1.28
IL6ST	-1	0.004669167	0.56 (0.37, 0.84)	6.00%	1.02	1.29

IL6ST	-1	0.004669167	0.56 (0.37, 0.84)	6.00%	1.02	1.29
IL6ST	-1	0.004669167	0.56 (0.37, 0.84)	6.00%	1.02	1.29
INCA1	-1	0.003958143	0.61 (0.43, 0.85)	5.50%	1.02	1.3
INCA1	-1	0.003958143	0.61 (0.43, 0.85)	5.50%	1.02	1.3
INCA1	-1	0.003958143	0.61 (0.43, 0.85)	5.50%	1.02	1.3
INCA1	-1	0.003958143	0.61 (0.43, 0.85)	5.50%	1.02	1.3
INO80	1	0.004710879	1.77 (1.19, 2.62)	6.00%	1.02	1.27
ISOC2	-1	0.006176895	0.61 (0.43, 0.87)	6.90%	1.02	1.28
ISOC2	-1	0.006176895	0.61 (0.43, 0.87)	6.90%	1.02	1.28
ISOC2	-1	0.006176895	0.61 (0.43, 0.87)	6.90%	1.02	1.28
KCNA4	1	0.004433861	1.41 (1.11, 1.79)	5.80%	1.02	1.26
KIAA1324	-1	0.005588146	0.68 (0.52, 0.89)	6.50%	1.02	1.27
KIF18A	1	0.005735098	1.80 (1.19, 2.72)	6.60%	1.02	1.26
KIF23	1	0.006540193	1.78 (1.17, 2.69)	7.10%	1.02	1.25
KIF23	1	0.006540193	1.78 (1.17, 2.69)	7.10%	1.02	1.25
KIF2C	1	0.005175206	1.97 (1.22, 3.17)	6.30%	1.02	1.25
KRCC1	-1	0.004567679	0.63 (0.46, 0.87)	5.90%	1.02	1.29
KRT16	1	0.004086786	1.43 (1.12, 1.83)	5.60%	1.02	1.26
KRT84	1	0.004004984	1.49 (1.14, 1.96)	5.50%	1.02	1.27
LACTB	-1	0.006101678	0.61 (0.43, 0.87)	6.90%	1.02	1.28
LACTB	-1	0.006101678	0.61 (0.43, 0.87)	6.90%	1.02	1.28
LAG3	-1	0.005742967	0.62 (0.45, 0.87)	6.60%	1.02	1.28
LIN9	1	0.004469851	1.73 (1.19, 2.53)	5.80%	1.02	1.27
LOC100190938	-1	0.005127469	0.64 (0.47, 0.88)	6.20%	1.02	1.29
LOC100190938	-1	0.005127469	0.64 (0.47, 0.88)	6.20%	1.02	1.29
LOC154860	1	0.004106036	1.50 (1.14, 1.98)	5.60%	1.02	1.27
LOC285735	1	0.003944073	1.43 (1.12, 1.82)	5.50%	1.02	1.26
LOC400643	1	0.004781617	1.30 (1.08, 1.55)	6.10%	1.02	1.22
LOC400657	-1	0.004993934	0.67 (0.50, 0.88)	6.20%	1.02	1.28
LY6D	1	0.004888422	1.46 (1.12, 1.90)	6.10%	1.02	1.26
LY6H	1	0.004151007	1.39 (1.11, 1.75)	5.60%	1.02	1.25
LY6H	1	0.004151007	1.39 (1.11, 1.75)	5.60%	1.02	1.25
LY6H	1	0.004151007	1.39 (1.11, 1.75)	5.60%	1.02	1.25
MAP2K2	-1	0.005892515	0.63 (0.46, 0.88)	6.70%	1.02	1.28
MAP3K4	1	0.004985634	1.43 (1.11, 1.84)	6.20%	1.02	1.26
MAP3K4	1	0.004985634	1.43 (1.11, 1.84)	6.20%	1.02	1.26
MAP7D2	1	0.005695576	1.53 (1.13, 2.06)	6.60%	1.02	1.26
MAP7D2	1	0.005695576	1.53 (1.13, 2.06)	6.60%	1.02	1.26
MAP7D2	1	0.005695576	1.53 (1.13, 2.06)	6.60%	1.02	1.26
MAP7D2	1	0.005695576	1.53 (1.13, 2.06)	6.60%	1.02	1.26
MCCC1	1	0.006217752	1.59 (1.14, 2.22)	6.90%	1.02	1.26
ME3	-1	0.005503433	0.61 (0.43, 0.86)	6.40%	1.02	1.29

ME3	-1	0.005503433	0.61 (0.43, 0.86)	6.40%	1.02	1.29
ME3	-1	0.005503433	0.61 (0.43, 0.86)	6.40%	1.02	1.29
MELK	1	0.006465586	1.77 (1.17, 2.66)	7.10%	1.02	1.26
MMP15	1	0.005850262	1.85 (1.19, 2.86)	6.70%	1.02	1.25
MOV10	-1	0.005238498	0.58 (0.39, 0.85)	6.30%	1.02	1.29
MOV10	-1	0.005238498	0.58 (0.39, 0.85)	6.30%	1.02	1.29
MRPL39	-1	0.003894605	0.61 (0.44, 0.85)	5.40%	1.02	1.3
MRPL39	-1	0.003894605	0.61 (0.44, 0.85)	5.40%	1.02	1.3
MSL3L2	1	0.005035426	1.60 (1.15, 2.23)	6.20%	1.02	1.27
MTBP	1	0.005853811	1.63 (1.15, 2.30)	6.70%	1.02	1.27
MTFR1	1	0.005110758	1.55 (1.14, 2.11)	6.20%	1.02	1.27
MTFR1	1	0.005110758	1.55 (1.14, 2.11)	6.20%	1.02	1.27
MTFR1	1	0.005110758	1.55 (1.14, 2.11)	6.20%	1.02	1.27
MTSS1L	1	0.004990967	1.65 (1.16, 2.34)	6.20%	1.02	1.27
MYOM3	-1	0.00522092	0.63 (0.46, 0.87)	6.30%	1.02	1.29
NCRNA00263	1	0.004190387	1.65 (1.17, 2.33)	5.60%	1.02	1.28
NDUFB10	-1	0.005128156	0.69 (0.54, 0.90)	6.20%	1.02	1.27
NEIL3	1	0.006472151	1.95 (1.21, 3.15)	7.10%	1.02	1.24
NKG7	1	0.003249298	1.34 (1.10, 1.62)	4.90%	1.02	1.24
NMNAT3	-1	0.004403783	0.56 (0.37, 0.83)	5.80%	1.02	1.29
NOD1	1	0.003051661	1.40 (1.12, 1.75)	4.70%	1.02	1.26
NPM1	1	0.004274784	1.78 (1.20, 2.66)	5.70%	1.02	1.27
NPM1	1	0.004274784	1.78 (1.20, 2.66)	5.70%	1.02	1.27
NPM1	1	0.004274784	1.78 (1.20, 2.66)	5.70%	1.02	1.27
NPY5R	-1	0.005397335	0.56 (0.37, 0.84)	6.40%	1.02	1.28
NRG2	1	0.005368867	1.65 (1.16, 2.34)	6.40%	1.02	1.27
NRG2	1	0.005368867	1.65 (1.16, 2.34)	6.40%	1.02	1.27
NRG2	1	0.005368867	1.65 (1.16, 2.34)	6.40%	1.02	1.27
NRG2	1	0.005368867	1.65 (1.16, 2.34)	6.40%	1.02	1.27
NRG2	1	0.005368867	1.65 (1.16, 2.34)	6.40%	1.02	1.27
NUDT16P1	-1	0.004513272	0.59 (0.41, 0.85)	5.90%	1.02	1.29
NUDT16P1	-1	0.004513272	0.59 (0.41, 0.85)	5.90%	1.02	1.29
NUF2	1	0.004146016	1.68 (1.18, 2.41)	5.60%	1.02	1.28
NUF2	1	0.004146016	1.68 (1.18, 2.41)	5.60%	1.02	1.28
NUSAP1	1	0.004608304	1.85 (1.21, 2.83)	6.00%	1.02	1.27
NUSAP1	1	0.004608304	1.85 (1.21, 2.83)	6.00%	1.02	1.27
NUSAP1	1	0.004608304	1.85 (1.21, 2.83)	6.00%	1.02	1.27
OIP5	1	0.00444449	1.74 (1.19, 2.54)	5.80%	1.02	1.27
PARD3	1	0.00638968	1.81 (1.18, 2.79)	7.10%	1.02	1.25
PARD3	1	0.00638968	1.81 (1.18, 2.79)	7.10%	1.02	1.25
PARD3	1	0.00638968	1.81 (1.18, 2.79)	7.10%	1.02	1.25
PARD3	1	0.00638968	1.81 (1.18, 2.79)	7.10%	1.02	1.25

PARD3	1	0.00638968	1.81 (1.18, 2.79)	7.10%	1.02	1.25
PARD3	1	0.00638968	1.81 (1.18, 2.79)	7.10%	1.02	1.25
PARD3	1	0.00638968	1.81 (1.18, 2.79)	7.10%	1.02	1.25
PARD3	1	0.00638968	1.81 (1.18, 2.79)	7.10%	1.02	1.25
PARD3	1	0.00638968	1.81 (1.18, 2.79)	7.10%	1.02	1.25
PARD3	1	0.00638968	1.81 (1.18, 2.79)	7.10%	1.02	1.25
PARD3	1	0.00638968	1.81 (1.18, 2.79)	7.10%	1.02	1.25
PCDH11X	1	0.003459139	1.50 (1.14, 1.96)	5.10%	1.02	1.28
PCDH11X	1	0.003459139	1.50 (1.14, 1.96)	5.10%	1.02	1.28
PCDH11X	1	0.003459139	1.50 (1.14, 1.96)	5.10%	1.02	1.28
PCDH11X	1	0.003459139	1.50 (1.14, 1.96)	5.10%	1.02	1.28
PCDH11X	1	0.003459139	1.50 (1.14, 1.96)	5.10%	1.02	1.28
PCDH11X	1	0.003459139	1.50 (1.14, 1.96)	5.10%	1.02	1.28
PCDH11X	1	0.003459139	1.50 (1.14, 1.96)	5.10%	1.02	1.28
PCDH11X	1	0.003459139	1.50 (1.14, 1.96)	5.10%	1.02	1.28
PDZD3	-1	0.004829406	0.57 (0.39, 0.84)	6.10%	1.02	1.29
PDZD3	-1	0.004829406	0.57 (0.39, 0.84)	6.10%	1.02	1.29
PDZD3	-1	0.004829406	0.57 (0.39, 0.84)	6.10%	1.02	1.29
PHIP	1	0.004453412	1.59 (1.16, 2.20)	5.80%	1.02	1.27
PHKB	1	0.00471534	1.49 (1.13, 1.96)	6.00%	1.02	1.27
PHKB	1	0.00471534	1.49 (1.13, 1.96)	6.00%	1.02	1.27
PHKG2	-1	0.006596304	0.52 (0.33, 0.83)	7.10%	1.02	1.27
PHKG2	-1	0.006596304	0.52 (0.33, 0.83)	7.10%	1.02	1.27
PIAS1	1	0.004108295	1.43 (1.12, 1.82)	5.60%	1.02	1.26
PLA2R1	-1	0.004141664	0.65 (0.48, 0.87)	5.60%	1.02	1.29
PLA2R1	-1	0.004141664	0.65 (0.48, 0.87)	5.60%	1.02	1.29
PLA2R1	-1	0.004141664	0.65 (0.48, 0.87)	5.60%	1.02	1.29
PLCD4	-1	0.005641861	0.60 (0.41, 0.86)	6.60%	1.02	1.28
POC1A	1	0.005505401	1.66 (1.16, 2.37)	6.40%	1.02	1.27
POC1A	1	0.005505401	1.66 (1.16, 2.37)	6.40%	1.02	1.27
POC1A	1	0.005505401	1.66 (1.16, 2.37)	6.40%	1.02	1.27
POMT2	-1	0.005356899	0.61 (0.43, 0.86)	6.40%	1.02	1.29
PPIL6	-1	0.00393157	0.60 (0.43, 0.85)	5.50%	1.02	1.3
PPIL6	-1	0.00393157	0.60 (0.43, 0.85)	5.50%	1.02	1.3
PPPDE1	1	0.004067992	1.62 (1.17, 2.26)	5.60%	1.02	1.28
PRPF8	-1	0.004322159	0.63 (0.46, 0.87)	5.70%	1.02	1.29
PSMC6	1	0.004415222	1.51 (1.14, 2.00)	5.80%	1.02	1.27
PTDSS1	1	0.005883984	1.64 (1.15, 2.33)	6.70%	1.02	1.26
PTGR1	-1	0.005430957	0.62 (0.44, 0.87)	6.40%	1.02	1.29
PTGR1	-1	0.005430957	0.62 (0.44, 0.87)	6.40%	1.02	1.29
PTGR1	-1	0.005430957	0.62 (0.44, 0.87)	6.40%	1.02	1.29
PTK2	1	0.003632816	1.53 (1.15, 2.04)	5.30%	1.02	1.28

PTK2	1	0.003632816	1.53 (1.15, 2.04)	5.30%	1.02	1.28
PTK2	1	0.003632816	1.53 (1.15, 2.04)	5.30%	1.02	1.28
PTPLB	1	0.003892716	1.62 (1.17, 2.25)	5.40%	1.02	1.28
PTRH2	1	0.004217013	1.50 (1.14, 1.99)	5.60%	1.02	1.27
RAB1A	1	0.005732236	1.58 (1.14, 2.19)	6.60%	1.02	1.27
RAB1A	1	0.005732236	1.58 (1.14, 2.19)	6.60%	1.02	1.27
RAB32	-1	0.004345803	0.68 (0.52, 0.89)	5.70%	1.02	1.28
RAD54B	1	0.004999815	1.60 (1.15, 2.23)	6.20%	1.02	1.27
RBM34	1	0.004614592	1.61 (1.16, 2.24)	6.00%	1.02	1.27
RBM34	1	0.004614592	1.61 (1.16, 2.24)	6.00%	1.02	1.27
RBM34	1	0.004614592	1.61 (1.16, 2.24)	6.00%	1.02	1.27
RERG	-1	0.006256771	0.60 (0.41, 0.86)	7.00%	1.02	1.28
RERG	-1	0.006256771	0.60 (0.41, 0.86)	7.00%	1.02	1.28
RG9MTD2	-1	0.005451293	0.68 (0.52, 0.89)	6.40%	1.02	1.27
RG9MTD2	-1	0.005451293	0.68 (0.52, 0.89)	6.40%	1.02	1.27
RG9MTD2	-1	0.005451293	0.68 (0.52, 0.89)	6.40%	1.02	1.27
RIBC1	-1	0.005090705	0.63 (0.46, 0.87)	6.20%	1.02	1.29
RIBC1	-1	0.005090705	0.63 (0.46, 0.87)	6.20%	1.02	1.29
RIPK2	1	0.004284645	1.66 (1.17, 2.34)	5.70%	1.02	1.28
RIPPLY2	1	0.00362128	1.39 (1.11, 1.73)	5.30%	1.02	1.26
RNF215	-1	0.003675247	0.65 (0.49, 0.87)	5.30%	1.02	1.29
RPL23AP82	1	0.003704396	1.41 (1.12, 1.78)	5.30%	1.02	1.26
RPL23AP82	1	0.003704396	1.41 (1.12, 1.78)	5.30%	1.02	1.26
RRM2	1	0.00530057	2.12 (1.25, 3.59)	6.30%	1.02	1.24
RRM2	1	0.00530057	2.12 (1.25, 3.59)	6.30%	1.02	1.24
RRP8	-1	0.004670198	0.63 (0.45, 0.87)	6.00%	1.02	1.29
RSPH1	-1	0.005024925	0.63 (0.45, 0.87)	6.20%	1.02	1.29
SAMD14	-1	0.003593798	0.73 (0.59, 0.90)	5.20%	1.02	1.26
SECISBP2	-1	0.00565347	0.56 (0.37, 0.85)	6.60%	1.02	1.28
SEPT1	-1	0.003777972	0.62 (0.45, 0.86)	5.40%	1.02	1.3
SEPT7	1	0.003942003	1.65 (1.17, 2.32)	5.50%	1.02	1.28
SEPT7	1	0.003942003	1.65 (1.17, 2.32)	5.50%	1.02	1.28
SET	-1	0.005433028	0.57 (0.39, 0.85)	6.40%	1.02	1.28
SET	-1	0.005433028	0.57 (0.39, 0.85)	6.40%	1.02	1.28
SH2B1	-1	0.004950832	0.65 (0.48, 0.88)	6.20%	1.02	1.29
SH2B1	-1	0.004950832	0.65 (0.48, 0.88)	6.20%	1.02	1.29
SH2B1	-1	0.004950832	0.65 (0.48, 0.88)	6.20%	1.02	1.29
SH2B1	-1	0.004950832	0.65 (0.48, 0.88)	6.20%	1.02	1.29
SH2B1	-1	0.004950832	0.65 (0.48, 0.88)	6.20%	1.02	1.29
SH2D6	1	0.004314207	1.42 (1.12, 1.82)	5.70%	1.02	1.26
SI	1	0.005422844	1.39 (1.10, 1.75)	6.40%	1.02	1.25
SIPA1L2	1	0.005953535	1.62 (1.15, 2.28)	6.80%	1.02	1.26

SLC28A1	1	0.005368187	1.71 (1.17, 2.50)	6.40%	1.02	1.27
SLC28A1	1	0.005368187	1.71 (1.17, 2.50)	6.40%	1.02	1.27
SLC6A10P	1	0.004304834	1.34 (1.10, 1.63)	5.70%	1.02	1.24
SLC7A8	-1	0.006012426	0.59 (0.40, 0.86)	6.80%	1.02	1.28
SLC7A8	-1	0.006012426	0.59 (0.40, 0.86)	6.80%	1.02	1.28
SLITRK2	1	0.004114097	1.45 (1.12, 1.86)	5.60%	1.02	1.27
SLITRK2	1	0.004114097	1.45 (1.12, 1.86)	5.60%	1.02	1.27
SLITRK2	1	0.004114097	1.45 (1.12, 1.86)	5.60%	1.02	1.27
SLITRK2	1	0.004114097	1.45 (1.12, 1.86)	5.60%	1.02	1.27
SLITRK2	1	0.004114097	1.45 (1.12, 1.86)	5.60%	1.02	1.27
SLITRK2	1	0.004114097	1.45 (1.12, 1.86)	5.60%	1.02	1.27
SLITRK2	1	0.004114097	1.45 (1.12, 1.86)	5.60%	1.02	1.27
SLITRK2	1	0.004114097	1.45 (1.12, 1.86)	5.60%	1.02	1.27
SMARCC1	1	0.004969555	1.61 (1.15, 2.24)	6.20%	1.02	1.27
SNRPB2	1	0.003112308	1.40 (1.12, 1.75)	4.80%	1.02	1.26
SNRPB2	1	0.003112308	1.40 (1.12, 1.75)	4.80%	1.02	1.26
SOCS6	-1	0.004297582	0.60 (0.42, 0.85)	5.70%	1.02	1.29
SOX17	-1	0.00472738	0.62 (0.44, 0.86)	6.00%	1.02	1.29
SOX2OT	-1	0.006142043	0.55 (0.35, 0.84)	6.90%	1.02	1.28
SPA17	-1	0.004800037	0.72 (0.57, 0.90)	6.10%	1.02	1.26
SPAG17	-1	0.006045057	0.60 (0.42, 0.86)	6.80%	1.02	1.28
SPINK8	1	0.005890681	1.59 (1.14, 2.22)	6.70%	1.02	1.27
SRBD1	1	0.003804838	1.55 (1.15, 2.09)	5.40%	1.02	1.28
SRD5A1	1	0.006103365	1.58 (1.14, 2.20)	6.90%	1.02	1.26
SRPRB	1	0.004270811	1.53 (1.14, 2.06)	5.70%	1.02	1.27
STK3	1	0.004308969	1.79 (1.20, 2.67)	5.70%	1.02	1.27
STON2	-1	0.005917452	0.55 (0.36, 0.84)	6.80%	1.02	1.28
TAF2	1	0.00478922	1.48 (1.13, 1.93)	6.10%	1.02	1.27
TBX3	-1	0.004788214	0.60 (0.43, 0.86)	6.10%	1.02	1.29
TBX3	-1	0.004788214	0.60 (0.43, 0.86)	6.10%	1.02	1.29
TDO2	1	0.005420059	1.57 (1.14, 2.16)	6.40%	1.02	1.27
TEKT2	-1	0.005472115	0.61 (0.43, 0.86)	6.40%	1.02	1.29
TEX101	-1	0.004405596	0.57 (0.39, 0.84)	5.80%	1.02	1.29
TEX101	-1	0.004405596	0.57 (0.39, 0.84)	5.80%	1.02	1.29
TFF2	1	0.002565639	1.30 (1.10, 1.53)	4.30%	1.02	1.23
TGFBR3	-1	0.005568795	0.59 (0.40, 0.86)	6.50%	1.02	1.28
TGFBR3	-1	0.005568795	0.59 (0.40, 0.86)	6.50%	1.02	1.28
TGFBR3	-1	0.005568795	0.59 (0.40, 0.86)	6.50%	1.02	1.28
TGFBR3	-1	0.005568795	0.59 (0.40, 0.86)	6.50%	1.02	1.28
TLX3	1	0.005429471	1.44 (1.11, 1.86)	6.40%	1.02	1.26
TM4SF20	-1	0.005502692	0.61 (0.43, 0.87)	6.40%	1.02	1.29
TMBIM1	-1	0.005802111	0.62 (0.44, 0.87)	6.70%	1.02	1.28

TMC6	1	0.004143969	1.69 (1.18, 2.42)	5.60%	1.02	1.28
TMC6	1	0.004143969	1.69 (1.18, 2.42)	5.60%	1.02	1.28
TMEM132B	1	0.003802933	1.57 (1.16, 2.13)	5.40%	1.02	1.28
TMEM165	1	0.003867527	1.49 (1.14, 1.96)	5.40%	1.02	1.27
TMEM167B	-1	0.005258342	0.67 (0.51, 0.89)	6.30%	1.02	1.28
TMEM49	1	0.005254418	1.54 (1.14, 2.09)	6.30%	1.02	1.27
TP53I3	-1	0.004119014	0.63 (0.47, 0.87)	5.60%	1.02	1.29
TP53I3	-1	0.004119014	0.63 (0.47, 0.87)	5.60%	1.02	1.29
TPH1	-1	0.004144358	0.59 (0.41, 0.85)	5.60%	1.02	1.3
TPRG1	-1	0.004865463	0.54 (0.35, 0.83)	6.10%	1.02	1.28
TRIP10	-1	0.004862787	0.66 (0.50, 0.88)	6.10%	1.02	1.28
TRYX3	1	0.005334529	1.48 (1.12, 1.95)	6.30%	1.02	1.26
TTLL9	-1	0.004802396	0.59 (0.41, 0.85)	6.10%	1.02	1.29
UBTF	-1	0.003797859	0.64 (0.48, 0.87)	5.40%	1.02	1.29
UBTF	-1	0.003797859	0.64 (0.48, 0.87)	5.40%	1.02	1.29
UBTF	-1	0.003797859	0.64 (0.48, 0.87)	5.40%	1.02	1.29
USP10	1	0.004974453	1.60 (1.15, 2.22)	6.20%	1.02	1.27
USP20	-1	0.006090279	0.52 (0.33, 0.83)	6.90%	1.02	1.27
USP20	-1	0.006090279	0.52 (0.33, 0.83)	6.90%	1.02	1.27
USP20	-1	0.006090279	0.52 (0.33, 0.83)	6.90%	1.02	1.27
USP6NL	1	0.005838641	1.62 (1.15, 2.28)	6.70%	1.02	1.27
USP6NL	1	0.005838641	1.62 (1.15, 2.28)	6.70%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VEGFA	1	0.004912488	1.55 (1.14, 2.11)	6.20%	1.02	1.27
VPS13D	1	0.00462902	1.61 (1.16, 2.25)	6.00%	1.02	1.27
VPS13D	1	0.00462902	1.61 (1.16, 2.25)	6.00%	1.02	1.27
WDR91	1	0.004652961	1.64 (1.16, 2.31)	6.00%	1.02	1.27
XPO1	1	0.0059138	1.68 (1.16, 2.43)	6.80%	1.02	1.26

ZNF197	-1	0.004824119	0.64 (0.47, 0.87)	6.10%	1.02	1.29
ZNF197	-1	0.004824119	0.64 (0.47, 0.87)	6.10%	1.02	1.29
ZNF239	-1	0.004350897	0.66 (0.50, 0.88)	5.80%	1.02	1.29
ZNF239	-1	0.004350897	0.66 (0.50, 0.88)	5.80%	1.02	1.29
ZNF239	-1	0.004350897	0.66 (0.50, 0.88)	5.80%	1.02	1.29
ZNF239	-1	0.004350897	0.66 (0.50, 0.88)	5.80%	1.02	1.29
ZNF346	1	0.005370981	1.47 (1.12, 1.94)	6.40%	1.02	1.26
ZNF434	-1	0.004137381	0.58 (0.40, 0.84)	5.60%	1.02	1.3
ZNF616	-1	0.004212388	0.57 (0.39, 0.84)	5.60%	1.02	1.29
ZNF619	-1	0.004847157	0.61 (0.43, 0.86)	6.10%	1.02	1.29
ZNF619	-1	0.004847157	0.61 (0.43, 0.86)	6.10%	1.02	1.29
ZNF619	-1	0.004847157	0.61 (0.43, 0.86)	6.10%	1.02	1.29
ZNF619	-1	0.004847157	0.61 (0.43, 0.86)	6.10%	1.02	1.29
ZNF710	1	0.004198366	1.37 (1.11, 1.71)	5.60%	1.02	1.25
ZNF738	-1	0.005996712	0.64 (0.47, 0.88)	6.80%	1.02	1.28
ZNRF2	1	0.002907072	1.35 (1.11, 1.64)	4.60%	1.02	1.25
ZSCAN16	-1	0.003648245	0.66 (0.50, 0.87)	5.30%	1.02	1.29
ZWILCH	1	0.006215321	1.62 (1.15, 2.28)	6.90%	1.02	1.26
ZWILCH	1	0.006215321	1.62 (1.15, 2.28)	6.90%	1.02	1.26
AARS	1	0.006581854	1.65 (1.15, 2.36)	7.10%	1.01	1.26
ABAT	-1	0.008694362	0.53 (0.33, 0.85)	8.20%	1.01	1.26
ABAT	-1	0.008694362	0.53 (0.33, 0.85)	8.20%	1.01	1.26
ABAT	-1	0.008694362	0.53 (0.33, 0.85)	8.20%	1.01	1.26
ABHD5	1	0.007921655	1.61 (1.13, 2.29)	7.80%	1.01	1.25
ABL1	-1	0.00834792	0.62 (0.44, 0.89)	8.00%	1.01	1.27
ABL1	-1	0.00834792	0.62 (0.44, 0.89)	8.00%	1.01	1.27
ABR	-1	0.007662518	0.60 (0.41, 0.87)	7.70%	1.01	1.27
ABR	-1	0.007662518	0.60 (0.41, 0.87)	7.70%	1.01	1.27
ABR	-1	0.007662518	0.60 (0.41, 0.87)	7.70%	1.01	1.27
ABTB2	1	0.008523209	1.52 (1.11, 2.07)	8.10%	1.01	1.25
ADAMTS8	-1	0.006436924	0.66 (0.48, 0.89)	7.10%	1.01	1.28
AFM	1	0.005145801	1.19 (1.05, 1.35)	6.20%	1.01	1.17
ALDH7A1	1	0.008021584	1.72 (1.15, 2.57)	7.90%	1.01	1.25
ALKBH3	-1	0.009889635	0.61 (0.42, 0.89)	8.70%	1.01	1.26
ALOX12	-1	0.00634658	0.62 (0.44, 0.88)	7.00%	1.01	1.28
ANTXRL	1	0.00868012	1.56 (1.12, 2.18)	8.20%	1.01	1.25
ARHGEF4	1	0.009414554	1.71 (1.14, 2.56)	8.50%	1.01	1.24
ARHGEF4	1	0.009414554	1.71 (1.14, 2.56)	8.50%	1.01	1.24
ASAH2B	-1	0.006655111	0.72 (0.57, 0.91)	7.10%	1.01	1.26
ASB13	-1	0.007573921	0.65 (0.47, 0.89)	7.70%	1.01	1.27
ASB13	-1	0.007573921	0.65 (0.47, 0.89)	7.70%	1.01	1.27
ASB13	-1	0.007573921	0.65 (0.47, 0.89)	7.70%	1.01	1.27

ASPM	1	0.006786143	1.91 (1.20, 3.05)	7.20%	1.01	1.24
ASTN2	-1	0.008824541	0.56 (0.36, 0.86)	8.20%	1.01	1.26
ASTN2	-1	0.008824541	0.56 (0.36, 0.86)	8.20%	1.01	1.26
ASTN2	-1	0.008824541	0.56 (0.36, 0.86)	8.20%	1.01	1.26
ASTN2	-1	0.008824541	0.56 (0.36, 0.86)	8.20%	1.01	1.26
ASTN2	-1	0.008824541	0.56 (0.36, 0.86)	8.20%	1.01	1.26
ASTN2	-1	0.008824541	0.56 (0.36, 0.86)	8.20%	1.01	1.26
ATL2	1	0.008592516	1.47 (1.10, 1.97)	8.10%	1.01	1.25
ATL2	1	0.008592516	1.47 (1.10, 1.97)	8.10%	1.01	1.25
ATL2	1	0.008592516	1.47 (1.10, 1.97)	8.10%	1.01	1.25
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
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ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
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ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
ATXN3	-1	0.009014078	0.62 (0.43, 0.89)	8.30%	1.01	1.27
AZIN1	1	0.009281268	1.47 (1.10, 1.95)	8.50%	1.01	1.25

AZIN1	1	0.009281268	1.47 (1.10, 1.95)	8.50%	1.01	1.25
BLOC1S1-RDH5	-1	0.00930281	0.62 (0.43, 0.89)	8.50%	1.01	1.27
BRD3	-1	0.008625203	0.58 (0.39, 0.87)	8.10%	1.01	1.27
BRD9	1	0.006755386	1.66 (1.15, 2.41)	7.20%	1.01	1.26
BRD9	1	0.006755386	1.66 (1.15, 2.41)	7.20%	1.01	1.26
BRD9	1	0.006755386	1.66 (1.15, 2.41)	7.20%	1.01	1.26
BUB1B	1	0.007054086	1.95 (1.20, 3.18)	7.30%	1.01	1.24
C12orf52	-1	0.006034719	0.72 (0.57, 0.91)	6.80%	1.01	1.26
C12orf53	-1	0.007888739	0.62 (0.43, 0.88)	7.80%	1.01	1.27
C12orf76	-1	0.006422511	0.60 (0.42, 0.87)	7.10%	1.01	1.28
C14orf132	-1	0.01017781	0.62 (0.43, 0.89)	8.90%	1.01	1.26
C14orf145	1	0.009860907	1.47 (1.10, 1.97)	8.70%	1.01	1.24
C14orf147	1	0.0076906	1.58 (1.13, 2.21)	7.70%	1.01	1.26
C14orf38	-1	0.008239414	0.63 (0.45, 0.89)	8.00%	1.01	1.27
C1orf174	-1	0.008033783	0.66 (0.48, 0.90)	7.90%	1.01	1.27
C1orf38	1	0.008713276	1.58 (1.12, 2.22)	8.20%	1.01	1.25
C1orf38	1	0.008713276	1.58 (1.12, 2.22)	8.20%	1.01	1.25
C1orf38	1	0.008713276	1.58 (1.12, 2.22)	8.20%	1.01	1.25
C1orf9	1	0.008402668	1.56 (1.12, 2.16)	8.10%	1.01	1.25
C1orf9	1	0.008402668	1.56 (1.12, 2.16)	8.10%	1.01	1.25
C1QTNF6	-1	0.006525076	0.67 (0.51, 0.90)	7.10%	1.01	1.27
C1QTNF6	-1	0.006525076	0.67 (0.51, 0.90)	7.10%	1.01	1.27
C4orf44	-1	0.007314886	0.66 (0.49, 0.89)	7.50%	1.01	1.27
C7orf63	-1	0.007739854	0.60 (0.41, 0.87)	7.70%	1.01	1.27
C7orf63	-1	0.007739854	0.60 (0.41, 0.87)	7.70%	1.01	1.27
C8orf73	1	0.00790054	1.92 (1.19, 3.12)	7.80%	1.01	1.24
C9orf46	-1	0.006592071	0.56 (0.37, 0.85)	7.10%	1.01	1.28
C9orf47	1	0.005586283	1.36 (1.09, 1.68)	6.50%	1.01	1.24
C9orf47	1	0.005586283	1.36 (1.09, 1.68)	6.50%	1.01	1.24
CACNA1B	1	0.008323894	1.47 (1.10, 1.97)	8.00%	1.01	1.25
CATSPERG	-1	0.0079658	0.62 (0.43, 0.88)	7.90%	1.01	1.27
CCDC101	-1	0.007432279	0.64 (0.46, 0.89)	7.60%	1.01	1.27
CCDC153	-1	0.007781985	0.61 (0.43, 0.88)	7.80%	1.01	1.27
CCDC28B	-1	0.009710454	0.62 (0.44, 0.89)	8.70%	1.01	1.26
CCDC66	-1	0.009413964	0.70 (0.54, 0.92)	8.50%	1.01	1.25
CCDC66	-1	0.009413964	0.70 (0.54, 0.92)	8.50%	1.01	1.25
CCDC66	-1	0.009413964	0.70 (0.54, 0.92)	8.50%	1.01	1.25
CCDC68	-1	0.006409628	0.65 (0.48, 0.89)	7.10%	1.01	1.28
CCDC68	-1	0.006409628	0.65 (0.48, 0.89)	7.10%	1.01	1.28
CCDC85A	-1	0.006939346	0.57 (0.38, 0.86)	7.30%	1.01	1.27
CCDC97	-1	0.008529916	0.62 (0.43, 0.88)	8.10%	1.01	1.27
CDC73	1	0.008041561	1.69 (1.15, 2.49)	7.90%	1.01	1.25

CDH8	1	0.008791148	1.52 (1.11, 2.08)	8.20%	1.01	1.25
CENPO	1	0.008398103	1.87 (1.17, 2.98)	8.10%	1.01	1.24
CENPO	1	0.008398103	1.87 (1.17, 2.98)	8.10%	1.01	1.24
CENPW	1	0.010108567	1.63 (1.12, 2.36)	8.90%	1.01	1.24
CFDP1	1	0.009181598	1.42 (1.09, 1.84)	8.50%	1.01	1.24
CHCHD10	1	0.007522027	2.38 (1.26, 4.50)	7.70%	1.01	1.2
CHI3L1	1	0.006668226	1.67 (1.15, 2.42)	7.10%	1.01	1.26
CIT	1	0.007377258	1.85 (1.18, 2.89)	7.60%	1.01	1.24
CLASRP	-1	0.008231783	0.66 (0.48, 0.90)	8.00%	1.01	1.27
CLCN5	1	0.009310865	1.55 (1.11, 2.16)	8.50%	1.01	1.25
CLCN5	1	0.009310865	1.55 (1.11, 2.16)	8.50%	1.01	1.25
CLCN5	1	0.009310865	1.55 (1.11, 2.16)	8.50%	1.01	1.25
CLEC16A	-1	0.010281483	0.56 (0.36, 0.87)	8.90%	1.01	1.26
CMA1	-1	0.008693923	0.61 (0.42, 0.88)	8.20%	1.01	1.27
CNGA1	1	0.00795389	1.47 (1.11, 1.95)	7.90%	1.01	1.25
CNGA1	1	0.00795389	1.47 (1.11, 1.95)	7.90%	1.01	1.25
COMMD9	-1	0.007675478	0.65 (0.48, 0.89)	7.70%	1.01	1.27
COMMD9	-1	0.007675478	0.65 (0.48, 0.89)	7.70%	1.01	1.27
CPLX2	1	0.008558358	1.51 (1.11, 2.05)	8.10%	1.01	1.25
CPLX2	1	0.008558358	1.51 (1.11, 2.05)	8.10%	1.01	1.25
CPLX4	1	0.00691338	1.42 (1.10, 1.84)	7.30%	1.01	1.25
CRABP1	1	0.006626223	1.53 (1.13, 2.09)	7.10%	1.01	1.26
CRMP1	-1	0.007392616	0.64 (0.46, 0.89)	7.60%	1.01	1.27
CRMP1	-1	0.007392616	0.64 (0.46, 0.89)	7.60%	1.01	1.27
CSPG5	1	0.009780303	1.84 (1.16, 2.92)	8.70%	1.01	1.23
CYB5D2	-1	0.006826525	0.64 (0.47, 0.88)	7.20%	1.01	1.28
CYB5D2	-1	0.006826525	0.64 (0.47, 0.88)	7.20%	1.01	1.28
CYB5D2	-1	0.006826525	0.64 (0.47, 0.88)	7.20%	1.01	1.28
CYP4F8	-1	0.006572164	0.56 (0.37, 0.85)	7.10%	1.01	1.28
DBF4	1	0.007605751	1.63 (1.14, 2.33)	7.70%	1.01	1.26
DCAF16	-1	0.006850158	0.56 (0.36, 0.85)	7.20%	1.01	1.27
DEFB126	1	0.009243031	1.35 (1.08, 1.70)	8.50%	1.01	1.23
DERA	-1	0.005991399	0.67 (0.51, 0.89)	6.80%	1.01	1.27
DHRS3	1	0.006553888	1.67 (1.15, 2.41)	7.10%	1.01	1.26
DHRS4	-1	0.007490633	0.65 (0.48, 0.89)	7.60%	1.01	1.27
DHX40	1	0.006401593	1.44 (1.11, 1.88)	7.10%	1.01	1.25
DHX40	1	0.006401593	1.44 (1.11, 1.88)	7.10%	1.01	1.25
DLEC1	-1	0.007441555	0.57 (0.37, 0.86)	7.60%	1.01	1.27
DLEC1	-1	0.007441555	0.57 (0.37, 0.86)	7.60%	1.01	1.27
DMXL2	1	0.006523881	1.39 (1.10, 1.77)	7.10%	1.01	1.25
DMXL2	1	0.006523881	1.39 (1.10, 1.77)	7.10%	1.01	1.25
DMXL2	1	0.006523881	1.39 (1.10, 1.77)	7.10%	1.01	1.25

DNAJC12	-1	0.008733264	0.61 (0.42, 0.88)	8.20%	1.01	1.27
DNAJC12	-1	0.008733264	0.61 (0.42, 0.88)	8.20%	1.01	1.27
DUS2L	1	0.006904869	1.58 (1.13, 2.21)	7.30%	1.01	1.26
ECT2	1	0.006333315	1.61 (1.14, 2.27)	7.00%	1.01	1.26
EIF2AK1	1	0.006304207	1.58 (1.14, 2.19)	7.00%	1.01	1.26
EIF2AK1	1	0.006304207	1.58 (1.14, 2.19)	7.00%	1.01	1.26
ELP3	-1	0.008530309	0.59 (0.40, 0.87)	8.10%	1.01	1.27
EML4	1	0.00939952	1.49 (1.10, 2.00)	8.50%	1.01	1.25
EML4	1	0.00939952	1.49 (1.10, 2.00)	8.50%	1.01	1.25
EMP3	-1	0.009949959	0.61 (0.42, 0.89)	8.80%	1.01	1.26
EXT1	1	0.008271434	1.54 (1.12, 2.12)	8.00%	1.01	1.25
EZR	1	0.006750056	1.45 (1.11, 1.91)	7.20%	1.01	1.25
EZR	1	0.006750056	1.45 (1.11, 1.91)	7.20%	1.01	1.25
FAF2	1	0.008604571	1.62 (1.13, 2.33)	8.10%	1.01	1.25
FAM179B	-1	0.007462783	0.57 (0.38, 0.86)	7.60%	1.01	1.27
FAM20A	1	0.008860107	1.62 (1.13, 2.32)	8.30%	1.01	1.25
FAM20A	1	0.008860107	1.62 (1.13, 2.32)	8.30%	1.01	1.25
FAM3C	1	0.006674997	1.57 (1.13, 2.18)	7.10%	1.01	1.26
FAM3C	1	0.006674997	1.57 (1.13, 2.18)	7.10%	1.01	1.26
FAM5C	1	0.007019078	1.54 (1.13, 2.11)	7.30%	1.01	1.26
FAM66A	-1	0.007271558	0.69 (0.53, 0.91)	7.50%	1.01	1.26
FAM71E1	-1	0.006859843	0.65 (0.47, 0.89)	7.20%	1.01	1.28
FANCI	1	0.006580511	1.50 (1.12, 2.01)	7.10%	1.01	1.26
FANCI	1	0.006580511	1.50 (1.12, 2.01)	7.10%	1.01	1.26
FBXL13	-1	0.007857688	0.65 (0.47, 0.89)	7.80%	1.01	1.27
FBXL13	-1	0.007857688	0.65 (0.47, 0.89)	7.80%	1.01	1.27
FBXL3	-1	0.006493504	0.58 (0.40, 0.86)	7.10%	1.01	1.28
FBXW7	1	0.006175921	1.49 (1.12, 1.99)	6.90%	1.01	1.26
FBXW7	1	0.006175921	1.49 (1.12, 1.99)	6.90%	1.01	1.26
FBXW7	1	0.006175921	1.49 (1.12, 1.99)	6.90%	1.01	1.26
FHAD1	-1	0.008426078	0.71 (0.54, 0.91)	8.10%	1.01	1.26
FIGF	1	0.009002018	1.69 (1.14, 2.50)	8.30%	1.01	1.25
FLII	-1	0.008128059	0.61 (0.43, 0.88)	7.90%	1.01	1.27
FLJ34503	1	0.006440243	1.52 (1.12, 2.05)	7.10%	1.01	1.26
FSD1L	-1	0.009083561	0.66 (0.49, 0.90)	8.40%	1.01	1.26
FSD1L	-1	0.009083561	0.66 (0.49, 0.90)	8.40%	1.01	1.26
FSD1L	-1	0.009083561	0.66 (0.49, 0.90)	8.40%	1.01	1.26
FST	-1	0.006099071	0.66 (0.48, 0.89)	6.90%	1.01	1.28
FST	-1	0.006099071	0.66 (0.48, 0.89)	6.90%	1.01	1.28
FXN	-1	0.00959081	0.63 (0.44, 0.89)	8.60%	1.01	1.26
FXN	-1	0.00959081	0.63 (0.44, 0.89)	8.60%	1.01	1.26
FXN	-1	0.00959081	0.63 (0.44, 0.89)	8.60%	1.01	1.26

GABRG2	1	0.00801239	1.48 (1.11, 1.97)	7.90%	1.01	1.25
GABRG2	1	0.00801239	1.48 (1.11, 1.97)	7.90%	1.01	1.25
GABRG2	1	0.00801239	1.48 (1.11, 1.97)	7.90%	1.01	1.25
GFPT1	1	0.006343975	1.56 (1.13, 2.14)	7.00%	1.01	1.26
GGT8P	1	0.00992679	1.62 (1.12, 2.33)	8.80%	1.01	1.24
GKN1	1	0.007050806	1.47 (1.11, 1.95)	7.30%	1.01	1.25
GLRX5	-1	0.008313892	0.65 (0.47, 0.89)	8.00%	1.01	1.27
GPR68	-1	0.009262259	0.62 (0.43, 0.89)	8.50%	1.01	1.27
GPR68	-1	0.009262259	0.62 (0.43, 0.89)	8.50%	1.01	1.27
GPS2	-1	0.007595274	0.66 (0.49, 0.90)	7.70%	1.01	1.27
GREB1L	-1	0.007839939	0.62 (0.43, 0.88)	7.80%	1.01	1.27
GRPEL1	-1	0.006700841	0.62 (0.44, 0.88)	7.10%	1.01	1.28
GSTM4	-1	0.005934056	0.71 (0.56, 0.91)	6.80%	1.01	1.26
GSTM4	-1	0.005934056	0.71 (0.56, 0.91)	6.80%	1.01	1.26
GSTM4	-1	0.005934056	0.71 (0.56, 0.91)	6.80%	1.01	1.26
GTF2IRD2	-1	0.006754304	0.60 (0.41, 0.87)	7.20%	1.01	1.28
HCN1	-1	0.009201866	0.58 (0.38, 0.87)	8.50%	1.01	1.26
HEATR6	1	0.009234691	1.43 (1.09, 1.87)	8.50%	1.01	1.24
HEBP1	-1	0.007381555	0.55 (0.35, 0.85)	7.60%	1.01	1.27
HEBP2	1	0.009915175	1.57 (1.11, 2.21)	8.80%	1.01	1.25
HERPUD1	1	0.008338896	1.48 (1.11, 1.98)	8.00%	1.01	1.25
HERPUD1	1	0.008338896	1.48 (1.11, 1.98)	8.00%	1.01	1.25
HERPUD1	1	0.008338896	1.48 (1.11, 1.98)	8.00%	1.01	1.25
HEXA	-1	0.006684966	0.59 (0.40, 0.86)	7.10%	1.01	1.28
HNRNPA2B1	1	0.006193844	1.35 (1.09, 1.68)	6.90%	1.01	1.24
HNRNPA2B1	1	0.006193844	1.35 (1.09, 1.68)	6.90%	1.01	1.24
HSPA1L	-1	0.009960713	0.66 (0.48, 0.91)	8.80%	1.01	1.26
IFT27	-1	0.008743864	0.65 (0.47, 0.90)	8.20%	1.01	1.27
IFT27	-1	0.008743864	0.65 (0.47, 0.90)	8.20%	1.01	1.27
IFT27	-1	0.008743864	0.65 (0.47, 0.90)	8.20%	1.01	1.27
IFT27	-1	0.008743864	0.65 (0.47, 0.90)	8.20%	1.01	1.27
IGF2R	1	0.009756773	1.63 (1.13, 2.37)	8.70%	1.01	1.24
IL1A	1	0.009440424	1.69 (1.14, 2.52)	8.50%	1.01	1.24
IL20RB	1	0.006998603	1.58 (1.13, 2.21)	7.30%	1.01	1.26
IQCC	-1	0.006678534	0.66 (0.48, 0.89)	7.10%	1.01	1.28
IQCC	-1	0.006678534	0.66 (0.48, 0.89)	7.10%	1.01	1.28
IQCF5	1	0.007048357	1.29 (1.07, 1.55)	7.30%	1.01	1.21
IQCG	1	0.00660325	1.25 (1.06, 1.48)	7.10%	1.01	1.2
IQCG	1	0.00660325	1.25 (1.06, 1.48)	7.10%	1.01	1.2
ITCH	1	0.007636272	1.69 (1.15, 2.47)	7.70%	1.01	1.25
ITFG1	1	0.006426544	1.46 (1.11, 1.91)	7.10%	1.01	1.26
JHDM1D	1	0.006479536	1.57 (1.14, 2.18)	7.10%	1.01	1.26

KCNK13	-1	0.007077097	0.52 (0.32, 0.84)	7.40%	1.01	1.26
KCNMB3	-1	0.006827703	0.78 (0.65, 0.93)	7.20%	1.01	1.22
KCNMB3	-1	0.006827703	0.78 (0.65, 0.93)	7.20%	1.01	1.22
KCNMB3	-1	0.006827703	0.78 (0.65, 0.93)	7.20%	1.01	1.22
KCNMB3	-1	0.006827703	0.78 (0.65, 0.93)	7.20%	1.01	1.22
KCNMB3	-1	0.006827703	0.78 (0.65, 0.93)	7.20%	1.01	1.22
KCNMB3	-1	0.006827703	0.78 (0.65, 0.93)	7.20%	1.01	1.22
KDM4D	-1	0.008522948	0.61 (0.43, 0.88)	8.10%	1.01	1.27
KIAA0753	-1	0.007526058	0.56 (0.36, 0.86)	7.70%	1.01	1.27
KIAA1024	1	0.006800873	1.56 (1.13, 2.16)	7.20%	1.01	1.26
KIF13B	-1	0.010103096	0.58 (0.39, 0.88)	8.90%	1.01	1.26
KIF20B	1	0.006596402	1.65 (1.15, 2.36)	7.10%	1.01	1.26
KITLG	-1	0.00932099	0.58 (0.39, 0.87)	8.50%	1.01	1.26
KITLG	-1	0.00932099	0.58 (0.39, 0.87)	8.50%	1.01	1.26
KLHDC1	-1	0.006587563	0.63 (0.45, 0.88)	7.10%	1.01	1.28
KRTCAP2	1	0.009481883	1.58 (1.12, 2.23)	8.60%	1.01	1.25
LCN2	1	0.007623799	1.54 (1.12, 2.13)	7.70%	1.01	1.26
LGSN	1	0.00714657	1.52 (1.12, 2.07)	7.40%	1.01	1.26
LGSN	1	0.00714657	1.52 (1.12, 2.07)	7.40%	1.01	1.26
LHX1	1	0.007831619	1.48 (1.11, 1.98)	7.80%	1.01	1.25
LIMA1	-1	0.008443232	0.60 (0.42, 0.88)	8.10%	1.01	1.27
LIMA1	-1	0.008443232	0.60 (0.42, 0.88)	8.10%	1.01	1.27
LIMA1	-1	0.008443232	0.60 (0.42, 0.88)	8.10%	1.01	1.27
LMAN2L	-1	0.009248927	0.63 (0.45, 0.89)	8.50%	1.01	1.27
LMAN2L	-1	0.009248927	0.63 (0.45, 0.89)	8.50%	1.01	1.27
LMAN2L	-1	0.009248927	0.63 (0.45, 0.89)	8.50%	1.01	1.27
LMAN2L	-1	0.009248927	0.63 (0.45, 0.89)	8.50%	1.01	1.27
LMAN2L	-1	0.009248927	0.63 (0.45, 0.89)	8.50%	1.01	1.27
LMAN2L	-1	0.009248927	0.63 (0.45, 0.89)	8.50%	1.01	1.27
LOC100188947	-1	0.00851099	0.61 (0.42, 0.88)	8.10%	1.01	1.27
LOC100288842	-1	0.00809771	0.63 (0.45, 0.89)	7.90%	1.01	1.27
LOC100379224	-1	0.009205722	0.64 (0.46, 0.90)	8.50%	1.01	1.27
LOC338799	-1	0.007972298	0.55 (0.35, 0.86)	7.90%	1.01	1.27
LOC440335	-1	0.00981157	0.63 (0.44, 0.89)	8.70%	1.01	1.26
LOC440335	-1	0.00981157	0.63 (0.44, 0.89)	8.70%	1.01	1.26
LOC440335	-1	0.00981157	0.63 (0.44, 0.89)	8.70%	1.01	1.26
LOC57653	-1	0.009455291	0.66 (0.48, 0.90)	8.60%	1.01	1.26
LOC57653	-1	0.009455291	0.66 (0.48, 0.90)	8.60%	1.01	1.26
LOC57653	-1	0.009455291	0.66 (0.48, 0.90)	8.60%	1.01	1.26
LOC595101	-1	0.006518385	0.58 (0.39, 0.86)	7.10%	1.01	1.28
LOC643037	1	0.009129291	1.46 (1.10, 1.93)	8.40%	1.01	1.24
LOC729375	-1	0.009550732	0.65 (0.47, 0.90)	8.60%	1.01	1.26

LOC729668	1	0.008925516	1.54 (1.11, 2.12)	8.30%	1.01	1.25
LRPPRC	1	0.009760881	1.55 (1.11, 2.17)	8.70%	1.01	1.25
LRRC28	1	0.009655452	1.58 (1.12, 2.23)	8.60%	1.01	1.25
LRRC42	-1	0.006569663	0.60 (0.42, 0.87)	7.10%	1.01	1.28
LRRC4C	-1	0.007662013	0.56 (0.37, 0.86)	7.70%	1.01	1.27
LSS	1	0.00963785	1.74 (1.14, 2.65)	8.60%	1.01	1.24
LSS	1	0.00963785	1.74 (1.14, 2.65)	8.60%	1.01	1.24
LSS	1	0.00963785	1.74 (1.14, 2.65)	8.60%	1.01	1.24
LSS	1	0.00963785	1.74 (1.14, 2.65)	8.60%	1.01	1.24
LYPD6	-1	0.006710307	0.68 (0.52, 0.90)	7.20%	1.01	1.27
LYPD6	-1	0.006710307	0.68 (0.52, 0.90)	7.20%	1.01	1.27
LYZL6	1	0.008275122	1.50 (1.11, 2.02)	8.00%	1.01	1.25
LYZL6	1	0.008275122	1.50 (1.11, 2.02)	8.00%	1.01	1.25
LZTFL1	-1	0.009526935	0.65 (0.47, 0.90)	8.60%	1.01	1.26
MAN2B2	-1	0.008606344	0.61 (0.42, 0.88)	8.10%	1.01	1.27
MAP2K7	-1	0.006674321	0.59 (0.41, 0.86)	7.10%	1.01	1.28
MAPK13	-1	0.007291857	0.66 (0.48, 0.89)	7.50%	1.01	1.27
MAT2A	1	0.009104483	1.60 (1.12, 2.27)	8.40%	1.01	1.25
MCF2	1	0.007384553	1.58 (1.13, 2.20)	7.60%	1.01	1.26
MCF2	1	0.007384553	1.58 (1.13, 2.20)	7.60%	1.01	1.26
MCF2	1	0.007384553	1.58 (1.13, 2.20)	7.60%	1.01	1.26
MCF2	1	0.007384553	1.58 (1.13, 2.20)	7.60%	1.01	1.26
MCF2	1	0.007384553	1.58 (1.13, 2.20)	7.60%	1.01	1.26
MCF2	1	0.007384553	1.58 (1.13, 2.20)	7.60%	1.01	1.26
MCM10	1	0.008326599	1.78 (1.16, 2.73)	8.00%	1.01	1.24
MCM10	1	0.008326599	1.78 (1.16, 2.73)	8.00%	1.01	1.24
ME1	1	0.00963294	1.57 (1.12, 2.21)	8.60%	1.01	1.25
MGC87042	1	0.009587863	1.43 (1.09, 1.88)	8.60%	1.01	1.24
MGC87042	1	0.009587863	1.43 (1.09, 1.88)	8.60%	1.01	1.24
MGRN1	-1	0.008635109	0.54 (0.34, 0.86)	8.10%	1.01	1.26
MGRN1	-1	0.008635109	0.54 (0.34, 0.86)	8.10%	1.01	1.26
MGRN1	-1	0.008635109	0.54 (0.34, 0.86)	8.10%	1.01	1.26
MGRN1	-1	0.008635109	0.54 (0.34, 0.86)	8.10%	1.01	1.26
MINK1	-1	0.0100436	0.66 (0.48, 0.91)	8.80%	1.01	1.26
MINK1	-1	0.0100436	0.66 (0.48, 0.91)	8.80%	1.01	1.26
MINK1	-1	0.0100436	0.66 (0.48, 0.91)	8.80%	1.01	1.26
MINK1	-1	0.0100436	0.66 (0.48, 0.91)	8.80%	1.01	1.26
MLLT1	-1	0.006613376	0.57 (0.38, 0.86)	7.10%	1.01	1.28
MR1	-1	0.008382286	0.58 (0.39, 0.87)	8.10%	1.01	1.27
MR1	-1	0.008382286	0.58 (0.39, 0.87)	8.10%	1.01	1.27
MR1	-1	0.008382286	0.58 (0.39, 0.87)	8.10%	1.01	1.27
MR1	-1	0.008382286	0.58 (0.39, 0.87)	8.10%	1.01	1.27

MST4	1	0.010303281	1.70 (1.13, 2.54)	8.90%	1.01	1.24
MST4	1	0.010303281	1.70 (1.13, 2.54)	8.90%	1.01	1.24
MST4	1	0.010303281	1.70 (1.13, 2.54)	8.90%	1.01	1.24
MTMR9LP	-1	0.007633717	0.60 (0.41, 0.87)	7.70%	1.01	1.27
MTRF1	-1	0.008816635	0.67 (0.50, 0.91)	8.20%	1.01	1.26
MTRR	1	0.007604837	1.45 (1.10, 1.90)	7.70%	1.01	1.25
MTRR	1	0.007604837	1.45 (1.10, 1.90)	7.70%	1.01	1.25
MVD	1	0.008760469	1.53 (1.11, 2.09)	8.20%	1.01	1.25
MYBPHL	-1	0.006565434	0.69 (0.53, 0.90)	7.10%	1.01	1.27
MYH3	-1	0.009625687	0.59 (0.40, 0.88)	8.60%	1.01	1.26
MYO1F	-1	0.007103603	0.64 (0.47, 0.89)	7.40%	1.01	1.27
MZT2B	-1	0.009962642	0.61 (0.41, 0.89)	8.80%	1.01	1.26
NAGPA	-1	0.009376889	0.65 (0.47, 0.90)	8.50%	1.01	1.26
NAT15	-1	0.006663053	0.56 (0.37, 0.85)	7.10%	1.01	1.28
NAT15	-1	0.006663053	0.56 (0.37, 0.85)	7.10%	1.01	1.28
NAT15	-1	0.006663053	0.56 (0.37, 0.85)	7.10%	1.01	1.28
NCAPH	1	0.008056556	1.81 (1.17, 2.80)	7.90%	1.01	1.24
NCOA3	1	0.007667051	1.43 (1.10, 1.86)	7.70%	1.01	1.25
NCOA3	1	0.007667051	1.43 (1.10, 1.86)	7.70%	1.01	1.25
NCOA3	1	0.007667051	1.43 (1.10, 1.86)	7.70%	1.01	1.25
NCOA3	1	0.007667051	1.43 (1.10, 1.86)	7.70%	1.01	1.25
NCRNA00160	-1	0.008094623	0.64 (0.45, 0.89)	7.90%	1.01	1.27
NCRNA00200	1	0.005171237	1.32 (1.09, 1.61)	6.30%	1.01	1.23
NDUFS6	1	0.00974941	1.54 (1.11, 2.15)	8.70%	1.01	1.25
NECAP1	-1	0.007788839	0.63 (0.45, 0.89)	7.80%	1.01	1.27
NECAP1	-1	0.007788839	0.63 (0.45, 0.89)	7.80%	1.01	1.27
NEK10	-1	0.008430987	0.59 (0.39, 0.87)	8.10%	1.01	1.27
NFIB	1	0.00819163	1.68 (1.14, 2.46)	8.00%	1.01	1.25
NFIB	1	0.00819163	1.68 (1.14, 2.46)	8.00%	1.01	1.25
NFIB	1	0.00819163	1.68 (1.14, 2.46)	8.00%	1.01	1.25
NME2	1	0.008082262	1.49 (1.11, 2.01)	7.90%	1.01	1.25
NME2	1	0.008082262	1.49 (1.11, 2.01)	7.90%	1.01	1.25
NME2	1	0.008082262	1.49 (1.11, 2.01)	7.90%	1.01	1.25
NME2	1	0.008082262	1.49 (1.11, 2.01)	7.90%	1.01	1.25
NME2	1	0.008082262	1.49 (1.11, 2.01)	7.90%	1.01	1.25
NOL11	1	0.00717401	1.48 (1.11, 1.98)	7.40%	1.01	1.25
NOMO2	-1	0.009847368	0.70 (0.54, 0.92)	8.70%	1.01	1.25
NOMO2	-1	0.009847368	0.70 (0.54, 0.92)	8.70%	1.01	1.25
NOSTRIN	-1	0.008395695	0.61 (0.43, 0.88)	8.10%	1.01	1.27
NOSTRIN	-1	0.008395695	0.61 (0.43, 0.88)	8.10%	1.01	1.27
NOSTRIN	-1	0.008395695	0.61 (0.43, 0.88)	8.10%	1.01	1.27
NOSTRIN	-1	0.008395695	0.61 (0.43, 0.88)	8.10%	1.01	1.27

NXNL2	-1	0.008196179	0.65 (0.47, 0.89)	8.00%	1.01	1.27
NXNL2	-1	0.008196179	0.65 (0.47, 0.89)	8.00%	1.01	1.27
NXPH4	1	0.009631141	1.73 (1.14, 2.63)	8.60%	1.01	1.24
OXR1	1	0.009643083	1.53 (1.11, 2.10)	8.60%	1.01	1.25
OXR1	1	0.009643083	1.53 (1.11, 2.10)	8.60%	1.01	1.25
OXR1	1	0.009643083	1.53 (1.11, 2.10)	8.60%	1.01	1.25
OXR1	1	0.009643083	1.53 (1.11, 2.10)	8.60%	1.01	1.25
OXR1	1	0.009643083	1.53 (1.11, 2.10)	8.60%	1.01	1.25
OXR1	1	0.009643083	1.53 (1.11, 2.10)	8.60%	1.01	1.25
PAQR7	-1	0.00769964	0.61 (0.43, 0.88)	7.70%	1.01	1.27
PCDHGA6	1	0.008575643	1.59 (1.12, 2.24)	8.10%	1.01	1.25
PCDHGA7	1	0.010164903	1.80 (1.15, 2.83)	8.90%	1.01	1.23
PCDHGB4	1	0.008741639	1.56 (1.12, 2.18)	8.20%	1.01	1.25
PDIA6	1	0.006612815	1.66 (1.15, 2.39)	7.10%	1.01	1.26
PECI	-1	0.008942033	0.71 (0.55, 0.92)	8.30%	1.01	1.25
PECI	-1	0.008942033	0.71 (0.55, 0.92)	8.30%	1.01	1.25
PECI	-1	0.008942033	0.71 (0.55, 0.92)	8.30%	1.01	1.25
PECI	-1	0.008942033	0.71 (0.55, 0.92)	8.30%	1.01	1.25
PGA3	1	0.007689689	1.29 (1.07, 1.55)	7.70%	1.01	1.21
PHF11	-1	0.008193688	0.62 (0.43, 0.88)	8.00%	1.01	1.27
PHF11	-1	0.008193688	0.62 (0.43, 0.88)	8.00%	1.01	1.27
PHTF1	-1	0.007951372	0.63 (0.44, 0.88)	7.90%	1.01	1.27
PIAS4	-1	0.008102516	0.62 (0.44, 0.88)	7.90%	1.01	1.27
PITX3	-1	0.007254858	0.64 (0.47, 0.89)	7.50%	1.01	1.27
PLEKHG1	1	0.00933219	1.67 (1.13, 2.45)	8.50%	1.01	1.25
POLR3K	-1	0.00967405	0.65 (0.47, 0.90)	8.60%	1.01	1.26
POU6F1	-1	0.007157717	0.65 (0.48, 0.89)	7.40%	1.01	1.27
POU6F1	-1	0.007157717	0.65 (0.48, 0.89)	7.40%	1.01	1.27
PPP6R2	1	0.006788571	1.38 (1.09, 1.75)	7.20%	1.01	1.24
PRDX4	1	0.00907468	1.58 (1.12, 2.23)	8.40%	1.01	1.25
PRELID2	-1	0.007576831	0.63 (0.45, 0.88)	7.70%	1.01	1.27
PRELID2	-1	0.007576831	0.63 (0.45, 0.88)	7.70%	1.01	1.27
PRELID2	-1	0.007576831	0.63 (0.45, 0.88)	7.70%	1.01	1.27
PSME4	1	0.008102155	1.51 (1.11, 2.06)	7.90%	1.01	1.25
PTGER3	-1	0.008081201	0.58 (0.39, 0.87)	7.90%	1.01	1.27
PTGER3	-1	0.008081201	0.58 (0.39, 0.87)	7.90%	1.01	1.27
PTGER3	-1	0.008081201	0.58 (0.39, 0.87)	7.90%	1.01	1.27
PTGER3	-1	0.008081201	0.58 (0.39, 0.87)	7.90%	1.01	1.27
PTGER3	-1	0.008081201	0.58 (0.39, 0.87)	7.90%	1.01	1.27
PTGER3	-1	0.008081201	0.58 (0.39, 0.87)	7.90%	1.01	1.27
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PTGER3	-1	0.008081201	0.58 (0.39, 0.87)	7.90%	1.01	1.27
PTGER3	-1	0.008081201	0.58 (0.39, 0.87)	7.90%	1.01	1.27
PYGO2	-1	0.007468171	0.71 (0.55, 0.91)	7.60%	1.01	1.26
RABEP1	-1	0.008329941	0.57 (0.37, 0.86)	8.00%	1.01	1.27
RABEP1	-1	0.008329941	0.57 (0.37, 0.86)	8.00%	1.01	1.27
RABGAP1L	1	0.006232014	1.54 (1.13, 2.10)	6.90%	1.01	1.26
RABGAP1L	1	0.006232014	1.54 (1.13, 2.10)	6.90%	1.01	1.26
RAD9A	-1	0.009330391	0.65 (0.46, 0.90)	8.50%	1.01	1.27
RAGE	-1	0.006700386	0.61 (0.42, 0.87)	7.10%	1.01	1.28
RAPGEF2	1	0.008912008	1.80 (1.16, 2.79)	8.30%	1.01	1.24
RASGEF1B	1	0.006561595	1.50 (1.12, 2.02)	7.10%	1.01	1.26
RCBTB1	-1	0.007874485	0.60 (0.41, 0.87)	7.80%	1.01	1.27
RFWD3	1	0.007383613	1.50 (1.12, 2.03)	7.60%	1.01	1.26
RGR	1	0.005959146	1.46 (1.12, 1.92)	6.80%	1.01	1.26
RGR	1	0.005959146	1.46 (1.12, 1.92)	6.80%	1.01	1.26
RGR	1	0.005959146	1.46 (1.12, 1.92)	6.80%	1.01	1.26
RGS14	-1	0.009804379	0.65 (0.46, 0.90)	8.70%	1.01	1.26
RHBDD3	1	0.009281818	1.97 (1.18, 3.28)	8.50%	1.01	1.22
RIPPLY1	1	0.010067371	1.60 (1.12, 2.30)	8.80%	1.01	1.24
RIPPLY1	1	0.010067371	1.60 (1.12, 2.30)	8.80%	1.01	1.24
RNASE11	1	0.007561084	1.36 (1.09, 1.71)	7.70%	1.01	1.24
RNF125	-1	0.006986535	0.65 (0.48, 0.89)	7.30%	1.01	1.27
RNF180	-1	0.00949659	0.64 (0.46, 0.90)	8.60%	1.01	1.26
RNF180	-1	0.00949659	0.64 (0.46, 0.90)	8.60%	1.01	1.26
RNF214	-1	0.005949891	0.69 (0.53, 0.90)	6.80%	1.01	1.27
RNF214	-1	0.005949891	0.69 (0.53, 0.90)	6.80%	1.01	1.27
RNF216L	1	0.006855698	1.79 (1.17, 2.73)	7.20%	1.01	1.25
RNF216L	1	0.006855698	1.79 (1.17, 2.73)	7.20%	1.01	1.25
RNF216L	1	0.006855698	1.79 (1.17, 2.73)	7.20%	1.01	1.25
RPH3A	1	0.007850074	1.42 (1.10, 1.85)	7.80%	1.01	1.25
RPH3A	1	0.007850074	1.42 (1.10, 1.85)	7.80%	1.01	1.25
RPL37	1	0.008922524	2.00 (1.19, 3.36)	8.30%	1.01	1.22
RPL3L	1	0.006219667	1.38 (1.10, 1.74)	6.90%	1.01	1.24
RPS27L	-1	0.009737503	0.63 (0.45, 0.90)	8.70%	1.01	1.26
RPS8	1	0.008439438	1.88 (1.18, 3.01)	8.10%	1.01	1.24
RPUSD3	-1	0.008911008	0.61 (0.42, 0.88)	8.30%	1.01	1.27
RPUSD3	-1	0.008911008	0.61 (0.42, 0.88)	8.30%	1.01	1.27
RUSC2	-1	0.009594773	0.66 (0.49, 0.91)	8.60%	1.01	1.26
RUSC2	-1	0.009594773	0.66 (0.49, 0.91)	8.60%	1.01	1.26
S100A8	1	0.008623961	1.47 (1.10, 1.96)	8.10%	1.01	1.25
SCAPER	1	0.009790827	1.64 (1.13, 2.38)	8.70%	1.01	1.24
SCAPER	1	0.009790827	1.64 (1.13, 2.38)	8.70%	1.01	1.24

SCFD2	1	0.009357868	1.56 (1.12, 2.18)	8.50%	1.01	1.25
SCUBE3	-1	0.00648237	0.65 (0.47, 0.89)	7.10%	1.01	1.28
SEC24D	1	0.007226299	1.76 (1.17, 2.67)	7.50%	1.01	1.25
SH3RF2	-1	0.008949805	0.59 (0.40, 0.88)	8.30%	1.01	1.27
SIX2	1	0.009940046	1.43 (1.09, 1.89)	8.80%	1.01	1.24
SLC14A2	-1	0.00688137	0.49 (0.29, 0.82)	7.20%	1.01	1.26
SLC25A13	1	0.008049299	1.62 (1.13, 2.32)	7.90%	1.01	1.25
SLC25A13	1	0.008049299	1.62 (1.13, 2.32)	7.90%	1.01	1.25
SLC25A13	1	0.008049299	1.62 (1.13, 2.32)	7.90%	1.01	1.25
SLC25A24	-1	0.006618756	0.59 (0.40, 0.86)	7.10%	1.01	1.28
SLC25A24	-1	0.006618756	0.59 (0.40, 0.86)	7.10%	1.01	1.28
SLC6A15	1	0.007451471	1.56 (1.13, 2.17)	7.60%	1.01	1.26
SLC6A15	1	0.007451471	1.56 (1.13, 2.17)	7.60%	1.01	1.26
SLC6A15	1	0.007451471	1.56 (1.13, 2.17)	7.60%	1.01	1.26
SLC7A13	-1	0.009306511	0.62 (0.43, 0.89)	8.50%	1.01	1.27
SLURP1	1	0.008042738	1.34 (1.08, 1.65)	7.90%	1.01	1.23
SPAM1	1	0.007221968	1.55 (1.13, 2.14)	7.50%	1.01	1.26
SPAM1	1	0.007221968	1.55 (1.13, 2.14)	7.50%	1.01	1.26
SPAM1	1	0.007221968	1.55 (1.13, 2.14)	7.50%	1.01	1.26
SPAM1	1	0.007221968	1.55 (1.13, 2.14)	7.50%	1.01	1.26
SPAM1	1	0.007221968	1.55 (1.13, 2.14)	7.50%	1.01	1.26
SSBP1	1	0.008145394	1.52 (1.11, 2.07)	7.90%	1.01	1.25
STAM2	-1	0.007611313	0.54 (0.34, 0.85)	7.70%	1.01	1.27
STARD13	-1	0.007388965	0.48 (0.28, 0.82)	7.60%	1.01	1.25
STARD13	-1	0.007388965	0.48 (0.28, 0.82)	7.60%	1.01	1.25
STARD13	-1	0.007388965	0.48 (0.28, 0.82)	7.60%	1.01	1.25
STC2	-1	0.007653482	0.57 (0.38, 0.86)	7.70%	1.01	1.27
STIL	1	0.008856454	1.65 (1.13, 2.41)	8.30%	1.01	1.25
STIL	1	0.008856454	1.65 (1.13, 2.41)	8.30%	1.01	1.25
STK11	-1	0.00927752	0.59 (0.40, 0.88)	8.50%	1.01	1.26
STK32B	-1	0.007770131	0.54 (0.34, 0.85)	7.80%	1.01	1.26
STOX1	-1	0.009373358	0.60 (0.41, 0.88)	8.50%	1.01	1.27
STOX1	-1	0.009373358	0.60 (0.41, 0.88)	8.50%	1.01	1.27
STOX1	-1	0.009373358	0.60 (0.41, 0.88)	8.50%	1.01	1.27
STOX1	-1	0.009373358	0.60 (0.41, 0.88)	8.50%	1.01	1.27
STOX1	-1	0.009373358	0.60 (0.41, 0.88)	8.50%	1.01	1.27
SURF2	-1	0.008281877	0.61 (0.43, 0.88)	8.00%	1.01	1.27
SYCN	1	0.009880133	1.46 (1.09, 1.94)	8.70%	1.01	1.24
TBC1D10B	-1	0.007813488	0.63 (0.44, 0.88)	7.80%	1.01	1.27
TCTN1	-1	0.008791552	0.63 (0.44, 0.89)	8.20%	1.01	1.27
TCTN1	-1	0.008791552	0.63 (0.44, 0.89)	8.20%	1.01	1.27
TCTN1	-1	0.008791552	0.63 (0.44, 0.89)	8.20%	1.01	1.27

TCTN1	-1	0.008791552	0.63 (0.44, 0.89)	8.20%	1.01	1.27
TCTN1	-1	0.008791552	0.63 (0.44, 0.89)	8.20%	1.01	1.27
TEX9	-1	0.009763575	0.62 (0.43, 0.89)	8.70%	1.01	1.26
TFG	1	0.007007574	1.72 (1.16, 2.54)	7.30%	1.01	1.26
TFG	1	0.007007574	1.72 (1.16, 2.54)	7.30%	1.01	1.26
TFG	1	0.007007574	1.72 (1.16, 2.54)	7.30%	1.01	1.26
TFG	1	0.007007574	1.72 (1.16, 2.54)	7.30%	1.01	1.26
TLR7	-1	0.007037628	0.68 (0.51, 0.90)	7.30%	1.01	1.27
TM6SF1	-1	0.0077869	0.63 (0.44, 0.88)	7.80%	1.01	1.27
TM6SF1	-1	0.0077869	0.63 (0.44, 0.88)	7.80%	1.01	1.27
TMEM132A	1	0.007152656	1.73 (1.16, 2.57)	7.40%	1.01	1.25
TMEM132A	1	0.007152656	1.73 (1.16, 2.57)	7.40%	1.01	1.25
TMEM140	1	0.009060643	1.48 (1.10, 1.99)	8.40%	1.01	1.25
TMEM91	-1	0.00674262	0.64 (0.46, 0.88)	7.20%	1.01	1.28
TMEM91	-1	0.00674262	0.64 (0.46, 0.88)	7.20%	1.01	1.28
TMEM91	-1	0.00674262	0.64 (0.46, 0.88)	7.20%	1.01	1.28
TMEM91	-1	0.00674262	0.64 (0.46, 0.88)	7.20%	1.01	1.28
TMEM91	-1	0.00674262	0.64 (0.46, 0.88)	7.20%	1.01	1.28
TMEM91	-1	0.00674262	0.64 (0.46, 0.88)	7.20%	1.01	1.28
TMPRSS13	1	0.008747326	1.84 (1.17, 2.89)	8.20%	1.01	1.24
TMUB2	-1	0.008171294	0.63 (0.45, 0.89)	8.00%	1.01	1.27
TMUB2	-1	0.008171294	0.63 (0.45, 0.89)	8.00%	1.01	1.27
TMUB2	-1	0.008171294	0.63 (0.45, 0.89)	8.00%	1.01	1.27
TNFRSF21	1	0.008234578	1.48 (1.11, 1.99)	8.00%	1.01	1.25
TNIP2	-1	0.008424446	0.60 (0.41, 0.88)	8.10%	1.01	1.27
TNIP2	-1	0.008424446	0.60 (0.41, 0.88)	8.10%	1.01	1.27
TOPORS	-1	0.009571277	0.61 (0.42, 0.89)	8.60%	1.01	1.26
TOPORS	-1	0.009571277	0.61 (0.42, 0.89)	8.60%	1.01	1.26
TPPP	1	0.006317198	1.57 (1.14, 2.18)	7.00%	1.01	1.26
TRAM1	1	0.010148341	1.56 (1.11, 2.20)	8.90%	1.01	1.24
TRIM35	-1	0.006782048	0.59 (0.40, 0.86)	7.20%	1.01	1.28
TRIM45	-1	0.009288628	0.55 (0.36, 0.86)	8.50%	1.01	1.26
TRIM45	-1	0.009288628	0.55 (0.36, 0.86)	8.50%	1.01	1.26
TRIM66	-1	0.006237676	0.63 (0.45, 0.88)	6.90%	1.01	1.28
TRPC4AP	1	0.007218558	1.63 (1.14, 2.32)	7.50%	1.01	1.26
TRPC4AP	1	0.007218558	1.63 (1.14, 2.32)	7.50%	1.01	1.26
TRPC7	1	0.010038406	1.63 (1.12, 2.36)	8.80%	1.01	1.24
TRPC7	1	0.010038406	1.63 (1.12, 2.36)	8.80%	1.01	1.24
TRPC7	1	0.010038406	1.63 (1.12, 2.36)	8.80%	1.01	1.24
TSC1	-1	0.008687639	0.58 (0.39, 0.87)	8.20%	1.01	1.27
TSC1	-1	0.008687639	0.58 (0.39, 0.87)	8.20%	1.01	1.27
TSC1	-1	0.008687639	0.58 (0.39, 0.87)	8.20%	1.01	1.27

TSGA10	-1	0.009624267	0.63 (0.44, 0.89)	8.60%	1.01	1.26
TSGA10	-1	0.009624267	0.63 (0.44, 0.89)	8.60%	1.01	1.26
TSPYL2	-1	0.008608205	0.61 (0.42, 0.88)	8.10%	1.01	1.27
TTC12	-1	0.00902816	0.53 (0.33, 0.86)	8.30%	1.01	1.26
TTC31	-1	0.008773497	0.65 (0.47, 0.90)	8.20%	1.01	1.27
TTC31	-1	0.008773497	0.65 (0.47, 0.90)	8.20%	1.01	1.27
TTC8	-1	0.0075677	0.64 (0.46, 0.89)	7.70%	1.01	1.27
TTC8	-1	0.0075677	0.64 (0.46, 0.89)	7.70%	1.01	1.27
TTC8	-1	0.0075677	0.64 (0.46, 0.89)	7.70%	1.01	1.27
UBA7	-1	0.008940825	0.61 (0.42, 0.88)	8.30%	1.01	1.27
UBR1	1	0.009723514	1.35 (1.08, 1.70)	8.70%	1.01	1.23
UCHL5	1	0.009364974	1.62 (1.13, 2.32)	8.50%	1.01	1.25
UCHL5	1	0.009364974	1.62 (1.13, 2.32)	8.50%	1.01	1.25
UCHL5	1	0.009364974	1.62 (1.13, 2.32)	8.50%	1.01	1.25
UCHL5	1	0.009364974	1.62 (1.13, 2.32)	8.50%	1.01	1.25
UFD1L	1	0.010119718	1.59 (1.12, 2.26)	8.90%	1.01	1.24
UFD1L	1	0.010119718	1.59 (1.12, 2.26)	8.90%	1.01	1.24
ULBP1	1	0.008659691	1.50 (1.11, 2.03)	8.20%	1.01	1.25
VDAC2	1	0.007637438	1.47 (1.11, 1.95)	7.70%	1.01	1.25
VDAC2	1	0.007637438	1.47 (1.11, 1.95)	7.70%	1.01	1.25
VDAC2	1	0.007637438	1.47 (1.11, 1.95)	7.70%	1.01	1.25
VDAC2	1	0.007637438	1.47 (1.11, 1.95)	7.70%	1.01	1.25
VPS13B	1	0.007972288	1.58 (1.13, 2.21)	7.90%	1.01	1.25
VPS13B	1	0.007972288	1.58 (1.13, 2.21)	7.90%	1.01	1.25
VPS13B	1	0.007972288	1.58 (1.13, 2.21)	7.90%	1.01	1.25
VPS13B	1	0.007972288	1.58 (1.13, 2.21)	7.90%	1.01	1.25
VPS24	-1	0.009864489	0.69 (0.52, 0.92)	8.70%	1.01	1.26
VPS24	-1	0.009864489	0.69 (0.52, 0.92)	8.70%	1.01	1.26
VPS24	-1	0.009864489	0.69 (0.52, 0.92)	8.70%	1.01	1.26
VPS24	-1	0.009864489	0.69 (0.52, 0.92)	8.70%	1.01	1.26
VPS37B	1	0.007784747	1.54 (1.12, 2.11)	7.80%	1.01	1.25
WDR67	1	0.007371765	1.70 (1.15, 2.49)	7.60%	1.01	1.25
WDR67	1	0.007371765	1.70 (1.15, 2.49)	7.60%	1.01	1.25
WDR75	-1	0.007896105	0.49 (0.29, 0.83)	7.80%	1.01	1.25
WDTC1	-1	0.008530846	0.63 (0.45, 0.89)	8.10%	1.01	1.27
XPOT	1	0.010160158	1.58 (1.11, 2.24)	8.90%	1.01	1.24
YEATS2	1	0.007348357	1.58 (1.13, 2.22)	7.60%	1.01	1.26
ZC3H18	1	0.007722884	1.66 (1.14, 2.41)	7.70%	1.01	1.25
ZCWPW1	-1	0.008302062	0.57 (0.37, 0.86)	8.00%	1.01	1.27
ZGPAT	1	0.008586682	1.47 (1.10, 1.96)	8.10%	1.01	1.25
ZGPAT	1	0.008586682	1.47 (1.10, 1.96)	8.10%	1.01	1.25
ZGPAT	1	0.008586682	1.47 (1.10, 1.96)	8.10%	1.01	1.25

ZGPAT	1	0.008586682	1.47 (1.10, 1.96)	8.10%	1.01	1.25
ZGPAT	1	0.008586682	1.47 (1.10, 1.96)	8.10%	1.01	1.25
ZNF189	-1	0.006959976	0.58 (0.39, 0.86)	7.30%	1.01	1.27
ZNF189	-1	0.006959976	0.58 (0.39, 0.86)	7.30%	1.01	1.27
ZNF425	-1	0.009534005	0.65 (0.47, 0.90)	8.60%	1.01	1.26
ZNF490	-1	0.006800138	0.57 (0.38, 0.86)	7.20%	1.01	1.27
ZNF528	-1	0.008402995	0.62 (0.43, 0.88)	8.10%	1.01	1.27
ZNF578	-1	0.00702429	0.61 (0.43, 0.88)	7.30%	1.01	1.28
ZNF695	1	0.009425745	1.87 (1.17, 2.99)	8.50%	1.01	1.23
ZNF71	-1	0.006488217	0.67 (0.50, 0.89)	7.10%	1.01	1.27
ZNF791	-1	0.006897515	0.60 (0.42, 0.87)	7.30%	1.01	1.28
ZNF813	-1	0.009651252	0.69 (0.52, 0.91)	8.60%	1.01	1.26
ZZEF1	-1	0.007161028	0.59 (0.41, 0.87)	7.40%	1.01	1.28
ABI1	1	0.011314556	1.53 (1.10, 2.12)	9.40%	1	1.24
ABI1	1	0.011314556	1.53 (1.10, 2.12)	9.40%	1	1.24
ABI1	1	0.011314556	1.53 (1.10, 2.12)	9.40%	1	1.24
ABI1	1	0.011314556	1.53 (1.10, 2.12)	9.40%	1	1.24
ABI1	1	0.011314556	1.53 (1.10, 2.12)	9.40%	1	1.24
ABI1	1	0.011314556	1.53 (1.10, 2.12)	9.40%	1	1.24
ABI1	1	0.011314556	1.53 (1.10, 2.12)	9.40%	1	1.24
ABI1	1	0.011314556	1.53 (1.10, 2.12)	9.40%	1	1.24
ABI1	1	0.011314556	1.53 (1.10, 2.12)	9.40%	1	1.24
ABI1	1	0.011314556	1.53 (1.10, 2.12)	9.40%	1	1.24
ABI1	1	0.011314556	1.53 (1.10, 2.12)	9.40%	1	1.24
ADCY4	-1	0.012746837	0.60 (0.40, 0.90)	9.90%	1	1.25
ADCY4	-1	0.012746837	0.60 (0.40, 0.90)	9.90%	1	1.25
ADCY4	-1	0.012746837	0.60 (0.40, 0.90)	9.90%	1	1.25
AGBL2	-1	0.012159989	0.69 (0.52, 0.92)	9.70%	1	1.25
AKAP13	1	0.010556574	1.48 (1.10, 2.01)	9.00%	1	1.24
AKAP13	1	0.010556574	1.48 (1.10, 2.01)	9.00%	1	1.24
AKAP13	1	0.010556574	1.48 (1.10, 2.01)	9.00%	1	1.24
AKR1A1	1	0.010860471	1.41 (1.08, 1.83)	9.20%	1	1.23
AKR1A1	1	0.010860471	1.41 (1.08, 1.83)	9.20%	1	1.23
ALDH1B1	-1	0.011726926	0.63 (0.44, 0.90)	9.50%	1	1.26
AMBN	1	0.011422064	1.45 (1.09, 1.94)	9.40%	1	1.24
AMTN	1	0.010260119	1.39 (1.08, 1.79)	8.90%	1	1.23
ANKRD30BP2	1	0.010303181	1.48 (1.10, 2.00)	8.90%	1	1.24
ARFGAP1	1	0.011829858	1.47 (1.09, 1.99)	9.60%	1	1.24
ARFGAP1	1	0.011829858	1.47 (1.09, 1.99)	9.60%	1	1.24
ARMC1	1	0.01157055	1.46 (1.09, 1.95)	9.50%	1	1.24
ARPP21	-1	0.011971679	0.56 (0.35, 0.88)	9.60%	1	1.25

ARPP21	-1	0.011971679	0.56 (0.35, 0.88)	9.60%	1	1.25
ARPP21	-1	0.011971679	0.56 (0.35, 0.88)	9.60%	1	1.25
ARPP21	-1	0.011971679	0.56 (0.35, 0.88)	9.60%	1	1.25
ARSD	-1	0.011023269	0.65 (0.47, 0.91)	9.20%	1	1.26
ARSD	-1	0.011023269	0.65 (0.47, 0.91)	9.20%	1	1.26
ATP11B	1	0.011169252	1.56 (1.11, 2.20)	9.30%	1	1.24
BCKDHA	-1	0.010291527	0.67 (0.49, 0.91)	8.90%	1	1.26
BCKDHA	-1	0.010291527	0.67 (0.49, 0.91)	8.90%	1	1.26
BRIP1	1	0.012952368	1.55 (1.10, 2.19)	10.00%	1	1.24
C11orf74	-1	0.010770379	0.66 (0.48, 0.91)	9.10%	1	1.26
C14orf23	1	0.011832502	1.39 (1.08, 1.80)	9.60%	1	1.23
C14orf23	1	0.011832502	1.39 (1.08, 1.80)	9.60%	1	1.23
C16orf5	-1	0.010242171	0.66 (0.48, 0.91)	8.90%	1	1.26
C16orf5	-1	0.010242171	0.66 (0.48, 0.91)	8.90%	1	1.26
C16orf5	-1	0.010242171	0.66 (0.48, 0.91)	8.90%	1	1.26
C16orf5	-1	0.010242171	0.66 (0.48, 0.91)	8.90%	1	1.26
C17orf97	-1	0.012338083	0.60 (0.40, 0.89)	9.80%	1	1.25
C18orf55	-1	0.011092298	0.68 (0.50, 0.91)	9.30%	1	1.26
C1orf124	1	0.012304896	1.61 (1.11, 2.33)	9.80%	1	1.24
C1orf124	1	0.012304896	1.61 (1.11, 2.33)	9.80%	1	1.24
C20orf30	1	0.011038247	1.55 (1.11, 2.17)	9.20%	1	1.24
C20orf30	1	0.011038247	1.55 (1.11, 2.17)	9.20%	1	1.24
C20orf30	1	0.011038247	1.55 (1.11, 2.17)	9.20%	1	1.24
C20orf30	1	0.011038247	1.55 (1.11, 2.17)	9.20%	1	1.24
C20orf96	-1	0.010956191	0.65 (0.46, 0.90)	9.20%	1	1.26
C22orf26	-1	0.011951339	0.68 (0.50, 0.92)	9.60%	1	1.25
C3orf24	1	0.011566363	1.65 (1.12, 2.44)	9.50%	1	1.24
C3orf24	1	0.011566363	1.65 (1.12, 2.44)	9.50%	1	1.24
C4orf21	1	0.012027146	1.57 (1.10, 2.24)	9.60%	1	1.24
C5orf38	-1	0.012871615	0.63 (0.44, 0.91)	10.00%	1	1.25
C9orf117	-1	0.012155809	0.66 (0.48, 0.91)	9.70%	1	1.25
C9orf68	-1	0.011881699	0.64 (0.45, 0.91)	9.60%	1	1.26
CAPG	-1	0.01139945	0.64 (0.45, 0.90)	9.40%	1	1.26
CASP14	1	0.011468521	1.45 (1.09, 1.94)	9.40%	1	1.24
CBX7	-1	0.010411793	0.64 (0.46, 0.90)	8.90%	1	1.26
CCDC11	-1	0.01124832	0.62 (0.42, 0.90)	9.30%	1	1.26
CD2BP2	-1	0.012203297	0.66 (0.48, 0.91)	9.70%	1	1.25
CD2BP2	-1	0.012203297	0.66 (0.48, 0.91)	9.70%	1	1.25
CDC25C	1	0.012973395	2.13 (1.17, 3.88)	10.00%	1	1.2
CDC25C	1	0.012973395	2.13 (1.17, 3.88)	10.00%	1	1.2
CDCA2	1	0.01062877	1.77 (1.14, 2.73)	9.00%	1	1.23
CHEK2	1	0.010238312	1.55 (1.11, 2.17)	8.90%	1	1.24

CHEK2	1	0.010238312	1.55 (1.11, 2.17)	8.90%	1	1.24
CHEK2	1	0.010238312	1.55 (1.11, 2.17)	8.90%	1	1.24
CHMP2A	-1	0.011849205	0.69 (0.52, 0.92)	9.60%	1	1.25
CHMP2A	-1	0.011849205	0.69 (0.52, 0.92)	9.60%	1	1.25
CIZ1	-1	0.011264428	0.64 (0.45, 0.90)	9.30%	1	1.26
CIZ1	-1	0.011264428	0.64 (0.45, 0.90)	9.30%	1	1.26
CIZ1	-1	0.011264428	0.64 (0.45, 0.90)	9.30%	1	1.26
CIZ1	-1	0.011264428	0.64 (0.45, 0.90)	9.30%	1	1.26
CIZ1	-1	0.011264428	0.64 (0.45, 0.90)	9.30%	1	1.26
CLEC6A	1	0.011311521	1.54 (1.10, 2.14)	9.40%	1	1.24
COL6A4P1	1	0.011152024	1.74 (1.13, 2.66)	9.30%	1	1.23
CPT2	-1	0.011138461	0.71 (0.55, 0.93)	9.30%	1	1.25
CYHR1	1	0.010619769	1.71 (1.13, 2.59)	9.00%	1	1.24
CYHR1	1	0.010619769	1.71 (1.13, 2.59)	9.00%	1	1.24
CYHR1	1	0.010619769	1.71 (1.13, 2.59)	9.00%	1	1.24
CYTH2	-1	0.010385083	0.61 (0.41, 0.89)	8.90%	1	1.26
CYTH2	-1	0.010385083	0.61 (0.41, 0.89)	8.90%	1	1.26
DDX47	-1	0.010917905	0.59 (0.40, 0.89)	9.20%	1	1.26
DDX47	-1	0.010917905	0.59 (0.40, 0.89)	9.20%	1	1.26
DEFB123	1	0.010229146	1.42 (1.09, 1.85)	8.90%	1	1.24
DIAPH1	1	0.012626509	1.59 (1.10, 2.28)	9.90%	1	1.24
DIAPH1	1	0.012626509	1.59 (1.10, 2.28)	9.90%	1	1.24
DIAPH2	1	0.012938831	1.64 (1.11, 2.41)	10.00%	1	1.23
DIAPH2	1	0.012938831	1.64 (1.11, 2.41)	10.00%	1	1.23
DIAPH3	1	0.011764308	1.73 (1.13, 2.65)	9.60%	1	1.23
DIAPH3	1	0.011764308	1.73 (1.13, 2.65)	9.60%	1	1.23
DIXDC1	-1	0.012908259	0.59 (0.39, 0.90)	10.00%	1	1.25
DIXDC1	-1	0.012908259	0.59 (0.39, 0.90)	10.00%	1	1.25
DMKN	-1	0.011852194	0.69 (0.52, 0.92)	9.60%	1	1.25
DMKN	-1	0.011852194	0.69 (0.52, 0.92)	9.60%	1	1.25
DMKN	-1	0.011852194	0.69 (0.52, 0.92)	9.60%	1	1.25
DMKN	-1	0.011852194	0.69 (0.52, 0.92)	9.60%	1	1.25
DMKN	-1	0.011852194	0.69 (0.52, 0.92)	9.60%	1	1.25
DMKN	-1	0.011852194	0.69 (0.52, 0.92)	9.60%	1	1.25
DMKN	-1	0.011852194	0.69 (0.52, 0.92)	9.60%	1	1.25
DMKN	-1	0.011852194	0.69 (0.52, 0.92)	9.60%	1	1.25
DMKN	-1	0.011852194	0.69 (0.52, 0.92)	9.60%	1	1.25
DNALI1	-1	0.011877008	0.64 (0.45, 0.91)	9.60%	1	1.26
DPCD	-1	0.012550805	0.65 (0.47, 0.91)	9.90%	1	1.25
DSCR8	1	0.010278294	1.47 (1.09, 1.97)	8.90%	1	1.24
DSCR8	1	0.010278294	1.47 (1.09, 1.97)	8.90%	1	1.24

DSCR8	1	0.010278294	1.47 (1.09, 1.97)	8.90%	1	1.24
DSCR8	1	0.010278294	1.47 (1.09, 1.97)	8.90%	1	1.24
DSCR8	1	0.010278294	1.47 (1.09, 1.97)	8.90%	1	1.24
DYNC1I2	-1	0.011091334	0.66 (0.48, 0.91)	9.30%	1	1.26
E2F1	1	0.012893985	1.55 (1.10, 2.18)	10.00%	1	1.24
EEF2K	-1	0.012968682	0.54 (0.33, 0.88)	10.00%	1	1.24
EIF3H	1	0.011777481	1.47 (1.09, 1.99)	9.60%	1	1.24
ENO3	-1	0.012599193	0.71 (0.55, 0.93)	9.90%	1	1.24
ENO3	-1	0.012599193	0.71 (0.55, 0.93)	9.90%	1	1.24
ENO3	-1	0.012599193	0.71 (0.55, 0.93)	9.90%	1	1.24
EPX	-1	0.012837554	0.67 (0.49, 0.92)	10.00%	1	1.25
EVL	-1	0.011561201	0.54 (0.34, 0.87)	9.50%	1	1.25
FAM115A	-1	0.010185752	0.69 (0.52, 0.92)	8.90%	1	1.26
FAM120A	-1	0.011120887	0.59 (0.39, 0.89)	9.30%	1	1.26
FAM126A	1	0.012480024	1.92 (1.15, 3.20)	9.80%	1	1.21
FAM170A	1	0.011370873	1.46 (1.09, 1.97)	9.40%	1	1.24
FAM170A	1	0.011370873	1.46 (1.09, 1.97)	9.40%	1	1.24
FGB	1	0.012651414	1.36 (1.07, 1.73)	9.90%	1	1.22
FGB	1	0.012651414	1.36 (1.07, 1.73)	9.90%	1	1.22
FMNL3	-1	0.010449305	0.68 (0.51, 0.91)	9.00%	1	1.26
FMNL3	-1	0.010449305	0.68 (0.51, 0.91)	9.00%	1	1.26
GJA1	-1	0.010395278	0.61 (0.42, 0.89)	8.90%	1	1.26
GJA5	-1	0.011769561	0.66 (0.48, 0.91)	9.60%	1	1.26
GJA5	-1	0.011769561	0.66 (0.48, 0.91)	9.60%	1	1.26
GMFB	-1	0.012184114	0.64 (0.45, 0.91)	9.70%	1	1.26
GPR180	1	0.011018759	1.78 (1.14, 2.79)	9.20%	1	1.23
GUCY2E	1	0.011410591	1.53 (1.10, 2.13)	9.40%	1	1.24
HOMER1	1	0.011336137	1.65 (1.12, 2.42)	9.40%	1	1.24
HOOK2	-1	0.011600713	0.67 (0.49, 0.92)	9.50%	1	1.25
HOOK2	-1	0.011600713	0.67 (0.49, 0.92)	9.50%	1	1.25
HOXA11	1	0.012018331	1.45 (1.09, 1.94)	9.60%	1	1.24
HSD11B1	1	0.010395781	1.46 (1.09, 1.94)	8.90%	1	1.24
HSD11B1	1	0.010395781	1.46 (1.09, 1.94)	8.90%	1	1.24
HSPA12B	-1	0.012610444	0.61 (0.41, 0.90)	9.90%	1	1.25
HSPA12B	-1	0.012610444	0.61 (0.41, 0.90)	9.90%	1	1.25
HSPG2	-1	0.010853095	0.61 (0.42, 0.89)	9.20%	1	1.26
HUWE1	1	0.011791679	1.59 (1.11, 2.29)	9.60%	1	1.24
HYAL2	-1	0.010655266	0.70 (0.54, 0.92)	9.00%	1	1.25
HYAL2	-1	0.010655266	0.70 (0.54, 0.92)	9.00%	1	1.25
IKBKAP	-1	0.011093127	0.59 (0.40, 0.89)	9.30%	1	1.26
IKBKB	-1	0.011775833	0.61 (0.42, 0.90)	9.60%	1	1.26
IKBKB	-1	0.011775833	0.61 (0.42, 0.90)	9.60%	1	1.26

IKBKB	-1	0.011775833	0.61 (0.42, 0.90)	9.60%	1	1.26
IKBKB	-1	0.011775833	0.61 (0.42, 0.90)	9.60%	1	1.26
IKBKB	-1	0.011775833	0.61 (0.42, 0.90)	9.60%	1	1.26
IKBKB	-1	0.011775833	0.61 (0.42, 0.90)	9.60%	1	1.26
IKBKB	-1	0.011775833	0.61 (0.42, 0.90)	9.60%	1	1.26
IL17C	1	0.010547784	1.50 (1.10, 2.04)	9.00%	1	1.24
ILF2	1	0.012045497	1.59 (1.11, 2.28)	9.60%	1	1.24
ITPRIP	1	0.010966603	1.63 (1.12, 2.36)	9.20%	1	1.24
KIAA0528	-1	0.0115925	0.64 (0.46, 0.91)	9.50%	1	1.26
KIAA1644	-1	0.010636853	0.65 (0.47, 0.91)	9.00%	1	1.26
KIF1C	-1	0.0120162	0.67 (0.49, 0.91)	9.60%	1	1.25
KRT6C	1	0.012814231	1.38 (1.07, 1.79)	10.00%	1	1.23
LGMN	1	0.011416167	1.45 (1.09, 1.94)	9.40%	1	1.24
LGMN	1	0.011416167	1.45 (1.09, 1.94)	9.40%	1	1.24
LINGO1	1	0.012057057	1.70 (1.12, 2.56)	9.60%	1	1.23
LIX1	1	0.01111679	1.59 (1.11, 2.28)	9.30%	1	1.24
LOC100129931	-1	0.011472246	0.65 (0.46, 0.91)	9.40%	1	1.26
LOC100233209	1	0.012607821	1.43 (1.08, 1.90)	9.90%	1	1.23
LOC144776	1	0.012325145	1.38 (1.07, 1.79)	9.80%	1	1.23
LOC283761	1	0.011585471	1.57 (1.11, 2.24)	9.50%	1	1.24
LOC283761	1	0.011585471	1.57 (1.11, 2.24)	9.50%	1	1.24
LOC283761	1	0.011585471	1.57 (1.11, 2.24)	9.50%	1	1.24
LOC283761	1	0.011585471	1.57 (1.11, 2.24)	9.50%	1	1.24
LOC400043	-1	0.011245964	0.65 (0.47, 0.91)	9.30%	1	1.26
LOC91316	1	0.011446822	1.67 (1.12, 2.48)	9.40%	1	1.24
LOXL3	-1	0.012709255	0.65 (0.46, 0.91)	9.90%	1	1.25
LRGUK	-1	0.010254375	0.65 (0.47, 0.90)	8.90%	1	1.26
LRPAP1	-1	0.011640785	0.60 (0.40, 0.89)	9.50%	1	1.26
LRRC23	-1	0.011607799	0.64 (0.45, 0.90)	9.50%	1	1.26
LRRC23	-1	0.011607799	0.64 (0.45, 0.90)	9.50%	1	1.26
LRRC23	-1	0.011607799	0.64 (0.45, 0.90)	9.50%	1	1.26
LRRC56	-1	0.010591983	0.68 (0.51, 0.92)	9.00%	1	1.26
LRTOMT	-1	0.010400431	0.59 (0.40, 0.88)	8.90%	1	1.26
LRTOMT	-1	0.010400431	0.59 (0.40, 0.88)	8.90%	1	1.26
LRTOMT	-1	0.010400431	0.59 (0.40, 0.88)	8.90%	1	1.26
LRTOMT	-1	0.010400431	0.59 (0.40, 0.88)	8.90%	1	1.26
LRTOMT	-1	0.010400431	0.59 (0.40, 0.88)	8.90%	1	1.26
LRTOMT	-1	0.010400431	0.59 (0.40, 0.88)	8.90%	1	1.26
LYRM1	-1	0.012839377	0.59 (0.38, 0.89)	10.00%	1	1.25
LYRM1	-1	0.012839377	0.59 (0.38, 0.89)	10.00%	1	1.25
LYRM1	-1	0.012839377	0.59 (0.38, 0.89)	10.00%	1	1.25
MAML1	1	0.012398823	1.60 (1.11, 2.31)	9.80%	1	1.24

MAP3K1	-1	0.012373459	0.60 (0.40, 0.90)	9.80%	1	1.25
MAPK14	1	0.012704887	1.45 (1.08, 1.94)	9.90%	1	1.23
MAPK14	1	0.012704887	1.45 (1.08, 1.94)	9.90%	1	1.23
MAPK14	1	0.012704887	1.45 (1.08, 1.94)	9.90%	1	1.23
MAPK14	1	0.012704887	1.45 (1.08, 1.94)	9.90%	1	1.23
MDH1B	-1	0.012649336	0.68 (0.51, 0.92)	9.90%	1	1.25
MEIS1	1	0.012898017	1.69 (1.12, 2.55)	10.00%	1	1.23
MEIS3	-1	0.012545351	0.63 (0.44, 0.91)	9.90%	1	1.25
MEIS3	-1	0.012545351	0.63 (0.44, 0.91)	9.90%	1	1.25
MORN1	-1	0.011397709	0.63 (0.45, 0.90)	9.40%	1	1.26
MPHOSPH9	1	0.012594163	1.53 (1.10, 2.15)	9.90%	1	1.24
MPZL1	1	0.012035119	1.49 (1.09, 2.04)	9.60%	1	1.24
MPZL1	1	0.012035119	1.49 (1.09, 2.04)	9.60%	1	1.24
MPZL1	1	0.012035119	1.49 (1.09, 2.04)	9.60%	1	1.24
MRPL34	1	0.012406647	1.51 (1.09, 2.08)	9.80%	1	1.24
MSTO1	1	0.012937941	1.59 (1.10, 2.29)	10.00%	1	1.23
MYLK2	1	0.010890821	1.66 (1.12, 2.45)	9.20%	1	1.24
MYO7A	1	0.012737066	1.56 (1.10, 2.22)	9.90%	1	1.24
MYO7A	1	0.012737066	1.56 (1.10, 2.22)	9.90%	1	1.24
MYO7A	1	0.012737066	1.56 (1.10, 2.22)	9.90%	1	1.24
MYOG	1	0.011353552	1.36 (1.07, 1.72)	9.40%	1	1.23
NAA15	1	0.012422722	1.54 (1.10, 2.16)	9.80%	1	1.24
NBAS	1	0.012672103	1.55 (1.10, 2.19)	9.90%	1	1.24
NBPF3	-1	0.012664759	0.70 (0.52, 0.93)	9.90%	1	1.25
NDUFB6	-1	0.012109776	0.66 (0.48, 0.91)	9.70%	1	1.25
NDUFB6	-1	0.012109776	0.66 (0.48, 0.91)	9.70%	1	1.25
NDUFB6	-1	0.012109776	0.66 (0.48, 0.91)	9.70%	1	1.25
NFE2L1	-1	0.010751476	0.65 (0.47, 0.91)	9.10%	1	1.26
NOL10	1	0.011705945	1.59 (1.11, 2.28)	9.50%	1	1.24
NPHS2	-1	0.011756253	0.58 (0.38, 0.89)	9.60%	1	1.25
NPLOC4	1	0.011913565	1.61 (1.11, 2.35)	9.60%	1	1.24
NUDT21	1	0.011032838	1.60 (1.11, 2.30)	9.20%	1	1.24
NUP188	-1	0.011639171	0.55 (0.34, 0.87)	9.50%	1	1.25
OTOL1	1	0.012763111	1.39 (1.07, 1.81)	9.90%	1	1.23
PARP3	-1	0.01013124	0.68 (0.50, 0.91)	8.90%	1	1.26
PARP3	-1	0.01013124	0.68 (0.50, 0.91)	8.90%	1	1.26
PCDH11Y	1	0.012243822	1.46 (1.09, 1.97)	9.70%	1	1.24
PCDH11Y	1	0.012243822	1.46 (1.09, 1.97)	9.70%	1	1.24
PCDH11Y	1	0.012243822	1.46 (1.09, 1.97)	9.70%	1	1.24
PDE2A	1	0.010557993	1.43 (1.09, 1.88)	9.00%	1	1.24
PDE2A	1	0.010557993	1.43 (1.09, 1.88)	9.00%	1	1.24
PDE2A	1	0.010557993	1.43 (1.09, 1.88)	9.00%	1	1.24

PDE2A	1	0.010557993	1.43 (1.09, 1.88)	9.00%	1	1.24
PDE4A	-1	0.01282959	0.66 (0.48, 0.92)	10.00%	1	1.25
PDE4A	-1	0.01282959	0.66 (0.48, 0.92)	10.00%	1	1.25
PDE4A	-1	0.01282959	0.66 (0.48, 0.92)	10.00%	1	1.25
PDE4A	-1	0.01282959	0.66 (0.48, 0.92)	10.00%	1	1.25
PERP	1	0.012898142	1.49 (1.09, 2.04)	10.00%	1	1.24
PHGR1	-1	0.010645275	0.68 (0.50, 0.91)	9.00%	1	1.26
PHLDB1	-1	0.010487792	0.62 (0.43, 0.90)	9.00%	1	1.26
PHLDB1	-1	0.010487792	0.62 (0.43, 0.90)	9.00%	1	1.26
PHLDB1	-1	0.010487792	0.62 (0.43, 0.90)	9.00%	1	1.26
PIGL	-1	0.012014368	0.68 (0.51, 0.92)	9.60%	1	1.25
PLA2G7	1	0.010739931	1.45 (1.09, 1.92)	9.10%	1	1.24
PLA2G7	1	0.010739931	1.45 (1.09, 1.92)	9.10%	1	1.24
PLEKHM2	-1	0.010229479	0.64 (0.46, 0.90)	8.90%	1	1.26
POPDC2	-1	0.011856189	0.66 (0.47, 0.91)	9.60%	1	1.26
PPM1B	1	0.011847581	1.59 (1.11, 2.29)	9.60%	1	1.24
PPM1B	1	0.011847581	1.59 (1.11, 2.29)	9.60%	1	1.24
PPM1B	1	0.011847581	1.59 (1.11, 2.29)	9.60%	1	1.24
PPM1B	1	0.011847581	1.59 (1.11, 2.29)	9.60%	1	1.24
PPM1B	1	0.011847581	1.59 (1.11, 2.29)	9.60%	1	1.24
PPP1R14C	1	0.010609549	1.69 (1.13, 2.54)	9.00%	1	1.24
PPP3R1	1	0.011797778	1.48 (1.09, 2.00)	9.60%	1	1.24
PPP6R3	1	0.01182462	1.46 (1.09, 1.96)	9.60%	1	1.24
PPP6R3	1	0.01182462	1.46 (1.09, 1.96)	9.60%	1	1.24
PPP6R3	1	0.01182462	1.46 (1.09, 1.96)	9.60%	1	1.24
PPP6R3	1	0.01182462	1.46 (1.09, 1.96)	9.60%	1	1.24
PPP6R3	1	0.01182462	1.46 (1.09, 1.96)	9.60%	1	1.24
PPP6R3	1	0.01182462	1.46 (1.09, 1.96)	9.60%	1	1.24
PRAME	1	0.012015796	1.56 (1.10, 2.20)	9.60%	1	1.24
PRAME	1	0.012015796	1.56 (1.10, 2.20)	9.60%	1	1.24
PRAME	1	0.012015796	1.56 (1.10, 2.20)	9.60%	1	1.24
PRAME	1	0.012015796	1.56 (1.10, 2.20)	9.60%	1	1.24
PRAME	1	0.012015796	1.56 (1.10, 2.20)	9.60%	1	1.24
PRDM1	1	0.010864619	1.56 (1.11, 2.21)	9.20%	1	1.24
PRDM1	1	0.010864619	1.56 (1.11, 2.21)	9.20%	1	1.24
PRIM2	1	0.01189465	1.53 (1.10, 2.13)	9.60%	1	1.24
PSMD11	1	0.012123119	1.56 (1.10, 2.21)	9.70%	1	1.24
PTPRT	-1	0.012542322	0.60 (0.40, 0.90)	9.90%	1	1.25
PTPRT	-1	0.012542322	0.60 (0.40, 0.90)	9.90%	1	1.25
QPRT	1	0.012915155	1.66 (1.11, 2.49)	10.00%	1	1.23
RACGAP1	1	0.012817548	1.63 (1.11, 2.40)	10.00%	1	1.23
RACGAP1	1	0.012817548	1.63 (1.11, 2.40)	10.00%	1	1.23

RACGAP1	1	0.012817548	1.63 (1.11, 2.40)	10.00%	1	1.23
RAMP2	-1	0.011709734	0.68 (0.50, 0.92)	9.50%	1	1.25
RARRES3	-1	0.012940159	0.54 (0.33, 0.88)	10.00%	1	1.24
RASGRF1	1	0.011225453	1.57 (1.11, 2.23)	9.30%	1	1.24
RASGRF1	1	0.011225453	1.57 (1.11, 2.23)	9.30%	1	1.24
RASGRF1	1	0.011225453	1.57 (1.11, 2.23)	9.30%	1	1.24
RBM45	-1	0.01057111	0.67 (0.49, 0.91)	9.00%	1	1.26
REPS1	1	0.010521625	1.55 (1.11, 2.16)	9.00%	1	1.24
REPS1	1	0.010521625	1.55 (1.11, 2.16)	9.00%	1	1.24
RFC4	1	0.010308541	1.53 (1.11, 2.11)	8.90%	1	1.24
RFC4	1	0.010308541	1.53 (1.11, 2.11)	8.90%	1	1.24
RHOXF1	-1	0.012326771	0.66 (0.48, 0.92)	9.80%	1	1.25
RNF126	-1	0.010822836	0.66 (0.48, 0.91)	9.10%	1	1.26
RNMTL1	-1	0.012150331	0.61 (0.41, 0.90)	9.70%	1	1.25
RSPO1	-1	0.010347188	0.61 (0.41, 0.89)	8.90%	1	1.26
SARS	-1	0.011466736	0.61 (0.42, 0.90)	9.40%	1	1.26
SARS	-1	0.011466736	0.61 (0.42, 0.90)	9.40%	1	1.26
SARS	-1	0.011466736	0.61 (0.42, 0.90)	9.40%	1	1.26
SAT1	1	0.012394064	1.48 (1.09, 2.02)	9.80%	1	1.24
SAT1	1	0.012394064	1.48 (1.09, 2.02)	9.80%	1	1.24
SATB2	1	0.011161894	1.72 (1.13, 2.61)	9.30%	1	1.23
SATB2	1	0.011161894	1.72 (1.13, 2.61)	9.30%	1	1.23
SATB2	1	0.011161894	1.72 (1.13, 2.61)	9.30%	1	1.23
SCARF1	-1	0.012672823	0.61 (0.41, 0.90)	9.90%	1	1.25
SCARF1	-1	0.012672823	0.61 (0.41, 0.90)	9.90%	1	1.25
SCARF1	-1	0.012672823	0.61 (0.41, 0.90)	9.90%	1	1.25
SCARF1	-1	0.012672823	0.61 (0.41, 0.90)	9.90%	1	1.25
SCARF1	-1	0.012672823	0.61 (0.41, 0.90)	9.90%	1	1.25
SERPINI1	-1	0.012995951	0.60 (0.40, 0.90)	10.00%	1	1.25
SERPINI1	-1	0.012995951	0.60 (0.40, 0.90)	10.00%	1	1.25
SGSM2	-1	0.012351408	0.61 (0.41, 0.90)	9.80%	1	1.25
SGSM2	-1	0.012351408	0.61 (0.41, 0.90)	9.80%	1	1.25
SHF	-1	0.010407548	0.64 (0.46, 0.90)	8.90%	1	1.26
SIRT3	-1	0.010395406	0.66 (0.48, 0.91)	8.90%	1	1.26
SIRT3	-1	0.010395406	0.66 (0.48, 0.91)	8.90%	1	1.26
SLC25A45	-1	0.01047703	0.67 (0.49, 0.91)	9.00%	1	1.26
SLC25A45	-1	0.01047703	0.67 (0.49, 0.91)	9.00%	1	1.26
SLC2A1	1	0.012060656	1.50 (1.09, 2.06)	9.60%	1	1.24
SLC2A8	-1	0.012758716	0.59 (0.39, 0.89)	9.90%	1	1.25
SLC30A3	1	0.012074545	1.47 (1.09, 1.98)	9.60%	1	1.24
SMG6	-1	0.011386009	0.56 (0.36, 0.88)	9.40%	1	1.25
SMG6	-1	0.011386009	0.56 (0.36, 0.88)	9.40%	1	1.25

SOCS4	-1	0.012820451	0.63 (0.44, 0.91)	10.00%	1	1.25
SOCS4	-1	0.012820451	0.63 (0.44, 0.91)	10.00%	1	1.25
SPANXN2	1	0.010765906	1.37 (1.08, 1.74)	9.10%	1	1.23
SPATA5L1	1	0.011141111	1.51 (1.10, 2.07)	9.30%	1	1.24
SPATA5L1	1	0.011141111	1.51 (1.10, 2.07)	9.30%	1	1.24
TCERG1	1	0.012536518	1.66 (1.12, 2.48)	9.90%	1	1.23
TCERG1	1	0.012536518	1.66 (1.12, 2.48)	9.90%	1	1.23
TMEM108	-1	0.010602477	0.58 (0.38, 0.88)	9.00%	1	1.26
TMEM108	-1	0.010602477	0.58 (0.38, 0.88)	9.00%	1	1.26
TMOD4	-1	0.010546039	0.66 (0.48, 0.91)	9.00%	1	1.26
TRAK1	-1	0.012552903	0.57 (0.37, 0.89)	9.90%	1	1.25
TRAK1	-1	0.012552903	0.57 (0.37, 0.89)	9.90%	1	1.25
TRAPPC6A	-1	0.012887833	0.72 (0.56, 0.93)	10.00%	1	1.24
TRPC6	-1	0.011288328	0.54 (0.34, 0.87)	9.40%	1	1.25
TTC13	1	0.011432765	1.76 (1.14, 2.72)	9.40%	1	1.23
TTC13	1	0.011432765	1.76 (1.14, 2.72)	9.40%	1	1.23
TTLL2	1	0.010400094	1.41 (1.08, 1.84)	8.90%	1	1.24
UBLCP1	1	0.010665655	1.72 (1.13, 2.62)	9.00%	1	1.24
VAT1	-1	0.011909359	0.69 (0.52, 0.92)	9.60%	1	1.25
VWA5A	-1	0.012389498	0.63 (0.44, 0.91)	9.80%	1	1.25
VWA5A	-1	0.012389498	0.63 (0.44, 0.91)	9.80%	1	1.25
VWA5A	-1	0.012389498	0.63 (0.44, 0.91)	9.80%	1	1.25
WASF3	1	0.011210635	1.68 (1.13, 2.52)	9.30%	1	1.24
WDR65	-1	0.010288387	0.67 (0.49, 0.91)	8.90%	1	1.26
WDR65	-1	0.010288387	0.67 (0.49, 0.91)	8.90%	1	1.26
WDR65	-1	0.010288387	0.67 (0.49, 0.91)	8.90%	1	1.26
WDR65	-1	0.010288387	0.67 (0.49, 0.91)	8.90%	1	1.26
WDR65	-1	0.010288387	0.67 (0.49, 0.91)	8.90%	1	1.26
ZNF217	1	0.011799956	1.62 (1.11, 2.35)	9.60%	1	1.24
ZNF223	-1	0.010393203	0.74 (0.58, 0.93)	8.90%	1	1.24
ZNF263	-1	0.010124367	0.68 (0.51, 0.91)	8.90%	1	1.26
ZNF384	-1	0.012231707	0.52 (0.32, 0.87)	9.70%	1	1.24
ZNF384	-1	0.012231707	0.52 (0.32, 0.87)	9.70%	1	1.24
ZNF384	-1	0.012231707	0.52 (0.32, 0.87)	9.70%	1	1.24
ZNF384	-1	0.012231707	0.52 (0.32, 0.87)	9.70%	1	1.24
ZNF384	-1	0.012231707	0.52 (0.32, 0.87)	9.70%	1	1.24
ZNF384	-1	0.012231707	0.52 (0.32, 0.87)	9.70%	1	1.24
ZNF384	-1	0.012231707	0.52 (0.32, 0.87)	9.70%	1	1.24
ZNF568	-1	0.010974016	0.65 (0.47, 0.91)	9.20%	1	1.26
ZNF594	-1	0.010316068	0.64 (0.45, 0.90)	8.90%	1	1.26
ZNF630	-1	0.011504134	0.71 (0.54, 0.93)	9.40%	1	1.25
ZNF630	-1	0.011504134	0.71 (0.54, 0.93)	9.40%	1	1.25

ZNF630	-1	0.011504134	0.71 (0.54, 0.93)	9.40%	1	1.25
ZNF716	1	0.010708479	1.34 (1.07, 1.68)	9.10%	1	1.22
ZNF763	-1	0.010793188	0.64 (0.45, 0.90)	9.10%	1	1.26
ZPBP2	1	0.010005183	1.44 (1.09, 1.90)	8.80%	1	1.24
ZPBP2	1	0.010005183	1.44 (1.09, 1.90)	8.80%	1	1.24

Table 4. LincRNAs Identified as Associated with Breast Cancer Recurrence in 136 Breast Cancer Patients

LincRNA	Chr	Start	End	Direction of Association (1 = Higher Expression Means Higher Risk)	*p*-value	Standardized Hazard Ratio Estimate (95% Confidence Interval)	*q*-value (FDR)	Maximum Lower Bound Std HR @ 10% FDR	Regression-to-the-Mean-Corrected Std HR
Khalil-787	15	49013058	49023258	1	6.10E-07	2.76 (1.85, 4.11)	0.1%	1.20	1.33
Khalil-2019	7	20876450	21120000	1	1.48E-08	1.75 (1.44, 2.12)	<0.1%	1.18	1.41
Khalil-748	14	95988347	96000872	-1	2.87E-06	0.39 (0.26, 0.58)	0.2%	1.18	1.30
Khalil-1961	6	138901082	139020207	1	1.14E-05	2.01 (1.47, 2.74)	0.6%	1.10	1.31
Khalil-1464	3	171491881	171537606	1	6.38E-05	1.58 (1.26, 1.98)	2.0%	1.04	1.29
Khalil-769	14	102051822	102062397	1	6.34E-05	1.54 (1.25, 1.91)	2.0%	1.04	1.28
Khalil-1542	4	26809677	26850102	-1	6.86E-05	0.55 (0.41, 0.74)	2.0%	1.04	1.28
Khalil-966	18	74178337	74202937	-1	1.15E-04	0.54 (0.39, 0.74)	2.6%	1.04	1.26
Khalil-1867	6	29238046	29248321	1	8.71E-05	1.53 (1.24, 1.90)	2.2%	1.04	1.28
Khalil-828	16	11294824	11305774	-1	1.97E-04	0.54 (0.39, 0.75)	3.7%	1.04	1.25
Khalil-1661	5	6829550	6853100	1	2.31E-04	1.99 (1.38, 2.88)	4.0%	1.04	1.24
Khalil-1697	5	55567468	55766893	-1	1.82E-04	0.49 (0.34, 0.71)	3.7%	1.04	1.24
Khalil-584	13	33888375	33923550	-1	2.72E-04	0.42 (0.27, 0.67)	4.3%	1.04	1.20
Khalil-96	1	119551052	119563877	-1	3.19E-04	0.57 (0.42, 0.77)	4.7%	1.03	1.24
Khalil-1797	5	147328132	147409407	1	3.51E-04	1.58 (1.23, 2.04)	4.8%	1.02	1.25
Khalil-933	18	42263052	42278652	-1	5.25E-04	0.48 (0.32, 0.73)	6.4%	1.02	1.21
Khalil-352	11	27594974	27650174	-1	4.49E-04	0.67 (0.54, 0.84)	5.8%	1.02	1.24
Khalil-207	1	239382227	239451677	1	6.35E-04	1.59 (1.22, 2.08)	7.3%	1.01	1.24
Khalil-2153	8	20826745	20929495	-1	7.42E-04	0.54 (0.38, 0.77)	8.0%	1.01	1.22
Khalil-1788	5	139092141	139092141	1	8.51E-04	1.63 (1.22, 2.16)	8.1%	1.01	1.23
Khalil-640	13	76462324	76475024	1	8.62E-04	1.76 (1.26, 2.46)	8.1%	1.01	1.22
Khalil-2253	8	111747974	111813899	1	8.55E-04	1.37 (1.14, 1.65)	8.1%	1.01	1.22
Khalil-139	1	192885227	192945802	1	1.09E-03	2.00 (1.32, 3.02)	9.7%	1.00	1.20

Table 5. Intergenic Region Locations Identified as Associated with Risk of Breast Cancer Recurrence in 136 Breast Cancer Patients

Region	Chromo-some	Start	Stop	Direction of Association (1 = Higher Expression Means Higher Risk)	*p*-value	Standardized Hazard Ratio Estimate (95% Confidence Interval)	*q*-value (FDR)	Maximum Lower Bound Std HR @ 10% FDR	Regression-to-the-Mean-Corrected Std HR
1	chr10	37,544,879	37,547,649	-1	0.00020	0.51 (0.36, 0.73)	1.9%	1.06	1.43
1	chr10	37,619,993	37,623,136	-1	0.00021	0.52 (0.36, 0.73)	1.9%	1.06	1.43
1	chr10	37,568,808	37,569,830	-1	0.00021	0.53 (0.38, 0.74)	1.9%	1.06	1.43
1	chr10	37,564,164	37,565,625	-1	0.00030	0.52 (0.37, 0.74)	1.9%	1.06	1.42
1	chr10	37,568,381	37,568,752	-1	0.00035	0.53 (0.38, 0.75)	1.9%	1.06	1.41
1	chr10	37,565,983	37,566,523	-1	0.00041	0.53 (0.37, 0.75)	1.9%	1.06	1.41
1	chr10	37,565,659	37,565,893	-1	0.00038	0.54 (0.39, 0.76)	1.9%	1.06	1.41
1	chr10	37,566,868	37,567,570	-1	0.00047	0.54 (0.38, 0.76)	1.9%	1.06	1.41
1	chr10	37,536,807	37,542,809	-1	0.00046	0.54 (0.38, 0.76)	1.9%	1.06	1.41
1	chr10	37,543,796	37,544,843	-1	0.00042	0.56 (0.40, 0.77)	1.9%	1.06	1.41
1	chr10	37,561,599	37,562,256	-1	0.00045	0.55 (0.39, 0.77)	1.9%	1.06	1.40
1	chr10	37,683,049	37,685,772	-1	0.00045	0.55 (0.39, 0.77)	1.9%	1.06	1.40
1	chr10	37,556,000	37,560,492	-1	0.00049	0.54 (0.38, 0.76)	1.9%	1.06	1.40
1	chr10	37,575,273	37,575,491	-1	0.00048	0.54 (0.38, 0.76)	1.9%	1.06	1.40
1	chr10	37,524,962	37,527,301	-1	0.00048	0.54 (0.39, 0.76)	1.9%	1.06	1.40
1	chr10	37,576,187	37,605,418	-1	0.00050	0.54 (0.38, 0.76)	1.9%	1.06	1.40
1	chr10	37,571,872	37,573,979	-1	0.00052	0.53 (0.37, 0.76)	1.9%	1.06	1.40
1	chr10	37,698,051	37,701,722	-1	0.00047	0.56 (0.41, 0.78)	1.9%	1.06	1.40
1	chr10	37,672,851	37,673,126	-1	0.00058	0.51 (0.35, 0.75)	1.9%	1.06	1.40
1	chr10	37,562,687	37,562,938	-1	0.00058	0.53 (0.37, 0.76)	1.9%	1.06	1.40
1	chr10	37,527,343	37,532,088	-1	0.00058	0.54 (0.38, 0.77)	1.9%	1.06	1.40
1	chr10	37,560,679	37,560,951	-1	0.00059	0.54 (0.37, 0.76)	1.9%	1.06	1.40
1	chr10	37,570,039	37,571,493	-1	0.00057	0.55 (0.39, 0.77)	1.9%	1.06	1.40
1	chr10	37,575,935	37,576,119	-1	0.00059	0.54 (0.38, 0.77)	1.9%	1.06	1.40
1	chr10	37,609,308	37,613,953	-1	0.00064	0.54 (0.38, 0.77)	2.0%	1.06	1.40
1	chr10	37,547,787	37,555,941	-1	0.00064	0.54 (0.38, 0.77)	2.0%	1.06	1.40

1	chr10	37,571,633	37,571,823	-1	0.00065	0.55 (0.39, 0.77)	2.0%	1.06	1.39
1	chr10	37,667,401	37,672,780	-1	0.00068	0.55 (0.39, 0.78)	2.0%	1.06	1.39
1	chr10	37,696,906	37,697,533	-1	0.00073	0.52 (0.36, 0.76)	2.0%	1.06	1.39
1	chr10	37,574,016	37,574,684	-1	0.00067	0.56 (0.40, 0.78)	2.0%	1.06	1.39
1	chr10	37,567,627	37,568,328	-1	0.00072	0.56 (0.41, 0.79)	2.0%	1.06	1.39
1	chr10	37,693,467	37,695,809	-1	0.00077	0.56 (0.40, 0.79)	2.1%	1.06	1.39
1	chr10	37,654,871	37,660,982	-1	0.00082	0.56 (0.40, 0.79)	2.2%	1.06	1.39
1	chr10	37,661,152	37,667,368	-1	0.00089	0.55 (0.39, 0.78)	2.2%	1.06	1.39
1	chr10	37,532,337	37,536,539	-1	0.00082	0.57 (0.41, 0.79)	2.2%	1.06	1.38
1	chr10	37,562,300	37,562,581	-1	0.00094	0.56 (0.39, 0.79)	2.2%	1.06	1.38
1	chr10	37,624,793	37,626,867	-1	0.00098	0.55 (0.39, 0.79)	2.2%	1.06	1.38
1	chr10	37,639,567	37,654,034	-1	0.00088	0.57 (0.41, 0.80)	2.2%	1.06	1.38
1	chr10	37,561,214	37,561,565	-1	0.00103	0.55 (0.39, 0.79)	2.2%	1.06	1.38
1	chr10	37,673,162	37,677,786	-1	0.00088	0.59 (0.43, 0.80)	2.2%	1.06	1.38
1	chr10	37,701,753	37,702,125	-1	0.00115	0.54 (0.37, 0.78)	2.3%	1.06	1.38
1	chr10	37,626,921	37,629,035	-1	0.00105	0.57 (0.41, 0.80)	2.2%	1.06	1.38
1	chr10	37,695,882	37,696,129	-1	0.00118	0.54 (0.37, 0.78)	2.4%	1.06	1.38
1	chr10	37,654,201	37,654,768	-1	0.00103	0.58 (0.42, 0.80)	2.2%	1.06	1.38
1	chr10	37,685,838	37,687,256	-1	0.00109	0.57 (0.41, 0.80)	2.3%	1.06	1.38
1	chr10	37,732,968	37,734,110	-1	0.00127	0.55 (0.38, 0.79)	2.4%	1.06	1.38
1	chr10	37,563,652	37,564,121	-1	0.00123	0.57 (0.41, 0.80)	2.4%	1.06	1.37
1	chr10	37,614,131	37,619,802	-1	0.00126	0.57 (0.40, 0.80)	2.4%	1.06	1.37
1	chr10	37,566,588	37,566,765	-1	0.00141	0.56 (0.39, 0.80)	2.5%	1.06	1.37
1	chr10	37,632,316	37,633,017	-1	0.00136	0.58 (0.41, 0.81)	2.4%	1.06	1.37
1	chr10	37,633,094	37,639,262	-1	0.00142	0.58 (0.42, 0.81)	2.5%	1.05	1.37
1	chr10	37,689,902	37,693,366	-1	0.00147	0.58 (0.42, 0.81)	2.5%	1.05	1.37
1	chr10	37,623,556	37,624,754	-1	0.00169	0.57 (0.40, 0.81)	2.8%	1.05	1.36
1	chr10	37,707,161	37,714,709	-1	0.00176	0.58 (0.41, 0.81)	2.9%	1.05	1.36
1	chr10	37,687,488	37,689,827	-1	0.00172	0.59 (0.42, 0.82)	2.9%	1.05	1.36
1	chr10	37,629,082	37,632,280	-1	0.00199	0.59 (0.42, 0.82)	3.2%	1.05	1.36
1	chr10	37,575,553	37,575,759	-1	0.00198	0.59 (0.42, 0.82)	3.2%	1.05	1.36
1	chr10	37,677,954	37,682,763	-1	0.00205	0.60 (0.43, 0.83)	3.3%	1.04	1.35
1	chr10	37,563,315	37,563,610	-1	0.00232	0.58 (0.40, 0.82)	3.5%	1.04	1.35

1	chr10	37,575,794	37,575,896	-1	0.00253	0.54 (0.36, 0.81)	3.7%	1.04	1.35
1	chr10	37,542,848	37,543,623	-1	0.00229	0.59 (0.42, 0.83)	3.5%	1.04	1.35
1	chr10	37,561,067	37,561,175	-1	0.00270	0.56 (0.38, 0.82)	3.8%	1.04	1.35
1	chr10	37,734,169	37,740,911	-1	0.00233	0.61 (0.44, 0.84)	3.5%	1.04	1.35
1	chr10	37,702,517	37,707,119	-1	0.00275	0.61 (0.44, 0.84)	3.8%	1.04	1.34
1	chr10	37,605,587	37,609,120	-1	0.00273	0.61 (0.44, 0.84)	3.8%	1.04	1.34
1	chr10	37,562,986	37,563,198	-1	0.00356	0.60 (0.43, 0.85)	4.6%	1.03	1.34
1	chr10	37,740,954	37,745,137	-1	0.00387	0.60 (0.43, 0.85)	4.8%	1.03	1.34
1	chr10	37,716,056	37,717,321	-1	0.00393	0.61 (0.44, 0.86)	4.9%	1.03	1.33
1	chr10	37,639,364	37,639,473	-1	0.00470	0.58 (0.40, 0.85)	5.4%	1.03	1.33
1	chr10	37,728,632	37,731,719	-1	0.00487	0.61 (0.43, 0.86)	5.4%	1.03	1.33
1	chr10	37,717,419	37,728,598	-1	0.00478	0.62 (0.45, 0.87)	5.4%	1.03	1.33
1	chr10	37,731,776	37,732,927	-1	0.00530	0.60 (0.42, 0.86)	5.7%	1.02	1.33
1	chr10	37,747,085	37,748,228	-1	0.00712	0.60 (0.42, 0.87)	6.9%	1.02	1.32
1	chr10	37,714,745	37,715,803	-1	0.00867	0.62 (0.43, 0.89)	7.7%	1.01	1.31
1	chr10	37,696,547	37,696,778	-1	0.01035	0.58 (0.38, 0.88)	8.6%	1.01	1.30
1	chr10	37,750,435	37,752,430	-1	0.01125	0.61 (0.42, 0.89)	9.1%	1.00	1.30
1	chr10	37,745,221	37,746,267	-1	0.01313	0.60 (0.40, 0.90)	9.8%	1.00	1.29
1	chr10	37,697,835	37,697,938	-1	0.01311	0.58 (0.38, 0.89)	9.8%	1.00	1.29
2	chr13	33,913,029	33,915,362	-1	0.00000	0.53 (0.41, 0.69)	0.1%	1.11	1.53
2	chr13	33,895,486	33,899,980	-1	0.00010	0.45 (0.30, 0.67)	1.7%	1.07	1.45
2	chr13	33,861,025	33,870,309	-1	0.00025	0.43 (0.28, 0.68)	1.9%	1.06	1.42
2	chr13	33,885,431	33,895,429	-1	0.00025	0.43 (0.27, 0.68)	1.9%	1.06	1.42
2	chr13	33,905,649	33,907,334	-1	0.00038	0.46 (0.30, 0.70)	1.9%	1.06	1.41
2	chr13	33,875,986	33,880,221	-1	0.00053	0.47 (0.31, 0.72)	1.9%	1.06	1.40
3	chr14	100,492,181	100,494,055	-1	0.00003	0.54 (0.41, 0.72)	0.8%	1.07	1.47
3	chr14	100,490,070	100,492,136	-1	0.00046	0.61 (0.46, 0.80)	1.9%	1.06	1.39
3	chr14	100,488,826	100,489,839	-1	0.00125	0.54 (0.37, 0.78)	2.4%	1.06	1.38
3	chr14	100,452,553	100,453,714	-1	0.00131	0.57 (0.40, 0.80)	2.4%	1.06	1.37
3	chr14	100,480,756	100,482,681	-1	0.00114	0.64 (0.48, 0.84)	2.3%	1.05	1.36
3	chr14	100,513,361	100,516,723	-1	0.00211	0.56 (0.38, 0.81)	3.3%	1.05	1.36
3	chr14	100,522,353	100,526,500	-1	0.00327	0.56 (0.38, 0.82)	4.3%	1.04	1.34
3	chr14	100,494,916	100,500,335	-1	0.00433	0.54 (0.35, 0.82)	5.3%	1.03	1.33

3	chr14	100,482,810	100,488,781	-1	0.00449	0.56 (0.37, 0.83)	5.3%	1.03	1.33
3	chr14	100,500,384	100,505,674	-1	0.00474	0.56 (0.37, 0.84)	5.4%	1.03	1.33
3	chr14	100,505,745	100,509,590	-1	0.00578	0.59 (0.41, 0.86)	6.0%	1.02	1.32
3	chr14	100,510,107	100,513,108	-1	0.00732	0.59 (0.40, 0.87)	6.9%	1.01	1.32
3	chr14	100,494,179	100,494,879	-1	0.00731	0.63 (0.45, 0.88)	6.9%	1.01	1.31
3	chr14	100,466,798	100,467,228	-1	0.00706	0.68 (0.51, 0.90)	6.9%	1.01	1.30
3	chr14	100,509,621	100,510,070	-1	0.01210	0.65 (0.47, 0.91)	9.5%	1.00	1.29
4	chr15	50,998,590	50,999,355	1	0.00000	1.46 (1.27, 1.67)	0.0%	1.11	1.36
4	chr15	50,995,854	50,996,481	1	0.00163	1.56 (1.18, 2.05)	2.8%	1.05	1.25
5	chr15	71,427,690	71,430,497	-1	0.00459	0.62 (0.44, 0.86)	5.4%	1.03	1.33
5	chr15	71,423,356	71,427,046	-1	0.00474	0.64 (0.47, 0.87)	5.4%	1.02	1.32
5	chr15	71,420,670	71,423,120	-1	0.00938	0.63 (0.45, 0.89)	8.1%	1.01	1.30
6	chr17	42,098,064	42,100,474	-1	0.00003	0.46 (0.32, 0.66)	0.8%	1.07	1.49
6	chr17	42,097,068	42,097,990	-1	0.00003	0.50 (0.36, 0.70)	0.8%	1.07	1.48
6	chr17	42,095,337	42,097,009	-1	0.00007	0.51 (0.36, 0.71)	1.4%	1.07	1.46
6	chr17	42,093,032	42,094,287	-1	0.00105	0.62 (0.47, 0.82)	2.2%	1.06	1.37
7	chr19	15,685,213	15,685,925	-1	0.00126	0.63 (0.47, 0.83)	2.4%	1.05	1.36
7	chr19	15,686,036	15,688,801	-1	0.00136	0.65 (0.49, 0.84)	2.4%	1.05	1.35
7	chr19	15,681,763	15,685,139	-1	0.00282	0.66 (0.51, 0.87)	3.9%	1.03	1.33
8	chr2	162,136,055	162,136,356	1	0.00049	1.67 (1.25, 2.24)	1.9%	1.06	1.28
8	chr2	162,135,070	162,135,249	1	0.00086	1.61 (1.22, 2.12)	2.2%	1.06	1.26
9	chr5	34,201,715	34,201,852	1	0.00323	1.91 (1.24, 2.94)	4.3%	1.04	1.19
9	chr5	34,170,829	34,170,949	1	0.00430	1.91 (1.22, 2.97)	5.3%	1.03	1.18
10	chr6	72,099,739	72,107,969	-1	0.00250	0.52 (0.34, 0.80)	3.7%	1.04	1.35
10	chr6	72,092,048	72,099,685	-1	0.00447	0.57 (0.39, 0.84)	5.3%	1.03	1.33
10	chr6	72,082,646	72,084,661	-1	0.00514	0.64 (0.47, 0.87)	5.6%	1.02	1.32
10	chr6	72,090,253	72,091,283	-1	0.01000	0.57 (0.37, 0.87)	8.5%	1.01	1.30
11	chr6	151,715,844	151,717,137	1	0.00002	1.51 (1.25, 1.83)	0.8%	1.07	1.33
11	chr6	151,717,215	151,718,164	1	0.00782	1.59 (1.13, 2.23)	7.2%	1.01	1.19
12	chr7	149,668,770	149,669,327	-1	0.00090	0.60 (0.44, 0.81)	2.2%	1.06	1.38
12	chr7	149,925,596	149,925,704	-1	0.00327	0.60 (0.43, 0.84)	4.3%	1.03	1.34
12	chr7	149,699,811	149,700,117	-1	0.00689	0.64 (0.47, 0.89)	6.8%	1.02	1.31

13	chr8	12,401,386	12,401,654	-1	0.00022	0.64 (0.51, 0.81)	1.9%	1.06	1.38
13	chr8	12,432,626	12,433,347	-1	0.00238	0.60 (0.43, 0.83)	3.5%	1.04	1.35
13	chr8	12,403,417	12,403,612	-1	0.00522	0.62 (0.45, 0.87)	5.6%	1.02	1.32
14	chr9	134,279,738	134,284,311	-1	0.00095	0.54 (0.38, 0.78)	2.2%	1.06	1.38
14	chr9	134,271,924	134,274,441	-1	0.00137	0.56 (0.40, 0.80)	2.4%	1.06	1.37
14	chr9	134,291,733	134,295,852	-1	0.00826	0.62 (0.43, 0.88)	7.5%	1.01	1.31
15	chrX	93,652,357	93,666,290	-1	0.00619	0.62 (0.44, 0.87)	6.3%	1.02	1.32
15	chrX	93,688,784	93,693,228	-1	0.00613	0.63 (0.45, 0.88)	6.3%	1.02	1.32
15	chrX	93,669,788	93,672,149	-1	0.00674	0.61 (0.43, 0.87)	6.8%	1.02	1.32
15	chrX	93,666,349	93,667,298	-1	0.01336	0.59 (0.39, 0.90)	10.0%	1.00	1.29
16	chrX	93,717,247	93,720,845	-1	0.00466	0.61 (0.44, 0.86)	5.4%	1.03	1.33
16	chrX	93,725,918	93,737,489	-1	0.00522	0.62 (0.44, 0.87)	5.6%	1.02	1.32
16	chrX	93,751,305	93,757,302	-1	0.00855	0.64 (0.45, 0.89)	7.7%	1.01	1.31
16	chrX	93,748,573	93,749,757	-1	0.01008	0.63 (0.44, 0.89)	8.5%	1.01	1.30
16	chrX	93,746,612	93,748,536	-1	0.01154	0.63 (0.45, 0.90)	9.1%	1.00	1.30
17	chrX	93,772,799	93,777,937	-1	0.00940	0.63 (0.44, 0.89)	8.1%	1.01	1.30
17	chrX	93,778,121	93,784,508	-1	0.01142	0.65 (0.47, 0.91)	9.1%	1.00	1.29
18	chrX	93,824,387	93,825,877	-1	0.00564	0.61 (0.43, 0.86)	5.9%	1.02	1.32
18	chrX	93,830,179	93,833,764	-1	0.00623	0.61 (0.43, 0.87)	6.3%	1.02	1.32
19	chr4	14,787,521	14,788,354	-1	0.00032	0.57 (0.41, 0.77)	1.9%	1.06	1.41
20	chr3	27,150,797	27,152,817	-1	0.00057	0.51 (0.35, 0.75)	1.9%	1.06	1.40
21	chr16	30,875,605	30,875,752	-1	0.00037	0.60 (0.45, 0.79)	1.9%	1.06	1.40
22	chr4	39,536,187	39,536,524	-1	0.00018	0.63 (0.49, 0.80)	1.9%	1.06	1.40
23	chr14	81,726,879	81,729,708	-1	0.00094	0.52 (0.36, 0.77)	2.2%	1.06	1.39
24	chr11	781,048	781,371	-1	0.00062	0.61 (0.46, 0.81)	2.0%	1.06	1.38
25	chr12	57,793,185	57,793,823	1	0.00042	1.49 (1.19, 1.86)	1.9%	1.06	1.28
26	chr8	81,525,870	81,526,021	1	0.00237	1.70 (1.21, 2.38)	3.5%	1.04	1.23
27	chr4	74,877,348	74,877,549	1	0.00276	1.69 (1.20, 2.37)	3.8%	1.04	1.22
28	chr1	36,798,999	36,802,115	-1	0.00305	0.60 (0.43, 0.84)	4.2%	1.04	1.34
29	chr19	12,378,905	12,380,075	-1	0.00340	0.58 (0.41, 0.84)	4.4%	1.03	1.34
30	chr21	9,837,324	9,837,442	1	0.00270	1.50 (1.15, 1.95)	3.8%	1.03	1.23
31	chr3	123,210,205	123,211,948	1	0.00339	1.72 (1.20, 2.48)	4.4%	1.03	1.21
32	chr8	12,054,779	12,054,926	-1	0.00359	0.59 (0.41, 0.84)	4.6%	1.03	1.34

33	chr11	63,336,814	63,339,112	-1	0.00382	0.62 (0.45, 0.86)	4.8%	1.03	1.33
34	chr6	36,575,163	36,576,155	-1	0.00332	0.72 (0.58, 0.90)	4.4%	1.03	1.29
35	chr14	38,291,258	38,299,693	-1	0.00440	0.65 (0.49, 0.88)	5.3%	1.03	1.32
36	chr1	168,218,748	168,220,325	1	0.00439	1.55 (1.15, 2.09)	5.3%	1.03	1.21
37	chr3	112,414,798	112,415,017	1	0.00494	1.80 (1.20, 2.71)	5.4%	1.03	1.19
38	chr10	133,732,921	133,733,113	-1	0.00553	0.64 (0.46, 0.88)	5.8%	1.02	1.32
39	chr3	195,671,271	195,671,479	1	0.00550	1.55 (1.14, 2.11)	5.8%	1.02	1.21
40	chr5	180,678,078	180,680,053	1	0.00682	1.65 (1.15, 2.38)	6.8%	1.02	1.19
41	chr10	29,738,073	29,738,359	-1	0.00621	0.71 (0.55, 0.91)	6.3%	1.02	1.29
42	chr2	91,816,094	91,819,627	-1	0.00735	0.63 (0.44, 0.88)	6.9%	1.01	1.31
43	chr15	39,777,520	39,813,177	-1	0.00738	0.63 (0.45, 0.88)	6.9%	1.01	1.31
44	chr16	21,527,242	21,527,480	-1	0.00715	0.68 (0.51, 0.90)	6.9%	1.01	1.30
45	chr1	222,906,688	222,910,172	1	0.00738	1.55 (1.13, 2.15)	6.9%	1.01	1.19
46	chr20	3,074,943	3,075,062	1	0.00770	1.67 (1.15, 2.43)	7.2%	1.01	1.18
47	chr15	50,653,452	50,656,894	1	0.00787	1.49 (1.11, 1.99)	7.2%	1.01	1.20
48	chr11	8,681,526	8,687,251	-1	0.00851	0.61 (0.42, 0.88)	7.7%	1.01	1.31
49	chr18	14,274,671	14,274,823	-1	0.00912	0.59 (0.39, 0.88)	7.9%	1.01	1.31
50	chr7	94,189,030	94,190,366	-1	0.00943	0.60 (0.41, 0.88)	8.1%	1.01	1.31
51	chr19	56,149,766	56,151,179	-1	0.00958	0.59 (0.39, 0.88)	8.1%	1.01	1.31
52	chr19	22,021,429	22,024,672	-1	0.00909	0.65 (0.47, 0.90)	7.9%	1.01	1.30
53	chr10	42,398,467	42,398,655	1	0.00822	1.37 (1.08, 1.73)	7.5%	1.01	1.19
54	chr1	15,936,663	15,936,819	1	0.00905	1.53 (1.11, 2.10)	7.9%	1.01	1.19
55	chr19	57,811,563	57,811,715	1	0.00906	1.61 (1.13, 2.29)	7.9%	1.01	1.18
56	chrX	115,108,909	115,109,012	1	0.01070	1.63 (1.12, 2.38)	8.9%	1.01	1.17
57	chr10	38,637,965	38,638,108	-1	0.01097	0.63 (0.44, 0.90)	8.9%	1.00	1.30
58	chr7	76,741,733	76,741,898	-1	0.01084	0.65 (0.47, 0.91)	8.9%	1.00	1.30
59	chr2	96,492,560	96,493,149	-1	0.01096	0.68 (0.50, 0.91)	8.9%	1.00	1.29
60	chr6	26,130,873	26,132,970	1	0.01081	1.58 (1.11, 2.25)	8.9%	1.00	1.18
61	chr16	25,271,035	25,272,071	-1	0.01152	0.61 (0.42, 0.90)	9.1%	1.00	1.30
62	chr5	10,435,961	10,438,476	1	0.01152	1.81 (1.14, 2.86)	9.1%	1.00	1.15
63	chr16	31,465,709	31,467,707	-1	0.01273	0.59 (0.39, 0.89)	9.8%	1.00	1.30
64	chr9	33,018,805	33,020,959	-1	0.01273	0.55 (0.35, 0.88)	9.8%	1.00	1.29
65	chr17	3,710,044	3,712,797	-1	0.01240	0.67 (0.48, 0.92)	9.7%	1.00	1.29

66	chr1	121,484,124	121,485,310	1	0.01262	1.56 (1.10, 2.21)	9.8%	1.00	1.17
67	chr17	41,379,297	41,379,450	-1	0.01286	0.68 (0.51, 0.92)	9.8%	1.00	1.28
68	chr6	138,982,087	138,982,527	1	0.01300	1.73 (1.12, 2.67)	9.8%	1.00	1.15
69	chr1	11,968,187	11,968,792	1	0.01310	1.78 (1.13, 2.81)	9.8%	1.00	1.14

Table A. Accession Nos. and Coordinates of Intronic RNAs Associated with Risk of Breast Cancer Recurrence

Intron	Accession No.	Chr. No.	Location
WBSCR17	NM_022479	chr7	70598027-70800534,70800720-70853219,70853388-70880873,70881050-70885892,70886092-71036268,71036388-71130394,71130582-71134955,71135095-71142194,71142292-71175744,71175914-71177001,
AACSP1	NR_024035	chr5	178193177-178194129,178194337-178195469,178195666-178199428,178199633-178201497,178201550-178202266,178202338-178203141,
AARS	NM_001605	chr16	70286810-70287169,70287285-70287615,70287704-70287820,70287942-70288522,70288638-70289629,70289740-70291934,70292121-70292881,70293090-70294945,70295061-70296247,70296428-70298859,70299006-70299439,70299566-70301560,70301713-70302172,70302283-70303519,70303667-70304097,70304244-70305682,70305876-70310387,70310535-70310867,70311058-70316521,70316688-70323322,
ABAT	NM_000663	chr16	8807723-8829554,8829667-8839856,8839956-8841963,8841995-8844277,8844397-8851612,8851664-8857924,8858007-8858593,8858688-8860063,8860128-8862048,8862114-8862680,8862831-8866635,8866775-8868745,8868915-8870199,8870348-8873334,8873448-8875164,
ABAT	NM_020686	chr16	8768569-8829554,8829667-8839856,8839956-8841963,8841995-8844277,8844397-8851612,8851664-8857924,8858007-8858593,8858688-8860063,8860128-8862048,8862114-8862680,8862831-8866635,8866775-8868745,8868915-8870199,8870348-8873334,8873448-8875164,
ABAT	NM_001127448	chr16	8814792-8829554,8829667-8839856,8839956-8841963,8841995-8844277,8844397-8851612,8851664-8857924,8858007-8858593,8858688-8860063,8860128-8862048,8862114-8862680,8862831-8866635,8866775-8868745,8868915-8870199,8870348-8873334,8873448-8875164,
ABCA12	NM_015657	chr2	215797466-215798800,215798940-215802232,215802340-215807647,215807742-215809723,215809829-215812144,215812281-215813318,215813462-215813762,215813874-215815601,215815808-215818576,215818832-215819924,215820086-215821385,215821503-215822999,215823179-215823746,215823803-215831570,215831678-215833442,215833532-215834995,215835125-215838671,215838767-215839500,215839589-215840507,215840762-215843038,215843191-215843526,215843765-215845205,215845368-215846909,215847108-215848369,215848590-215851264,215851453-215852369,215852518-215854051,215854188-215854274,215854346-215855424,215855756-215862417,215862534-215865427,215865745-215866280,215866462-215868931,215869024-215872449,215872571-215875053,215875195-215876161,215876374-215876693,215876860-215880212,215880388-215882730,215882857-215884058,215884173-215884262,215884521-215890395,215890504-215891542,215891663-215896543,
ABCA12	NM_173076	chr2	215797466-215798800,215798940-215802232,215802340-215807647,215807742-215809723,215809829-215812144,215812281-215813318,215813462-215813762,215813874-215815601,215815808-215818576,215818832-215819924,215820086-215821385,215821503-215822999,215823179-215823746,215823803-215831570,215831678-215833442,215833532-215834995,215835125-215838671,215838767-215839500,215839589-215840507,215840762-215843038,215843191-215843526,215843765-215845205,215845368-215846909,215847108-215848369,215848590-215851264,215851453-215852369,215852518-215854051,215854188-215854274,215854346-215855424,215855756-215862417,215862534-215865427,215865745-215866280,215866462-215868931,215869024-215872449,215872571-215875053,215875195-215876161,215876374-215876693,215876860-215880212,215880388-215882730,215882857-215884058,215884173-215884262,215884521-215890395,215890504-215891542,215891663-215896543,215896621-215901675,215901790-215910559,215910740-215914348,215914536-215917209,215917309-215919295,215919389-215928787,215928943-215976318,215976414-216002861,
ABHD5	NM_016006	chr3	43732532-43740766,43740854-43743705,43744080-43753199,43753356-43756437,43756551-43759161,43759350-43759933,
ABI1	NM_001178121	chr10	27037675-27040525,27040713-27047989,27048165-27054145,27054248-27057779,27057922-27059172,27059275-27065992,27066171-27112065,27112235-27149674,
ABI1	NM_001012750	chr10	27037675-27040525,27040713-27044582,27044671-27047989,27048168-27054145,27054248-27057779,27057922-27059172,27059275-

			27060002,27060019-27065992,27066171-27112065,27112235-27149674,
ABI1	NM_005470	chr10	27037675-27040525,27040713-27044582,27044671-27047989,27048168-27052807,27052890-27054145,27054248-27057779,27057922-27059172,27059275-27060002,27060019-27065992,27066171-27112065,27112235-27149674,
ABI1	NM_001178120	chr10	27037675-27040525,27040713-27047989,27048165-27054145,27054248-27057779,27057922-27059172,27059275-27060002,27060019-27065992,27066171-27112065,27112235-27149674,
ABI1	NM_001178119	chr10	27037675-27040525,27040713-27044582,27044671-27047989,27048165-27054145,27054248-27057779,27057922-27059172,27059275-27060002,27060019-27065992,27066171-27112065,27112235-27149674,
ABI1	NM_001178116	chr10	27037675-27040525,27040713-27047989,27048168-27052807,27052890-27054145,27054248-27057779,27057922-27059172,27059275-27060002,27060019-27065992,27066171-27112065,27112235-27128660,27128713-27149674,
ABI1	NM_001178123	chr10	27037675-27040525,27040713-27054145,27054248-27057779,27057922-27059172,27059275-27060002,27060019-27065992,27066171-27112065,27112235-27149674,
ABI1	NM_001178122	chr10	27037675-27040525,27040713-27044582,27044671-27054145,27054248-27057779,27057922-27059172,27059275-27060002,27060019-27065992,27066171-27112065,27112235-27149674,
ABI1	NM_001012752	chr10	27037675-27040525,27040713-27044582,27044671-27047989,27048168-27054145,27054248-27057779,27057922-27059172,27059275-27065992,27066171-27112065,27112235-27149674,
ABI1	NM_001012751	chr10	27037675-27040525,27040713-27047989,27048168-27054145,27054248-27057779,27057922-27059172,27059275-27060002,27060019-27065992,27066171-27112065,27112235-27149674,
ABI1	NM_001178124	chr10	27037675-27040525,27040713-27054145,27054248-27057779,27057922-27059172,27059275-27065992,27066171-27112065,27112235-27149674,
ABI1	NM_001178125	chr10	27037675-27040525,27040713-27054145,27054248-27057779,27057922-27059172,27059275-27112065,27112235-27149674,
ABL1	NM_007313	chr9	133589843-133729449,133729625-133730186,133730484-133738148,133738423-133747514,133747601-133748245,133748425-133750253,133750440-133753800,133753955-133755453,133755545-133755885,133756052-133759354,
ABL1	NM_005157	chr9	133710913-133729449,133729625-133730186,133730484-133738148,133738423-133747514,133747601-133748245,133748425-133750253,133750440-133753800,133753955-133755453,133755545-133755885,133756052-133759354,
ABR	NM_001092	chr17	909410-910403,910553-912917,913025-913967,914104-915084,915226-915926,916038-916343,916405-953288,953422-953775,953875-959273,959350-960236,960343-961208,961286-961983,962108-970315,970483-973207,973331-975852,975995-976863,976918-982568,982631-986758,986868-994903,995091-1003875,1003976-1012172,
ABR	NM_001159746	chr17	909410-910403,910553-912917,913025-913967,914104-915084,915226-915926,916038-916343,916405-953288,953422-953775,953875-959273,959350-960236,960343-961208,961286-961983,962108-970315,970483-973207,973331-975852,975995-976863,976918-982568,982631-986758,986868-994903,995091-1003875,1003976-1028516,1028703-1090092,
ABR	NM_021962	chr17	909410-910403,910553-912917,913025-913967,914104-915084,915226-915926,916038-916343,916405-953288,953422-953775,953875-959273,959350-960236,960343-961208,961286-961983,962108-970315,970483-973207,973331-975852,975995-976863,976918-982568,982631-986758,986868-994903,995091-1003875,1003976-1028516,1028703-1082959,
ABTB2	NM_145804	chr11	34174132-34175810,34175926-34176246,34176317-34180841,34180934-34181451,34181556-34181793,34181901-34182448,34182629-34184121,34184353-34186231,34186369-34186805,34186904-34188804,34188908-34189448,34189540-34192451,34192619-34194700,34194855-34218870,34219086-34226089,34226238-34378246,
ACAP2	NM_012287	chr3	195000158-195006523,195006587-195009848,195009961-195012433,195012545-195012992,195013182-195015446,195015541-195016435,195016622-195017917,195018011-195022302,195022374-195022693,195022904-195027238,195027346-195027950,195028053-195029513,195029567-195041428,195041543-195047612,195047689-195053755,195053853-195057659,195057706-195063198,195063384-195065986,195066047-195101736,195101792-195102630,195102752-195112817,195112877-195163522,
ACBD3	NM_022735	chr1	226334523-226340034,226340321-226342346,226342535-226346883,226347060-226349230,226349391-226352488,226352631-226353558,226353702-226374089,
ACBD4	NM_001135704	chr17	43210031-43212706,43212964-43213207,43213321-43213473,43213600-43213865,43213988-43214057,43214144-43214384,43214507-43214733,43214822-43215087,43215198-43215278,43215356-43216386,43216528-43220808,

ACBD4	NM_001135707	chr17	43213321-43213473,43213600-43213865,43213988-43214057,43214144-43214384,43214507-43214733,43214822-43215125,43215198-43215288,43215356-43216386,43216528-43219948,
ACBD4	NM_024722	chr17	43213600-43213865,43213988-43214057,43214144-43214384,43214507-43214733,43214822-43215125,43215198-43215278,43215356-43216386,43216528-43220808,
ACBD4	NM_001135706	chr17	43213321-43213473,43213600-43213865,43213988-43214057,43214144-43214384,43214507-43214733,43214822-43215087,43215198-43215278,43215356-43216386,43216528-43220808,
ACBD4	NM_001135705	chr17	43213321-43213473,43213600-43213865,43213988-43214057,43214144-43214384,43214507-43214733,43214822-43215125,43215198-43215278,43215356-43216386,43216528-43220808,
ACCN5	NM_017419	chr4	156751199-156752974,156753068-156757839,156758010-156759963,156760022-156763357,156763507-156764831,156764983-156773341,156773469-156775227,156775467-156784598,156784907-156787337,
ACER2	NM_001010887	chr9	19409191-19423858,19423975-19424696,19424840-19434943,19435083-19446277,19446417-19450446,
ACRBP	NM_032489	chr12	6747571-6748118,6748204-6749224,6749394-6749507,6749689-6752703,6752838-6753301,6753772-6754384,6754504-6755647,6755744-6755958,6756179-6756488,
ACSBG2	NM_030924	chr19	6135921-6141522,6141622-6147455,6147687-6151716,6151807-6156440,6156563-6161224,6161307-6165875,6166027-6177238,6177408-6182760,6182944-6183048,6183284-6185445,6185665-6187292,6187434-6187608,6187857-6190593,6190704-6192677,
ACSM5	NM_017888	chr16	20420988-20422790,20423011-20429379,20429592-20430548,20430758-20432578,20432724-20435236,20435392-20439108,20439190-20440998,20441124-20442313,20442396-20442540,20442644-20448372,20448502-20448588,20448690-20451120,20451242-20451664,
ACTL8	NM_030812	chr1	18082000-18149478,18149852-18152260,
ADAM17	NM_003183	chr2	9630648-9631228,9631281-9633025,9633116-9633874,9633955-9634764,9634897-9637241,9637378-9642300,9642406-9645293,9645495-9650106,9650261-9658028,9658119-9658230,9658377-9661330,9661446-9663376,9663468-9666238,9666374-9667913,9668084-9675961,9676052-9676825,9676958-9683280,9683415-9695636,
ADAMTS8	NM_007037	chr11	130276024-130278357,130278535-130278661,130278836-130281310,130281496-130284424,130284728-130286056,130286226-130286833,130286971-130288946,130289188-130297460,
ADAMTSL2	NM_001145320	chr9	136397693-136401683,136401925-136402525,136402670-136403469,136403547-136404891,136404996-136405718,136405866-136405998,136406124-136409590,136409673-136412158,136412336-136419477,136419816-136420678,136421053-136426318,136426418-136432056,136432185-136433393,136433609-136433723,136433881-136434528,136434701-136435451,136435630-136438963,136439110-136439866,
ADAMTSL2	NM_014694	chr9	136400040-136401683,136401925-136402525,136402670-136403469,136403547-136404891,136404996-136405718,136405866-136405998,136406124-136409590,136409673-136412158,136412336-136419477,136419816-136420678,136421053-136426318,136426418-136432056,136432185-136433393,136433609-136433723,136433881-136434528,136434701-136435451,136435630-136438963,136439110-136439866,
ADC	NM_052998	chr1	33546896-33546987,33547110-33547200,33547414-33547777,33547956-33549553,33549729-33557649,33557824-33558881,33559018-33560147,33560315-33562306,33562471-33563666,33563781-33583501,33583718-33585643,
ADCK5	NM_174922	chr8	145597797-145603074,145603180-145608280,145608432-145615869,145615947-145616054,145616257-145616332,145616475-145616559,145616675-145616778,145616912-145616981,145617067-145617139,145617223-145617290,145617371-145617452,145617546-145617658,145617913-145617989,145618108-145618182,
ADCY4	NM_139247	chr14	24787775-24787858,24787985-24788302,24788419-24788533,24788643-24788946,24789095-24791270,24791431-24791828,24791915-24792108,24792295-24792548,24792661-24793266,24793406-24793511,24793598-24794581,24794681-24795022,24795094-24795283,24795372-24795503,24795549-24798265,24798441-24798605,24798740-24799064,24799225-24799372,24799502-24800222,24800336-24800412,24800563-24800992,24801144-24801726,24801890-24801995,24802195-24803698,24803885-24804188,
ADCY4	NM_001198592	chr14	24787775-24787858,24787985-24788302,24788419-24788533,24788643-24788946,24789095-24791270,24791431-24791828,24791915-24792108,24792295-24792548,24792661-24793266,24793406-24793511,24793598-24794581,24794681-24795022,24795094-24795283,24795372-24795503,24795549-24798265,24798441-24798605,24798740-24799064,24799225-24799372,24799502-24800222,24800336-24800412,24800563-24800992,24801144-24801726,24801890-24801995,24802195-24803698,24803889-24804188,

ADCY4	NM_001198568	chr14	24787775-24787858,24787985-24788302,24788419-24788533,24788643-24788946,24789095-24791270,24791431-24791828,24791915-24792108,24792295-24792548,24792661-24793266,24793406-24793511,24793598-24794581,24794681-24795022,24795094-24795283,24795372-24795503,24795549-24798265,24798441-24798605,24798740-24799064,24799225-24799372,24799502-24800222,24800336-24800412,24800563-24800992,24801144-24801726,24801890-24801995,24802195-24803698,
ADHFE1	NM_144650	chr8	67344811-67352395,67352435-67355031,67355080-67356600,67356656-67356827,67356984-67357451,67357650-67359497,67359577-67361098,67361206-67364186,67364341-67366292,67366393-67369050,67369131-67369303,67369402-67372541,67372701-67380502,
ADM2	NM_024866	chr22	50920387-50920994,
AFF3	NM_001025108	chr2	100168058-100170771,100170997-100171143,100171195-100175335,100175431-100176825,100176899-100181947,100182086-100185312,100185378-100194787,100194914-100199258,100199462-100203614,100203741-100209655,100210752-100217895,100218084-100266086,100266129-100288998,100289052-100343537,100343591-100360564,100360603-100368681,100368764-100453937,100453987-100623092,100623480-100623608,100623923-100625272,100625395-100627957,100628034-100720862,100720981-100721964,
AFF3	NM_002285	chr2	100168058-100170771,100170997-100171143,100171195-100175335,100175431-100176825,100176899-100181947,100182086-100185312,100185378-100194787,100194914-100199258,100199462-100203614,100203741-100209655,100210752-100217895,100218084-100266086,100266129-100288998,100289052-100343537,100343591-100360564,100360603-100368681,100368764-100453937,100453987-100623092,100623480-100623608,100623923-100625272,100625395-100720862,100720981-100721964,100722046-100758944,
AFM	NM_001133	chr4	74347581-74349656,74349707-74349973,74350108-74351577,74351791-74352682,74352817-74353439,74353539-74354345,74354477-74357587,74357804-74361015,74361150-74363367,74363467-74364829,74364964-74365719,74365945-74367502,74367637-74368765,74368828-74369591,
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AGTR1	NM_004835	chr3	148415915-148447965,148448025-148458774,
AGTR1	NM_009585	chr3	148415915-148458774,
AGTR1	NM_000685	chr3	148415915-148425729,148425815-148458774,
AGTR1	NM_032049	chr3	148448025-148457585,148457744-148458774,
AGTR1	NM_031850	chr3	148415915-148425729,148425815-148447965,148448025-148458774,
AGTR2	NM_000686	chrX	115302070-115302219,115302281-115303497,
AHCTF1	NM_015446	chr1	247004301-247005994,247006079-247007095,247007231-247012915,247014745-247016391,247016602-247019030,247019130-247020991,247021117-247024199,247024598-247025259,247025456-247027224,247027419-247030544,247030654-247030961,247031114-247039337,247039490-247040250,247040384-247040458,247040605-247048793,247048983-247050511,247050660-247051477,247051536-247051694,247051820-247053266,247053362-247054256,247054363-247055079,247055222-247057959,247058051-247059135,247059228-247061508,247061639-247062751,247062815-247063365,247063549-247063637,247063772-247065825,247065978-247067249,247067336-247068841,247068960-247070851,247071061-247076532,247076715-247079442,247079698-247081550,247081680-247094608,
AIDA	NM_022831	chr1	222843332-222843473,222843593-222846653,222846778-222849436,222849561-222860270,222860379-222860935,222861001-222867129,222867186-222867550,222867606-222876488,222876560-222885548,
AK7	NM_152327	chr14	96858597-96864410,96864601-96871092,96871203-96875182,96875279-96887157,96887270-96904170,96904253-96909065,96909156-96912852,96912945-96916137,96916217-96917756,96917908-96922682,96922813-96924418,96924550-96937813,96937944-96939022,96939093-96944800,96945000-96949334,96949557-96953233,96953394-96954640,
AK8	NM_152572	chr9	135601313-135602839,135602922-135668019,135668163-135690023,135690115-135698590,135698724-135702239,135702442-135703398,135703472-135704030,135704114-135730242,135730313-135739050,135739166-135742289,135742341-135750500,135750587-135753557,

AKAP13	NM_006738	chr15	85924030-86028939,86028985-86064657,86064807-86076813,86077112-86087001,86087187-86118360,86118561-86122159,86125339-86128931,86129055-86182603,86182681-86189047,86189186-86198646,86199019-86205617,86205685-86207792,86207987-86212951,86213062-86225387,86225444-86227970,86228105-86236506,86236683-86251248,86251318-86253808,86253877-86259017,86259155-86260519,86260634-86261236,86261391-86262305,86262558-86265220,86265348-86265459,86265579-86266301,86266552-86269639,86269718-86270295,86270479-86270610,86270695-86273742,86273939-86278221,86278382-86278789,86278862-86279319,86279366-86283451,86283504-86284275,86284727-86286721,86287057-86287857,
AKAP13	NM_144767	chr15	86220330-86225387,86225444-86227970,86228105-86236506,86236683-86251248,86251318-86253808,86253877-86259017,86259155-86260519,86260634-86261236,86261391-86262305,86262558-86265220,86265348-86265459,86265579-86266301,86266552-86269639,86269718-86270295,86270479-86270610,86270695-86273742,86273939-86278221,86278382-86278789,86278862-86279319,86279366-86283451,86283504-86284275,86284727-86286721,86287057-86287857,
AKAP13	NM_007200	chr15	85924030-86028939,86028985-86064657,86064807-86076813,86077112-86087001,86087187-86118360,86118561-86122159,86125339-86128931,86129055-86182603,86182681-86189047,86189186-86198646,86199019-86201766,86201822-86207792,86207987-86212951,86213062-86225387,86225444-86227970,86228105-86236506,86236683-86251248,86251318-86253808,86253877-86259017,86259155-86260519,86260634-86261236,86261391-86262305,86262558-86265220,86265348-86265459,86265579-86266301,86266552-86269639,86269718-86270295,86270479-86270610,86270695-86273742,86273939-86278221,86278382-86278789,86278862-86279319,86279366-86283451,86283504-86284275,86284727-86286721,86287057-86287857,
AKD1	NM_001145128	chr6	109814775-109815182,109815299-109816539,109816644-109818666,109818767-109818997,109819169-109820245,109820444-109827528,109827751-109827855,109828004-109830380,109830584-109835425,109835641-109837058,109837279-109837631,109837846-109850212,109850277-109854452,109854674-109863248,109863375-109867068,109867331-109871291,109871506-109884798,109884916-109885281,109885484-109885957,109886049-109894643,109894798-109900751,109900830-109906324,109906441-109907117,109907276-109931566,109931717-109933211,109933297-109935384,109935500-109935586,109935684-109940293,109940440-109954124,109954307-109954385,109954527-109962719,109962820-109965815,109965892-109977957,109978088-109980429,109980617-109983752,109983867-109993120,109993219-109993316,109993371-109995399,109995465-109996830,109996960-110012348,
AKD1	NM_145025	chr6	109954307-109954385,109954527-109962719,109962820-109965815,109965892-109977957,109978088-109980429,109980617-109983752,109983867-109993120,109993219-109993316,109993371-109995399,109995465-109996830,109996960-110012348,
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ALB	NM_000477	chr4	74270124-74270831,74270891-74272344,74272479-74274309,74274523-74275070,74275205-74276027,74276127-74277711,74277843-74279135,74279352-74280750,74280885-74281971,74282071-74283246,74283387-74283803,74284029-74285222,74285357-74285969,74286039-74286807,
ALDH1B1	NM_000692	chr9	38392805-38395735,
ALDH3A1	NM_001135168	chr17	19641549-19641634,19641767-19642307,19642409-19642819,19642988-19643647,19643791-19644404,19644524-19645315,19645526-19645856,19645944-19646543,19646777-19648279,
ALDH3A1	NM_001135167	chr17	19641549-19641634,19641767-19642307,19642409-19642819,19642988-19643647,19643791-19644404,19644524-19645315,19645526-19645856,19645944-19646543,19646777-19648279,19648448-19648754,
ALDH3A1	NM_000691	chr17	19641549-19641634,19641767-19642307,19642409-19642819,19642988-19643647,19643791-19644404,19644524-19645315,19645526-19645856,19645944-19646543,19646777-19648279,19648448-19651570,
ALDH7A1	NM_001182	chr5	125880712-125882014,125882092-125885619,125885695-125885886,125885986-125887711,125887830-125889977,125890086-125891621,125891708-125894930,125895027-125896773,125896817-125903949,125904049-125906472,125906552-125911110,125911157-125912769,125912904-125918541,125918667-125919622,125919705-125928354,125928422-125929041,125929097-125930697,
ALG14	NM_144988	chr1	95448863-95492683,95492817-95530420,95530574-95538317,
ALG1L	NM_001015050	chr3	125648411-125649398,125649473-125650479,125650506-125651491,125651553-125652416,125652540-125655739,

ALG1L	NM_001195223	chr3	125648411-125649398,125649473-125650479,125650596-125651491,125651553-125652416,125652540-125653277,125653390-125655739,
ALKBH3	NM_139178	chr11	43902730-43904131,43904282-43904633,43904739-43905531,43905568-43908154,43908204-43911273,43911379-43913589,43913680-43923064,43923276-43940586,43940687-43941466,
ALKBH5	NM_017758	chr17	18088328-18098267,18098350-18110127,18110285-18111531,
ALOX12	NM_000697	chr17	6899572-6900143,6900347-6901826,6901910-6902032,6902157-6902270,6902376-6902623,6902786-6903653,6903799-6904919,6905131-6908574,6908663-6909175,6909347-6909803,6909927-6913064,6913167-6913273,6913446-6913561,
AMBN	NM_016519	chr4	71458091-71459042,71459113-71462714,71462767-71464071,71464121-71465251,71465364-71467133,71467372-71468339,71468380-71468513,71468554-71468687,71468728-71468975,71469037-71469131,71469178-71469592,71469639-71471900,
AMDHD1	NM_152435	chr12	96337314-96346493,96346602-96348687,96348754-96350461,96350741-96354174,96354402-96356131,96356258-96359462,96359558-96360124,96360287-96361532,
AMN1	NM_001113402	chr12	31825312-31841939,31842053-31850293,31850352-31850672,31850892-31854795,31854942-31862225,31862360-31881903,
AMN1	NR_004854	chr12	31825312-31841939,31842053-31850293,31850352-31850672,31850892-31854795,31854942-31862225,31862360-31881923,
AMTN	NM_212557	chr4	71384372-71384478,71384549-71388470,71388556-71389583,71389651-71390587,71390679-71394438,71394476-71394899,71394928-71396754,71397018-71398170,
ANKAR	NM_144708	chr2	190540764-190541180,190541818-190554251,190554691-190556979,190557145-190557798,190557904-190558705,190559888-190560874,190561096-190569747,190569951-190571662,190571873-190575773,190575880-190584296,190584540-190585343,190585514-190592580,190592824-190592991,190593147-190593384,190593548-190595219,190595328-190597831,190597956-190602407,190602568-190603289,190603409-190606066,190606178-190607999,190608201-190609466,190609515-190611104,
ANKK1	NM_178510	chr11	113258792-113264201,113264498-113265649,113265803-113266079,113266131-113266787,113266945-113267944,113268065-113268700,113268739-113269684,
ANKMY1	NM_017844	chr2	241419073-241420352,241420515-241421598,241421679-241439373,241439541-241439867,241439983-241446975,241447109-241452217,241452360-241459777,241459951-241463300,241463799-241465100,241465267-241492329,241492475-241494281,241494473-241496605,241496770-241497296,
ANKMY1	NM_016552	chr2	241419073-241420352,241420515-241421598,241421679-241439373,241439541-241439867,241439983-241446975,241447109-241448763,241448873-241451276,241451419-241452217,241452360-241459777,241459951-241463300,241463799-241465100,241465267-241465644,241465863-241468452,241468927-241492329,241492475-241494281,241494473-241497296,
ANKRD11	NM_013275	chr16	89335072-89337223,89337318-89341220,89341366-89341499,89341600-89345478,89352058-89352445,89352595-89354934,89355079-89357031,89357237-89357419,89357592-89371612,89371753-89383339,89383487-89484690,89484777-89556651,
ANKRD17	NM_198889	chr4	73942008-73942655,73942822-73943070,73943251-73944357,73944608-73950964,73951164-73956382,73958018-73959794,73959946-73962832,73962990-73963788,73964238-73968091,73968265-73979507,73979626-73981536,73981634-73984403,73984568-73985877,73986055-73986596,73986812-73987332,73987477-73990628,73990776-73990916,73991030-74000832,74000983-74007456,74007561-74007957,74008103-74008355,74008485-74010460,74010550-74012479,74012591-74012956,74013150-74014528,74014768-74017145,74017242-74019595,74019831-74021346,74021496-74021734,74021884-74026907,74027066-74043095,74043251-74123991,
ANKRD17	NM_032217	chr4	73942008-73942655,73942822-73943070,73943251-73944357,73944608-73950964,73951164-73956382,73958018-73959794,73959946-73962832,73962990-73963788,73964238-73968091,73968265-73979507,73979626-73981536,73981634-73984403,73984568-73985877,73986055-73986596,73986812-73987332,73987477-73990628,73990776-73990916,73991030-74000832,74000983-74005246,74006001-74007456,74007561-74007957,74008103-74008355,74008485-74010460,74010550-74012479,74012591-74012956,74013150-74014528,74014768-74017145,74017242-74019595,74019831-74021346,74021496-74021734,74021884-74026907,74027066-74043095,74043251-74123991,
ANKRD19	NR_026868	chr9	95572153-95575876,95575993-95576154,95576330-95580598,95580707-95581522,95581662-95584490,95584560-95588805,95588861-95591218,95591446-95599057,95600023-95600537,
ANKRD24	NM_133475	chr19	4183475-4186269,4186459-4199678,4199767-4199870,4200003-4200078,4200169-4202021,4202088-4202864,4202924-4207237,4207310-4207496,4207605-4207776,4207966-4208759,4208799-4210053,4210136-4210260,4210370-4212470,4212511-4212595,4212696-4215973,4216048-4216279,4216400-4216545,4218161-4219586,4219756-4222665,4222793-4224122,4224190-4224423,

ANKRD27	NM_032139	chr19	33089285-33090608,33090683-33090876,33090957-33092919,33093033-33095167,33095331-33096739,33096861-33098539,33098739-33106562,33106687-33108493,33108540-33110164,33110286-33110398,33110460-33113326,33113526-33116778,33116873-33117616,33117734-33118987,33119072-33119626,33119756-33122306,33122401-33130260,33130395-33131211,33131292-33132928,33133052-33134027,33134106-33134191,33134259-33134335,33134391-33134476,33134538-33135229,33135386-33137363,33137522-33140586,33140699-33149818,33149952-33165975,
ANKRD30A	NM_052997	chr10	37414937-37418819,37418936-37419131,37419307-37421166,37421275-37422842,37422982-37425533,37425600-37430644,37431219-37433921,37433985-37436296,37436386-37438577,37438608-37438703,37438778-37440986,37441050-37442498,37442591-37447318,37447349-37447440,37447515-37451575,37451606-37451702,37451777-37454020,37454084-37455531,37455624-37470248,37470279-37470370,37470445-37474439,37474470-37474566,37474641-37476884,37476948-37478393,37478486-37481990,37482021-37482112,37482187-37486207,37486238-37486334,37486409-37488653,37488717-37490161,37490254-37505107,37505323-37506621,37506807-37507906,37508826-37520387,37520609-37521425,
ANKRD30BP2	NR_026916	chr21	14410746-14414821,14414938-14415098,14415274-14417482,14417592-14421284,14421351-14424115,14425024-14432785,14433205-14435159,14435280-14437494,14438021-14439171,14439370-14441494,14441614-14490157,
ANKRD37	NM_181726	chr4	186318105-186318302,186318457-186320089,186320183-186320722,186320928-186321169,
ANKRD5	NM_022096	chr20	10015982-10016225,10016291-10018904,10019296-10023768,10023970-10025040,10025192-10026220,10026346-10030036,10030861-10032309,10032538-10033758,10033924-10035108,10035248-10036148,
ANKRD5	NM_198798	chr20	10015982-10018904,10019296-10023768,10023970-10025040,10025192-10026220,10026346-10030036,10030861-10032309,10032538-10033758,10033924-10035108,10035248-10036148,
ANKS6	NM_173551	chr9	101498906-101507839,101507958-101513309,101513379-101518700,101518886-101530361,101530533-101533176,101533329-101536157,101536363-101539685,101539737-101540506,101540707-101542469,101542620-101544747,101544856-101546233,101546440-101547112,101547159-101552384,101552889-101558413,
ANKZF1	NM_018089	chr2	220094623-220094948,220095128-220096648,220096763-220096980,220097085-220097210,220097406-220097799,220097914-220098006,220098156-220098435,220098666-220098853,220099011-220099546,220100035-220100194,220100308-220100428,220100598-220100730,220100818-220101042,
ANKZF1	NM_001042410	chr2	220094681-220094948,220095128-220096648,220096763-220096980,220097085-220097210,220097406-220097799,220097914-220098006,220098156-220098435,220098666-220098853,220099011-220099546,220100035-220100194,220100308-220100428,220100598-220100730,220100818-220101042,
ANLN	NM_018685	chr7	36429654-36435873,36436029-36438686,36439003-36445788,36446176-36447341,36447566-36450121,36450314-36450666,36450776-36455365,36455494-36456687,36456800-36458851,36459089-36459776,36459924-36460204,36460354-36461464,36461602-36462240,36462419-36463424,36463553-36464152,36464203-36464293,36464352-36465309,36465350-36465622,36465646-36466523,36466638-36478811,36478900-36483362,36483472-36489272,36489447-36492084,
ANO10	NM_018075	chr3	43408467-43474101,43474220-43591210,43591341-43596768,43596962-43602710,43602895-43607143,43607220-43616299,43616357-43618182,43618754-43621843,43621965-43640022,43640159-43641874,43642074-43647204,43647356-43663399,
ANTXRL	NR_003601	chr10	47658278-47658574,47658747-47663292,47663366-47665063,47665137-47667253,47667337-47667453,47667489-47668486,47668565-47668640,47668711-47669065,47669148-47669236,47669299-47673956,47674057-47678037,47678109-47678636,47678717-47679692,47679903-47680347,47680439-47681695,47681736-47682744,47682902-47684470,47684553-47700833,47701018-47701085,
ANUBL1	NM_001128324	chr10	46112020-46113586,46113709-46120029,46120086-46121397,46122554-46135262,46135412-46143740,46143983-46147412,46147482-46148430,46148508-46158988,46159291-46168125,
ANUBL1	NM_174890	chr10	46112020-46113586,46113709-46120029,46120086-46121397,46122554-46135262,46135412-46143740,46143983-46147412,46147482-46148430,46148508-46158988,46159291-46167696,
AP1G1	NM_001128	chr16	71767063-71768510,71768611-71772843,71773006-71773135,71773245-71779045,71779174-71779374,71779518-71780489,71780596-71782152,71782282-71783795,71783887-71784111,71784236-71787734,71787791-71789920,71790063-71792709,71792825-71795413,71795471-71798251,71798352-71798547,71798630-71799390,71799488-71803524,71803603-71805057,71805156-71807122,71807266-71808369,71808496-71823180,71823386-71842664,

AP1G1	NM_001030007	chr16	71767063-71768510,71768611-71772843,71773006-71773135,71773245-71779045,71779174-71779374,71779518-71780489,71780596-71782152,71782282-71783795,71783887-71784111,71784236-71787734,71787791-71789920,71790063-71792709,71792825-71795413,71795471-71798251,71798352-71798547,71798630-71799390,71799490-71800340,71800349-71803524,71803603-71805057,71805156-71807122,71807266-71808369,71808496-71823180,71823386-71842664,
AP4E1	NM_007347	chr15	51201126-51204273,51204347-51207643,51207769-51216126,51216202-51217293,51217417-51221204,51221366-51223000,51223169-51226819,51226895-51233637,51233762-51233861,51233973-51240215,51240357-51242021,51242136-51242246,51242367-51250687,51250992-51260458,51260575-51276217,51276343-51285565,51285823-51289521,51290081-51291267,51291460-51293221,51293381-51294697,
APOF	NM_001638	chr12	56755974-56756512,
ARFGAP1	NM_018209	chr20	61904273-61906927,61906993-61907441,61907553-61907830,61908004-61908555,61908658-61909467,61909556-61910249,61910348-61912641,61912700-61914169,61914204-61916216,61916275-61917004,61917066-61917716,61917795-61918914,
ARFGAP1	NM_175609	chr20	61904273-61906927,61906993-61907441,61907553-61907830,61908004-61908555,61908658-61909467,61909556-61910249,61910348-61912641,61912700-61914169,61914204-61915201,61915233-61916216,61916275-61917004,61917066-61917722,61917795-61918914,
ARHGEF4	NM_032995	chr2	131674635-131674968,131675072-131688523,131688831-131704080,131704209-131785516,131785658-131796424,131796606-131797587,131797766-131797832,131798014-131798801,131799036-131799386,131799518-131801023,131801157-131801870,131802116-131802940,
ARHGEF4	NM_015320	chr2	131674635-131674968,131675072-131688523,131688831-131704080,131704209-131785516,131785658-131796424,131796606-131797587,131797766-131797832,131798014-131798801,131799036-131799386,131799518-131801023,131801157-131801870,131802116-131802940,131803020-131803609,
ARHGEF6	NM_004840	chrX	135750329-135751639,135751696-135754177,135754279-135757164,135757256-135758781,135758877-135760093,135760116-135761692,135761820-135762888,135763036-135764047,135764128-135764915,135765004-135767834,135767983-135770089,135770151-135772767,135772908-135789065,135789190-135790832,135790930-135795433,135795530-135814259,135814332-135825742,135825946-135827380,135827507-135829665,135829752-135861571,135861657-135862875,
ARMC1	NM_018120	chr8	66516821-66517496,66517573-66517655,66517774-66525477,66525669-66534496,66534590-66539449,66539669-66546231,
ARMC9	NM_025139	chr2	232063413-232070909,232071003-232072838,232072966-232079542,232079715-232081349,232081507-232087439,232087534-232091485,232091512-232099935,232100095-232104654,232104755-232121297,232121334-232123702,232123816-232127017,232127112-232135693,232135786-232137666,232137792-232141347,232141489-232143093,232143172-232146770,232146847-232156064,232156157-232160909,232160967-232196503,232196610-232209685,
ARMCX4	NR_028407	chrX	100673359-100673896,100673989-100699038,100699144-100700984,100701033-100741008,100741080-100742178,100742260-100742593,100742679-100742993,100743087-100743429,100744303-100753130,100754354-100759922,100760343-100764344,100764415-100764575,100764666-100766010,100766043-100779189,100779420-100786629,
ARPP19	NM_006628	chr15	52844302-52849295,52849420-52861043,
ARPP21	NM_001025069	chr3	35721194-35721277,35721453-35723204,35723373-35724338,35724382-35725216,35725308-35725511,
ARPP21	NM_016300	chr3	35683901-35721277,35721453-35723204,35723373-35724338,35724382-35725216,35725308-35729229,35729376-35730797,35730878-35731571,35731633-35732355,35732498-35748464,35748575-35750459,35750563-35756929,35756969-35758788,35758850-35763095,35763327-35770793,35771029-35778668,35778855-35780807,35781070-35785329,35785458-35833872,35834023-35835191,
ARPP21	NM_198399	chr3	35722663-35723204,35723373-35724338,35724382-35725216,35725308-35725511,
ARPP21	NM_001025068	chr3	35721185-35721277,35721453-35723204,35723373-35724338,35724382-35725216,35725308-35725511,
ARRDC3	NM_020801	chr5	90667274-90669499,90669656-90669929,90670094-90670737,90670996-90671326,90671431-90672436,90672586-90674509,90674593-90678628,
ARSD	NM_009589	chrX	2832815-2833595,2833734-2835843,2836269-2838640,2838765-2839942,2840066-2843655,2843807-2847271,
ARSD	NM_001669	chrX	2825674-2826760,2826884-2827856,2828021-2828698,2828835-2833595,2833734-2835843,2836269-2838640,2838765-2839942,2840066-2843655,2843807-2847271,
ASAH2B	NM_001079516	chr10	52499763-52502673,52502771-52504960,52505035-52509101,52509163-52512226,52512317-52514309,
ASB13	NM_024701	chr10	5682794-5683731,5683925-5690931,5691068-5693174,5693327-5694824,5695014-5708470,
ASB13	NR_037164	chr10	5682794-5683731,5683925-5684434,5684517-5690931,5691068-5693174,5693327-5694824,5695014-5708470,

ASB13	NR_024581	chr10	5682794-5683731,5683925-5690931,5691068-5694824,5695014-5708470,
ASB18	NM_212556	chr2	237103701-237104913,237105029-237123003,237123510-237146330,237146600-237149921,237150046-237172782,
ASPM	NM_018136	chr1	197053557-197055931,197056103-197057384,197057563-197059058,197059215-197059324,197059519-197059978,197060172-197061035,197061187-197062180,197062392-197063212,197063311-197065126,197065295-197069559,197074316-197086917,197087114-197091043,197091174-197091287,197091432-197091516,197091726-197093238,197093462-197093998,197094086-197094174,197094322-197097618,197097796-197098315,197098448-197099043,197099187-197101413,197101483-197102478,197102726-197104224,197104373-197108895,197109002-197111459,197112941-197113085,197113231-197115269,
ASTN2	NM_001184735	chr9	119375885-119380601,119380752-119382587,119382723-119413805,119414073-119449343,
ASTN2	NM_198188	chr9	119187906-119188153,119188368-119202886,119203072-119204730,119204833-119249636,119249780-119380601,119380752-119382587,119382723-119413805,119414073-119449343,
ASTN2	NM_001184734	chr9	119187906-119188187,119188368-119202886,119203072-119204730,119204833-119249636,119249780-119380601,119380752-119382587,119382723-119413805,119414073-119449343,
ASTN2	NM_014010	chr9	119188368-119202886,119203072-119204730,119204833-119249636,119249780-119380601,119380752-119382587,119382723-119413805,119414073-119488048,119488230-119491269,119491376-119495676,119495803-119567909,119568100-119582894,119583063-119625860,119626013-119737485,119737625-119738391,119738468-119738978,119739065-119770369,119770539-119802096,119802245-119858321,119858431-119976635,119977022-120053603,120053793-120176773,
ASTN2	NM_198187	chr9	119187906-119188132,119188368-119202886,119203072-119204730,119204833-119249636,119249780-119380601,119380752-119382587,119382723-119413805,119414073-119449343,
ASTN2	NM_198186	chr9	119188368-119202886,119203072-119204730,119204833-119249636,119249780-119380601,119380752-119382587,119382723-119413805,119414073-119448974,
ATAD2B	NM_017552	chr2	23974958-23977047,23977178-23977515,23977645-23980286,23980972-23985077,23985217-23988374,23988499-24005737,24005899-24008895,24009094-24011380,24011518-24021006,24021194-24033184,24033373-24042615,24042753-24046126,24046440-24051717,24051810-24056787,24056949-24080283,24080374-24086249,24086426-24087677,24087795-24090703,24090817-24092531,24092632-24098697,24098775-24103507,24103626-24107633,24107744-24108595,24108700-24110700,24110856-24111218,24111270-24118687,24118841-24149423,
ATG5	NM_004849	chr6	106634552-106649845,106649965-106696023,106696120-106727534,106727699-106740901,106740982-106756237,106756367-106763974,106764142-106773399,
ATL2	NM_022374	chr2	38523733-38525284,38525718-38526396,38526470-38527412,38527471-38536519,38536649-38537449,38537590-38540291,38540386-38541748,38541807-38542424,38542477-38545675,38545782-38546025,38546162-38570408,38570655-38604283,
ATL2	NM_001135673	chr2	38523256-38525284,38525718-38526396,38526470-38527412,38527471-38536519,38536649-38537449,38537590-38540291,38540386-38541748,38541807-38542424,38542477-38545675,38545782-38546025,38546162-38570408,38570655-38604283,
ATL2	NR_024191	chr2	38523256-38525284,38525718-38526396,38526470-38527412,38527471-38536519,38536649-38537449,38537590-38540291,38540386-38541748,38541807-38542424,38542477-38545675,38545782-38546025,38546162-38604283,
ATN1	NM_001007026	chr12	7033701-7043001,7043192-7043337,7043477-7043626,7043742-7044708,7046725-7047006,7047231-7047642,7048341-7050041,7050187-7050535,7050718-7050908,
ATN1	NM_001940	chr12	7037548-7043001,7043192-7043337,7043477-7043626,7043742-7044708,7046725-7047006,7047231-7047642,7048341-7050041,7050187-7050535,7050718-7050908,
ATP11B	NM_014616	chr3	182511575-182538046,182538165-182545906,182545998-182547458,182547541-182553821,182553931-182554128,182554259-182554857,182554963-182559861,182559911-182563244,182563311-182566262,182566346-182575664,182575817-182576948,182577148-182583242,182583487-182584054,182584232-182585162,182585233-182586864,182586940-182587014,182587120-182590142,182590326-182591598,182591804-182597282,182597438-182598665,182598770-182602539,182602687-182603737,182603799-182605372,182605502-182607196,182607337-182614486,182614554-182615089,182615195-182616393,182616561-182631647,182631783-182635809,
ATP1A1OS	NR_027646	chr1	116935649-116943516,116943754-116961079,
ATP1A1OS	NR_027645	chr1	116941937-116943516,116943754-116961079,
ATP1A1OS	NR_024124	chr1	116948771-116961079,

ATP1A1OS	NR_024126	chr1	116948771-116953881,116953938-116961079,
ATP1A1OS	NR_024125	chr1	116948771-116949548,116949818-116961079,
ATP1A3	NM_152296	chr19	42471118-42471399,42471493-42471812,42471916-42472935,42473068-42473585,42473733-42474335,42474461-42474538,42474695-42479779,42479950-42480566,42480719-42482086,42482225-42482301,42482479-42482756,42482951-42485652,42485789-42485872,42485984-42486058,42486259-42489068,42489339-42489456,42489576-42490014,42490151-42490266,42490382-42492086,42492292-42492468,42492530-42492626,42492715-42498221,
ATP2A2	NM_001681	chr12	110719713-110720407,110720427-110720516,110720601-110729823,110729930-110734402,110734543-110760795,110760878-110764193,110764281-110765356,110765823-110770400,110770491-110770984,110771089-110771815,110771949-110777084,110777209-110777306,110777527-110778462,110778800-110780031,110780254-110781035,110781240-110782689,110782777-110783052,110783188-110783804,110783924-110784004,110784127-110788095,
ATP2A2	NM_001135765	chr12	110719713-110720407,110720427-110720516,110720601-110729823,110729930-110734402,110734543-110764193,110764281-110765356,110765823-110770400,110770491-110770984,110771089-110771815,110771949-110777084,110777209-110777306,110777527-110778462,110778800-110780031,110780254-110781035,110781240-110782689,110782777-110783052,110783188-110783804,110783924-110784004,
ATP2A2	NM_170665	chr12	110719713-110720407,110720427-110720516,110720601-110729823,110729930-110734402,110734543-110760795,110760878-110764193,110764281-110765356,110765823-110770400,110770491-110770984,110771089-110771815,110771949-110777084,110777209-110777306,110777527-110778462,110778800-110780031,110780254-110781035,110781240-110782689,110782777-110783052,110783188-110783804,110783924-110784004,
ATP5S	NM_001003805	chr14	50779779-50788199,50788313-50789227,50789438-50792325,
ATP5S	NR_033761	chr14	50779779-50781307,50781345-50788199,50788313-50789227,50789438-50790661,50790835-50792325,
ATP5S	NM_015684	chr14	50779779-50788199,50788313-50789227,
ATP5S	NM_001003803	chr14	50779779-50788199,50788313-50789227,50789438-50790661,50790835-50792325,
ATP6V0C	NM_001694	chr16	2564184-2569217,2569403-2569540,
ATP6V0C	NM_001198569	chr16	2563778-2564079,2564184-2569217,2569403-2569540,
ATP7B	NM_001005918	chr13	52509166-52509727,52509832-52511410,52511530-52511610,52511816-52513185,52513330-52515215,52515361-52516520,52516691-52518243,52518428-52520418,52520615-52524141,52524298-52524406,52524536-52531650,52531744-52539006,52539170-52542578,52542744-52544626,52544886-52548069,52549305-52585421,
ATP7B	NM_000053	chr13	52509166-52509727,52509832-52511410,52511530-52511610,52511816-52513185,52513330-52515215,52515361-52516520,52516691-52518243,52518428-52520418,52520615-52523796,52523933-52524141,52524298-52524406,52524536-52531650,52531744-52532445,52532681-52534282,52534459-52535971,52536050-52539006,52539170-52542578,52542744-52544626,52544886-52548069,52549305-52585421,
ATXN3	NR_028457	chr14	92530759-92537277,92537398-92545757,92545813-92547307,92547406-92548642,92548811-92549468,92549603-92549755,92549848-92555072,92555162-92559594,92559663-92562435,92562482-92563016,92563183-92572871,
ATXN3	NR_028455	chr14	92530759-92537277,92537398-92545757,92545813-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92559594,92559663-92562435,92562482-92563016,92563183-92572871,
ATXN3	NR_028462	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549580-92555072,92555162-92559594,92559663-92562435,92562482-92563016,92563183-92572871,
ATXN3	NR_028461	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549603-92559594,92559663-92560088,92560176-92562435,92562482-92563016,92563183-92572871,
ATXN3	NM_030660	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92559594,92559663-92560088,92560176-92562435,92562482-92572871,
ATXN3	NM_001164774	chr14	92530759-92537277,92537398-92563016,92563183-92572871,
ATXN3	NM_001164778	chr14	92530759-92537277,92537398-92559594,92559663-92560088,92560176-92562435,92562482-92563016,92563183-92572871,
ATXN3	NM_001164781	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92559594,92559663-92560088,92560176-92572871,

ATXN3	NM_001164782	chr14	92530759-92537277,92537398-92572871,
ATXN3	NM_001164777	chr14	92530759-92537277,92537398-92562435,92562482-92572871,
ATXN3	NM_001164780	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92559594,92559663-92572871,
ATXN3	NM_001164779	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92572871,
ATXN3	NR_028470	chr14	92530759-92537277,92537398-92559594,92559663-92572871,
ATXN3	NR_028469	chr14	92530759-92537277,92537398-92547295,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92559594,92559663-92562435,92562482-92572871,
ATXN3	NM_001127697	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92562435,92562482-92563016,92563183-92572871,
ATXN3	NR_028468	chr14	92530759-92537277,92537398-92547307,92547406-92549468,92549603-92555072,92555162-92559594,92559663-92562435,92562482-92563016,92563183-92572871,
ATXN3	NR_028467	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549580-92549755,92549848-92555072,92555162-92562435,92562482-92563016,92563183-92572871,
ATXN3	NR_028466	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549603-92572871,
ATXN3	NR_028465	chr14	92530759-92537277,92537398-92545757,92545813-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92559594,92559663-92563016,92563183-92572871,
ATXN3	NM_004993	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92559594,92559663-92560088,92560176-92562435,92562482-92563016,92563183-92572871,
ATXN3	NR_028460	chr14	92530759-92537277,92537398-92559594,92559663-92562435,92562482-92563016,92563183-92572871,
ATXN3	NR_028459	chr14	92530759-92537277,92537398-92545757,92545813-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92559594,92559663-92560088,92560176-92562435,92562482-92563016,92563183-92572871,
ATXN3	NR_028458	chr14	92530759-92537277,92537398-92547295,92547406-92548642,92548811-92549468,92549580-92555072,92555162-92559594,92559663-92562435,92562482-92563016,92563183-92572871,
ATXN3	NM_001164776	chr14	92530759-92537277,92537398-92562435,92562482-92563016,92563183-92572871,
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ATXN3	NR_028456	chr14	92530759-92537277,92537398-92545757,92545813-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92559594,92559663-92562435,92562482-92572871,
ATXN3	NM_001127696	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92559594,92559663-92560088,92560176-92563016,92563183-92572871,
ATXN3	NR_028454	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92559594,92559663-92562435,92562482-92572871,
ATXN3	NR_028464	chr14	92530759-92537277,92537398-92545757,92545813-92547307,92547406-92548642,92548811-92549468,92549603-92555072,92555162-92562435,92562482-92563016,92563183-92572871,
ATXN3	NR_031765	chr14	92530759-92537277,92537398-92547307,92547406-92548642,92548811-92572871,
ATXN3	NR_028463	chr14	92530759-92537277,92537398-92545757,92545813-92547307,92547406-92548642,92548811-92549468,92549603-92572871,
AURKA	NM_198437	chr20	54945397-54945539,54945716-54948462,54948613-54956487,54956628-54958039,54958233-54959324,54959381-54961311,54961590-54963210,54963259-54967222,
AURKA	NM_198436	chr20	54945397-54945539,54945716-54948462,54948613-54956487,54956628-54958039,54958233-54959324,54959381-54961311,54961590-54963210,54963259-54965610,54965722-54967222,
AURKA	NM_198435	chr20	54945397-54945539,54945716-54948462,54948613-54956487,54956628-54958039,54958233-54959324,54959381-54961311,54961590-54963210,54963259-54967208,
AURKA	NM_198434	chr20	54945397-54945539,54945716-54948462,54948613-54956487,54956628-54958039,54958233-54959324,54959381-54961311,54961590-54963210,54963259-54965610,54965722-549[illegible]

AURKA	NM_003600	chr20	54945397-54945539,54945716-54948462,54948613-54956487,54956628-54958039,54958233-54959324,54959381-54961311,54961590-54963210,54963259-54966997,
AURKA	NM_198433	chr20	54945397-54945539,54945716-54948462,54948613-54956487,54956628-54958039,54958233-54959324,54959381-54961311,54961590-54963210,54963259-54963741,54963841-54965610,54965722-54966997,
AZI2	NM_022461	chr3	28365946-28368321,28368442-28373858,28373919-28378226,28378377-28379426,28379528-28379982,28380107-28381891,28382114-28390090,
AZI2	NM_001134432	chr3	28373446-28373858,28373919-28378226,28378377-28379426,28379528-28379982,28380107-28381891,28382114-28390090,
AZI2	NM_001134433	chr3	28373442-28373858,28373919-28378226,28378377-28379426,28379528-28379982,28380107-28381891,28382114-28390090,
AZIN1	NM_015878	chr8	103840907-103841498,103841715-103842047,103842165-103845282,103845447-103846415,103846492-103846892,103846976-103848482,103848619-103850970,103851145-103851876,103852052-103855777,103855976-103862225,103862373-103870239,103870379-103876033,
AZIN1	NM_148174	chr8	103840907-103841498,103841715-103842047,103842165-103845282,103845447-103846415,103846492-103846892,103846976-103848482,103848619-103850970,103851145-103851876,103852052-103855777,103855976-103870239,103870379-103876033,
B3GALNT2	NM_152490	chr1	235613656-235616400,235616459-235617466,235617628-235618869,235618997-235621909,235622095-235628951,235629032-235634162,235634275-235643368,235643466-235647636,235647832-235652471,235652574-235657989,235658139-235667439,
B3GNT8	NM_198540	chr19	41932716-41933187,41933476-41934499,
B9D2	NM_030578	chr19	41860919-41863800,41863928-41869335,41869429-41869861,
BAGE	NM_001187	chr21	11058324-11059724,11059818-11089740,11089754-11097541,11097648-11098722,
BAI2	NM_001703	chr1	32193207-32193624,32193683-32193781,32193882-32194197,32194235-32196399,32197021-32197714,32197756-32198116,32198214-32198571,32198745-32200782,32200883-32201179,32201267-32201426,32201495-32201920,32201992-32202172,32202325-32203028,32203133-32203251,32203357-32203799,32203928-32204186,32204232-32204431,32204539-32204907,32205237-32205525,32205636-32205709,32205780-32205946,32206143-32206972,32207081-32207223,32207327-32207399,32207569-32207652,32207819-32208437,32208604-32209792,32209959-32210247,32210333-32221598,32222417-32222800,32222883-32222981,32223113-32229483,
BANP	NM_001173543	chr16	88003777-88008652,88008792-88014640,88014734-88017688,88017866-88037899,88038018-88039694,88039872-88052032,88052274-88061087,88061257-88066713,88066852-88068936,88069001-88071577,88071618-88098871,88098939-88105673,88105819-88110194,
BANP	NM_079837	chr16	87985122-88008652,88008792-88014640,88014734-88017664,88017866-88039694,88039872-88052032,88052274-88061087,88061257-88066713,88066852-88068927,88069001-88071577,88071618-88098871,88098939-88105673,88105819-88110194,
BANP	NM_017869	chr16	87985122-88008652,88008792-88014640,88014734-88017664,88017866-88039694,88039872-88052032,88052274-88061087,88061257-88066713,88066852-88068927,88069001-88071577,88071618-88105673,88105819-88110194,
BANP	NM_001173542	chr16	87993600-88008652,88008792-88014640,88014734-88017664,88017866-88037899,88038018-88039694,88039872-88052032,88052274-88061087,88061257-88066713,88066852-88068927,88069001-88071577,88071618-88105673,88105819-88110194,
BANP	NM_001173541	chr16	87985122-88008652,88008792-88014640,88014734-88017664,88017866-88039694,88039872-88052032,88052274-88061087,88061257-88066713,88066852-88068936,88069001-88071577,88071618-88105673,88105819-88110194,
BANP	NM_001173539	chr16	87985122-88008652,88008792-88014640,88014734-88017664,88017866-88037899,88038018-88039694,88039872-88052032,88052274-88061087,88061257-88066713,88066852-88068936,88069001-88071577,88071618-88105673,88105819-88110194,
BANP	NM_001173540	chr16	87985122-88008652,88008810-88014640,88014734-88017664,88017866-88039694,88039872-88052032,88052274-88061087,88061257-88066713,88066852-88068927,88069001-88071577,88071618-88098871,88098939-88105673,88105819-88110194,
BBS12	NM_152618	chr4	123654040-123663036,
BBS12	NM_001178007	chr4	123654040-123655057,123655247-123663036,
BBS5	NM_152384	chr2	170336123-170338759,170338844-170343577,170343645-170344314,170344366-170344495,170344625-170349382,170349520-170350249,170350347-170354135,170354200-170355994,170356131-170359603,170359689-170360811,170360837-170360989,
BCAR3	NM_003567	chr1	94027977-94032834,94033049-94033295,94033409-94037225,94037399-94041569,94041687-94047856,94048511-94049573,94049679-94054532,94054977-94057820,94057951-94107858,94107900-94140168,94140498-94147152,

BCAS3	NM_001099432	chr17	58755276-58756812,58756902-58761341,58761398-58767045,58767123-58786578,58786687-58824557,58824641-58885363,58885438-58945935,58946045-58952021,58952100-58967054,58967133-58979979,58980065-58987891,58988064-59001766,59001862-59024578,59024714-59067330,59067597-59093110,59093263-59104225,59104272-59112025,59112152-59115248,59115416-59118151,59118254-59152279,59152382-59155692,59155891-59161826,59161926-59445686,59445856-59469336,
BCAS3	NM_017679	chr17	58755276-58756812,58756902-58761341,58761398-58767045,58767123-58786578,58786687-58824557,58824641-58885363,58885438-58945935,58946045-58952021,58952100-58967054,58967133-58979979,58980065-58987891,58988064-59001766,59001862-59024578,59024714-59067330,59067597-59093110,59093263-59112025,59112152-59115248,59115416-59118151,59118254-59152279,59152382-59155692,59155891-59161826,59161926-59445686,59445856-59469336,
BCKDHA	NM_001164783	chr19	41903841-41916540,41916722-41916826,41916915-41919952,41920063-41925038,41925202-41928067,41928276-41928535,41928676-41928901,41929075-41930341,
BCKDHA	NM_000709	chr19	41903841-41916540,41916722-41916826,41916915-41919952,41920063-41925038,41925202-41928067,41928276-41928532,41928676-41928901,41929075-41930341,
BCL2	NM_000657	chr18	60986186-60986405,
BCL2	NM_000633	chr18	60795993-60985313,60986186-60986405,
BCL7C	NM_004765	chr16	30899312-30900179,30900267-30903905,30904069-30904159,30904270-30904531,30904612-30905172,
BDNF-AS1	NR_002832	chr11	27528446-27561565,27561664-27605814,27605885-27661390,27661553-27679786,27680010-27680716,27680776-27696842,27697688-27698527,
BDNF-AS1	NR_033314	chr11	27528446-27561565,27561664-27605814,27605885-27661390,27661553-27679786,27680010-27680716,27680776-27698527,
BDNF-AS1	NR_033312	chr11	27528446-27561565,27561664-27661390,27661553-27679786,27680010-27680716,27680776-27697122,27697688-27698527,27698687-27712651,27712688-27719023,
BDNF-AS1	NR_033313	chr11	27528446-27561565,27561664-27661390,27661553-27679786,27680010-27680716,27680776-27719023,
BDNF-AS1	NR_033315	chr11	27528446-27561565,27561664-27661390,27661553-27679786,27680010-27680716,27680776-27698527,27698687-27719023,
BGN	NM_001711	chrX	152760572-152770077,152770328-152770694,152770809-152771319,152771535-152771985,152772098-152772286,152772382-152772503,152772644-152773704,
BICD2	NM_001003800	chr9	95477746-95480077,95480231-95480819,95481865-95482580,95483038-95484936,95485091-95491304,95491519-95526785,
BICD2	NM_015250	chr9	95475744-95477533,95477746-95480077,95480231-95480819,95481865-95482580,95483038-95484936,95485091-95491304,95491519-95526785,
BNRC6	NM_016252	chr2	32582555-32602654,32602838-32605219,32605359-32613816,32614012-32617105,32617219-32620577,32620662-32626229,32626454-32626529,32626692-32631565,32631626-32639835,32641232-32654212,32654364-32655931,32656159-32658710,32658873-32660562,32660654-32661119,32661253-32664574,32664755-32666395,32666531-32667131,32667295-32667390,32667524-32668557,32668657-32670587,32670737-32673861,32673997-32678874,32679011-32688260,32688450-32689575,32689892-32690131,32690233-32692591,32692808-32692969,32693180-32693503,32693852-32694461,32694683-32695234,32695370-32696080,32696193-32698178,32698308-32701279,32701413-32702434,32702652-32703701,32703887-32704528,32704686-32706386,32706522-32707495,32707651-32710708,32710827-32712712,32712869-32713653,32713782-32715106,32715219-32716490,32716626-32718605,32718735-32724612,32725177-32726778,32726956-32727860,32727959-32728107,32728304-32730070,32730273-32733045,32733327-32734803,32735062-32735591,32735702-32737998,32738222-32740055,32740838-32743319,32743465-32743882,32744014-32749953,32750087-32750529,32750696-32754716,32754892-32756420,32756619-32768306,32768609-32770708,32770928-32772915,32773082-32774378,32774549-32800221,32800434-32818980,32819128-32820099,32820212-32822816,32823036-32824804,32824968-32828071,32828151-32832520,32832711-32836513,32836650-32842790,
BLM	NM_000057	chr15	91260672-91290617,91290721-91292595,91293298-91295015,91295177-91298039,91298169-91303375,91303510-91303822,91304486-91306194,91306388-91308524,91308645-91310138,91310254-91312361,91312462-91312666,91312817-91326050,91326159-91328149,91328312-91333877,91334075-91337395,91337588-91341418,91341568-91346749,91346951-91347395,91347590-91352365,91352490-91354433,91354637-91358330,
BLOC1S1-RDH5	NR_037658	chr12	56109981-56110715,56110790-56112873,56113008-56115471,56115732-56117668,56117834-56118104,

BPTF	NM_182641	chr17	65822454-65850054,65850879-65862578,65862804-65870931,65871137-65887958,65888151-65889484,65889842-65890148,65890282-65899903,65900035-65900816,65900957-65905696,65905878-65906991,65909304-65914828,65914955-65916129,65916260-65918954,65919107-65920661,65920706-65924469,65924718-65925450,65925604-65928025,65928136-65936553,65936773-65940264,65940489-65941523,65942442-65943840,65943925-65944195,65944423-65955655,65955992-65960326,65960521-65962686,65962773-65971886,65972075-65978366,
BPTF	NM_004459	chr17	65822454-65850054,65850879-65862578,65862804-65870931,65871137-65871670,65871861-65882242,65882433-65887958,65888151-65889484,65889842-65890148,65890282-65899903,65900035-65900816,65900957-65905696,65905878-65906991,65909304-65914828,65914955-65916129,65916260-65918954,65919107-65920661,65920706-65924469,65924718-65925450,65925604-65928025,65928136-65936553,65936773-65940264,65940489-65941523,65942013-65943840,65943925-65944195,65944423-65955655,65955992-65960326,65960521-65962686,65962773-65971886,65972075-65978366,
BRD1	NM_014577	chr22	50168065-50169237,50169394-50169696,50169808-50170680,50170810-50171324,50171462-50181036,50181143-50187680,50187943-50191451,50191766-50192204,50192335-50192634,50192768-50197850,50198009-50216597,
BRD3	NM_007371	chr9	136898828-136899821,136899952-136901152,136901447-136905154,136905392-136906880,136907074-136910413,136910544-136913203,136913577-136915494,136915711-136916682,136916832-136917426,136917566-136918385,136918713-136933065,
BRD7	NM_001173984	chr16	50353178-50353796,50353942-50354157,50354303-50354572,50354689-50355891,50355950-50357496,50357610-50359657,50359795-50360193,50360303-50362578,50362656-50367483,50367609-50368620,50368807-50373885,50373998-50383932,50384079-50388334,50388394-50388702,50388834-50401999,50402210-50402635,
BRD7	NM_013263	chr16	50353178-50353796,50353942-50354157,50354303-50354572,50354686-50355891,50355950-50357496,50357610-50359657,50359795-50360193,50360303-50362578,50362656-50367483,50367609-50368620,50368807-50373885,50373998-50383932,50384079-50388334,50388394-50388702,50388834-50401999,50402210-50402635,
BRD9	NR_027633	chr5	864684-865527,865697-870586,870691-871639,871680-876214,876328-878468,878603-879907,880005-881220,881298-884051,884186-886705,886883-887474,887587-889134,889281-889700,889882-891268,891403-891753,891970-892719,
BRD9	NM_001009877	chr5	864684-865527,865697-870586,870691-871639,871680-876214,876328-878468,878603-879907,880005-881220,881298-884051,884186-886705,886823-887474,887587-889134,889276-889700,889763-891268,891403-891753,891970-892622,
BRD9	NM_023924	chr5	864684-865527,865697-870586,870691-871639,871680-876214,876328-878468,878603-879907,880005-881220,881298-884051,884186-886705,886823-887474,887587-889134,889281-889700,889763-891268,891403-891753,891970-892719,
BRIP1	NM_032043	chr17	59761502-59763195,59763527-59770789,59770874-59793310,59793425-59820372,59820496-59821791,59821953-59853760,59853924-59857620,59857763-59858199,59858367-59861629,59861786-59870956,59871091-59876459,59876661-59878612,59878836-59885826,59886119-59924460,59924582-59926488,59926618-59934417,59934593-59937155,59937269-59938806,59938931-59940643,
BTG3	NM_006806	chr21	18966651-18970933,18971143-18977176,18977316-18981288,18981471-18985015,
BTG3	NM_001130914	chr21	18966651-18970933,18971143-18976461,18976595-18977176,18977316-18981288,18981471-18985015,
BUB1	NM_004336	chr2	111395737-111397317,111397426-111398609,111398783-111398882,111399042-111399217,111399381-111399694,111399812-111406809,111406955-111408121,111408362-111411011,111411101-111413314,111413494-111414611,111414695-111415121,111415223-111415985,111416098-111416189,111416320-111417553,111417614-111419157,111419419-111423838,111423992-111425096,111425283-111425372,111425427-111427028,111427131-111428100,111428146-111430236,111430435-111431661,111431802-111431881,111431943-111435545,
BUB1B	NM_001211	chr15	40453457-40457252,40457398-40462261,40462323-40462736,40462883-40468676,40468875-40475913,40476085-40477364,40477581-40477750,40477844-40488744,40488976-40491814,40491929-40492443,40492561-40493130,40493182-40494604,40494667-40494788,40494896-40498383,40498660-40500836,40500972-40501834,40501977-40502309,40502412-40504698,40504850-40505531,40505676-40509695,40509869-40510655,40510764-40512763,
BZRAP1	NM_004758	chr17	56379809-56381697,56381761-56382420,56382533-56382746,56382820-56382899,56383005-56383192,56383227-56383701,56383775-56384159,56384330-56384970,56385124-56385201,56385303-56385900,56386742-56387326,56387520-56387871,56388113-56388195,56388575-56388930,56389084-56389251,56390084-56393382,56393494-56393784,56393902-56395639,56395814-56396449,56396656-56397468,56397491-56397890,56397943-56399667,56399774-56400013,56400138-56400309,56400401-56400657,56400743-56400827,56400907-56402170,56402364-56402893,56403075-56403652,56403783-56404042,56404152-56404947,

BZRAP1	NM_024418	chr17	56379809-56381697,56381761-56382420,56382533-56382746,56382820-56382899,56383005-56383192,56383227-56383701,56383775-56384159,56384330-56384970,56385124-56385201,56385303-56385900,56386742-56387326,56387520-56387871,56388113-56388195,56388575-56388930,56389084-56389251,56390084-56393382,56393494-56393784,56393902-56395639,56395814-56396449,56396656-56397468,56397491-56397890,56397943-56399667,56399774-56400013,56400138-56400309,56400401-56400657,56400743-56400827,56400907-56402170,56402364-56403652,56403783-56404042,56404152-56404947,
C10orf18	NM_017782	chr10	5727139-5754784,5754882-5759620,5759714-5762505,5762632-5762716,5762738-5762832,5762934-5765638,5765741-5766391,5766497-5768846,5768921-5769022,5769087-5772448,5773167-5777265,5777510-5781579,5782461-5784058,5784490-5788140,5791991-5798574,5798702-5799481,5799637-5800848,5800956-5803251,5803435-5804493,5804610-5804990,
C10orf79	NM_025145	chr10	105890064-105891087,105891243-105891872,105891955-105893376,105893543-105900598,105900760-105902037,105902152-105903182,105903398-105905232,105905323-105906019,105906108-105907647,105907757-105912363,105912485-105920793,105920921-105921717,105921800-105922073,105922162-105923850,105924059-105926244,105926477-105927377,105927496-105928500,105928607-105932166,105932294-105938785,105938865-105939596,105939691-105942122,105942272-105944772,105944905-105945730,105945882-105947076,105947251-105948026,105948169-105951955,105952061-105953622,105953773-105956609,105956692-105957678,105957797-105963428,105963562-105965719,105965789-105967421,105967583-105971763,105971916-105974015,105974185-105985217,105985316-105990346,105990602-105991938,
C10orf82	NM_144661	chr10	118423685-118424270,118424459-118425117,118425338-118427767,118427835-118429436,
C10orf93	NM_173572	chr10	134743309-134748254,134748367-134750463,134750560-134751054,134751180-134752091,134752258-134754498,134754565-134755093,134755227-134755482,134755609-134755938,
C11orf24	NM_022338	chr11	68030387-68031158,68031335-68035520,68035720-68039323,
C11orf34	NM_001145024	chr11	112119698-112123069,112123133-112126109,112126313-112131127,
C11orf40	NM_144663	chr11	4592860-4593384,4593525-4594534,4594703-4598908,
C11orf70	NM_032930	chr11	101918312-101918544,101918628-101929609,101929687-101937214,101937383-101946602,101946777-101951944,101952013-101953800,
C11orf70	NM_001195005	chr11	101918312-101918544,101918628-101929609,101929687-101946602,
C11orf74	NM_138787	chr11	36616143-36631629,36631790-36654832,36654989-36657599,36657668-36669564,36669706-36680567,
C12orf26	NM_032230	chr12	82752604-82780580,82780747-82783593,82783702-82792572,82793174-82796760,82796910-82824670,82824767-82828472,82828504-82832495,82832571-82850504,82850600-82870421,82870498-82871058,82871132-82872709,
C12orf35	NM_018169	chr12	32112426-32113709,32113806-32123121,32123291-32133810,32138892-32140171,32140257-32145310,
C12orf47	NR_015404	chr12	112278282-112279129,
C12orf48	NM_017915	chr12	102514065-102517662,102517820-102542006,102542242-102547645,102547755-102558214,102558387-102559505,102559662-102569259,102569445-102572368,102572549-102576325,102576406-102589088,102589226-102589727,
C12orf5	NM_020375	chr12	4430470-4440444,4440484-4446203,4446327-4458983,4459063-4460431,4460544-4461424,
C12orf52	NM_032848	chr12	113623827-113623988,113624122-113624486,113624854-113629113,
C12orf53	NM_153685	chr12	6804224-6804594,6804818-6805607,6805691-6806451,6806959-6807209,6807271-6809778,
C12orf57	NM_138425	chr12	7053337-7053637,7053816-7054932,
C12orf76	NM_207435	chr12	110480265-110494992,110495102-110496791,110496969-110503663,110503839-110505293,
C14orf105	NM_018168	chr14	57938309-57947311,57947473-57948275,57948379-57949781,57949870-57957705,57957790-57960209,
C14orf132	NR_023938	chr14	96505865-96552846,
C14orf135	NM_022495	chr14	60559138-60581416,60581598-60581690,60582180-60582435,60582538-60582657,60582779-60585045,60585411-60587912,60588018-60590934,60591970-60592353,60592542-60600686,
C14orf145	NM_152446	chr14	80963926-80971253,80971364-80993211,80993327-80997151,80997231-81025621,81025647-81046716,81046768-81209417,81209612-81223234,81223296-81227779,81227958-81244224,81244391-81251237,81251890-81259102,81259455-81297485,81297639-81302547,81302682-81304546,81304623-81307024,81307113-81329099,81329218-81362060,81362135-81366280,81366374-81371155,81371276-81372297,81372426-81380664,81380753-81382743,81382907-81405727,
C14orf147	NM_138288	chr14	34904511-34931300,

C14orf23	NR_026732	chr14	29242062-29242564,29242640-29247062,29247198-29247310,
C14orf23	NR_026731	chr14	29242062-29242564,29242640-29261084,
C14orf38	NM_001164399	chr14	59972034-59977362,59977527-59978476,59978522-59988290,59988395-59991998,59992153-59993811,59993893-59998488,59998629-60004739,60004873-60005421,60005559-60007391,60007465-60010060,60010173-60011879,60012018-60018071,60018155-60027835,60027947-60030453,60030578-60031763,60031994-60034961,60035099-60039418,60039532-60041659,60041747-60043335,
C14orf50	NM_172365	chr14	65016785-65017637,65017704-65019530,65019580-65031467,65031556-65032073,65032173-65032342,65032411-65035065,65035166-65041171,65041308-65053553,65053598-65053910,65054091-65054820,65055014-65055868,
C14orf79	NM_174891	chr14	105453192-105455278,105455426-105457826,105457958-105459283,105459402-105460933,
C15orf23	NM_001142762	chr15	40675246-40675427,40675524-40678561,40678696-40679358,40679408-40681705,40681813-40682035,40682131-40684148,40684225-40685668,
C15orf23	NM_033286	chr15	40675246-40675427,40675524-40678561,40678696-40679358,40679408-40681705,40681813-40682035,40682131-40683692,40683756-40684148,40684225-40685668,
C15orf23	NM_001142761	chr15	40675246-40675427,40675524-40678561,40678696-40679358,40679408-40681705,40681813-40682035,40682131-40683692,40683756-40684148,40684225-40685392,
C15orf42	NM_152259	chr15	90119472-90125915,90126197-90127515,90127759-90128937,90129174-90135276,90135408-90137644,90137786-90138622,90138843-90142553,90142707-90143814,90143917-90144527,90144623-90144718,90144800-90144966,90145208-90146025,90146124-90149997,90150057-90152032,90152181-90159634,90159727-90161381,90161442-90162937,90163074-90164622,90164782-90166852,90169018-90169165,90169293-90170185,
C16orf5	NM_013399	chr16	4562685-4562790,4563066-4563695,4563853-4564045,4564146-4564574,4564666-4588701,
C16orf5	NM_001199054	chr16	4562685-4562790,4563066-4563695,4563853-4564045,4564146-4564574,4564666-4588324,
C16orf5	NM_001199055	chr16	4562685-4562790,4562949-4563695,4563853-4564045,4564146-4564574,4564666-4588701,
C16orf5	NM_001199056	chr16	4562685-4562790,4562949-4563815,4563853-4564045,4564146-4564574,4564666-4588701,
C16orf52	NM_001164579	chr16	22019729-22086806,22087021-22092015,
C16orf58	NM_022744	chr16	31502254-31503328,31503408-31503516,31503662-31504297,31504370-31504786,31504846-31504922,31505109-31505185,31505258-31508168,31508272-31510621,31510729-31510812,31510847-31512005,31512053-31519083,31519200-31519393,
C16orf61	NM_020188	chr16	81010077-81015409,81015483-81030917,81031035-81040337,
C16orf71	NM_139170	chr16	4784700-4786463,4786645-4787799,4787948-4790152,4790661-4793042,4793162-4794869,4795013-4796374,4796514-4796926,4797027-4797342,4797636-4798724,
C17orf102	NM_207454	chr17	32904640-32905888,
C17orf49	NM_001142798	chr17	6918198-6918379,6918476-6919091,6919195-6919812,6920005-6920227,6920334-6920574,
C17orf49	NM_174893	chr17	6918198-6918379,6918476-6919091,6919195-6919812,6920005-6920227,6920334-6920578,
C17orf49	NM_001142799	chr17	6918198-6918379,6918476-6919812,6920005-6920227,6920334-6920578,
C17orf64	NM_181707	chr17	58500005-58503142,58503246-58503520,58503698-58504077,58504179-58506721,58506919-58508540,
C17orf68	NM_025099	chr17	8131638-8131819,8131948-8132043,8132211-8132458,8132525-8132618,8132765-8133207,8133287-8133610,8133787-8133879,8133970-8134592,8134788-8135042,8135134-8135219,8135546-8135677,8135794-8136222,8136351-8137771,8137974-8138065,8138245-8138369,8138604-8139147,8139278-8139374,8139661-8140691,8140838-8141347,8141561-8141708,8141948-8146301,8146467-8151320,
C17orf85	NM_001114118	chr17	3716574-3717614,3717778-3719408,3719565-3721555,3721867-3724541,3724647-3725245,3725347-3728234,3728345-3729059,3729138-3729379,3729510-3732535,3732663-3743392,3743500-3746378,3746446-3749333,
C17orf85	NM_018553	chr17	3716574-3717614,3717778-3719408,3719565-3721555,3721867-3724541,3724647-3725245,3725347-3727352,3727387-3728234,3728345-3729059,3729138-3729379,3729510-3732535,3732663-3743392,3743500-3746378,3746446-3749333,
C17orf97	NM_001013672	chr17	260438-262937,
C18orf26	NM_173629	chr18	52258571-52262168,52262335-52265042,
C18orf54	NM_173529	chr18	51885241-51886895,51887226-51888011,51888319-51889139,51889292-51892087,51892192-51898834,51898968-51900582,51900655-51904542,
C18orf55	NM_014177	chr18	71816345-71822378,71822443-71822539,71822639-71825247,71825323-71825404,71825512-71825609,
C18orf62	NM_001037331	chr18	73122865-73130739,73130872-73139388,

C19orf20	NM_033513	chr19	507845-518887,
C19orf76	NM_001101340	chr19	50193169-50193361,
C1orf106	NM_018265	chr1	200860830-200867433,200867584-200868599,200868726-200869230,200869349-200870063,200870288-200876960,200877016-200877856,200878069-200878350,200878526-200880579,200881266-200882663,
C1orf105	NM_001142569	chr1	200864216-200867433,200867584-200868599,200868726-200869230,200869349-200870063,200870288-200876960,200877016-200877856,200878069-200878350,200878526-200880579,200881266-200882663,
C1orf124	NM_032018	chr1	231474351-231475513,231475615-231483541,231483672-231487048,231487318-231488354,
C1orf124	NM_001010984	chr1	231474351-231475513,231475615-231483541,231483672-231487048,
C1orf146	NM_001012425	chr1	92683606-92696937,92697044-92707767,92707863-92709772,92709943-92710334,92710415-92711095,
C1orf168	NM_001004303	chr1	57185366-57185693,57185729-57185844,57186003-57189259,57189355-57192168,57192257-57202758,57202821-57204296,57204327-57206368,57206469-57207832,57207895-57209697,57209740-57209823,57209940-57216715,57216877-57219510,57219609-57221567,57221601-57224387,57224424-57233500,57233612-57252846,57252882-57254644,57254808-57257727,57258477-57284953,
C1orf173	NM_001002912	chr1	75036124-75036781,75039176-75042577,75042621-75055313,75055765-75065377,75065616-75072283,75072587-75078305,75078494-75086416,75086599-75097395,75097613-75101962,75102123-75107013,75107144-75108709,75108783-75112349,75112477-75114904,75115000-75139179,
C1orf174	NM_207356	chr1	3806638-3807131,3807622-3809445,3809561-3816734,
C1orf198	NM_032800	chr1	230975655-230979098,230979643-230991412,230991465-231003924,
C1orf198	NM_001136495	chr1	230975655-230979098,230979643-230991412,230991465-230991622,
C1orf198	NM_001136494	chr1	230975655-230979098,230979643-230991412,230991465-231003924,231004149-231004556,231004662-231005226,
C1orf38	NM_001039477	chr1	28199177-28203097,28203240-28211804,28211963-28212376,
C1orf38	NM_001105556	chr1	28199177-28203097,28203240-28206153,28206566-28208480,28209555-28211804,28211963-28212376,
C1orf38	NM_004848	chr1	28199177-28203097,28203240-28206153,28206566-28211804,28211963-28212376,
C1orf9	NM_016227	chr1	172502638-172520650,172520767-172525007,172525164-172526418,172526558-172526782,172526935-172538157,172538283-172539185,172539312-172539801,172539871-172543029,172543139-172544656,172544764-172546902,172546960-172547436,172547530-172548340,172548408-172554156,172554227-172554996,172555089-172557898,172559067-172560122,172560212-172569202,172569309-172571202,172571359-172571834,172571928-172577885,172577943-172578954,
C1orf9	NM_014283	chr1	172502638-172520650,172520767-172522398,172522511-172525007,172525164-172526418,172526558-172526782,172526935-172538157,172538283-172539185,172539312-172539801,172539871-172543029,172543139-172544656,172544764-172546677,172546700-172546902,172546960-172547436,172547530-172548340,172548408-172554156,172554227-172554996,172555089-172557898,172559067-172560122,172560212-172569202,172569309-172571202,172571359-172571834,172571928-172577885,172577943-172578954,
C1QTNF6	NM_031910	chr22	37578776-37581256,37581496-37584201,
C1QTNF6	NM_182486	chr22	37576908-37578190,37578776-37581256,37581496-37584201,
C20orf132	NM_213631	chr20	35757571-35766211,35766374-35769563,35769718-35772118,35772245-35776175,35776313-35783464,35783571-35786261,35786359-35787293,35787440-35788498,35788580-35796522,35796647-35800313,35800461-35802396,35802520-35807624,
C20orf132	NM_152503	chr20	35729822-35731065,35731239-35737000,35737068-35738657,35738759-35740725,35740850-35742391,35742549-35743574,35743741-35748099,35748242-35748905,35749022-35749300,35749440-35752010,35752203-35757433,35757571-35766211,35766374-35769563,35769718-35772118,35772245-35776175,35776313-35783464,35783571-35786261,35786359-35787293,35787440-35788498,35788580-35796522,35796647-35800313,35800461-35802396,35802520-35807624,
C20orf132	NM_213632	chr20	35757571-35766211,35766374-35769563,35769718-35772118,35772245-35776175,35776313-35786261,35786359-35787293,35787440-35788498,35788580-35796522,35796647-35800313,35800461-35802396,35802520-35807624,
C20orf185	NM_182658	chr20	31643354-31644346,31644505-31647182,31647289-31647695,31647838-31649572,31649638-31651419,31651482-31652261,31652355-31652470,31652652-31654628,31654684-31656607,31656780-31657692,31657762-31659057,31659102-31659908,31659974-31660521,31660600-31661380,
C20orf191	NR_003678	chr20	26084308-26094513,

C20orf26	NM_001167816	chr20	20037441-20051496,20051649-20054944,20055023-20055831,20055901-20056131,20056260-20071486,20071621-20079297,20079459-20123499,20123593-20140012,20140089-20144692,20144873-20147039,20147081-20149963,20150105-20152423,
C20orf26	NM_015585	chr20	20033236-20037260,20037441-20051496,20051649-20054944,20055023-20055831,20055901-20056131,20056260-20071486,20071621-20079297,20079459-20123499,20123593-20140012,20140089-20144692,20144873-20147039,20147081-20149963,20150105-20168572,20168701-20171984,20172064-20177212,20177421-20180410,20180547-20208891,20209021-20226759,20226860-20232237,20232408-20243598,20243775-20257808,20258103-20269251,20269581-20270942,20271036-20278823,20279031-20322473,20322566-20340852,
C20orf30	NM_001009924	chr20	5081578-5086832,5086957-5089976,5090092-5092144,5092252-5093387,
C20orf30	NM_001009925	chr20	5081578-5086832,5086957-5089976,5090092-5093605,
C20orf30	NM_001009923	chr20	5081578-5086832,5086957-5089976,5090092-5092144,5092252-5093605,
C20orf30	NM_014145	chr20	5081578-5086832,5086957-5089976,5090092-5093374,
C20orf96	NM_153269	chr20	251909-256607,256728-257432,257521-257683,257787-257865,258025-258969,259071-259811,259972-264602,264723-270198,270318-270898,270949-271230,
C21orf29	NM_144991	chr21	45919820-45924661,45924765-45929080,45929270-45941764,45941996-45945534,45945723-45947173,45947402-45948333,45948467-45949679,45949838-45950924,45951017-45953566,45953807-45987667,45987890-46131346,
C22orf26	NM_018280	chr22	46447780-46449628,
C22orf9	NM_001009880	chr22	45593098-45593669,45593830-45595752,45595917-45598869,45599066-45599724,45599867-45601096,45601200-45601509,45601589-45601672,45601794-45607835,45607989-45636519,
C22orf9	NM_015264	chr22	45593098-45593669,45593830-45595752,45595917-45598869,45599066-45599724,45599867-45601096,45601200-45601509,45601589-45601672,45601794-45607835,45607989-45608144,
C2orf34	NM_024766	chr2	44589285-44599853,44600028-44617378,44617445-44931420,44931483-44933424,44933481-44934536,44934602-44942424,44942493-44970759,44970836-44981192,44981258-44993567,44993701-44999173,
C2orf65	NM_138804	chr2	74786002-74786823,74786837-74787276,74787419-74789342,74789551-74802563,74802707-74803581,74803746-74808799,74808975-74834180,74834351-74842089,74842277-74867161,74867455-74875098,
C2orf73	NM_001100396	chr2	54558139-54561952,54562162-54570855,54571011-54586094,54586212-54587338,
C2orf77	NM_001085447	chr2	170502693-170505690,170505857-170506837,170507032-170510583,170510725-170518788,170518947-170531084,170531280-170531375,170531551-170537515,170537744-170550769,
C2orf78	NM_001080474	chr2	74011534-74040602,74041354-74042196,
C2orf84	NM_001040710	chr2	24398044-24398334,24398443-24400669,24400740-24406152,24406242-24406362,24406515-24413279,
C3orf15	NM_033364	chr3	119422070-119425654,119425733-119426249,119426409-119427436,119427522-119428684,119428743-119434407,119434591-119445016,119445196-119449065,119449225-119451139,119451324-119452209,119452354-119456211,119456330-119458100,119458174-119459394,119459543-119462820,119463044-119465960,119466111-119466656,119466750-119469782,119469946-119483897,
C3orf24	NM_173472	chr3	10123216-10145880,10146467-10149697,
C3orf24	NM_001164839	chr3	10146467-10149697,
C4orf21	NM_018392	chr4	113460846-113461017,113461281-113461975,113462112-113462246,113462425-113468439,113468565-113469407,113469537-113474989,113475139-113475859,113475939-113479304,113479466-113481887,113482152-113483525,113483642-113484285,113484431-113502817,113502959-113505132,113505331-113506695,113506882-113507599,113507740-113508434,113509086-113510878,113511031-113524678,113524854-113527162,113527248-113530533,113530586-113533678,113533745-113538594,113540847-113541156,113541347-113544971,113545033-113553084,113553167-113554310,113554399-113558005,
C4orf32	NM_152400	chr4	113066890-113107847,
C4orf44	NM_001042690	chr4	3251270-3254932,3255210-3257450,
C4orf45	NM_152543	chr4	159814870-159836320,159836512-159881436,159881497-159894229,159894464-159956183,

C5	NM_001735	chr9	123715147-123716006,123716147-123719561,123719647-123722524,123722616-123723758,123723844-123724947,123725055-123725169,123725246-123725912,123726017-123731337,123731397-123732446,123732530-123734206,123734271-123737055,123737210-123738976,123739184-123742359,123742533-123744120,123744218-123744931,123745093-123751322,123751400-123751844,123752059-123753467,123753559-123758516,123758579-123759823,123760053-123768195,123768337-123769180,123769256-123770684,123770777-123776149,123776349-123777475,123777540-123778530,123778662-123779638,123779790-123779919,123780131-123782252,123782458-123783785,123783973-123785680,123785798-123787730,123787859-123789436,123789553-123792673,123792766-123794389,123794474-123797079,123797173-123800157,123800230-123805280,123805445-123808467,123808662-123812458,
C5orf22	NM_018356	chr5	31532581-31534377,31534525-31535849,31536001-31538365,31538797-31541054,31541119-31541386,31541510-31545751,31545820-31551398,31551540-31552878,
C5orf30	NM_033211	chr5	102594598-102601607,102601699-102611596,
C5orf38	NM_178569	chr5	2752579-2752734,2752869-2753397,2753470-2755141,
C6orf103	NM_024694	chr6	146920251-146956509,146956674-146965907,146966002-146975269,146975343-146977905,146978117-146985335,146985477-146987950,146988039-146993354,146993604-146997447,146997578-147006868,147006965-147012250,147012427-147013959,147014052-147022075,147022207-147036516,147036552-147038017,147038206-147038670,147038736-147042537,147042642-147045320,147045464-147047217,147047334-147049708,147049878-147054254,147054392-147055027,147055167-147057632,147057728-147061593,147061730-147062252,147062408-147067056,147067246-147073664,147073851-147085035,147085237-147090154,147090268-147103154,147103329-147105752,147105931-147106744,147106849-147109523,147109747-147122317,147122416-147122962,147123148-147136166,
C6orf124	NR_027906	chr6	168225487-168226081,
C6orf155	NR_026807	chr6	72126263-72127021,72127096-72128390,72128458-72129767,
C6orf225	NM_001033564	chr6	112408924-112418242,112418405-112420471,112420612-112421871,
C6orf58	NM_001010905	chr6	127898632-127899829,127899918-127901408,127901595-127902325,127902428-127911230,127911471-127912686,
C7orf30	NM_138446	chr7	23339228-23340456,23340637-23347485,23347569-23348973,
C7orf53	NM_001134468	chr7	112121038-112124865,112124999-112126976,112127107-112129863,
C7orf53	NM_182597	chr7	112121402-112124865,112124999-112126976,112127107-112129863,
C7orf63	NM_001160138	chr7	89874859-89884735,89884797-89887410,89887478-89891259,89891371-89894613,89894692-89897598,89897645-89900838,89900990-89901093,89901273-89903299,89903425-89906385,89906436-89906525,89906649-89908989,89909208-89912204,89912371-89915593,89915714-89917546,89917667-89927061,89927145-89929179,89929374-89933281,89933421-89934056,89934135-89936213,89936413-89937080,89937169-89938575,89938682-89939380,
C7orf63	NM_001039706	chr7	89874859-89884735,89884797-89887410,89887478-89891259,89891371-89894613,89894692-89897598,89897699-89900838,89900990-89901093,89901273-89903299,89903425-89906385,89906436-89906525,89906649-89908989,89909208-89912204,89912371-89915593,89915714-89917546,89917667-89927061,89927145-89929179,89929374-89933281,89933421-89934056,89934135-89936213,89936413-89937080,89937169-89938575,89938682-89939380,
C8orf73	NM_001100878	chr8	144649636-144649779,144649847-144649954,144650059-144650310,144650432-144650720,144650890-144651609,144651785-144651865,144652011-144652119,144652236-144652411,144652551-144652641,144652828-144653045,144653165-144653835,144653992-144654201,144654356-144654589,
C8orf75	NR_026765	chr8	29579668-29582391,29582536-29583670,29583940-29605529,
C9orf102	NM_001010895	chr9	98638367-98643149,98643576-98660129,98660254-98669358,98669554-98677948,98678112-98678507,98678717-98683455,98683598-98684585,98684701-98685540,98685662-98690359,98690433-98690999,98691147-98703734,98703832-98718194,98718296-98728842,
C9orf117	NM_001012502	chr9	130469472-130471699,130471973-130472878,130473034-130473506,130473776-130474097,130474230-130474476,130474629-130474986,130475155-130475297,130475486-130476111,
C9orf130	NR_023389	chr9	98632724-98636789,98636905-98637260,
C9orf130	NR_023390	chr9	98576205-98612507,98612575-98638145,
C9orf156	NM_016481	chr9	100667275-100672240,100672899-100675681,100675841-100678444,100678621-100684698,
C9orf27	NR_024032	chr9	118650760-118666648,118666922-118687300

C9orf43	NM_152786	chr9	116173419-116175723,116175925-116176037,116176175-116181386,116181446-116183381,116183484-116184827,116184866-116185604,116185779-116186444,116186597-116187297,116187357-116187622,116187701-116187921,116188011-116190425,116190504-116191178,116191244-116191450,
C9orf46	NM_018465	chr9	5358361-5361076,5361188-5361756,5361889-5431895,5431984-5436567,5436695-5437787,
C9orf47	NM_001142413	chr9	91606100-91606383,91606611-91606765,
C9orf47	NM_001001938	chr9	91606157-91606383,91606611-91606765,
C9orf64	NM_032307	chr9	86554659-86559707,86559905-86570294,86570556-86571077,
C9orf68	NM_001039395	chr9	4600810-4604177,4604270-4605345,4605441-4617921,4618111-4618862,4618899-4622406,4622511-4625325,4625567-4629089,4629169-4661897,4662037-4666210,4666257-4666433,
C9orf80	NM_021218	chr9	115449914-115451805,115451898-115456409,115456514-115478739,115478822-115480265,
C9orf89	NM_032310	chr9	95858635-95869954,95870099-95872848,95873004-95874159,95874221-95874498,95874572-95875272,
C9orf9	NM_018956	chr9	135754402-135759296,135759479-135762754,135762959-135763675,135763825-135765342,
CA10	NM_001082534	chr17	49708968-49710835,49711012-49713214,49713371-49726541,49726616-49731000,49731098-49824991,49825179-50008348,50008493-50149677,50149754-50235084,50235730-50237282,
CA10	NM_001082533	chr17	49708968-49710835,49711012-49713214,49713371-49726541,49726616-49731000,49731098-49824991,49825179-50008348,50008493-50149677,50149754-50235084,50235730-50236631,
CA10	NM_020178	chr17	49708968-49710835,49711012-49713214,49713371-49726541,49726616-49731000,49731098-49824991,49825179-50008348,50008493-50149677,50149754-50235084,
CACNA1B	NM_000718	chr9	140772670-140773504,140773612-140777194,140777336-140807630,140807724-140809104,140809259-140811691,140811884-140846724,140846830-140850148,140850266-140851221,140851280-140852048,140852140-140865833,140866045-140870357,140870472-140878588,140878703-140880863,140880997-140881232,140881307-140901217,140901337-140904460,140904530-140907579,140907688-140917461,140918264-140919405,140919625-140938224,140938353-140941354,140941486-140941849,140941911-140943659,140943768-140946542,140946641-140948296,140948459-140952182,140952322-140952499,140952703-140953019,140953186-140953529,140953642-140954104,140954194-140967936,140968057-140968451,140968519-140970269,140970363-140972564,140972711-140990934,140991064-140997161,140997260-141000149,141000260-141006848,141006958-141008828,141008943-141010002,141010132-141012396,141012534-141013102,141013221-141014615,141014825-141015081,141015334-141015919,
CADM4	NM_145296	chr19	44127592-44128264,44128395-44129228,44129403-44130061,44130154-44130274,44130441-44130934,44131071-44131316,44131471-44131794,44131943-44143877,
CALCOCO1	NM_020898	chr12	54105906-54106882,54106991-54107483,54107685-54107915,54108026-54108380,54108478-54108982,54109110-54109575,54109832-54110042,54110200-54113521,54113614-54115249,54115400-54115807,54115968-54117375,54117568-54118427,54118532-54118869,54119051-54121186,
CALCOCO1	NM_001143682	chr12	54105906-54106882,54106991-54107483,54107685-54107915,54108026-54108380,54108478-54108982,54109110-54109575,54109832-54113521,54113614-54115249,54115400-54115807,54115968-54117375,54117469-54118427,54118532-54118869,54119051-54121186,
CALCOCO1	NR_026554	chr12	54105906-54106882,54106991-54107483,54107685-54107915,54108026-54108380,54108478-54108982,54109110-54109575,54109832-54110042,54110200-54113521,54113614-54115249,54115400-54115807,54115968-54117375,54117568-54118869,54119051-54121186,
CALCOCO2	NM_005831	chr17	46908441-46919058,46919250-46925424,46925529-46925682,46925818-46926612,46926740-46928449,46928540-46928919,46928991-46929866,46929991-46930286,46930375-46933452,46933550-46937674,46937812-46939636,46939667-46940198,
CALHM2	NR_024552	chr10	105207326-105209155,105209857-105210838,105210940-105211911,
CALHM2	NM_015916	chr10	105207326-105209142,105209857-105210838,105211043-105211911,
CALU	NM_001130674	chr7	128379487-128388625,128388859-128394581,128394777-128398923,128399092-128399844,128399907-128407508,128407710-128409115,
CALU	NM_001219	chr7	128379487-128388625,128388859-128394314,128394510-128398923,128399092-128399844,128399907-128407508,128407710-128409115,
CALU	NM_001199671	chr7	128379487-128387605,128388422-128388625,128388859-128394314,128394510-128398923,128399092-128399844,128399907-128407508,128407710-128409115,
CALU	NM_001199674	chr7	128379487-128398923,128399092-128399844,128399907-128407508,128407710-128409115,

CALU	NM_001199673	chr7	128379487-128388625,128388859-128394314,128394510-128398923,128399092-128399844,128399907-128409115,
CALU	NM_001199672	chr7	128379487-128387605,128388422-128388625,128388859-128394581,128394777-128398923,128399092-128399844,128399907-128407508,128407710-128409115,
CAMTA2	NM_001171166	chr17	4872115-4872200,4872277-4872443,4872633-4872923,4872997-4873195,4873381-4873633,4873832-4875525,4875832-4876062,4876287-4876468,4876549-4876878,4877065-4877678,4877796-4880351,4880488-4881797,4881926-4882977,4883917-4884518,4884655-4884971,4885127-4885382,4885456-4886050,4886188-4886269,4886339-4889173,4889279-4890886,
CAMTA2	NM_001171168	chr17	4872115-4872200,4872277-4872443,4872633-4872793,4872816-4872923,4872997-4873195,4873381-4873633,4873832-4875525,4875832-4876062,4876287-4876468,4876549-4876878,4877065-4877678,4877796-4880351,4880488-4881797,4881926-4882977,4883917-4884518,4884655-4884971,4885127-4886050,4886188-4886269,4886339-4889173,4889279-4889485,4889582-4890247,
CAMTA2	NM_001171167	chr17	4872115-4872200,4872275-4872443,4872633-4872793,4872816-4872923,4872997-4873195,4873381-4873633,4873832-4875525,4875832-4876062,4876287-4876468,4876549-4876878,4877065-4877678,4877796-4880351,4880488-4881797,4881926-4882977,4883917-4884518,4884655-4884971,4885127-4885382,4885456-4886050,4886188-4886269,4886339-4889173,4889279-4889485,4889582-4890247,
CAMTA2	NM_015099	chr17	4872115-4872200,4872277-4872443,4872633-4872793,4872816-4872923,4872997-4873195,4873381-4873633,4873832-4875525,4875832-4876062,4876287-4876468,4876549-4876878,4877065-4877678,4877796-4880351,4880488-4881797,4881926-4882977,4883917-4884518,4884655-4884971,4885127-4885382,4885456-4886050,4886188-4886269,4886339-4889173,4889279-4889485,4889582-4890886,
CANX	NM_001746	chr5	179126104-179132678,179132854-179133257,179133333-179134131,179134192-179135238,179135382-179135977,179136061-179136872,179137067-179143104,179143296-179146667,179146783-179147403,179147562-179149803,179150021-179150659,179150781-179151656,179151785-179153679,179153761-179155590,
CANX	NM_001024649	chr5	179126051-179132678,179132854-179133257,179133333-179134131,179134192-179135238,179135382-179135977,179136061-179136872,179137067-179143104,179143296-179146667,179146783-179147403,179147562-179149803,179150021-179150659,179150781-179151656,179151785-179153679,179153761-179155590,
CAPG	NM_001747	chr2	85622082-85622659,85622750-85625141,85625276-85625811,85625906-85626257,85626409-85628286,85628453-85628650,85628807-85628906,85629081-85629244,85629282-85637438,
CARD18	NM_021571	chr11	105008826-105009537,105009806-105010445,
CASC1	NM_018272	chr12	25261758-25263059,25263175-25264704,25264874-25267588,25267805-25272077,25272236-25274685,25274848-25276143,25276221-25297297,25297612-25299933,25300039-25302560,25302709-25307251,25307391-25308243,25308347-25311404,25311498-25314045,25314132-25343546,25343566-25348008,
CASC1	NM_001082972	chr12	25261696-25263059,25263175-25264704,25264874-25267588,25267805-25272077,25272236-25274685,25274848-25276143,25276221-25297297,25297612-25299933,25300039-25302560,25302709-25307251,25307391-25308243,25308347-25311404,25311498-25314045,25314132-25343546,25343566-25347818,
CASC1	NM_001082973	chr12	25261758-25263059,25263175-25264704,25264874-25267588,25267805-25272077,25272236-25274685,25274848-25276143,25276221-25297297,25297612-25299933,25300039-25302560,25302709-25307251,25307391-25308243,25308347-25311404,25311498-25314045,25314132-25348008,
CASC5	NM_170589	chr15	40886591-40895111,40895165-40897306,40897348-40898589,40898651-40901043,40901107-40902441,40902496-40902995,40903075-40903674,40903710-40907537,40907577-40911155,40911210-40912836,40917839-40920266,40920407-40920807,40920877-40921469,40921570-40933108,40933226-40937193,40937286-40937852,40937971-40939183,40939273-40942497,40942577-40942740,40942782-40943667,40943771-40944201,40944304-40947105,40947176-40949238,40949350-40949551,40949672-40951535,40951660-40954270,
CASC5	NM_144508	chr15	40886591-40895111,40895165-40897306,40897348-40898589,40898651-40901043,40901107-40902441,40902496-40903674,40903710-40907537,40907577-40911155,40911210-40912836,40917839-40920266,40920407-40920807,40920877-40921469,40921570-40933108,40933226-40937193,40937286-40937852,40937971-40939183,40939273-40942497,40942577-40942740,40942782-40943667,40943771-40944201,40944304-40947105,40947176-40949238,40949350-40949551,40949672-40951535,40951660-40954270,
CASK	NM_001126055	chrX	41379850-41383202,41383288-41390258,41390463-41393957,41394040-41394144,41394227-41401942,41402060-41412970,41413169-41414851,41414889-41419030,41419101-41420810,41420898-41428919,41429000-41437591,41437782-41446158,41446241-41448766,41448846-41469155,41469279-41485855,41485957-41495839,41495915-41519690,41519815-41524528,41524706-41530679,41530784-41598635,41598710-

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CASK	NM_001126054	chrX	41379850-41383202,41383288-41390258,41390463-41393957,41394040-41394144,41394212-41401942,41402060-41412970,41413169-41414851,41414889-41419030,41419101-41420810,41420898-41428919,41429000-41437591,41437782-41446158,41446241-41448766,41448846-41469155,41469279-41481868,41481888-41485855,41485957-41495829,41495915-41519690,41519815-41524528,41524706-41530679,41530784-41598635,41598710-41604775,41604855-41646429,41646537-41712366,41712481-41782181,
CASK	NM_003688	chrX	41379850-41383202,41383288-41390258,41390463-41393957,41394040-41394144,41394212-41401942,41402060-41412970,41413169-41414851,41414889-41416283,41416354-41419030,41419101-41420810,41420898-41428919,41429000-41437591,41437782-41446158,41446241-41448766,41448846-41469155,41469279-41481868,41481888-41485855,41485957-41495829,41495915-41519690,41519815-41524528,41524706-41530679,41530784-41598635,41598710-41604775,41604855-41646429,41646537-41712366,41712481-41782181,
CASP14	NM_012114	chr19	15160457-15163015,15163090-15164291,15164443-15164542,15164770-15165967,15166086-15166239,15166345-15166794,
CATSPERG	NM_021185	chr19	38826516-38827859,38828145-38828231,38828287-38834218,38834365-38834631,38834760-38834934,38835009-38837088,38837246-38842899,38843073-38845348,38845488-38847122,38847184-38847380,38847502-38848916,38848969-38849070,38849202-38850108,38850222-38851127,38851288-38851369,38851484-38852286,38852502-38852848,38852913-38853014,38853215-38853352,38853473-38855529,38855612-38855699,38855758-38857794,38857953-38858147,38858213-38858319,38858417-38858686,38858778-38860610,38860705-38860797,38860899-38861164,
CBFB	NM_022845	chr16	67063389-67063628,67063717-67070540,67070659-67100583,67100702-67116114,67116212-67132611,
CBFB	NM_001755	chr16	67063389-67063628,67063717-67070540,67070659-67100583,67100702-67116114,67116243-67132611,
CBLN4	NM_080617	chr20	54573811-54575785,54575904-54578935,
CBX3	NM_007276	chr7	26241182-26242589,26242643-26245986,26246131-26248011,26248176-26251280,26251377-26251700,
CBX3	NM_016587	chr7	26241447-26242589,26242643-26245986,26246131-26248011,26248176-26251280,26251377-26251700,
CBX7	NM_175709	chr22	39530054-39530404,39530758-39534639,39534708-39537374,39537442-39545792,39545838-39548379,
CCDC101	NM_138414	chr16	28565419-28592374,28592466-28596232,28596310-28596967,28597042-28600419,28600486-28601415,28601547-28601615,28601764-28601950,28601988-28602092,28602257-28602909,
CCDC11	NM_145020	chr18	47753980-47764971,47765076-47769268,47769487-47777126,47777347-47777849,47778155-47787432,47787608-47788358,47788590-47792704,
CCDC144NL	NM_001004306	chr17	20768823-20769859,20770017-20796703,20796776-20798988,
CCDC153	NM_001145018	chr11	119061162-119061417,119061550-119063859,119063954-119064474,119064596-119065631,119065705-119066132,119066210-119066507,
CCDC28B	NM_024296	chr1	32666311-32667512,32667701-32669478,32669647-32669785,32669981-32670197,32670222-32670793,
CCDC40	NM_017950	chr17	78010491-78011920,78011986-78013609,78014070-78021076,78021202-78022380,78022561-78023703,78023789-78023861,78024083-78032291,78032451-78032655,78032780-78039282,78039406-78055343,78055589-78055673,78055858-78058540,78058788-78059800,78060016-78061404,78061576-78061808,78061902-78063561,78063684-78069060,78069251-78071042,78071203-78073324,
CCDC45	NM_138363	chr17	62503235-62504708,62504839-62506289,62506399-62510364,62510477-62512839,62512947-62515437,62515555-62517518,62517646-62518818,62519014-62521886,62522001-62522187,62522319-62523227,62523383-62525404,62525546-62527042,62527137-62528006,62528141-62528955,62529127-62529233,62529310-62530701,62530856-62532718,62532867-62533157,62533231-62533719,
CCDC47	NM_020198	chr17	61824322-61829298,61829468-61829678,61829790-61830099,61830160-61831791,61831879-61833598,61833711-61833827,61833931-61838272,61838340-61838588,61838712-61841374,61841551-61842098,61842208-61843270,61843555-61850770,
CCDC66	NM_001141947	chr3	56591282-56592872,56592939-56593595,56593623-56597710,56598154-56600620,56600788-56600976,56601082-56605207,56605331-56626996,56627130-56627517,56627770-56627970,56628057-56647615,56647779-56649154,56649301-56649948,56650082-56651138,56651634-56652198,56652241-56653297,56653556-56653803,56653930-56655558,
CCDC66	NR_024460	chr3	56591282-56592872,56592939-56593595,56593623-56597710,56598154-56600620,56600769-56600976,56601082-56605207,56605331-56626996,56627130-56627517,56627770-56627970,56628057-56647615,56647779-56649154,56649301-56649948,56650082-56651138,56651634-56652198,56652241-56653297,56653556-56653803,56653930-56655558,
CCDC66	NM_001012506	chr3	56591263-56592872,56592939-56593595,56593623-56597710,56598154-56600620,56600788-56600976,56601082-56605207,56605331-

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CCDC68	NM_025214	chr18	52571647-52575015,52575094-52585142,52585228-52586500,52586608-52596029,52596114-52602049,52602180-52604062,52604190-52605186,52605329-52608226,52608315-52609904,52610035-52612617,52612709-52626565,
CCDC76	NM_019083	chr1	100598872-100602436,100602485-100602573,100602642-100605203,100605268-100605736,100605808-100605962,100606071-100606406,100606576-100608691,100608766-100609623,100609700-100613448,100613883-100614179,
CCDC85A	NM_001080433	chr2	56412036-56419610,56420576-56570012,56570091-56599477,56599614-56602949,56603071-56611399,
CCDC92	NM_025140	chr12	124422378-124427289,124427333-124427892,124428041-124428817,124428912-124457074,
CCDC97	NM_052848	chr19	41816262-41822287,41822745-41825477,41825758-41826244,41826376-41828498,
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CCNB2	NM_004701	chr15	59397492-59399519,59399650-59399754,59399870-59406641,59406814-59406915,59407076-59408887,59409126-59409425,59409568-59415714,59415827-59416964,
CD2BP2	NR_024465	chr16	30364417-30364500,30364609-30364687,30365122-30365220,30365380-30365503,30365644-30365923,
CD2BP2	NM_006110	chr16	30364417-30364500,30364609-30364687,30365122-30365220,30365380-30365503,30365644-30365923,30366029-30366531,
CD300C	NM_006678	chr17	72537876-72538998,72539127-72540746,72541087-72541859,
CD33	NM_001772	chr19	51728412-51728472,51728855-51729057,51729338-51729563,51729613-51738410,51738509-51738848,51738932-51742771,
CD33	NM_001082618	chr19	51728412-51729057,51729338-51729563,51729613-51738410,51738509-51738848,51738932-51742771,
CD33	NM_001177608	chr19	51728412-51728472,51728855-51729057,51729338-51729563,51729613-51738410,51738509-51738848,51738932-51739076,
CDC25C	NM_022809	chr5	137621531-137621709,137621823-137622184,137622320-137622856,137622957-137625188,137625253-137626326,137626430-137627657,137627806-137654906,137655064-137664171,137664219-137666674,137666908-137667282,
CDC25C	NM_001790	chr5	137621531-137621709,137621823-137622184,137622320-137622856,137622957-137625188,137625253-137626326,137626430-137627657,137627806-137654906,137655064-137661502,137661594-137661708,137661744-137664171,137664219-137665240,137665337-137666674,137666908-137667282,
CDC45	NM_001178011	chr22	19467543-19467679,19467741-19468474,19468569-19471383,19471529-19481848,19481906-19483502,19483553-19484907,19484971-19486622,19486675-19492883,19493005-19494907,19495041-19495287,19495388-19496051,19496215-19502270,19502411-19502486,19502572-19504048,19504169-19504338,19504417-19506365,19506433-19508002,
CDC45	NM_001178010	chr22	19467543-19467679,19467741-19468474,19468569-19470211,19470351-19471383,19471529-19481848,19481906-19482028,19482126-19483502,19483553-19484907,19484971-19486622,19486675-19492883,19493005-19494907,19495041-19495287,19495388-19496051,19496215-19502270,19502411-19502486,19502572-19504048,19504169-19504338,19504417-19506365,19506433-19508002,
CDC45	NM_003504	chr22	19467543-19467679,19467741-19468474,19468569-19470211,19470351-19471383,19471529-19481848,19481906-19483502,19483553-19484907,19484971-19486622,19486675-19492883,19493005-19494907,19495041-19495287,19495388-19496051,19496215-19502270,19502411-19502486,19502572-19504048,19504169-19504338,19504417-19506365,19506433-19508002,
CDC73	NM_024529	chr1	193091462-193094240,193094348-193099302,193099374-193104519,193104584-193104665,193104720-193107213,193107304-193110978,193111197-193116995,193117096-193119432,193119513-193121508,193121575-193172923,193172983-193181193,193181231-193181518,193181608-193202121,193202285-193205384,193205487-193218858,193219002-193219804,
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CDCA8	NM_018101	chr1	38158251-38158346,38158457-38158575,38158706-38161580,38161623-38164575,38164650-38166106,38166194-38167424,38167491-38168922,38169020-38171111,38171240-38172648,38172737-38173992,
CDH8	NM_001796	chr16	61688006-61689372,61689626-61747743,61747863-61760996,61761120-61823248,61823387-61851381,61851637-61854828,61855018-61858914,61859084-61891021,61891143-619[illegible]61935378-62055054,62055507-62069982,

CDHR2	NM_017675	chr5	175976416-175992337,175992406-175992671,175992745-175995677,175995819-175995959,175996012-175998212,175998304-176001082,176001174-176002083,176002211-176002279,176002428-176002505,176002583-176002723,176002841-176002951,176003187-*176004398,176004556-176004636,176004800-176005033,176005097-176005364,176005610-176008342,176008584-176011189,176011261*-176011409,176012017-176012953,176013027-176013792,176013844-176016030,176016184-176016329,176016440-176016527,176016618-176017077,176017148-176017252,176017332-176017424,176017487-176017562,176017689-176018209,176018325-176018403,176018486-176019722,176019782-176022531,
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CDK13	NM_003718	chr7	39991452-40027196,40027858-40037091,40037264-40038958,40039100-40041458,40041631-40085433,40085625-40087418,40087477-40102423,40102527-40102620,40102700-40117602,40117721-40118317,40118451-40127723,40127931-40132382,40132837-40133727,
CDK13	NM_031267	chr7	39991452-40027196,40027858-40037091,40037264-40038958,40039100-40041458,40041631-40085433,40085625-40087418,40087477-40102423,40102527-40102620,40102700-40117602,40117721-40118317,40118451-40127723,40127931-40132562,40132837-40133727,
CDK20	NM_001170639	chr9	90582547-90584107,90584265-90584709,90584835-90585689,90585813-90586060,90586251-90588835,90588951-90589285,
CDK20	NM_178432	chr9	90582575-90584107,90584265-90584709,90584835-90585689,90585813-90586060,90586251-90588835,90588990-90589285,
CDK20	NM_001170640	chr9	90582575-90584107,90584265-90585689,90585813-90586060,90586251-90588835,90588951-90589285,
CDK20	NM_001039803	chr9	90582575-90584107,90584265-90584709,90584835-90585481,90585546-90585689,90585813-90586060,90586251-90588835,90588951-90589285,
CDK20	NM_012119	chr9	90582575-90584107,90584265-90584709,90584835-90585689,90585813-90586060,90586251-90588835,90588951-90589285,
CDKN3	NM_005192	chr14	54863796-54866610,54866695-54868240,54868298-54875461,54875508-54878200,54878425-54882615,54882649-54884564,54884670-54886708,
CDKN3	NM_001130851	chr14	54863796-54866610,54866631-54875461,54875508-54878200,54878425-54882615,54882649-54884564,54884670-54886708,
CELA2B	NM_015849	chr1	15802661-15802950,15803041-15807591,15807691-15808758,15808889-15809757,15809896-15812394,15812542-15813778,15813933-15817788,
CELF6	NM_052840	chr15	72578684-72579576,72579734-72580647,72580793-72580877,72580960-72581207,72581272-72581477,72581629-72581714,72581849-72581966,72582112-72582278,72582360-72582466,72582597-72597085,72597136-72608184,72608269-72611952,
CELF6	NM_001172684	chr15	72578684-72579576,72579734-72580647,72580793-72581207,72581272-72581477,72581629-72581714,72581849-72581966,72582112-72582278,72582360-72582466,72582597-72597085,72597136-72608184,72608269-72611952,
CELF6	NM_001172685	chr15	72578684-72579576,72579734-72580647,72580793-72580877,72580960-72581477,72581626-72581714,72581849-72581966,72582112-72582278,72582360-72582466,72582597-72597085,72597136-72598480,
CENPE	NM_001813	chr4	104027474-104029958,104030247-104031983,104032169-104035610,104035710-104037732,104037847-104041303,104041491-104044026,104044247-104053848,104054054-104054850,104055050-104057296,104057517-104059506,104059607-104060944,104061237-104061411,104061572-104061969,104062262-104062905,104063066-104064403,104064564-104065486,104065776-104066205,104066492-104066678,104066839-104066984,104067265-104068511,104068804-104069999,104070157-104070273,104070566-104072374,104072535-104074202,104074408-104079455,104079616-104079769,104080044-104080165,104080482-104081780,104081937-104082241,104082409-104082490,104082615-104084292,104084414-104084634,104084711-104095891,104096061-104097115,104097206-104098054,104098204-104101466,104101627-104102492,104102614-104103917,104104049-104104356,104104446-104106965,104107019-104115384,104115452-104115529,104115599-104115758,104115842-104116269,104116391-104117075,104117196-104117318,104117410-104117914,104118008-104119419,
CENPF	NM_016343	chr1	214776665-214787055,214787260-214788173,214788372-214791914,214792038-214792470,214792564-214793996,214794290-214795420,214795625-214802387,214802515-214803875,214804006-214805821,214805946-214811207,214811345-214813262,214816668-214817898,214820744-214822016,214822171-214825051,214825230-214826169,214826333-214828582,214828747-214830274,214830753-214832191,214832372-214836932,

CENPI	NM_006733	chrX	100355055-100356045,100356286-100357261,100357401-100364460,100364581-100364878,100364988-100375389,100375440-100375725,100375774-100381696,100381788-100382125,100382256-100382485,100382655-100383703,100383826-100384969,100385063-100387177,100387297-100387379,100387446-100395653,100395750-100400051,100400189-100401140,100401267-100402750,100402801-100402930,100403151-100416515,100416559-100417820,
CENPN	NM_001100625	chr16	81040883-81045533,81045716-81047739,81047787-81050929,81050991-81051361,81051440-81053703,81053882-81056200,81056304-81058318,81058384-81060129,81060244-81061774,81061903-81066173,
CENPN	NM_018455	chr16	81040883-81045533,81045716-81047739,81047787-81050929,81050991-81051361,81051440-81053703,81053882-81056358,
CENPN	NM_001100624	chr16	81040883-81045533,81045716-81047739,81047787-81050929,81050991-81051361,81051440-81053703,81053882-81056200,81056304-81058318,81058384-81060129,81060244-81061774,81061903-81062172,
CENPO	NM_024322	chr2	25016390-25016719,25016835-25022542,25022714-25037243,25037363-25038364,25038626-25039513,25039687-25040537,25040711-25042221,
CENPO	NM_001199803	chr2	25016371-25022542,25022714-25037243,25037363-25038364,25038626-25039513,25039687-25040537,25040711-25042221,
CENPP	NM_001012267	chr9	95088388-95094450,95094634-95099821,95099912-95107979,95108070-95142043,95142142-95373594,95373676-95374803,95374897-95375299,
CENPV	NM_181716	chr17	16246256-16247909,16248026-16251928,16252000-16253243,16253344-16256339,
CENPW	NM_001012507	chr6	126661546-126667349,126667465-126669610,
CEP110	NM_007018	chr9	123850822-123852551,123852684-123857164,123857297-123858698,123858842-123860662,123860851-123870078,123870274-123874735,123874857-123875778,123876003-123877367,123877479-123880622,123880819-123886207,123886363-123887992,123888215-123898082,123898261-123900821,123900958-123902917,123903065-123903657,123903867-123904367,123904549-123906179,123906361-123907119,123907238-123907520,123907664-123908384,123908535-123910948,123911140-123912446,123912762-123914761,123914972-123916997,123917192-123919746,123919879-123920016,123920159-123920259,123920388-123921131,123921298-123922419,123922581-123924132,123924250-123924330,123924550-123927219,123927379-123928383,123928459-123929765,123929956-123930372,123930600-123931887,123932095-123933684,123933827-123935519,123935788-123935951,123936016-123937294,123937503-123939439,
CEP152	NM_001194998	chr15	49031486-49033796,49033902-49034142,49034298-49036435,49036541-49037091,49037190-49040638,49040808-49044544,49044667-49048098,49048751-49052330,49052464-49054586,49054870-49059255,49059390-49059530,49059661-49060414,49060526-49061151,49061279-49064682,49064889-49073391,49073557-49074334,49074428-49076168,49076318-49080996,49081199-49083432,49083574-49085516,49085659-49088205,49088358-49089496,49089777-49089856,49089928-49090143,49090249-49097758,49097854-49103156,
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CEP72	NM_018140	chr5	612559-619103,619233-620182,620377-624584,624695-633882,634063-635485,635700-637630,637934-639202,639340-640521,640720-644412,644541-647918,648032-653101,
CFDP1	NM_006324	chr16	75327941-75338920,75339081-75428986,75429108-75445721,75445851-75446431,75446653-75448474,75448594-75467185,
CFHR1	NM_002113	chr1	196789033-196794605,196794802-196795957,196796136-196797198,196797377-196799528,196799813-196800925,
CFHR5	NM_030787	chr1	196946853-196952013,196952210-196953089,196953268-196963208,196963387-196964845,196965030-196965150,196965332-196967256,196967435-196971610,196971795-196973789,196973974-196977615,
CGRRF1	NM_006568	chr14	54976782-54989170,54989312-54996765,54996945-54997619,54997769-55004438,55004548-55004779,
CHCHD10	NM_213720	chr22	24108214-24108313,24108463-24109559,24109781-24110019,
CHEK2	NM_007194	chr22	29083975-29085121,29085204-29090018,29090106-29091113,29091231-29091696,29091862-29092887,29092976-29095824,29095926-29099491,29099555-29105992,29106048-29107895,29108006-29115381,29115474-29120963,29121113-29121229,29121356-29130389,29130716-29137755,
CHEK2	NM_001005735	chr22	29083975-29085121,29085204-29090018,29090106-29091113,29091231-29091696,29091862-29092887,29092976-29095824,29095926-29099491,29099555-29105992,29106048-29107895,29108006-29115381,29115474-29120963,29121113-29121229,29121356-29126406,29126537-29130389,29130716-29137755,

CHEK2	NM_145862	chr22	29083975-29085121,29085204-29090018,29090106-29091113,29091231-29091696,29091862-29095824,29095926-29099491,29099555-29105992,29106048-29107895,29108006-29115381,29115474-29120963,29121113-29121229,29121356-29130389,29130716-29137755,
CHI3L1	NM_001276	chr1	203148714-203148887,203149006-203149596,203149781-203150288,203150414-203151857,203151981-203152767,203152920-203153702,203153761-203154310,203154514-203155442,203155474-203155725,
CHKA	NM_001277	chr11	67821515-67829418,67829502-67831990,67832099-67833251,67833362-67833894,67833984-67836344,67836405-67837654,67837761-67838189,67838325-67842182,67842298-67848869,67848925-67864484,67864598-67888293,
CHKA	NM_212469	chr11	67821515-67829418,67829502-67831990,67832099-67833251,67833362-67833894,67833984-67836344,67836405-67837654,67837761-67838189,67838325-67842182,67842298-67864484,67864598-67888293,
CHMP2A	NM_014453	chr19	59063144-59063271,59063335-59063420,59063553-59063624,59063806-59065410,59065604-59066353,
CHMP2A	NM_198426	chr19	59063144-59063271,59063335-59063420,59063553-59063624,59063806-59065410,59065604-59066230,
CHP	NM_007236	chr15	41523648-41535863,41535938-41549106,41549189-41554952,41555082-41562753,41562817-41570963,41571088-41571532,
CHRM3	NM_000740	chr1	239792840-239795522,239795587-239841484,239841589-239990550,239990679-240070731,
CHRNA6	NM_004198	chr8	42608454-42610987,42611968-42612069,42612181-42614210,42614257-42620206,42620348-42623493,
CHRNA6	NM_001199279	chr8	42608454-42610987,42611968-42612069,42612181-42620206,42620348-42623493,
CIC	NM_015125	chr19	42788924-42790921,42791073-42791156,42791393-42791470,42791602-42791695,42791880-42791960,42792128-42793038,42793243-42793331,42793559-42793998,42794104-42794383,42795619-42795708,42795898-42796236,42796360-42796450,42796619-42796716,42797012-42797106,42797434-42797742,42797989-42798085,42798242-42798323,42798457-42798754,42798888-42798974,
CIT	NM_007174	chr12	120126061-120127954,120128260-120135462,120135644-120135779,120135860-120138548,120138631-120139427,120139558-120139653,120139764-120142166,120142261-120145982,120146124-120148054,120148192-120148343,120148426-120149981,120150153-120150394,120150501-120151006,120151100-120151271,120151454-120152000,120152140-120156048,120156215-120156502,120156667-120158281,120158391-120159112,120159255-120166305,120166412-120168298,120168436-120171967,120172163-120172963,120173163-120180214,120180270-120189853,120190053-120195173,120195350-120196393,120196505-120198741,120198860-120204889,120204987-120210572,120210715-120213588,120213644-120214160,120214213-120214474,120214647-120220320,120220442-120221710,120221856-120222762,120222870-120241008,120241194-120260622,120260778-120262967,120263173-120270573,120270669-120271888,120272033-120287976,120288080-120295325,120295503-120306862,120307006-120313875,120313986-120315051,
CIZ1	NM_012127	chr9	130928686-130929036,130929160-130929372,130929444-130931329,130931481-130931683,130931799-130932297,130932387-130938628,130938755-130939843,130940043-130940646,130940770-130940986,130941695-130942692,130942803-130942998,130943094-130947824,130948056-130950140,130950214-130952606,130952724-130952965,130953142-130966463,
CIZ1	NM_001131015	chr9	130928686-130929036,130929160-130929372,130929444-130931329,130931481-130931683,130931799-130932297,130932387-130938628,130938755-130939843,130940043-130940646,130940770-130940986,130941184-130941350,130941695-130942692,130942803-130942998,130943094-130947824,130948056-130950140,130950214-130952606,130952724-130952965,130953142-130966463,
CIZ1	NM_001131016	chr9	130928686-130929036,130929160-130929372,130929444-130931329,130931481-130931683,130931799-130932297,130932387-130938628,130938755-130939843,130940043-130940646,130940770-130940986,130941695-130942692,130942803-130942998,130943094-130947824,130948056-130950140,130950214-130952606,130952724-130952965,130953142-130953709,
CIZ1	NM_001131018	chr9	130928686-130929036,130929160-130929372,130929444-130931329,130931481-130931683,130931799-130932297,130932387-130938628,130938755-130939843,130940043-130940646,130940770-130940986,130941184-130941350,130941695-130942692,130942803-130942998,130943094-130947824,130948056-130952606,130952724-130952965,130953142-130953709,
CIZ1	NM_001131017	chr9	130928686-130929036,130929160-130929372,130929444-130931329,130931481-130931683,130931799-130932297,130932387-130938628,130938755-130939843,130940043-130940646,130940770-130940986,130941184-130941350,130941695-130942692,130942803-130942998,130943079-130947824,130948056-130950140,130950214-130952606,130952724-130952965,130953142-130953709,
CKAP2L	NM_152515	chr2	113496626-113498393,113498585-113500281,113500347-113503995,113504153-113509842,113510052-113513552,113514792-113518288,113518342-113520078,113520147-113522137,

CLASRP	NM_007056	chr19	45542367-45543440,45543570-45555327,45555427-45556047,45556151-45556354,45556436-45559706,45559793-45561006,45561157-45562524,45562623-45563645,45563726-45563810,45563886-45565410,45565454-45567268,45567486-45567599,45567889-45570593,45570853-45571271,45571313-45571676,45571739-45572322,45572383-45572458,45572507-45573278,45573363-45573793,45573820-45574059,
CLCN5	NM_000084	chrX	49832416-49834532,49834686-49837142,49837244-49840448,49840638-49845249,49845374-49846296,49846505-49850635,49850718-49850983,49851528-49853353,49853542-49854771,49855172-49855325,49855544-49856784,
CLCN5	NM_001127899	chrX	49687403-49688014,49688351-49689779,49689925-49806923,49807072-49834532,49834686-49837142,49837244-49840448,49840638-49845249,49845374-49846296,49846505-49850635,49850718-49850983,49851528-49853353,49853542-49854771,49855172-49855325,49855544-49856784,
CLCN5	NM_001127898	chrX	49687403-49688014,49688092-49689779,49689925-49806923,49807072-49834532,49834686-49837142,49837244-49840448,49840638-49845249,49845374-49846296,49846505-49850635,49850718-49850983,49851528-49853353,49853542-49854771,49855172-49855325,49855544-49856784,
CLDN6	NM_021195	chr16	3066044-3068148,
CLEC10A	NM_182906	chr17	6978542-6978677,6978786-6979048,6979205-6979302,6979472-6980050,6980124-6980209,6980307-6981314,6981433-6982063,6982205-6983369,
CLEC10A	NM_006344	chr17	6978542-6978677,6978786-6979048,6979205-6979293,6979391-6980050,6980124-6980209,6980307-6981314,6981433-6982063,6982205-6983369,
CLEC16A	NM_015226	chr16	11038655-11051637,11051768-11056310,11056446-11063016,11063167-11064980,11065088-11066787,11066919-11071080,11071257-11073184,11073240-11076733,11076849-11096929,11097163-11114048,11114183-11118676,11118779-11133609,11133734-11136109,11136221-11137883,11137930-11141147,11141200-11145368,11145499-11154757,11154880-11214470,11214624-11217597,11217804-11219834,11220004-11260243,11260410-11272190,
CLEC4A	NM_016184	chr12	8276557-8278155,8278274-8281858,8281959-8288179,8288333-8289382,8289500-8290734,
CLEC4A	NM_194450	chr12	8276557-8278155,8278274-8288179,8288333-8289382,8289500-8290734,
CLEC4A	NM_194448	chr12	8276557-8288179,8288333-8289382,8289500-8290734,
CLEC4A	NM_194447	chr12	8276557-8281858,8281959-8288179,8288333-8289382,8289500-8290734,
CLEC6A	NM_001007033	chr12	8608739-8610492,8610584-8612191,8612295-8618078,8618226-8628719,8628837-8629914,
CLIC6	NM_053277	chr21	36043062-36079576,36079688-36080240,36080368-36080996,36081105-36081653,36081837-36088617,
CLINT1	NM_014666	chr5	157215001-157216369,157216522-157218709,157219004-157221904,157221981-157230656,157230728-157232872,157233121-157236634,157236814-157240069,157240236-157241191,157241302-157243740,157243839-157244449,157244556-157285936,
CLINT1	NM_001195556	chr5	157215001-157216369,157216576-157218709,157219004-157221904,157221981-157230656,157230728-157232872,157233121-157236634,157236814-157240069,157240236-157241191,157241302-157243740,157243839-157244449,157244556-157285959,
CLINT1	NM_001195555	chr5	157215001-157216369,157216576-157218709,157219004-157221904,157221981-157230656,157230728-157232872,157233121-157236634,157236814-157240069,157240236-157241191,157241302-157243740,157243839-157244449,157244556-157285936,
CLPTM1	NM_001199468	chr19	45458725-45465218,45465333-45476342,45476468-45477694,45477855-45480598,45480718-45488474,45488562-45489711,45489834-45490435,45490682-45491336,45491432-45493651,45493844-45494106,45494204-45494494,45494632-45495489,45495659-45495867,45496114-45496323,
CLPTM1	NM_001294	chr19	45458725-45465218,45465333-45476342,45476468-45477694,45477855-45480598,45480718-45488474,45488562-45489711,45489834-45490435,45490682-45491336,45491432-45493651,45493844-45494106,45494204-45494494,45494632-45495489,45495659-45495867,
CLRN1	NM_052995	chr3	150644660-150645850,150645989-150659367,150659549-150661605,
CLRN1	NM_174878	chr3	150645989-150659367,150659549-150690241,
CLRN1	NM_001195794	chr3	150645989-150658266,150658307-150659367,150659549-150690241,
CLTC	NM_004859	chr17	57697535-57721635,57721845-57724757,57725028-57725599,57725763-57728562,57728678-57733213,57733389-57737750,57737950-57738802,57739005-57741201,57741356-57742146,57742271-57743462,57743602-57743839,57744006-57744156,57744339-57746136,57746302-57751006,57751134-57752060,57752205-57754313,57754550-57756756,57756881-57758271,57758419-57758654,57758840-57759006,57759201-57759630,57759790-57759988,57760155-57760266,57760376-57760454,57760624-57760746,57760898-57760984,57761118-57761234,57761347-57762415,57762588-57762946,57763170-57767995,57768073-57771087,
CMA1	NM_001836	chr14	24974866-24975232,24975489-24975673,24975811-24976560,24976713-24977382,

CNGA1	NM_001142564	chr4	47939847-47942778,47942887-47944056,47944166-47945196,47945306-47945386,47945430-47951848,47951913-47953368,47953487-47954598,47954721-47972911,47973118-47983408,
CNGA1	NM_000087	chr4	47939847-47942778,47942887-47944056,47944166-47945196,47945306-47945386,47945430-47951848,47951913-47953368,47953487-*47954598,47954721-47983408,47983518-48012809,48012911-48014904*,
CNGB3	NM_019098	chr8	87588359-87590915,87591092-87591332,87591481-87616319,87616440-87623814,87623900-87638209,87638309-87641145,87641307-87644978,87645122-87655977,87656102-87656848,87656915-87660027,87660116-87666238,87666291-87679151,87679362-87680245,87680397-87683170,87683327-87738757,87738886-87751881,87751965-87755725,
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CNTNAP1	NM_003632	chr17	40834915-40835837,40835941-40836052,40836248-40837007,40837157-40837233,40837439-40837973,40838160-40838919,40839065-40839736,40840000-40840478,40840630-40840892,40841066-40841537,40841646-40842104,40842226-40842755,40842961-40843153,40843312-40843400,40843530-40843822,40844010-40844515,40844739-40845313,40845555-40847537,40847893-40848041,40848171-40849290,40849386-40849570,40849818-40849919,40849969-40850634,
COG4	NM_001195139	chr16	70515048-70515260,70515391-70515665,70515769-70515993,70516079-70516630,70516725-70517754,70517873-70530167,70530335-70531122,70531291-70531838,70531959-70534859,70534995-70542307,70542368-70543132,70543292-70543817,70543925-70546140,70546336-70548236,70548413-70551527,70551644-70553550,70553635-70557274,
COG4	NM_015386	chr16	70515048-70515260,70515391-70515665,70515769-70515993,70516079-70516630,70516725-70517754,70517873-70524231,70524296-70530167,70530335-70531122,70531291-70531838,70531959-70534859,70534995-70542307,70542368-70543132,70543292-70543817,70543925-70546140,70546336-70548236,70548413-70551527,70551644-70553550,70553635-70557274,
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COL11A2	NM_080681	chr6	33131596-33132042,33132251-33132627,33132742-33133324,33133594-33133706,33133762-33133946,33133984-33134288,33134344-33134495,33134605-33134845,33134901-33135039,33135095-33135201,33135311-33135574,33135630-33136294,33136350-33136481,33136537-33136730,33136786-33137158,33137268-33137606,33137662-33137822,33137878-33138101,33138157-33138332,33138388-33138585,33138695-33138889,33138945-33139046,33139102-33139242,33139352-33139488,33139598-33139825,33139881-33140064,33140156-33140305,33140415-33140835,33140891-33141123,33141179-33141277,33141333-33141476,33141523-33141648,33141704-33141786,33141833-33141940,33141996-33142302,33142358-33143349,33143459-33143791,33143847-33144034,33144081-33144208,33144264-33144496,33144543-33144767,33144823-33144956,33145003-33145187,33145243-33145437,33145484-33145907,33145963-33146083,33146130-33146210,33146266-33146454,33146510-33146695,33146751-33146848,33146904-33147006,33147062-33147206,33147265-33147494,33147583-33148033,33148110-33148443,33148508-33148739,33148783-33148886,33148948-33152767,33152832-33154402,33154596-33156137,33156302-33156753,33156966-33157095,33157247-33159934,
COL11A2	NM_080679	chr6	33131596-33132042,33132251-33132627,33132742-33133324,33133594-33133706,33133762-33133946,33133984-33134288,33134344-33134495,33134605-33134845,33134901-33135039,33135095-33135201,33135311-33135574,33135630-33136294,33136350-33136481,33136537-33136730,33136786-33137158,33137268-33137606,33137662-33137822,33137878-33138101,33138157-33138332,33138388-33138585,33138695-33138889,33138945-33139046,33139102-33139242,33139352-33139488,33139598-33139825,33139881-33140064,33140156-33140305,33140415-33140835,33140891-33141123,33141179-33141277,33141333-33141476,33141523-33141648,33141704-33141786,33141833-33141940,33141996-33142302,33142358-33143349,33143459-33143791,33143847-33144034,33144081-33144208,33144264-33144496,33144543-33144767,33144823-33144956,33145003-33145187,33145243-33145437,33145484-33145907,33145963-33146083,33146130-33146210,33146266-33146454,33146510-33146695,33146751-33146848,33146904-33147006,33147062-33147206,33147265-33147494,33147583-33148033,33148110-33148443,33148508-33148739,33148783-33148886,33148948-33154402,33154596-33156137,33156302-33156753,33156966-33157095,33157247-33159934,
COL11A2	NM_001163771	chr6	33154596-33156137,33156302-33156753,33156966-33157095,33157247-33159934,
COL20A1	NM_020882	chr20	61924628-61926448,61926542-61929260,61929373-61936767,61936913-61937231,61937392-61938840,61939001-61939321,61939443-61939892,61940059-61940683,61940850-61941108,61941268-61941731,61941863-61942744,61942892-61942975,61943101-61943266,61943408-61943770,61943902-61944142,61944287-61944467,61944602-61945093,61945244-61945422,61945554-61946754,61946792-61947903,61948044-61950408,61950553-61950837,61950949-61951389,61951550-61951641,61951721-61952363,61952452-61953408,61953464-61956791,61956847-61957018,61957074-61957446,61957502-61958102,61958176-61959302,61959340-61959429,61959480-61959681,61959851-61960935,61961014-61962070,
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COL6A4P1	NR_027927	chr3	15207047-15211453,15212085-15216268,15216859-15219090,15219695-15247216,
COMMD9	NM_014186	chr11	36296323-36297685,36297791-36298637,36298674-36300025,36300167-36302260,36302388-36310910,
COMMD9	NM_001101653	chr11	36296323-36297685,36297791-36298637,36298674-36300025,36300167-36310910,
COMP	NM_000095	chr19	18893772-18893862,18894004-18894999,18895174-18895704,18895903-18896306,18896357-18896481,18896662-18896773,18896957-18897047,18897102-18897340,18897461-18898298,18898460-18899019,18899129-18899217,18899324-18899399,18899560-18899646,18899723-18899967,18900107-18900749,18900924-18901369,18901423-18901657,18901745-18901998,
COPB1	NM_001144061	chr11	14479430-14480076,14480234-14481752,14481844-14482730,14482878-14486455,14486577-14487826,14487973-14490225,14490407-14490880,14491110-14496039,14496162-14497329,14497492-14498463,14498562-14501113,14501261-14502303,14502452-14502534,14502644-14504576,14504698-14507911,14508051-14510036,14510131-14512109,14512226-14515186,14515358-14515754,14515986-14520382,14520532-14521251,
COPB1	NM_001144062	chr11	14479430-14480076,14480234-14481752,14481844-14482730,14482878-14486455,14486577-14487826,14487973-14490225,14490407-14490880,14491110-14496039,14496162-14497329,14497492-14498463,14498562-14501113,14501261-14502303,14502452-14502534,14502644-14504576,14504698-14507911,14508051-14510036,14510131-14512109,14512226-14515186,14515358-14515754,14515986-14520382,14520532-14521286,
COPB1	NM_016451	chr11	14479430-14480076,14480234-14481752,14481844-14482730,14482878-14486455,14486577-14487826,14487973-14490225,14490407-14490880,14491110-14496039,14496162-14497329,14497492-14498463,14498562-14501113,14501261-14502303,14502452-14502534,14502644-14504576,14504698-14507911,14508051-14510036,14510131-14512109,14512226-14515186,14515358-14515754,14515986-14520382,14520532-14521153,
COQ9	NM_020312	chr16	57481491-57484950,57485121-57486711,57486849-57490414,57490559-57490841,57490928-57492156,57492263-57493475,57493633-57493961,57494017-57494499,
COX4I1	NM_001861	chr16	85833359-85834809,85834885-85838541,85838711-85839337,85839471-85840342,
COX5A	NM_004255	chr15	75212784-75215987,75216112-75219105,75219229-75221455,75221574-75230254,
CPA3	NM_001870	chr3	148583163-148583258,148583336-148586700,148586827-148596226,148596331-148596432,148596536-148597573,148597677-148599307,148599420-148600290,148600383-148601398,148601603-148603878,148603965-148614305,
CPLX2	NM_006650	chr5	175223788-175235990,175236072-175305653,175305774-175305909,175306087-175306849,
CPLX2	NM_001008220	chr5	175298709-175305653,175305774-175305909,175306087-175306849,
CPLX3	NM_001030005	chr15	75119209-75120373,75120463-75122469,
CPLX4	NM_181654	chr18	56964158-56979915,56980005-56985526,
CPT2	NM_000098	chr1	53662768-53666389,53666472-53667993,53668102-53675685,53676992-53678934,
CRABP1	NM_004378	chr15	78632841-78633383,78633564-78635839,78635955-78640267,
CREB3	NM_006368	chr9	35732899-35732991,35733141-35733210,35733280-35733391,35733483-35735104,35735213-35735301,35735372-35736043,35736130-35736222,35736309-35736387,
CREB3L2	NM_194071	chr7	137565298-137567156,137567375-137569739,137569868-137570147,137570249-137586098,137586169-137588703,137588764-137590446,137590595-137592996,137593183-137597735,137597825-137600581,137600759-137612894,137613113-137686348,
CREBBP	NM_004380	chr16	3779876-3781191,3781475-3781775,3781939-3786035,3786205-3786649,3786817-3788558,3788674-3789577,3789726-3790398,3790551-3794893,3794963-3795276,3795356-3799626,3799685-3801725,3801808-3807287,3807378-3807808,3808050-3808853,3808974-3817719,3817911-3819173,3819355-3820569,3820988-3823750,3823932-3824568,3824695-3827612,3827659-3828010,3828184-3828699,3828819-3830731,3830880-3831203,3831308-3832683,3832928-3841980,3842096-3843385,3843628-3860602,3860781-3900296,3901011-3929831,
CREBBP	NM_001079846	chr16	3779876-3781191,3781475-3781775,3781939-3786035,3786205-3786649,3786817-3788558,3788674-3789577,3789726-3790398,3790551-3794893,3794963-3795276,3795356-3799626,3799685-3801725,3801808-3807287,3807378-3807808,3808050-3808853,3808974-3817719,3817911-3819173,3819355-3820569,3820988-3823750,3823932-3824568,3824695-3827612,3827659-3828010,3828184-3828699,3828819-3830731,3830880-3831203,3831308-3832683,3832928-3843385,3843628-3860602,3860781-3900296,3901011-3929831,
CREBL2	NM_001310	chr12	12765122-12788709,12788909-12790502,12790649-12794926,

CRMP1	NM_001014809	chr4	5823579-5827219,5827387-5830214,5830396-5837640,5837813-5838490,5838634-5841247,5841406-5843033,5843156-5844818,5844889-5851117,5851200-5853133,5853197-5857868,5858035-5862751,5862938-5868393,5868484-5894314,
CRMP1	NM_001313	chr4	5823579-5827219,5827387-5830214,5830396-5837640,5837813-5838490,5838634-5841247,5841406-5843033,5843156-5844818,5844889-5851117,5851200-5853133,5853197-5857868,5858035-5862751,5862938-5868393,5868484-5889953,
CRNN	NM_016190	chr1	152383420-152384570,152384723-152386688,
CROCC	NM_014675	chr1	17248574-17249156,17249294-17250818,17250975-17256339,17256527-17256617,17256703-17256779,17256843-17256922,17257090-17257784,17257893-17263130,17263369-17264134,17264233-17264893,17264979-17265402,17265638-17266387,17266589-17270593,17270778-17271955,17272102-17272752,17272901-17273254,17273487-17274824,17275020-17275292,17275422-17277446,17277618-17279795,17279977-17280716,17280853-17281227,17281373-17281805,17282046-17282490,17282652-17285076,17285246-17287251,17287626-17292216,17292388-17292492,17292615-17292901,17293067-17294696,17294914-17295609,17295836-17296278,17296430-17296746,17296949-17297129,17297263-17297958,17298143-17298853,
CRYZ	NM_001130042	chr1	75172142-75172581,75172679-75172785,75172889-75175780,75175932-75180261,75180315-75184891,75185057-75188800,75188955-75190393,75190519-75196064,75196105-75198638,
CRYZ	NM_001130043	chr1	75172142-75172581,75172679-75175780,75175932-75180261,75180315-75184891,75185057-75188800,75188955-75190393,75190519-75198638,
CRYZ	NM_001889	chr1	75172142-75172581,75172679-75172785,75172889-75175780,75175932-75180261,75180315-75184891,75185057-75188800,75188955-75190393,75190519-75198638,
CRYZ	NM_001134759	chr1	75172142-75172581,75172679-75172785,75172889-75175780,75175932-75180261,75180315-75188800,75188955-75198638,
CSHL1	NM_001318	chr17	61987269-61987520,61987687-61987778,61987900-61988545,
CSHL1	NM_022579	chr17	61987269-61987520,61987687-61987778,61987896-61988103,61988285-61988545,
CSHL1	NM_022581	chr17	61987269-61987520,61987687-61987778,61987827-61988103,61988285-61988545,
CSHL1	NM_022580	chr17	61987269-61987520,61987687-61987778,61987827-61988545,
CSPG5	NM_006574	chr3	47604252-47610640,47610718-47614174,47614365-47618321,47619419-47620085,
CT62	NM_001102658	chr15	71403766-71404485,71404634-71405972,71406103-71407466,
CTDSP1	NM_021198	chr2	219264881-219266285,219266436-219266832,219266939-219267070,219267129-219267756,219267851-219267953,219268141-219269018,
CTDSP1	NM_182642	chr2	219264881-219266285,219266436-219266835,219266939-219267070,219267129-219267756,219267851-219267953,219268141-219269018,
CTXN2	NM_001145668	chr15	48484051-48493439,
CX3CR1	NM_001171171	chr3	39308010-39322532,
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CX3CR1	NM_001171174	chr3	39308010-39323098,
CX3CR1	NM_001337	chr3	39308010-39321443,
CXCL13	NM_006419	chr4	78432943-78526976,78527084-78528855,78528990-78531766,78531849-78532140,
CXorf64	NM_001122716	chrX	125953847-125954640,
CYB5D1	NM_144607	chr17	7761613-7761719,7761798-7761922,7762143-7762698,
CYB5D2	NR_023346	chr17	4047058-4053183,4053326-4057966,4058155-4060158,
CYB5D2	NR_023347	chr17	4046608-4053183,4053326-4057966,4058155-4060158,
CYB5D2	NM_144611	chr17	4047300-4053183,4053326-4057966,4058155-4060158,
CYB5R1	NM_016243	chr1	202931828-202932192,202932294-202932768,202932856-202933738,202933824-202934497,202934629-202935013,202935122-202935654,202935729-202935875,202936027-202936317,
CYBRD1	NM_001127383	chr2	172379249-172409854,172410011-172411032,
CYBRD1	NM_024843	chr2	172379249-172398093,172398304-172409854,172410011-172411032,
CYHR1	NM_001129888	chr8	145689996-145690190,145690480-145690952,
CYHR1	NM_138496	chr8	145676154-145677740,145677954-145678603,145678844-145689841,145689996-145690190,
CYHR1	NM_032687	chr8	145689996-145690190,145690480-145690734,
CYP19A1	NM_000103	chr15	51503254-51504515,51504759-51507265,51507430-51507898,51508015-51510736,51510853-51514544,51514723-51519974,51520131-

			51529054,51529207-51534963,51535148-51630690,
CYP19A1	NM_031226	chr15	51503254-51504515,51504759-51507265,51507430-51507898,51508015-51510736,51510853-51514544,51514723-51519974,51520131-51529054,51529207-51534963,51535148-51616011,51616122-51630690,
CYP4B1	NM_001099772	chr1	47264934-47276478,47276622-47276810,47276857-47278166,47278296-47279152,47279279-47279579,47279736-47279879,47279988-47280744,47280937-47282718,47282854-47283635,47283702-47283801,47283886-47284301,
CYP4B1	NM_000779	chr1	47264934-47276478,47276622-47276810,47276857-47278166,47278296-47279152,47279279-47279582,47279736-47279879,47279988-47280744,47280937-47282718,47282854-47283635,47283702-47283801,47283886-47284301,
CYP4F8	NM_007253	chr19	15726092-15726425,15726626-15728809,15728956-15730299,15730355-15730444,15730573-15733027,15733151-15733913,15734186-15734507,15734576-15734773,15734905-15739110,15739246-15739339,15739406-15739569,15739654-15740001,
CYTH2	NM_017457	chr19	48972784-48973608,48973758-48973858,48973927-48975580,48975701-48976553,48976636-48977160,48977275-48977437,48977588-48978093,48978208-48981322,48981403-48981530,48981604-48981693,48981850-48982378,
CYTH2	NM_004228	chr19	48972784-48973608,48973758-48973858,48973927-48975580,48975701-48976553,48976636-48977160,48977275-48977437,48977588-48978093,48978207-48981324,48981403-48981530,48981604-48981693,48981850-48982378,
DAB1	NM_021080	chr1	57463802-57476351,57476464-57476816,57476946-57480554,57481105-57489202,57489313-57491652,57491717-57528555,57528617-57535031,57535099-57536694,57536735-57537193,57537315-57537954,57538088-57602214,57602315-57610961,57611103-57756634,57756839-58115262,58115338-58349669,58349835-58715910,
DAP	NM_004394	chr5	10681282-10683639,10683684-10748285,10748384-10761124,
DARS2	NM_018122	chr1	173794495-173795823,173795925-173797469,173797538-173799796,173799900-173800671,173800769-173802512,173802638-173803609,173803658-173806076,173806185-173807326,173807398-173808503,173808685-173810002,173810112-173814365,173814430-173819463,173819618-173822485,173822706-173822931,173823044-173825802,173825880-173826654,
DBF4	NM_006716	chr7	87506094-87507366,87507541-87514292,87514474-87516157,87516210-87516642,87516714-87517296,87517375-87525787,87525826-87526607,87526655-87529534,87529665-87530077,87530194-87533605,87533732-87536501,
DCAF16	NM_017741	chr4	17806395-17806728,17806849-17812068,
DCDC1	NM_181807	chr11	31284621-31287052,31287148-31312192,31312400-31327160,31327325-31327777,31327936-31329184,31329456-31349662,31349834-31356992,31357112-31391242,
DCDC2	NM_001195610	chr6	24175063-24178556,24178861-24205228,24205331-24278275,24278440-24289078,24289135-24291158,24291307-24301941,24302075-24302194,24302273-24353795,24353852-24357684,24358076-24383407,
DCDC2	NM_016356	chr6	24175063-24178556,24178861-24205228,24205331-24278275,24278440-24289078,24289135-24291158,24291307-24301941,24302075-24302194,24302273-24353795,24353852-24357684,
DCDC5	NM_020869	chr11	30886880-30900089,30900259-30902703,30902856-30914363,30914545-30915793,30915932-30921086,30921190-30921891,30922046-30925027,30925231-30926506,30926691-30928085,30928273-30930491,30930664-30932872,30932968-30935062,30935193-30937056,30937259-30938415,30938576-30942321,30942471-30943322,30943477-30944048,30944186-30946854,30946956-30947341,30947559-30953316,
DCHS1	NM_003737	chr11	6645622-6645959,6646100-6646427,6646713-6646826,6646959-6647149,6647306-6647398,6647612-6647781,6647897-6648018,6648899-6649850,6650062-6650681,6650809-6650901,6651143-6651228,6652095-6652282,6652442-6652540,6652639-6652845,6653041-6653260,6654288-6654641,6654880-6655018,6655252-6655347,6655538-6661046,6662965-6676792,
DCP1B	NM_152640	chr12	2055453-2058250,2058501-2061580,2062455-2064596,2064727-2074722,2074860-2077008,2077077-2102428,2102558-2107099,2107142-2113446,
DCTD	NM_001921	chr4	183812631-183814182,183814281-183815640,183815759-183836074,183836212-183836612,183836729-183838462,
DCTD	NM_001012732	chr4	183812631-183814182,183814281-183815640,183815759-183836074,183836212-183836612,183836729-183838439,
DCTN3	NM_007234	chr9	34613869-34614037,34614099-34614705,34614766-34616025,34616111-34617880,34617969-34618671,34618758-34620364,
DCTN3	NM_024348	chr9	34613869-34614037,34614196-34614705,34614766-34616025,34616111-34617880,34617969-34618671,34618758-34620364,
DDIT4	NM_019058	chr10	74033819-74033913,74034180-74034451,
DDX12	NR_033399	chr12	9571296-9571369,9571526-9571706,9571787-9572083,9572170-9572575,9572678-9572767,9572852-9573109,9573261-9573982,9574088-9574412,9574487-9577122,9577237-9578065,9578199-9578310,9578421-9578676,9578717-9580227,9580297-9580415,9580462-9581726,9581808-9582154,9582203-9583182,9583337-9584960 9585171-9585563,9585653-9585902,9586012-9586689,9586737-9589541,9589701-9589997,9590086-

			9590605,9590856-9596129,9596279-9600576,
DDX19A	NM_018332	chr16	70380952-70384458,70384509-70389386,70389439-70390013,70390151-70395319,70395414-70398444,70398549-70398918,70399035-70399986,70400166-70400525,70400765-70404124,70404289-70405273,70405467-70405826,
DDX42	NM_007372	chr17	61851737-61852466,61852539-61864392,61864631-61869770,61869923-61875396,61875460-61876947,61876986-61877826,61877978-61882429,61882536-61883893,61884015-61885082,61885261-61886178,61886309-61886918,61887020-61887871,61887921-61888434,61888534-61889290,61889569-61890586,61890815-61892921,61893034-61894226,61894327-61895052,
DDX42	NM_203499	chr17	61851737-61864392,61864631-61869770,61869923-61875396,61875460-61876947,61876986-61877826,61877978-61882429,61882536-61883893,61884015-61885082,61885261-61886178,61886309-61886918,61887020-61887871,61887921-61888434,61888534-61889290,61889569-61890586,61890815-61892921,61893034-61894226,61894327-61895052,
DDX47	NM_016355	chr12	12966389-12967063,12967159-12974140,12974331-12974587,12974661-12974897,12975018-12975593,12975667-12976135,12976254-12976802,12976951-12977472,12977612-12978932,12979005-12980178,12980310-12982355,
DDX47	NM_201224	chr12	12966389-12967063,12967159-12974140,12974331-12974587,12974661-12974897,12975018-12975593,12975667-12976135,12976254-12977472,12977612-12978932,12979005-12980178,12980310-12982355,
DDX5	NM_004396	chr17	62496445-62496665,62496892-62498126,62498188-62498278,62498342-62498555,62498668-62499042,62499217-62499304,62499467-62499546,62499690-62499919,62499987-62500099,62500235-62500338,62500437-62500793,62500961-62502192,
DEFB112	NM_001037498	chr6	50011515-50016248,
DEFB123	NM_153324	chr20	30028560-30037830,
DEFB126	NM_030931	chr20	123328-126054,
DEGS2	NM_206918	chr14	100613245-100615303,100616048-100625841,
DEPDC1B	NM_001145208	chr5	59893742-59899216,59899395-59901515,59901684-59934575,59934718-59938637,59938687-59940570,59940703-59941317,59941447-59943223,59943361-59982787,59983055-59995871,
DEPDC1B	NM_018369	chr5	59893742-59894900,59895088-59899216,59899395-59901515,59901684-59934575,59934718-59938637,59938687-59940570,59940703-59941317,59941447-59943223,59943361-59982787,59983055-59995871,
DERA	NM_015954	chr12	16064349-16109868,16109968-16111120,16111270-16112761,16112859-16115745,16115882-16135240,16135371-16185474,16185589-16189164,16189316-16189622,
DET1	NM_017996	chr15	89056372-89060011,89060205-89070828,89071018-89073852,89074947-89079541,89079613-89089769,
DET1	NM_001144074	chr15	89056372-89060011,89060205-89070828,89071018-89073852,89074947-89089769,
DET1	NR_026645	chr15	89056372-89060011,89060205-89073852,89074705-89074842,89074947-89089769,
DFNA5	NM_004403	chr7	24738879-24742377,24742453-24745801,24745996-24747744,24747874-24749841,24750008-24756871,24756994-24758664,24758838-24784179,24784374-24789181,24789413-24797324,
DFNA5	NM_001127453	chr7	24738879-24742377,24742453-24745801,24745996-24747744,24747874-24749841,24750008-24756871,24756994-24758664,24758838-24784179,24784374-24789181,24789413-24797013,
DFNA5	NM_001127454	chr7	24738879-24742377,24742453-24745801,24745996-24747744,24747874-24749841,24750008-24756871,24756994-24758664,24758838-24784179,24784374-24797324,
DHCR7	NM_001360	chr11	71146886-71148856,71148990-71149923,71150130-71152271,71152487-71153307,71153400-71155037,71155262-71155899,71156005-71158654,71158781-71159334,
DHCR7	NM_001163817	chr11	71146886-71148856,71148990-71149923,71150130-71152271,71152487-71153307,71153400-71155037,71155262-71155899,71156005-71158654,71158781-71159357,
DHRS3	NM_004753	chr1	12628454-12632754,12632882-12638744,12638985-12639319,12639441-12640549,12640695-12677157,
DHRS4	NM_021004	chr14	24423126-24424242,24424422-24429109,24429213-24434969,24435042-24435139,24435193-24435490,24435627-24436418,24436476-24437964,
DHX40	NM_001166301	chr17	57643145-57643986,57644071-57650475,57650597-57651099,57651329-57651547,57651616-57652699,57652833-57654625,57654727-57656831,57656920-57657056,57657241-57663512,57663595-57665255,57665415-57676096,57676213-57676734,57676845-57679881,57679978-

			57682474,57682546-57682805,57683036-57684392,
DHX40	NM_024612	chr17	57643145-57643986,57644156-57647877,57648025-57650475,57650597-57651099,57651329-57651547,57651616-57652699,57652833-57654625,57654727-57656831,57656920-57657056,57657241-57663512,57663595-57665255,57665415-57676096,57676213-57676734,57676845-57679881,57679978-57682474,57682546-57682805,57683036-57684392,
DIAPH1	NM_005219	chr5	140896576-140903708,140903797-140905603,140905741-140905862,140906029-140907138,140907265-140908018,140908150-140908267,140908509-140908737,140908841-140909168,140909265-140913900,140914001-140915619,140915630-140951491,140951608-140953057,140953776-140954532,140954714-140955795,140955862-140956321,140956439-140957040,140957159-140957790,140957911-140958080,140958193-140958653,140958764-140960309,140960451-140961877,140961943-140962771,140962860-140963050,140963183-140963689,140963793-140966607,140966765-140967789,140967818-140998363,
DIAPH1	NM_001079812	chr5	140896576-140903708,140903797-140905603,140905741-140905862,140906029-140907138,140907265-140908018,140908150-140908267,140908509-140908737,140908841-140909168,140909265-140913900,140914001-140915619,140915630-140951491,140951608-140953057,140953776-140954532,140954714-140955795,140955862-140956321,140956439-140957040,140957159-140957790,140957911-140958080,140958193-140958653,140958764-140960309,140960451-140961877,140961943-140962771,140962860-140963050,140963183-140963689,140963793-140966607,140966765-140998363,
DIAPH2	NM_006729	chrX	95940190-95990755,95990790-95993583,95993762-96013151,96013258-96136576,96136718-96167325,96167402-96167480,96167552-96171435,96171574-96173506,96173617-96185730,96185843-96192230,96192351-96194263,96194382-96197015,96197136-96200524,96200591-96203932,96204039-96212825,96213148-96220090,96220207-96327938,96328042-96330164,96330261-96354691,96354795-96369723,96369965-96396662,96396794-96502712,96502839-96603113,96603280-96638906,96639044-96684647,96684745-96854250,
DIAPH2	NM_007309	chrX	95940190-95990755,95990790-95993583,95993762-96013151,96013258-96136576,96136718-96167325,96167402-96167480,96167552-96171435,96171574-96173506,96173617-96185730,96185843-96192230,96192351-96194263,96194382-96197015,96197136-96200524,96200591-96203932,96204039-96212825,96213148-96220090,96220207-96327938,96328042-96330164,96330261-96354691,96354795-96369723,96369965-96396662,96396794-96502712,96502839-96603113,96603280-96638906,96639044-96684647,96684745-96724691,
DIAPH3	NM_030932	chr13	60348383-60348860,60348958-60384920,60385058-60407239,60407406-60413456,60413583-60435539,60435671-60453361,60453603-60485867,60485971-60490287,60490384-60498907,60499005-60544076,60544193-60544984,60545295-60548484,60548591-60554927,60554994-60557901,60558022-60565290,60565409-60566200,60566321-60566605,60566718-60582676,60582784-60584665,60584804-60587181,
DIAPH3	NM_001042517	chr13	60240981-60348321,60348383-60348860,60348958-60384920,60385058-60407239,60407406-60413456,60413583-60435539,60435671-60453361,60453603-60485867,60485971-60490287,60490384-60498907,60499005-60544076,60544193-60544984,60545295-60548484,60548591-60554927,60554994-60557901,60558022-60565290,60565409-60566200,60566321-60566605,60566718-60582676,60582784-60584665,60584804-60590045,60590117-60590203,60590280-60616822,60616955-60667760,60667867-60686142,60686321-60707089,60707124-60737719,
DIO1	NM_213593	chr1	54360029-54370337,54370483-54371766,54371968-54375602,
DIO1	NM_001039716	chr1	54360221-54370337,54370483-54375602,
DIO1	NM_001039715	chr1	54360221-54371766,54371968-54375602,
DIO1	NM_000792	chr1	54360221-54370337,54370483-54371766,54371968-54375602,
DIS3L	NM_001143688	chr15	66586074-66587324,66587480-66599160,66599291-66601045,66601183-66604060,66604239-66606375,66606456-66607372,66607554-66610785,66610957-66612907,66613071-66615023,66615273-66615829,66615924-66618167,66618703-66621306,66621463-66621557,66621738-66624211,66624359-66625072,66625249-66625340,
DIS3L	NM_133375	chr15	66585706-66587324,66587480-66599160,66599291-66601045,66601183-66604060,66604239-66606375,66606456-66607372,66607554-66610785,66610957-66612907,66613071-66615023,66615273-66615829,66615924-66618167,66618703-66621306,66621463-66621557,66621738-66624211,66624359-66625072,66625249-66625340,
DIXDC1	NM_001037954	chr11	111808284-111835271,111835403-111839235,111839363-111844745,111844979-111845598,111845708-111851460,111851575-111853062,111853212-111855954,111856046-111857593,111857649-111859727,111859780-111863137,111863244-111863673,111863729-111864218,111864313-111864391,111864465-111865741,111865833-111866125,111866289-111866802,111866871-111887413,111887521-111888499,111888610-111889678,

DIXDC1	NM_033425	chr11	111848520-111851460,111851575-111853062,111853212-111855954,111856046-111857593,111857649-111859727,111859780-111863137,111863244-111863673,111863729-111864218,111864313-111864391,111864465-111865741,111865833-111866125,111866289-111866802,111866871-111887413,111887521-111888499,111888610-111889678,
DLEC1	NM_007335	chr3	38081128-38087032,38087185-38101231,38101344-38103658,38103860-38104070,38104293-38105330,38105411-38125647,38125737-38126763,38126939-38127730,38127869-38129785,38129880-38134279,38134372-38135094,38135259-38136368,38136563-38137377,38137438-38138058,38138229-38138671,38138767-38138996,38139129-38139233,38139394-38141775,38141917-38149073,38149229-38149894,38150007-38150921,38151054-38151588,38151773-38153166,38153239-38153699,38153853-38155831,38155952-38156472,38156545-38157942,38158150-38158262,38158381-38158464,38158592-38158697,38158794-38159016,38159103-38159295,38159516-38161937,38162101-38163117,38163273-38163560,38163686-38163778,
DLEC1	NM_007337	chr3	38081128-38087032,38087185-38101231,38101344-38103658,38103860-38104070,38104293-38105330,38105411-38125647,38125737-38126763,38126939-38127730,38127869-38129785,38129880-38134279,38134372-38135094,38135259-38136368,38136563-38137377,38137438-38138058,38138229-38138671,38138767-38138996,38139129-38139233,38139394-38141775,38141917-38149073,38149229-38149894,38150007-38150921,38151054-38151588,38151773-38153166,38153239-38153699,38153853-38155831,38155952-38156472,38156545-38157942,38158150-38158262,38158381-38158464,38158592-38158697,38158794-38159016,38159103-38159295,38159516-38161937,38162101-38163117,38163273-38163778,
DLG1	NM_004087	chr3	196771601-196778446,196778540-196786758,196786870-196792145,196792320-196792577,196792681-196793573,196793626-196796088,196796132-196803455,196803557-196807920,196807989-196812449,196812628-196817781,196817898-196831772,196831877-196842796,196842955-196846279,196846402-196857396,196857543-196863411,196863550-196865091,196865263-196867009,196867136-196869587,196869640-196876612,196876668-196888509,196888610-196921294,196921461-197009548,197009717-197023215,197023349-197024055,197024107-197025287,
DLG1	NM_001098424	chr3	196771601-196778446,196778540-196786758,196786870-196792145,196792320-196792577,196792681-196793573,196793626-196796088,196796132-196802706,196802742-196807920,196807989-196812449,196812628-196817781,196817898-196831772,196831877-196842796,196842955-196846279,196846402-196857396,196857543-196863411,196863550-196865091,196865263-196867009,196867136-196869587,196869640-196876612,196876668-196888509,196888610-196921294,196921461-197009548,197009717-197023215,197023349-197024055,197024107-197025287,
DLGAP5	NM_001146015	chr14	55615192-55615310,55615403-55617515,55617567-55618411,55618660-55619306,55619366-55621333,55621525-55625238,55625460-55629687,55629794-55636115,55636278-55637418,55637506-55642062,55642191-55642610,55642737-55643778,55644055-55646345,55646418-55647372,55647497-55647929,55648016-55649086,55649151-55650276,55650472-55655658,55655899-55658179,
DLGAP5	NM_014750	chr14	55615192-55617515,55617567-55618411,55618660-55619306,55619366-55621333,55621525-55625238,55625460-55629687,55629794-55636115,55636278-55637418,55637506-55642062,55642191-55642610,55642737-55643778,55644055-55646345,55646418-55647372,55647497-55647929,55648016-55649086,55649151-55650276,55650472-55655658,55655899-55658179,
DLX4	NM_138281	chr17	48047116-48050435,48050634-48051063,
DLX4	NM_001934	chr17	48050634-48051063,
DMKN	NR_033746	chr19	35988441-35988547,35988584-35989616,35989666-35989774,35989800-35990858,35990932-35991278,35991322-35991433,35991483-35993036,35993086-35993730,35993789-35996618,35996668-35996839,35996889-36000811,36000864-36001084,36001155-36001279,
DMKN	NM_001126056	chr19	35988441-35989616,35989666-35989774,35989800-35990858,35990932-35991433,35991483-35993036,35993086-35993730,35993789-35996618,35996668-35996839,35996889-35997026,35997088-35998358,35998414-35999105,35999143-36000811,36000864-36001084,36001155-36002663,36002716-36003321,36003380-36003490,36003693-36003950,
DMKN	NM_001190348	chr19	35994350-35996618,35996668-35996839,35996889-35997026,35997088-35998358,35998414-35999105,35999143-36000811,36000864-36001084,36001155-36002311,36002496-36002663,36002716-36003321,36003380-36003490,36003693-36003950,
DMKN	NM_001126057	chr19	35994350-35996618,35996668-35996839,35996889-35999105,35999143-36000811,36000864-36001084,36001155-36002311,36002496-36002663,36002716-36003321,36003380-36003490,36003693-36003950,
DMKN	NM_001190349	chr19	35994350-35996618,35996668-35996839,35996889-36001084,36001155-36002311,36002496-36002663,36002716-36003321,36003380-36003490,36003693-36003950,

DMKN	NM_001126059	chr19	35988441-35989616,35989666-35989774,35989800-35990858,35990932-35991433,35991483-35993036,35993086-35993730,35993789-35996618,35996668-35996839,35996889-36000811,36000864-36001084,36001155-36001271,
DMKN	NM_033317	chr19	35988441-35989616,35989666-35989774,35989800-35990858,35990932-35991433,35991483-35993036,35993086-35993730,35993789-35996618,35996668-35996839,35996889-36000811,36000864-36001084,36001155-36002311,36002496-36002663,36002716-36003321,36003380-36003490,36003693-36003950,
DMKN	NM_001190347	chr19	35988441-35989616,35989666-35989774,35989800-35990858,35990932-35991278,35991322-35991433,35991483-35993036,35993086-35993730,35993789-35996618,35996668-35996839,35996889-35997026,35997088-36000811,36000864-36001084,36001155-36002663,36002716-36003321,36003380-36003490,36003693-36003950,
DMKN	NM_001035516	chr19	35988441-35989616,35989666-35989774,35989800-35990858,35990932-35991433,35991483-35992723,
DMKN	NM_001126058	chr19	35994350-35996618,35996668-35996839,35996889-36000811,36000864-36001084,36001155-36002311,36002496-36002663,36002716-36003321,36003380-36003490,36003693-36003950,
DMRTC2	NM_001040283	chr19	42349165-42351491,42351721-42351802,42351950-42352518,42352597-42352861,42353044-42353196,42353325-42354378,42354441-42354592,42354769-42355650,
DMWD	NM_004943	chr19	46287549-46287897,46287974-46288850,46290130-46294161,46294346-46295572,
DMXL2	NM_001174117	chr15	51741391-51742324,51742544-51743840,51743895-51745745,51745839-51747346,51747426-51748261,51748391-51748504,51748567-51749523,51749664-51750701,51750825-51750904,51750993-51755574,51755694-51756870,51757074-51757761,51757849-51758379,51758509-51763418,51763599-51766539,51766790-51768784,51768914-51770466,51770545-51772143,51772337-51772737,51773821-51778268,51778535-51780149,51780317-51780743,51780843-51783773,51783945-51787219,51787332-51799329,51799451-51806637,51806757-51809273,51809365-51827858,51827982-51828361,51829060-51829683,51829957-51830408,51830650-51834528,51834705-51837778,51837964-51839425,51839606-51855576,51855645-51856320,51856458-51857283,51857364-51860682,51860756-51868251,51868379-51914654,
DMXL2	NM_015263	chr15	51741391-51742324,51742544-51743840,51743895-51745745,51745839-51747346,51747426-51748261,51748391-51748504,51748567-51749523,51749664-51750701,51750825-51750904,51750993-51755574,51755694-51756870,51757074-51757761,51757849-51758379,51758509-51763418,51763599-51766539,51766790-51768784,51768914-51770466,51770545-51772143,51772337-51772737,51773821-51778268,51778535-51780149,51780317-51780743,51780843-51783773,51783945-51787219,51787332-51790747,51792429-51795001,51795231-51799329,51799451-51806637,51806757-51809273,51809365-51827858,51827982-51828361,51829060-51829683,51829957-51830408,51830650-51834528,51834705-51837778,51837964-51839425,51839606-51855576,51855645-51856320,51856458-51857283,51857364-51860682,51860756-51868251,51868379-51914654,
DMXL2	NM_001174116	chr15	51741391-51742324,51742544-51743840,51743895-51745745,51745839-51747346,51747426-51748261,51748391-51748504,51748567-51749523,51749664-51750701,51750825-51750904,51750993-51755574,51755694-51756870,51757074-51757761,51757849-51758379,51758509-51763418,51763599-51766539,51766790-51768784,51768917-51770466,51770545-51772143,51772337-51772737,51773821-51778268,51778535-51780149,51780317-51780743,51780843-51783773,51783945-51787219,51787332-51790747,51792429-51795001,51795231-51799329,51799451-51806637,51806757-51809273,51809365-51827858,51827982-51828361,51829060-51829683,51829957-51830408,51830650-51834528,51834705-51837778,51837964-51839425,51839606-51855576,51855645-51856320,51856458-51857283,51857364-51860682,51860756-51868251,51868379-51914654,
DNAH6	NM_001370	chr2	84743708-84744941,84745176-84752687,84752863-84756026,84756291-84771355,84771625-84774390,84774527-84774614,84774737-84775410,84775542-84777011,84777182-84780040,84780159-84784857,84785060-84800589,84800712-84804379,84804533-84806649,84806804-84811121,84811375-84815948,84816079-84821094,84821210-84822768,84822914-84831461,84831676-84832622,84832717-84834098,84834220-84838796,84838979-84844008,84844107-84846807,84847029-84848313,84848480-84848560,84848676-84851387,84851515-84851587,84851745-84852024,84852188-84861626,84861766-84864332,84864502-84867552,84867703-84869069,84869179-84880441,84880999-84881782,84881907-84885414,84885599-84886148,84886294-84896411,84896635-84897450,84897600-84899449,84899609-84904127,84904261-84908479,84908653-84912448,84912597-84913606,84913682-84915561,84915718-84921371,84921605-84924697,84924852-84926716,84926859-84928219,84928464-84930517,84930687-84931189,84931427-84932608,84932872-84934018,84934144-84934642,84934841-84936465,84936671-84937409,84937537-84940217,84940384-84942682,84942752-84945326,84945509-84949747,84949929-84954791,84955027-84960566,84960704-84972202,84972374-84989877,84990070-85008615,85008778-85011844,85011935-85012732,85012881-85014286,85014427-85023428,85023550-85024659,85024783-

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DNAH7	NM_018897	chr2	196602852-196605488,196605594-196619059,196619239-196620855,196621010-196636382,196636615-196640568,196640708-196642522,196642710-196651732,196651896-196659060,196659263-196661298,196661462-196664018,196664197-196671462,196671557-196673404,196673601-196674467,196674596-196681350,196681688-196682418,196682554-196688977,196689170-196698928,196699085-196709724,196709890-196718065,196718253-196720533,196720716-196722099,196722448-196723196,196723529-196726439,196726671-196728871,196729746-196736972,196737194-196738290,196738419-196740397,196740568-196741266,196741424-196746517,196746717-196749307,196749534-196750863,196750997-196752980,196753159-196753521,196753706-196756377,196756529-196759698,196759949-196762389,196762490-196765004,196765219-196771381,196771511-196771629,196771734-196774749,196774920-196786810,196786922-196788317,196788532-196791148,196791291-196799313,196799514-196801321,196801517-196821983,196822172-196824982,196825670-196834670,196834819-196836964,196837191-196849354,196849435-196851788,196851918-196852679,196852954-196865426,196865608-196866397,196866583-196877509,196877631-196883892,196884020-196889151,196889229-196891482,196891665-196892682,196892772-196912074,196912224-196913018,196913129-196915909,196915974-196922776,196922841-196933419,
DNAJA1	NM_001539	chr9	33025382-33026471,33026615-33026809,33026989-33029881,33029988-33030436,33030666-33034212,33034329-33036570,33036688-33037011,33037114-33038681,
DNAJC12	NM_021800	chr10	69556969-69565339,69565546-69571280,69571422-69583070,69583151-69597690,
DNAJC12	NM_201262	chr10	69571422-69583070,69583151-69597690,
DNAJC16	NM_015291	chr1	15853454-15855581,15855768-15860730,15860799-15862968,15863310-15870892,15871079-15873260,15873367-15874763,15874924-15886019,15886152-15888635,15888821-15890422,15890607-15890776,15890855-15892412,15892495-15892575,15892676-15893592,15893765-15894271,
DNAJC24	NM_181706	chr11	31391460-31392261,31392407-31436356,31436497-31447832,31447903-31451816,
DNAJC5	NM_025219	chr20	62526677-62559686,62559806-62560663,62560879-62562202,62562376-62562816,
DNAL1	NM_031427	chr14	74111746-74121548,74121589-74125548,74125660-74128688,74128746-74138243,74138301-74153960,74154089-74156076,74156219-74162603,
DNALI1	NM_003462	chr1	38022677-38023202,38023350-38024926,38025098-38027156,38027337-38027680,38027847-38030625,
DNMT3B	NM_175848	chr20	31350506-31368122,31368272-31369157,31369221-31372562,31372666-31374306,31374434-31375034,31375258-31376658,31376819-31379405,31379515-31380430,31380577-31383213,31383341-31383454,31383501-31384594,31384676-31384991,31385106-31386264,31386450-31387048,31387135-31387957,31388105-31388639,31388732-31389082,31389233-31390189,31390277-31393142,31393214-31394013,31394134-31395566,
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DNMT3B	NM_175849	chr20	31350506-31368122,31368272-31369157,31369221-31372562,31372666-31374306,31374434-31375034,31375258-31376658,31376819-31379405,31379515-31380430,31380577-31383213,31383341-31383454,31383501-31384594,31384676-31384991,31385106-31386264,31386450-31387048,31387135-31387957,31388105-31388639,31388732-31389082,31389233-31390189,31390277-31395566,
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DPCD	NM_015448	chr10	103348158-103354413,103354496-103360493,103360620-103360958,103361094-103368590,103368695-103369122,
DPM3	NM_153741	chr1	155112722-155112965,
DROSHA	NM_013235	chr5	31401670-31405782,31405831-31406958,31407053-31409161,31409267-31409355,31409440-31410851,31410995-31421377,31421485-31422892,31423052-31424532,31424579-31429580,31429653-31431681,31431786-31435870,31435972-31437344,31437406-31448652,31448715-31449386,31449527-31451638,31451748-31464341,31464451-31466287,31466389-31468044,31468171-31472168,31472340-31483659,31483736-31484986,31485070-31486596,31486670-31493312,31493401-31495391,31495480-31504660,31504743-31508726,31508883-31511140,31511284-31515093,31515327-31515559,31515672-31521228,31521323-31526184,31527020-31529145,31529213-31530903,31531032-31532095,
DROSHA	NM_001100412	chr5	31401670-31405782,31405831-31406958,31407053-31409161,31409267-31409355,31409440-31410851,31410995-31421377,31421485-31422892,31423052-31424532,31424579-31429580,31429653-31431681,31431786-31435870,31435972-31437344,31437406-31448652,31448715-31449386,31449527-31451638,31451748-31464341,31464451-31466287,31466389-31468044,31468171-31472168,31472340-31483659,31483736-31484986,31485070-31486596,31486670-31493312,31493401-31495391,31495480-31504660,31504743-31508726,31508883-31511140,31511284-31515093,31515327-31521228,31521323-31526184,31527020-31529145,31529213-31530903,31531032-31531555,31531633-31532095,
DSCR10	NR_027695	chr21	39578455-39578564,39578711-39580227,
DSCR4	NM_005867	chr21	39427076-39492399,39492503-39493220,
DSCR8	NR_026840	chr21	39493696-39494404,39494506-39526507,39526624-39528396,
DSCR8	NR_026841	chr21	39493696-39494404,39494506-39526525,39526624-39528396,
DSCR8	NR_026842	chr21	39493696-39494404,39494506-39528396,
DSCR8	NR_026838	chr21	39493696-39494404,39494763-39526525,39526624-39528396,
DSCR8	NR_026839	chr21	39493696-39494404,39494763-39528396,
DSG4	NM_001134453	chr18	28956923-28965097,28965135-28966649,28966783-28968328,28968486-28968835,28968982-28970617,28970786-28971039,28971176-28972116,28972304-28979233,28979507-28980842,28980984-28983377,28983598-28986038,28986337-28989413,28989555-28991071,28991412-28992789,
DSG4	NM_177986	chr18	28956923-28965097,28965135-28966649,28966783-28968328,28968486-28968835,28968982-28970617,28970786-28971039,28971176-28972116,28972304-28979233,28979507-28980842,28980984-28983377,28983598-28986038,28986337-28989413,28989555-28989706,28989772-28991192,28991412-28992789,
DUS2L	NM_017803	chr16	68057255-68059316,68059398-68071907,68072053-68083406,68083454-68087465,68087559-68088475,68088521-68090265,68090328-68094967,68095017-68100218,68100286-68100467,68100540-68104035,68104124-68104841,68105012-68107935,68108059-68109256,68109408-68110533,68110623-68112346,68112422-68112650,
DYNC1I2	NM_001378	chr2	172544138-172546655,172546774-172549285,172549405-172563055,172563075-172563795,172563888-172569275,172569337-172571836,172571954-172582126,172582224-172582427,172582592-172582702,172582804-172583299,172583427-172584329,172584478-172584813,172584929-172585225,172585361-172586217,172586364-172600557,172600700-172602310,172602438-172604284,
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DYNLL1	NM_001037494	chr12	120907908-120934217,120934357-120935874,
DYNLL1	NM_001037495	chr12	120934020-120934203,120934357-120935874,
DYNLL1	NM_003746	chr12	120934020-120934217,120934357-120935874,
DYNLRB2	NM_130897	chr16	80574977-80577171,80577249-80583379,80583549-80584410,
DYX1C1	NM_130810	chr15	55722978-55724693,55724801-55727101,55727257-55731668,55731780-55742418,55742566-55759126,55759360-55783319,55783455-55789908,55790058-55790403,55790783-55800318,
DYX1C1	NM_001033560	chr15	55710332-55727101,55727257-55731668,55731780-55742418,55742566-55759126,55759360-55783319,55783455-55789908,55790058-55790403,55790783-55800318,
DYX1C1	NM_001033559	chr15	55722978-55727101,55727257-55731668,55731780-55742418,55742566-55759126,55759360-55783319,55783455-55789908,55790058-55790403,55790783-55800318,
E2F1	NM_005225	chr20	32264786-32264909,32265137-32265230,32265347-32266005,32266160-32267559,32267781-32268130,32268223-32273808,

E2F8	NM_024680	chr11	19246388-19246766,19247163-19247277,19247412-19250999,19251536-19251786,19251876-19252176,19252382-19253779,19253919-19255905,19256069-19256289,19256606-19258859,19259018-19259399,19259680-19261652,19261778-19262093,
EBF4	NM_001110514	chr20	2673795-2674305,2674429-2686221,2686380-2686618,2686684-2686853,2686911-2688591,2688667-2690218,2690289-2729193,2729277-2730045,2730165-2730264,2730400-2730491,2730620-2732344,2732435-2732566,2732634-2732730,2732910-2733001,2733192-2736271,2736471-2739553,2739631-2739912,
ECEL1	NM_004826	chr2	233344963-233345107,233345186-233345426,233345524-233345799,233345867-233346214,233346341-233346490,233346560-233347126,233347180-233347258,233347319-233347559,233347665-233347813,233347890-233348124,233348225-233348709,233348934-233349180,233349307-233349509,233349604-233349689,233349802-233349907,233349978-233350576,233351465-233352427,
ECT2	NM_018098	chr3	172472451-172473083,172473165-172474771,172474956-172476768,172476860-172477944,172478054-172479398,172479474-172480204,172480337-172480479,172480597-172480698,172480763-172482066,172482291-172486795,172486934-172491691,172491813-172499951,172500022-172501587,172501700-172502495,172502594-172504281,172504365-172520404,172520485-172520649,172520771-172523519,172523660-172525558,172525715-172533392,172533502-172534479,172534628-172537936,
EEF2K	NM_013302	chr16	22218001-22236973,22237297-22255949,22256052-22260074,22260137-22261973,22262013-22262470,22262644-22268067,22268219-22268572,22268707-22268962,22269092-22269813,22270017-22271781,22271851-22274429,22274509-22276137,22276202-22277709,22277846-22278007,22278198-22284945,22285072-22291517,22291698-22295206,
EFCAB6	NM_022785	chr22	43924856-43926693,43926845-43930566,43930753-43933255,43933426-43936005,43936238-43950747,43950977-43972175,43972369-43976342,43976540-43985952,43986110-43995947,43996144-44004360,44004481-44011704,44011803-44022325,44022560-44027983,44028119-44030980,44031097-44062982,44063153-44064750,44064926-44067851,44068014-44068124,44068186-44073874,44074044-44079625,44079736-44083349,44083462-44107353,44107504-44112726,44112853-44127577,44127692-44131735,44131874-44151644,44151713-44161183,44161274-44168770,44168984-44178058,44178206-44204873,44205012-44208046,
EFCAB6	NM_198856	chr22	43924856-43926693,43926845-43930566,43930753-43933255,43933426-43936005,43936238-43950747,43950977-43972175,43972369-43976342,43976540-43985952,43986110-43995947,43996144-44004360,44004481-44011704,44011803-44022325,44022560-44027983,44028119-44030980,44031097-44062982,44063153-44064750,44064926-44067851,44068014-44068124,44068186-44073874,44074044-44079625,44079736-44083349,44083462-44107353,44107504-44112726,44112853-44127577,44127692-44131735,44131874-44151644,44151713-44161183,44161274-44204873,44205012-44208046,
EFNA2	NM_001405	chr19	1286308-1295542,1295858-1298548,1298616-1299821,
EFNA5	NM_001962	chr5	106717078-106722934,106723017-106723405,106723473-106762916,106763211-107006188,
EGFEM1P	NR_021485	chr3	167967816-168027091,168027228-168031857,168031965-168237322,168237429-168363036,168363161-168427050,168427175-168509988,168510110-168511801,168511951-168520687,168520827-168525315,168525440-168527505,168527628-168527994,168528191-168530140,168530274-168538979,168539116-168542589,168542714-168546864,
EGLN1	NM_022051	chr1	231502222-231503313,231503383-231506306,231506445-231509724,231509846-231556742,
EIF2AK1	NM_001134335	chr7	6064433-6066357,6066593-6068244,6068329-6068547,6068664-6077053,6077156-6078189,6078303-6080521,6080851-6082562,6082622-6084191,6084293-6085700,6085783-6086621,6086723-6088436,6088476-6089541,6089677-6094175,6094336-6098595,
EIF2AK1	NM_014413	chr7	6064433-6066357,6066593-6068244,6068329-6068547,6068664-6077053,6077156-6078189,6078303-6080521,6080851-6082562,6082625-6084191,6084293-6085700,6085783-6086621,6086723-6088436,6088476-6089541,6089677-6094175,6094336-6098595,
EIF2B2	NM_014239	chr14	75469857-75469976,75470099-75470252,75470403-75471438,75471604-75472567,75472665-75473278,75473418-75474423,75474492-75475732,
EIF3B	NM_003751	chr7	2395056-2400343,2400538-2402278,2402400-2402703,2402763-2403265,2403396-2404005,2404165-2405950,2406084-2406158,2406227-2406632,2406681-2409105,2409318-2411410,2411485-2412306,2412431-2414161,2414242-2415022,2415163-2416583,2416711-2418322,2418402-2418767,2418878-2419027,2419147-2419912,
EIF3B	NM_001037283	chr7	2395056-2400343,2400538-2402278,2402400-2402703,2402763-2403265,2403396-2404005,2404165-2405950,2406084-2406158,2406227-2406632,2406681-2409105,2409318-2411410,2411485-2412306,2412431-2414161,2414242-2415022,2415163-2416583,2416711-2418322,2418402-2418767,2418878-2419027,2419147-2419837,
EIF3E	NM_001568	chr8	109214153-109215210,109215347-109215628,109215733-109226834,109226946-109228639,109228743-109229561,109229690-109240494,109240621-109241297,109241425-109247225,109247332-109248388,109248433-109252185,109252305-109254026,109254143-

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EIF3H	NM_003756	chr8	117657343-117658708,117658843-117661043,117661166-117668093,117668245-117669452,117669554-117671050,117671220-117738253,117738412-117767903,
ELL3	NM_025165	chr15	44065425-44065500,44065547-44066378,44066552-44066672,44066717-44066792,44066972-44067502,44067580-44067721,44067809-44067918,44068122-44068235,44068350-44068705,44068743-44068966,
ELOVL2	NM_017770	chr6	10984140-10989934,10990071-10990549,10990676-10995238,10995412-11000318,11000398-11005603,11005793-11010977,11011043-11044459,
ELP3	NM_018091	chr8	27950751-27954734,27954836-27957343,27957484-27964228,27964301-27965428,27965494-27967885,27967956-27970534,27970691-27987017,27987181-27989793,27989922-27995213,27995409-28013457,28013550-28016083,28016151-28017744,28017974-28019512,28019596-28047164,
EML4	NM_001145076	chr2	42396777-42472643,42472828-42483639,42483771-42490316,42490447-42491844,42491872-42507988,42508114-42509961,42510113-42511772,42511844-42513407,42513520-42515365,42515463-42522263,42522400-42522519,42522657-42528379,42528533-42530242,42530370-42530453,42530587-42531622,42531692-42543100,42543191-42544565,42544665-42552605,42552695-42553292,42553393-42556024,42556157-42556872,
EML4	NM_019063	chr2	42396777-42472643,42472828-42483639,42483771-42488259,42488435-42490316,42490447-42491844,42491872-42507988,42508114-42509961,42510113-42511772,42511844-42513407,42513520-42515365,42515463-42522263,42522400-42522519,42522657-42528379,42528533-42530242,42530370-42530453,42530587-42531622,42531692-42543100,42543191-42544565,42544665-42552605,42552695-42553292,42553393-42556024,42556157-42556872,
EMP3	NM_001425	chr19	48828868-48830085,48830180-48830776,48830881-48832607,48832750-48833556,
ENDOG	NM_004435	chr9	131581465-131583016,131583128-131584605,
ENO1	NM_001428	chr1	8921489-8922944,8923005-8923292,8923403-8923948,8924152-8925342,8925542-8926336,8926561-8927174,8927310-8928045,8928117-8930509,8930570-8931948,8932046-8934881,8934977-8938637,
ENO2	NM_001975	chr12	7023824-7024983,7025082-7025579,7025677-7025833,7025894-7026200,7026272-7026743,7026879-7027102,7027327-7028728,7028928-7030742,7030946-7031217,7031328-7031505,7031566-7031892,
ENO3	NM_053013	chr17	4854478-4855121,4855210-4856088,4856186-4856344,4856405-4856565,4856637-4857005,4857141-4858368,4858593-4858700,4858900-4859235,4859439-4859866,4859977-4860124,4860185-4860271,
ENO3	NM_001976	chr17	4854520-4855121,4855210-4856088,4856186-4856344,4856405-4856565,4856637-4857005,4857141-4858368,4858593-4858700,4858900-4859235,4859439-4859866,4859977-4860124,4860185-4860271,
ENO3	NM_001193503	chr17	4854478-4855121,4855210-4856088,4856186-4857005,4857141-4858368,4858593-4858700,4858900-4859235,4859439-4859866,4859977-4860124,4860185-4860271,
EPGN	NM_001013442	chr4	75174294-75174808,75174873-75177900,75178023-75178733,
EPOR	NM_000121	chr19	11489272-11489365,11489455-11491558,11491648-11491730,11491886-11492366,11492526-11492604,11492782-11493771,11493909-11494767,
EPOR	NR_033663	chr19	11489272-11489365,11489455-11491558,11491648-11491730,11491886-11492366,11492526-11492604,11492782-11493521,11493909-11494767,
EPRS	NM_004446	chr1	220142299-220142398,220142465-220145409,220145490-220146578,220146741-220151886,220152062-220152758,220152958-220153425,220153583-220154096,220154200-220154718,220154800-220156112,220156187-220156529,220156741-220157546,220157600-220160482,220160747-220161930,220162166-220170323,220170685-220174478,220174598-220178588,220178703-220179446,220179656-220180542,220180681-220184286,220184399-220191789,220191851-220192335,220192422-220193328,220193564-220195687,220195861-220197604,220197799-220198472,220198601-220203726,220203823-220205727,220205869-220206842,220207001-220208254,220208356-220213525,220213612-220219683,
EPX	NM_000502	chr17	56270284-56270397,56270493-56270730,56270908-56271073,56271193-56271322,56271454-56272323,56272532-56274298,56274619-56276399,56276562-56276898,56277156-56277584,56277757-56280440,56280680-56281581,56281795-56282095,
ERBB4	NM_005235	chr2	212248786-212251576,212251876-212252668,212252718-212285164,212285337-212286730,212286830-212288878,212289027-212293131,212293209-212295668,212295826-212426626,212426814-212483900,212484001-212488645,212488770-212495185,212495320-212522477,212522554-212530046,212530203-212537887,212537983-212543775,212543910-212566690,212566892-212568827,212568920-

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ERBB4	NM_001042599	chr2	212248786-212251576,212251876-212285164,212285337-212286730,212286830-212288878,212289027-212293131,212293209-212295668,212295826-212426626,212426814-212483900,212484001-212488645,212488770-212495185,212495320-212522477,212522554-212530046,212530203-212537887,212537983-212543775,212543910-212566690,212566892-212568827,212568920-212570041,212570117-212576773,212576902-212578258,212578374-212587116,212587260-212589799,212589920-212615362,212615430-212652748,212652885-212812153,212812342-212989475,212989629-213403171,
ERRFI1	NM_018948	chr1	8074457-8075366,8075445-8075553,8075753-8086216,
ESRP1	NM_001122827	chr8	95653679-95654182,95654313-95655529,95655645-95658394,95658511-95674498,95674599-95674727,95674784-95676923,95677036-95677153,95677288-95677380,95677425-95680175,95680479-95683679,95683900-95686534,95686723-95690429,95690600-95718151,
ESRP1	NM_017697	chr8	95653679-95654182,95654313-95655529,95655645-95658394,95658511-95674498,95674599-95674727,95674784-95676923,95677036-95677153,95677288-95677380,95677425-95680175,95680479-95683679,95683900-95686534,95686735-95690429,95690600-95704903,95705056-95709078,95709190-95718151,
ESRP1	NM_001122825	chr8	95653679-95654182,95654313-95655529,95655645-95658394,95658511-95674498,95674599-95674727,95674784-95676923,95677036-95677153,95677288-95677380,95677425-95680175,95680479-95683679,95683900-95686534,95686735-95690429,95690600-95718151,
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ESRP2	NM_024939	chr16	68264219-68264290,68264458-68264742,68264931-68265079,68265280-68265383,68265598-68265703,68266007-68266147,68266192-68266272,68266407-68266478,68266591-68266662,68266719-68267228,68267329-68267669,68267786-68267895,68268011-68269535,68269666-68269749,
ETFDH	NM_004453	chr4	159593643-159601617,159601760-159603345,159603577-159605742,159605826-159606251,159606372-159611498,159611578-159616647,159616796-159618709,159618852-159620137,159620283-159624573,159624744-159627339,159627524-159627779,159628003-159629514,
EVL	NM_016337	chr14	100531849-100551022,100551193-100563816,100563996-100589874,100589940-100593042,100593109-100594854,100595086-100595898,100596022-100599054,100599117-100602240,100602306-100603913,100603982-100604075,100604140-100607515,100607584-100608071,100608131-100610036,
EVX1	NM_001989	chr7	27283077-27284665,27284924-27285503,
EXD2	NM_001193360	chr14	69658309-69670632,69670718-69676139,69676521-69695531,69695790-69697187,69697316-69701415,69701749-69702761,69702870-69703122,69703260-69704290,69704649-69707599,
EXD2	NR_034165	chr14	69658757-69670632,69670718-69676139,69676521-69676827,69676919-69695531,69695790-69697187,69697316-69701415,69701749-69702761,69702870-69703122,69703260-69704290,69704649-69707599,
EXD2	NR_034164	chr14	69658309-69670632,69670718-69676139,69676521-69676827,69676919-69695531,69695790-69697187,69697316-69701415,69701749-69702761,69702870-69703122,69703260-69704290,69704649-69707599,
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EXD2	NM_001193362	chr14	69658757-69670632,69670718-69676139,69676521-69695531,69695790-69697187,69697316-69701415,69701749-69702761,69702870-

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EXO1	NM_003686	chr1	242012330-242013709,242013889-242015592,242015714-242016658,242016784-242020645,242020785-242021806,242022021-242023817,242024007-242024706,242024805-242030130,242030358-242035332,242035581-242042049,242042646-242045216,242045320-242048614,242048810-242052767,
EXO1	NM_006027	chr1	242012330-242013709,242013889-242015592,242015714-242016658,242016784-242020645,242020785-242021806,242022021-242023817,242024007-242024706,242024805-242030130,242030358-242035332,242035581-242042049,242042646-242045216,242045320-242048614,242048810-242052765,
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EXOC3L	NM_178516	chr16	67218508-67218587,67218714-67218803,67218961-67219037,67219162-67219262,67219394-67220138,67220251-67220458,67220561-67220660,67220788-67220922,67221042-67221126,67221741-67222622,67222844-67222921,67223084-67223532,67223587-67223872,
EXT1	NM_000127	chr8	118812137-118816959,118817133-118819454,118819617-118825109,118825201-118830672,118830770-118831913,118832034-118834702,118834837-118842467,118842589-118847681,118847791-118849345,118849441-119122322,
EZR	NM_001111077	chr6	159188111-159188291,159188545-159190356,159190451-159190814,159190977-159191794,159191927-159192274,159192440-159197438,159197537-159204550,159204699-159205674,159205760-159206339,159206616-159208138,159208236-159210318,159210404-159239112,159239199-159240347,
EZR	NM_003379	chr6	159188111-159188291,159188545-159190356,159190451-159190814,159190977-159191794,159191927-159192274,159192440-159197438,159197537-159204550,159204699-159205674,159205760-159206339,159206616-159208138,159208236-159210318,159210404-159239112,
FADS2	NM_004265	chr11	61595070-61605248,61605361-61607804,61608004-61608094,61608198-61615629,61615757-61624481,61624544-61624924,61625003-61630442,61630542-61630752,61630851-61631177,61631259-61632622,61632750-61633108,
FAF2	NM_014613	chr5	175875472-175906187,175906258-175913354,175913491-175915950,175916029-175919193,175919334-175920998,175921086-175921183,175921277-175923485,175923665-175925913,175926087-175927002,175927148-175933767,
FAHD1	NM_001018104	chr16	1877867-1888015,1888136-1889261,
FAHD1	NM_001142398	chr16	1877867-1889261,
FAM115A	NM_014719	chr7	143551236-143554191,143554444-143555915,143556255-143557299,143557541-143558186,143558402-143559507,143559607-143559893,143560890-143573080,143573716-143599052,
FAM120A	NM_014612	chr9	96214672-96233421,96233670-96238536,96238621-96259751,96259882-96261070,96261169-96277947,96278050-96278263,96278552-96289435,96289525-96291633,96291863-96294435,96294612-96305502,96305754-96312857,96312974-96318662,96318874-96320107,96320293-96320861,96321001-96323389,96323533-96324488,96324587-96326509,
FAM126A	NM_032581	chr7	22985783-22999873,23000035-23000852,23000942-23004032,23004151-23015827,23015925-23016310,23016428-23016958,23017041-23017886,23018068-23023561,23023665-23030678,23030759-23053542,
FAM131C	NM_182623	chr1	16385213-16385987,16386100-16386362,16386547-16388592,16388688-16388992,16389030-16390014,16390132-16399914,
FAM149A	NM_015398	chr4	187066267-187070325,187070438-187070718,187070859-187073055,187073200-187074797,187074925-187075620,187075793-187077152,187077345-187078717,187078874-187083997,187084103-187084576,187084788-187086496,187086619-187088120,187088251-187088333,187088417-187093066,
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FAM170A	NM_182761	chr5	118965534-118968441,118968584-118969653,118970430-118970724,118970782-118971393,
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FAM179B	NM_015091	chr14	45433671-45464947,45465106-45468564,45468701-45473262,45473570-45475209,45475471-45478114,45478349-45481176,45481279-45494984,45495076-45496500,45496678-45497377,45497533-45501424,45501580-45512887,45512995-45513836,45514074-45521637,45521766-

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FAM19A1	NM_213609	chr3	68053846-68055765,68055888-68466428,68466571-68587905,68588032-68593635,
FAM20A	NM_017565	chr17	66533883-66535476,66535538-66536024,66536108-66536988,66537100-66538124,66538307-66538833,66538951-66539768,66539863-66548012,66548093-66550916,66550969-66551698,66551885-66596402,
FAM20A	NR_027751	chr17	66533883-66535476,66535538-66536024,66536108-66536988,66537125-66538124,66538307-66538833,66538951-66539768,66539859-66548012,66548093-66550916,66550969-66551698,66551885-66554469,
FAM24A	NM_001029888	chr10	124670336-124671147,124671276-124672276,
FAM35A	NM_019054	chr10	88855006-88856689,88856747-88911105,88912637-88917803,88917913-88930233,88930430-88930595,88930732-88939830,88940061-88946840,88946958-88950239,
FAM38B	NM_022068	chr18	10671777-10672685,10672871-10675204,10675286-10677742,10677873-10680194,10680369-10681656,10681751-10682099,10682290-10689651,10689801-10691221,10691382-10696070,10696287-10696388,10696538-10697744,10697879-10698921,10699176-10701985,10702170-10704390,10704651-10705332,10705745-10714760,10714929-10715646,10715815-10718196,10718258-10731403,10731520-10736600,10736709-10741027,10741101-10742490,10742614-10744138,10744230-10748467,10748629-10750087,10750186-10752632,10752878-10757965,10758133-10759478,10759582-10759701,10759908-10760907,10761110-10762496,10762624-10762918,10763097-10770144,10770307-10773408,10773628-10784780,10784956-10787032,10787183-10789075,10789364-10791197,10791323-10794768,10795001-10797370,10797521-10800333,10800474-10801386,10801427-10803871,10803993-10807108,10807273-10855349,10855565-10856997,10857210-10871249,10871414-10911182,10911227-10979531,10979659-11066124,11066222-11148522,
FAM3C	NM_014888	chr7	120990605-120991195,120991324-121000095,121000182-121002949,121003002-121004182,121004243-121011352,121011478-121012162,121012194-121018962,121019069-121023009,121023065-121036214,
FAM3C	NM_001040020	chr7	120990605-120991195,120991324-121000095,121000182-121002949,121003002-121004182,121004243-121011352,121011478-121012162,121012194-121018962,121019069-121023009,121023065-121036254,
FAM5C	NM_199051	chr1	190068265-190129796,190130021-190195210,190195449-190203500,190203608-190233993,190234186-190250688,190250881-190423783,190424071-190446576,
FAM66A	NR_026789	chr8	12220072-12225746,12225812-12245465,12245529-12245774,12245844-12268472,
FAM66C	NR_026788	chr12	8333349-8340326,8340822-8341066,8341242-8346114,8346252-8346797,8347078-8347307,8347393-8348851,8349115-8352302,
FAM71E1	NM_138411	chr19	50970213-50970877,50971087-50978580,50978713-50979088,50979191-50979385,
FAM73A	NM_198549	chr1	78245422-78248921,78249037-78267014,78267194-78268953,78269092-78272658,78272787-78279417,78279553-78280791,78280917-78308990,78309093-78324621,78324742-78324997,78325072-78325723,78325812-78326907,78327008-78329577,78329714-78332021,78332077-78338687,78338806-78340529,
FAM75C1	NM_001145124	chr9	90533095-90534168,90534264-90534829,90534892-90535165,
FAM83A	NM_032899	chr8	124195577-124204041,124204211-124206262,124206389-124219395,
FAM83A	NM_207006	chr8	124195577-124204041,124204211-124206262,124206389-124219395,124219657-124221664,
FAM83D	NM_030919	chr20	37555569-37570600,37570770-37576517,37576644-37580180,
FAM98A	NM_015475	chr2	33810512-33810595,33810765-33811627,33811746-33812305,33812388-33813400,33813587-33817145,33817282-33820554,33820705-33824234,
FAM9C	NM_174901	chrX	13054138-13056533,13056623-13057925,13058036-13058875,13058992-13061035,13061069-13061245,13061368-13061846,13061977-13062657,
FANCA	NM_000135	chr16	89805117-89805288,89805383-89805539,89805698-89805884,89805962-89806400,89806508-89807210,89807275-89809206,89809347-89811365,89811480-89812990,89813097-89813237,89813299-89815065,89815176-89816136,89816311-89818544,89818631-89824983,89825114-89828355,89828431-89831296,89831475-89833547,89833646-89836243,89836433-89836572,89836668-89836970,89837043-89838084,89838223-89839677,89839793-89842148,89842224-89845207,89845259-89845349,89845412-89846275,89846366-89849265,89849327-89849413,89849511-89851260,89851373-89857809,89857945-89858333,89858477-89858877,89858956-89862312,89862427-89865572,89865641-89866011,89866047-89869665,89869750-89871686,89871801-89874700,89874776-89877113,89877211-89877335,89877480-89880926,89881022-89882283,89882395-89882943,
FANCA	NM_001018112	chr16	89865488-89865572,89865641-89866011,89866047-89869665,89869750-89871686,89871801-89874700,89874776-89877113,89877211-

			89877335,89877480-89880926,89881022-89882283,89882395-89882943,
FANCI	NM_001113378	chr15	89787265-89790858,89790963-89801933,89802008-89803942,89804075-89804814,89804973-89805050,89805110-89806648,89806692-89807132,89807258-89807751,89807839-89811628,89811757-89816606,89816701-89817397,89817536-89819940,89820123-89821916,89822006-89824399,89824532-89824994,89825067-89826365,89826482-89828325,89828450-89833442,89833513-89834842,89834946-89835917,89836096-89836171,89836295-89837062,89837229-89838144,89838326-89843029,89843198-89843529,89843617-89844555,89844674-89847093,89847147-89848344,89848474-89848570,89848641-89848834,89848930-89849236,89849426-89850705,89850761-89850842,89850904-89856133,89856204-89857841,89857939-89858511,89858621-89859626,
FANCI	NM_018193	chr15	89787265-89790858,89790963-89801933,89802008-89803942,89804075-89804814,89804973-89805050,89805110-89806648,89806692-89807132,89807258-89807751,89807839-89811628,89811757-89816606,89816701-89817397,89817536-89819940,89820123-89821916,89822006-89824399,89824532-89824994,89825067-89826365,89826482-89828325,89828450-89833442,89833513-89834842,89834946-89835917,89836096-89836171,89836295-89837062,89837229-89843029,89843198-89843529,89843617-89844555,89844674-89847093,89847147-89848344,89848474-89848570,89848641-89848834,89848930-89849236,89849426-89850705,89850761-89850842,89850904-89856133,89856204-89857841,89857939-89858511,89858621-89859626,
FANK1	NM_145235	chr10	127585225-127668728,127668908-127677118,127677245-127683984,127684068-127685117,127685194-127685987,127686055-127693451,127693619-127696974,127697120-127697621,127697701-127697789,127697836-127697940,
FARP2	NM_014808	chr2	242295804-242312497,242312706-242343241,242343348-242344212,242344257-242346950,242347031-242350446,242350546-242352720,242352837-242357375,242357525-242371092,242371190-242373571,242373737-242374375,242374446-242375894,242375954-242380717,242380972-242396160,242396338-242401936,242402028-242402748,242402884-242403312,242403396-242407553,242407793-242415270,242415403-242422878,242422949-242423655,242423747-242429375,242429460-242430474,242430595-242430929,242431095-242432342,242432452-242432706,242437860-242433421,
FBN3	NM_032447	chr19	8131145-8136930,8137083-8137945,8138182-8139953,8140075-8140165,8140296-8145885,8146004-8146240,8146365-8148129,8148257-8150245,8150454-8151082,8151210-8151959,8152096-8152707,8152832-8152942,8153064-8154427,8154555-8154776,8154844-8154981,8155136-8156347,8156475-8159328,8159450-8160257,8160388-8160846,8160965-8161326,8161454-8161763,8161891-8162171,8162299-8165783,8165857-8167606,8167758-8168444,8168572-8170990,8171118-8173052,8173123-8174109,8174273-8174513,8174638-8175727,8175852-8175940,8176068-8176530,8176655-8176859,8176984-8180397,8180525-8181556,8181684-8182051,8182176-8182346,8182474-8183779,8183907-8186140,8186271-8188346,8188474-8188666,8188893-8190774,8190902-8191179,8191232-8191350,8191490-8191595,8191717-8193910,8194038-8194122,8194250-8196117,8196173-8196436,8196714-8197866,8197991-8200843,8200971-8201072,8201194-8201270,8201416-8203023,8203208-8203294,8203449-8206599,8206727-8206822,8207022-8209759,8209857-8210725,8210823-8211009,8211110-8211986,8212071-8212196,
FBP1	NM_000507	chr9	97365855-97367737,97367859-97369095,97369235-97372201,97372344-97380048,97380143-97382609,97382774-97401421,
FBP1	NM_001127628	chr9	97365855-97367737,97367859-97369095,97369235-97372201,97372344-97380048,97380143-97382609,97382774-97401421,97401617-97402324,
FBXL13	NM_145032	chr7	102453979-102462485,102462651-102473285,102473422-102495222,102495308-102517912,102518041-102518776,102518898-102523750,102523915-102524013,102524133-102524659,102524760-102553531,102553663-102566719,102566822-102572326,102572381-102603978,102604113-102608467,102608565-102665508,102665678-102667894,102668006-102669045,102669196-102669796,102669866-102696089,102696195-102714691,
FBXL13	NM_001111038	chr7	102453979-102462485,102462651-102495222,102495308-102517912,102518041-102518776,102518898-102523750,102523915-102524013,102524133-102524659,102524760-102553531,102553663-102566719,102566822-102572326,102572381-102603978,102604113-102608467,102608565-102665508,102665678-102667894,102668006-102669045,102669196-102669796,102669866-102696089,102696195-102715141,
FBXL3	NM_012158	chr13	77581924-77589542,77589716-77592733,77592858-77595646,77595997-77600960,
FBXO15	NM_152676	chr18	71740966-71749160,71749287-71790601,71790746-71791722,71791807-71793208,71793337-71796638,71796850-71797649,71797894-71802995,71803102-71807435,71807548-71814774,
FBXO15	NM_001142958	chr18	71740966-71749160,71749287-71790601,71790746-71791722,71791807-71793208,71793337-71796638,71796850-71797649,71797894-71802995,71803102-71807435,71807548-71814903,

FBXO22	NM_012170	chr15	76196445-76196830,76196971-76205542,76205632-76206449,76206547-76209569,76209736-76222223,
FBXO22	NR_037623	chr15	76196445-76205542,76205632-76206449,76206547-76209569,76209736-76222223,76222391-76225024,
FBXO22	NM_147188	chr15	76196445-76196830,76196971-76205542,76205632-76206449,76206547-76209569,76209736-76222223,76222391-76225024,
FBXO36	NM_174899	chr2	230787326-230840955,230841066-230861465,230861640-230875410,
FBXO5	NM_012177	chr6	153292550-153293405,153293590-153294179,153294272-153296040,153296757-153303990,
FBXO5	NM_001142522	chr6	153292550-153293405,153293590-153294179,153294272-153296040,153296757-153304367,
FBXO8	NM_012180	chr4	175158751-175160143,175160342-175162249,175162370-175180848,175180977-175183913,175184252-175204559,
FBXW7	NM_001013415	chr4	153244302-153245334,153245547-153247156,153247384-153249358,153249542-153250822,153250938-153251882,153252021-153253746,153253872-153258952,153259089-153268080,153268224-153271192,153271277-153303339,
FBXW7	NM_018315	chr4	153244302-153245334,153245547-153247156,153247384-153249358,153249542-153250822,153250938-153251882,153252021-153253746,153253872-153258952,153259089-153268080,153268224-153271192,153271277-153273620,
FBXW7	NM_033632	chr4	153244302-153245334,153245547-153247156,153247384-153249358,153249542-153250822,153250938-153251882,153252021-153253746,153253872-153258952,153259089-153268080,153268224-153271192,153271277-153332453,153333025-153456091,
FCGBP	NM_003890	chr19	40354137-40354259,40354533-40357375,40357761-40360854,40361056-40362716,40363292-40363862,40364436-40366026,40366572-40367296,40367915-40368301,40368877-40370193,40370533-40373943,40374087-40376311,40376513-40376629,40377226-40380117,40380712-40382281,40382827-40383549,40384168-40384560,40385136-40386444,40386784-40389650,40389794-40391996,40392198-40392314,40392911-40395802,40396397-40397965,40398511-40399237,40399856-40400248,40400824-40402132,40402472-40405917,40406061-40407934,40408136-40408252,40408849-40411636,40412231-40419595,40420165-40421090,40421697-40423977,40424550-40430288,40430640-40432964,40434214-40440469,
FGB	NM_001184741	chr4	155484285-155486958,155487011-155487675,155487825-155488743,155488973-155489531,155489647-155490332,155490460-155490664,155490952-155491569,
FGB	NM_005141	chr4	155484285-155486958,155487152-155487639,155487825-155488743,155488973-155489531,155489647-155490332,155490460-155490664,155490952-155491569,
FGD3	NM_001083536	chr9	95710012-95737518,95737688-95738488,95738992-95765205,95765297-95766281,95766420-95768304,95768463-95772526,95772667-95773494,95773555-95776132,95776281-95778017,95778112-95780416,95780498-95782111,95782144-95782597,95782707-95784607,95784672-95792154,95792279-95795049,95795156-95796821,95796964-95797618,
FGD3	NM_033086	chr9	95737029-95737518,95737688-95738488,95738992-95765205,95765297-95766281,95766420-95768304,95768463-95772526,95772667-95773494,95773555-95776132,95776281-95778017,95778112-95780416,95780498-95782111,95782144-95782597,95782707-95784607,95784672-95792154,95792279-95795049,95795156-95796821,95796964-95797618,
FGF12	NM_021032	chr3	191861917-191888245,191888446-192053148,192053254-192078215,192078328-192125812,
FGF12	NM_004113	chr3	191861917-191888245,191888446-192053148,192053254-192078215,192078328-192444968,192445113-192445271,
FGFRL1	NM_021923	chr4	1006353-1015989,1016264-1017427,1017510-1017603,1017890-1018097,1018453-1018691,
FGFRL1	NM_001004358	chr4	1005776-1006256,1006353-1015989,1016264-1017427,1017510-1017603,1017890-1018097,1018453-1018691,
FGFRL1	NM_001004356	chr4	1005743-1006256,1006353-1015989,1016264-1017427,1017510-1017603,1017890-1018097,1018453-1018691,
FGG	NM_021870	chr4	155526219-155527855,155528135-155529616,155529803-155530780,155530916-155531217,155531350-155532955,155533051-155533168,155533354-155533541,155533588-155533682,
FGG	NM_000509	chr4	155525507-155526047,155526219-155527855,155528135-155529616,155529803-155530780,155530916-155531217,155531350-155532955,155533051-155533168,155533354-155533541,155533588-155533682,
FHAD1	NM_052929	chr1	15573892-15578265,15578374-15598817,15599026-15615893,15616163-15623178,15623290-15627699,15627938-15635107,15635233-15639551,15639684-15642872,15642964-15644318,15644425-15650946,15651056-15653553,15653639-15654771,15654926-15655840,15656038-15668230,15668390-15671577,15671687-15671910,15672020-15675536,15675646-15679371,15679481-15684604,15684780-15686972,15687200-15689136,15689223-15692321,15692430-15693957,15694119-15695864,15695999-15700996,15701128-15702097,15702227-15707195,15707293-15707725,15707948-15708522,15708690-15723791,
FIGF	NM_004469	chrX	15364382-15365284,15365482-15371188,15371291-15373270,15373421-15376123,15376316-15381229,15381442-15401977,

FLI	NM_002018	chr17	18148587-18148666,18148734-18148867,18148975-18149056,18149165-18149246,18149377-18149474,18149537-18149620,18149777-18149906,18150143-18150225,18150367-18150481,18150672-18150969,18151163-18151241,18151348-18151862,18152036-18152112,18152198-18152439,18152516-18152638,18152723-18154150,18154332-18154577,18154792-18154992,18155131-18155311,18155461-18155784,18155871-18156613,18156773-18156856,18157034-18157391,18157497-18157833,18157997-18158081,18158169-18158495,18158578-18159838,18159912-18160221,18160334-18161940,
FLJ14186	NR_037596	chr4	120331294-120331385,120331445-120331670,
FLJ21408	NR_037184	chr16	27279566-27292855,27292957-27297981,27298066-27300119,27300275-27301564,
FLJ26245	NR_033985	chr16	34981198-34983130,34983209-34989748,
FLJ31306	NR_029435	chr14	58734112-58740695,58740854-58758351,58758426-58764671,
FLJ31306	NR_029434	chr14	58734112-58740695,58740729-58752307,58752475-58758351,58758426-58764671,
FLJ34503	NR_027060	chr6	114225909-114238105,114238217-114240269,114240622-114241618,
FLJ42969	NR_033962	chr8	102065065-102066724,102066808-102087395,
FLJ46361	NR_003570	chr10	124516540-124516675,124516749-124516911,124517011-124520939,124521010-124521274,124521345-124524298,124524330-124525837,124525887-124528840,124528872-124530557,124530631-124531612,124531762-124534264,124534457-124535649,124535681-124536328,124536372-124537249,124537567-124538800,124538832-124539572,124539892-124540371,124540406-124542477,124542512-124543832,124543988-124544550,124544922-124545475,124545695-124548425,124548469-124551264,124551296-124551801,124551957-124554045,124554264-124554783,124555003-124556160,124556267-124556884,
FLYWCH2	NM_001142500	chr16	2933364-2945219,2945322-2946351,2946773-2949048,
FLYWCH2	NM_001142499	chr16	2933274-2945219,2945322-2946351,2946773-2949048,
FLYWCH2	NM_138439	chr16	2933368-2945219,2945322-2946351,2946773-2949048,
FMNL3	NM_175736	chr12	50039687-50040667,50040793-50041057,50041152-50041484,50041588-50041974,50042137-50042810,50042942-50043040,50043123-50043251,50043322-50043472,50043709-50044457,50044662-50044949,50045076-50045163,50045234-50045714,50045996-50047007,50047111-50047506,50047658-50047973,50048086-50048691,50048768-50050185,50050281-50050604,50050683-50050863,50050974-50052223,50052378-50055747,50055833-50059613,50059692-50059908,50059991-50062252,50062338-50100836,
FMNL3	NM_198900	chr12	50039687-50040667,50040793-50041057,50041152-50041484,50041588-50041974,50042137-50042810,50042942-50043040,50043123-50043251,50043322-50043472,50043709-50044457,50044662-50044949,50045076-50045163,50045234-50045714,50045996-50047007,50047111-50047506,50047658-50047973,50048086-50048691,50048768-50050185,50050281-50050604,50050683-50050863,50050974-50055747,50055833-50059613,50059692-50059908,50059991-50062252,50062338-50100836,
FOXH1	NM_003923	chr8	145700440-145700538,145700645-145700964,
FOXJ2	NM_018416	chr12	8186430-8192413,8192762-8195252,8195329-8196295,8196366-8196545,8196688-8197354,8197555-8200476,8200886-8201291,8201395-8201956,8202168-8203116,8203217-8205356,
FRMD8	NM_031904	chr11	65154233-65154506,65154593-65156830,65157000-65161042,65161146-65161510,65161571-65161728,65161897-65164268,65164492-65167205,65167331-65168193,65168339-65172333,65172540-65178711,
FRMPD2	NM_001018071	chr10	49365414-49371369,49371715-49376636,49376737-49379035,49379252-49380987,49381137-49382911,49382999-49383887,49383983-49386088,49386195-49388844,49389052-49392607,49392726-49392815,49392925-49393594,49393689-49395233,49395336-49400725,49400938-49409269,49409428-49414789,49414977-49419995,49420153-49430354,49430495-49431164,49431314-49440156,49440333-49444523,49444597-49446032,49446167-49447646,49447736-49448401,49448536-49450202,49450396-49452825,49452893-49457062,49457222-49459607,49459735-49482584,
FRMPD2	NR_033178	chr10	49365414-49371369,49371715-49376636,49376737-49379035,49379252-49380987,49381137-49382911,
FRS3	NM_006653	chr6	41739272-41739552,41739703-41740534,41740698-41743155,41743344-41744658,41744749-41745769,41745915-41747552,
FSD1L	NM_001145313	chr9	108210517-108223799,108223897-108226515,108226613-108230472,108230606-108234183,108234287-108241633,108241658-108246660,108246784-108268678,108268890-108270896,108270997-108275086,108275218-108296772,108296875-108297346,108297600-108301542,108301633-108308637,
FSD1L	NM_031919	chr9	108210517-108226515,108226613-108230472,108230606-108234183,

FSD1L	NM_207647	chr9	108210517-108226515,108226613-108230472,108230606-108234183,108234287-108241633,108241658-108246660,108246784-108268678,108268890-108270896,108270997-108275086,108275218-108296772,108296875-108297346,108297600-108301542,108301633-108308637,
FST	NM_013409	chr5	52776707-52778708,52778902-52779332,52779553-52779897,52780124-52780825,52781058-52781779,
FST	NM_006350	chr5	52776707-52778708,52778902-52779332,52779553-52779897,52780124-52780825,52781058-52781515,
FSTL3	NM_005860	chr19	676527-677790,677978-680272,680490-681331,681561-681648,
FTSJ3	NM_017647	chr17	61897355-61897437,61897534-61897613,61897799-61898197,61898299-61898388,61898476-61898712,61899004-61899081,61899204-61899342,61899529-61901175,61901313-61901442,61901600-61901689,61901772-61901995,61902098-61902183,61902290-61902406,61902524-61902600,61902797-61902894,61902996-61903414,61903496-61903616,61903665-61903925,61904033-61904194,61904289-61904410,
FXN	NM_001161706	chr9	71650864-71661299,71661399-71668054,71668177-71679852,71679952-71714815,
FXN	NM_000144	chr9	71650864-71661299,71661399-71668054,71668177-71679852,71679952-71687526,
FXN	NM_181425	chr9	71650864-71661299,71661399-71668054,71668177-71679852,71679960-71687526,
G3BP2	NM_203504	chr4	76570887-76571520,76571641-76572211,76572342-76573821,76573926-76580248,76580431-76580950,76581055-76582106,76582199-76582739,76582915-76584025,76584109-76587113,76587234-76598390,
G3BP2	NM_203505	chr4	76570887-76571520,76571641-76572211,76572342-76573821,76573926-76579165,76579266-76580248,76580431-76580950,76581055-76582106,76582199-76582739,76582915-76584025,76584109-76587113,76587234-76598390,
G3BP2	NM_012297	chr4	76570887-76571520,76571641-76572211,76572342-76573821,76573926-76579165,76579266-76580248,76580431-76580950,76581055-76582106,76582199-76582739,76582915-76584025,76584109-76587113,76587234-76598201,
GABPB1	NM_016654	chr15	50570982-50578263,50578381-50581678,50581866-50592984,50593100-50593452,50593566-50595124,50595321-50596161,50596331-50601886,50601996-50647180,
GABPB1	NM_181427	chr15	50578381-50581678,50581866-50592984,50593100-50593452,50593566-50595124,50595321-50596161,50596331-50601886,50601996-50638567,50638593-50647180,
GABPB1	NM_005254	chr15	50570982-50578263,50578381-50581678,50581866-50592984,50593100-50593416,50593566-50595124,50595321-50596161,50596331-50601886,50601996-50647180,
GABPB1	NM_002041	chr15	50578381-50581678,50581866-50592984,50593100-50593416,50593566-50595124,50595321-50596161,50596331-50601886,50601996-50647180,
GABPB1	NM_016655	chr15	50578381-50581678,50581866-50592984,50593100-50593452,50593566-50595124,50595321-50596161,50596331-50601886,50601996-50647180,
GABRG2	NM_198904	chr5	161495113-161520832,161520986-161522499,161522569-161524642,161524865-161528239,161528324-161530893,161531033-161569168,161569323-161576112,161576320-161578734,161578760-161580097,
GABRG2	NM_198903	chr5	161495113-161520832,161520986-161522499,161522569-161524642,161524865-161528239,161528324-161529558,161529680-161530893,161531033-161569168,161569323-161576112,161576320-161578734,161578760-161580097,
GABRG2	NM_000816	chr5	161495113-161520832,161520986-161522499,161522569-161524642,161524865-161528239,161528324-161530893,161531033-161569168,161569323-161576112,161576320-161580097,
GALC	NM_000153	chr14	88401223-88406247,88406326-88407737,88407903-88411895,88412078-88414070,88414223-88416187,88416276-88417001,88417093-88429726,88429850-88431847,88431974-88434677,88434835-88442700,88442833-88448547,88448588-88450736,88450878-88452831,88452947-88454486,88454552-88454797,88454868-88459312,
GALC	NM_001037525	chr14	88429856-88431847,88431974-88434677,88434835-88442700,88442833-88448547,88448588-88450736,88450878-88452831,88452947-88454486,88454552-88454797,88454868-88459312,
GALK2	NM_002044	chr15	49462573-49493357,49493448-49509385,49509511-49528046,49528139-49531416,49531565-49574182,49574283-49575761,49575916-49584522,49584735-49611799,49612003-49620147,
GALK2	NM_001001556	chr15	49448214-49493357,49493448-49509385,49509511-49528046,49528139-49531416,49531565-49574182,49574283-49575761,49575916-49584522,49584735-49611799,49612003-49620147,
GALNT12	NM_024642	chr9	101570352-101585536,101585708-101589032,101589224-101594052,101594240-101597529,101597649-101599252,101599431-101602282,101602416-101606376,101606492-101608257,101608406-101611232,

GALNT13	NM_052917	chr2	154728817-154757447,154757521-154800905,154801153-154996848,154997019-155098541,155098710-155099209,155099419-155102323,155102496-155115532,155115652-155157920,155158103-155252501,155252643-155265494,155265595-155295102,155295239-155306921,
GALNT14	NM_024572	chr2	31133926-31135087,31135209-31146983,31147130-31147604,31147690-31152259,31152354-31154932,31155061-31165065,31165171-31167722,31167809-31168647,31168737-31178482,31178606-31178776,31178844-31181261,31181331-31189068,31189169-31215702,31215874-31360822,
GALNT5	NM_014568	chr2	158116049-158140792,158140961-158142525,158142647-158152173,158152311-158152904,158153026-158156058,158156178-158157186,158157512-158162259,158162342-158165077,158165241-158167718,
GALNTL1	NM_001168368	chr14	69727185-69787426,69787586-69791407,69791508-69792052,69792122-69792677,69792745-69795165,69795289-69798179,69798269-69799800,69799887-69800212,69800318-69805366,69805495-69806242,69806337-69808396,69808482-69813755,69813899-69814592,69814720-69818746,
GALNTL1	NM_020692	chr14	69727185-69787426,69787586-69791407,69791508-69792052,69792122-69792677,69792745-69795165,69795289-69798179,69798269-69799800,69799887-69800212,69800318-69805366,69805495-69806242,69806337-69808396,69808482-69813755,69813899-69814592,69814720-69818746,69818888-69820047,
GAN	NM_022041	chr16	81348886-81385186,81385303-81388008,81388361-81390388,81390608-81391413,81391537-81396102,81396217-81397397,81397549-81398577,81398716-81398953,81399084-81410822,81410934-81411018,
GARS	NM_002047	chr7	30634760-30638410,30638514-30639561,30639666-30640673,30640817-30642648,30642739-30643110,30643189-30649199,30649347-30651710,30651862-30655510,30655675-30656728,30656895-30661007,30661117-30661931,30662079-30665848,30665936-30668174,30668286-30671062,30671158-30671861,30672054-30673349,
GDAP1L1	NM_024034	chr20	42876155-42885791,42885986-42887072,42887248-42891868,42891968-42893083,42893200-42907595,
GFOD2	NM_030819	chr16	67709957-67719358,67719706-67753064,
GFOD2	NR_027398	chr16	67709957-67753064,
GFOD2	NR_027399	chr16	67719706-67753064,
GFPT1	NM_002056	chr2	69553366-69554044,69554208-69555401,69555571-69556427,69556557-69556814,69556931-69565028,69565188-69565575,69565698-69569282,69569382-69573034,69573132-69575301,69575467-69577208,69577316-69581619,69581701-69583626,69583690-69585459,69585596-69586398,69586459-69590675,69590803-69597131,69597241-69601136,69601246-69614195,
GGCT	NR_037669	chr7	30536852-30538417,30538555-30544183,
GGCT	NM_001199815	chr7	30536852-30537355,30537513-30540150,30540298-30544183,
GGCT	NM_001199817	chr7	30536852-30544183,
GGCT	NM_001199816	chr7	30536852-30540150,30540298-30544183,
GGCT	NM_024051	chr7	30536852-30538417,30538555-30540150,30540298-30544183,
GGT8P	NR_003503	chr2	91964134-91968434,
GJA1	NM_000165	chr6	121756979-121767976,
GJA5	NM_005266	chr1	147231380-147245354,
GJA5	NM_181703	chr1	147231380-147232605,
GJB6	NM_001110219	chr13	20797635-20803717,20803889-20804835,20804947-20805519,20805645-20806331,
GJB6	NM_001110221	chr13	20797635-20803717,20803889-20806331,
GJB6	NM_001110220	chr13	20797635-20803717,20803889-20805519,20805645-20806331,
GJB6	NM_006783	chr13	20797635-20803717,20803889-20805003,
GJC3	NM_181538	chr7	99521227-99526461,
GKN1	NM_019617	chr2	69201822-69204625,69204681-69204767,69204907-69206001,69206114-69207043,69207193-69207859,
GLG1	NM_012201	chr16	74486030-74487067,74487233-74490545,74490654-74491770,74491893-74493578,74493688-74495990,74496094-74496384,74496529-74497252,74497378-74499572,74499712-74501652,74501747-74502842,74502962-74503881,74503972-74505069,74505185-74506245,74506310-74508442,74508531-74511292,74511432-74514137,74514293-74516919,74517023-74519692,74519816-74524897,74525114-74526853,74527039-

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GLG1	NR_027265	chr16	74487233-74490545,74490654-74491770,74491893-74493578,74493688-74495990,74496094-74496384,74496529-74497252,74497378-74499572,74499712-74501652,74501747-74502842,74502962-74503881,74503972-74505069,74505185-74506245,74506310-74508442,74508531-74511292,74511432-74514137,74514173-74530525,74530543-74537427,74537645-74542735,74542824-74566017,74566052-74640553,
GLG1	NM_001145667	chr16	74487233-74490545,74490654-74491770,74491893-74493578,74493688-74495990,74496094-74496384,74496529-74497252,74497378-74499572,74499712-74501652,74501747-74502842,74502962-74503881,74503972-74505069,74505185-74506245,74506310-74508442,74508531-74511292,74511432-74514137,74514293-74516919,74517023-74519692,74519816-74524897,74525114-74526853,74527039-74528656,74528730-74530337,74530543-74537427,74537645-74542735,74542824-74566017,74566052-74640553,
GLG1	NM_001145666	chr16	74486030-74487067,74487233-74490545,74490654-74491770,74491893-74493578,74493688-74495990,74496094-74496384,74496529-74497252,74497378-74499572,74499712-74501652,74501747-74502842,74502962-74503881,74503972-74505069,74505185-74506245,74506310-74508442,74508531-74511292,74511432-74514137,74514293-74516919,74517023-74519692,74519816-74524897,74525114-74526853,74527039-74528656,74528730-74530337,74530543-74537427,74537645-74542735,74542824-74640553,
GLIPR1L2	NM_152436	chr12	75785131-75804212,75804460-75807376,75807482-75816682,
GLRA1	NM_000171	chr5	151202525-151208480,151208629-151230949,151231166-151234599,151234739-151235860,151235945-151239344,151239570-151266280,151266350-151271870,151272000-151304053,
GLRA1	NM_001146040	chr5	151202549-151208480,151208629-151230949,151231166-151234599,151234739-151235860,151235945-151239344,151239570-151266280,151266350-151271870,151272000-151304053,
GLRX5	NM_016417	chr14	96001722-96010282,
GMFB	NM_004124	chr14	54944878-54946502,54946578-54947590,54947675-54948125,54948177-54948869,54948921-54950387,54950486-54955641,
GMPR2	NM_001002001	chr14	24701995-24702423,24702547-24702683,24702805-24704941,24705027-24705171,24705347-24706275,24706359-24706449,24706558-24706724,24706769-24707450,24707612-24707793,
GMPR2	NM_016576	chr14	24702547-24702683,24702805-24704941,24705027-24705171,24705347-24706275,24706359-24706449,24706558-24706724,24706769-24707450,24707612-24707793,
GMPR2	NM_001002000	chr14	24702054-24702423,24702547-24702683,24702805-24704941,24705027-24705171,24705347-24706275,24706359-24706449,24706558-24706724,24706769-24707450,24707612-24707793,
GMPR2	NM_001002002	chr14	24702184-24702423,24702547-24702683,24702805-24704941,24705027-24705171,24705347-24706275,24706359-24706449,24706558-24706724,24706769-24707450,24707612-24707793,
GNAI1	NM_002069	chr7	79764595-79818265,79818310-79818404,79818548-79828539,79828699-79833018,79833149-79840283,79840415-79842030,79842186-79846617,
GNB2L1	NM_006098	chr5	180664043-180664607,180664720-180665097,180665240-180666065,180666178-180666485,180666583-180668490,180668640-180669172,180669346-180670690,
GNN	NR_027249	chr12	104238198-104238287,104238428-104250886,104251022-104254894,104255049-104255920,104256070-104260156,104260330-104264047,104264189-104276308,104276489-104277380,104277593-104283177,104283409-104286727,104287175-104290747,104290902-104299906,104300131-104305094,104305277-104308854,104309862-104323658,
GNPDA2	NM_138335	chr4	44705160-44709767,44709944-44712968,44713155-44719128,44719313-44720324,44720428-44724099,44724260-44728489,
GOLPH3	NM_022130	chr5	32126743-32135676,32135793-32143853,32143987-32173914,
GOT1L1	NM_152413	chr8	37792005-37792589,37792734-37793220,37793388-37794236,37794389-37794481,37794576-37794793,37794905-37795154,37795268-37796216,37796400-37797431,
GP9	NM_000174	chr3	128779694-128780335,128780463-128780569,

GPR107	NM_020960	chr9	132816353-132837913,132838029-132838689,132838742-132839576,132839658-132841907,132842049-132845842,132845882-132848697,132848756-132853153,132853263-132854525,132854661-132861734,132861812-132862906,132862982-132863383,132863503-132866697,132866830-132869773,132869819-132887192,132887244-132889760,132889846-132890917,132891041-132897302,
GPR107	NM_001136557	chr9	132816353-132837913,132838029-132838689,132838742-132839576,132839658-132841907,132842049-132845842,132845882-132848697,132848756-132853153,132853263-132854525,132854661-132861734,132861812-132862906,132862982-132863383,132863503-132866697,132866830-132869773,132869819-132872647,132872706-132876854,132876943-132887192,132887244-132889760,132889846-132890917,132891041-132897302,
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GPR126	NM_198569	chr6	142623469-142630679,142630782-142688704,142689048-142691305,142691931-142703086,142703157-142704895,142704981-142711393,142711481-142714083,142714138-142715031,142715096-142718748,142718893-142721620,142721734-142723129,142723196-142723755,142723968-142724937,142725111-142726823,142726966-142729285,142729407-142731009,142731057-142732440,142732549-142736104,142736234-142736931,142737202-142738408,142738507-142740956,142741242-142758569,142758673-142759347,142759502-142764472,
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GPR126	NM_001032394	chr6	142623469-142630679,142630782-142688704,142689048-142691305,142691931-142703086,142703157-142711393,142711481-142714083,142714138-142715031,142715096-142718748,142718893-142721620,142721734-142723129,142723196-142723755,142723968-142724937,142725111-142726823,142726966-142729285,142729407-142731009,142731057-142732440,142732549-142736104,142736234-142736931,142737202-142738408,142738507-142740956,142741242-142758569,142758673-142759347,142759502-142762043,142762091-142764472,
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GPR56	NM_001145774	chr16	57673583-57675501,57675621-57684163,57684264-57685110,57685535-57687113,57687248-57687896,57688046-57689309,57689443-57689786,57689905-57690136,57690184-57690424,57690530-57691283,57691404-57693323,57693594-57694678,57694789-57695607,57695878-57697362,
GPR56	NM_201524	chr16	57662715-57675497,57675621-57684163,57684264-57685110,57685535-57687113,57687248-57687896,57688046-57689309,57689443-57689786,57689905-57690136,57690184-57690424,57690530-57691283,57691404-57693323,57693594-57694678,57694789-57695607,57695878-57697362,
GPR56	NM_005682	chr16	57654049-57675501,57675621-57684163,57684264-57685110,57685535-57687113,57687248-57687896,57688046-57689309,57689443-57689786,57689905-57690136,57690184-57690424,57690530-57691283,57691404-57693305,57693594-57694678,57694789-57695607,57695878-57697362,
GPR56	NM_001145771	chr16	57662715-57675501,57675621-57684163,57684264-57685110,57685535-57687113,57687248-57687896,57688046-57689309,57689443-57689786,57689905-57690136,57690184-57690424,57690530-57691283,57691404-57693305,57693594-57694678,57694789-57695607,57695878-57697362,

GPR56	NM_001145770	chr16	57654049-57675501,57675621-57684163,57684264-57685110,57685535-57687113,57687248-57687896,57688046-57689309,57689443-57689786,57689905-57690136,57690184-57690424,57690530-57691283,57691404-57693323,57693594-57694678,57694789-57695607,57695878-57697362,
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GPR56	NM_001145772	chr16	57662741-57675501,57675621-57684163,57684264-57685110,57685535-57687113,57687248-57687896,57688046-57689309,57689443-57689786,57689905-57690136,57690184-57690424,57690530-57691283,57691404-57693323,57693594-57694678,57694789-57695607,57695878-57697362,
GPR56	NM_201525	chr16	57662715-57684163,57684264-57685110,57685535-57687113,57687248-57687896,57688046-57689309,57689443-57689786,57689905-57690136,57690184-57690424,57690530-57691283,57691404-57693323,57693594-57694678,57694789-57695607,57695878-57697362,
GPR68	NM_001177676	chr14	91701524-91710639,
GPR68	NM_003485	chr14	91701524-91720057,
GPR78	NM_080819	chr4	8583378-8584256,8584372-8588779,
GPRIN1	NM_052899	chr5	176026879-176036998,
GPS2	NM_004489	chr17	7216159-7216346,7216444-7216529,7216611-7216697,7216789-7216885,7217041-7217223,7217308-7217397,7217479-7217608,7217723-7217805,7217917-7218276,7218439-7218648,
GREB1L	NM_001142966	chr18	18822355-18945986,18946098-18963469,18963637-18964165,18964365-18975344,18975523-18981109,18981288-18983831,18983956-19019480,19019599-19020228,19020350-19021359,19021499-19024183,19024371-19029469,19029798-19030982,19031113-19032042,19032179-19034325,19034525-19052990,19053173-19057123,19057318-19065579,19065715-19069971,19070313-19075629,19075747-19076413,19076660-19079688,19080268-19080499,19080604-19085371,19085529-19085769,19085911-19088077,19088241-19088346,19088553-19093780,19093948-19095376,19095606-19096572,19096716-19097993,19098196-19100647,19100785-19102617,
GRHL2	NM_024915	chr8	102505018-102555467,102555665-102564941,102565011-102570645,102571041-102582565,102582623-102585894,102586053-102589634,102589748-102611283,102611380-102631765,102631926-102643863,102643953-102644452,102644594-102649123,102649157-102656357,102656454-102661640,102661728-102676680,102676747-102678815,
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GSTA5	NM_153699	chr6	52696769-52697655,52697789-52698937,52699081-52701032,52701167-52702354,52702408-52705523,52705642-52710852,
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GSTM2	NM_000848	chr1	110210774-110211045,110211123-110211545,110211612-110211910,110211994-110212091,110212194-110213907,110214005-110214093,110214206-110217367,
GSTM4	NR_024538	chr1	110199048-110199332,110199410-110199835,110199902-110200392,110200495-110201434,110201532-110201620,110201733-110203785,
GSTM4	NM_147148	chr1	110199048-110199332,110199410-110199835,110199902-110200210,110200294-110200392,110200495-110201434,110201532-110201620,110201733-110207631,
GSTM4	NM_000850	chr1	110199048-110199332,110199410-110199835,110199902-110200210,110200294-110200392,110200495-110201434,110201532-110201620,110201733-110203785,
GTF2F1	NM_002096	chr19	6380497-6380582,6380702-6380913,6381054-6381131,6381207-6381368,6381490-6381563,6381627-6381706,6381862-6383320,6383507-6387398,6387571-6389453,6389649-6391911,6391986-6392866,6392915-6392993,
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GTF2NRD2B	NM_001003795	chr7	74508557-74524750,74524856-74528189,74528330-74536690,74536812-74538935,74539121-74539287,74539318-74541715,74541772-74542141,74542187-74548941,74549021-74550809,74550868-74552590,74552658-74554756,74554836-74556908,74556994-74558287,74558473-74559755,74559786-74563498,
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GUCA2B	NM_007102	chr1	42619212-42620349,42620538-42621204,
GUCY2E	NR_024042	chr11	76391414-76393816,76393845-76400077,76400272-76402646,76402733-76405100,76405180-76405580,76405704-76406405,76406594-76407783,76407960-76414377,76414572-76415203,76415369-76418547,76418606-76418648,76418730-76419292,76419487-76423309,76423460-76423758,76423789-76427451,76427506-76427588,76427687-76427772,76427943-76428976,76429071-76430540,76430910-76432749,
HAUS1	NR_026978	chr18	43684408-43685158,43685375-43698145,43698283-43699890,43700027-43702431,43702557-43703263,43703331-43704786,43704860-43705708,43705758-43708039,
HAUS1	NM_138443	chr18	43684408-43685158,43685335-43698145,43698283-43699890,43700027-43702431,43702557-43703263,43703331-43704786,43704860-43705708,43705758-43708039,
HCN1	NM_021072	chr5	45262913-45267189,45267356-45303699,45303942-45353200,45353349-45396592,45396813-45461946,45462110-45645285,45645711-45695769,
HDAC7	NM_001098416	chr12	48177670-48177860,48178001-48179168,48179255-48179533,48179669-48180366,48180487-48181493,48181593-48181826,48181948-48183042,48183132-48183304,48183362-48183594,48183704-48185040,48185092-48185367,48185490-48185652,48185788-48187150,48187372-48188541,48188717-48188965,48189164-48189368,48189551-48189988,48190082-48190798,48190926-48191165,48191283-48191889,48192003-48192343,48192436-48192566,48192756-48196005,48196058-48213548,
HDAC7	NM_015401	chr12	48177670-48177860,48178001-48179168,48179255-48179533,48179669-48180366,48180487-48181493,48181593-48181826,48181948-48183042,48183132-48183304,48183362-48183594,48183704-48185040,48185092-48185367,48185490-48185652,48185788-48187150,48187372-48188541,48188717-48188965,48189164-48189368,48189551-48189687,48189800-48189988,48190082-48190798,48190926-48191165,48191283-48191889,48192003-48192343,48192436-48192566,48192756-48196005,48196058-48213548,
HDGFRP2	NM_001001520	chr19	4472420-4475270,4475349-4475440,4475581-4488671,4488874-4491561,4491680-4491759,4491833-4493698,4493860-4493977,4494055-4494161,4494473-4496297,4496403-4497953,4498029-4498301,4498374-4498809,4498913-4499486,4499635-4499648,4499717-4501201,4501330-4501921,
HDGFRP2	NM_032631	chr19	4472420-4475270,4475349-4475440,4475581-4488671,4488874-4491561,4491680-4491759,4491833-4493698,4493860-4493977,4494055-4494161,4494473-4496297,4496403-4497953,4498029-4498301,4498374-4498809,4498913-4499486,4499635-4499648,4499717-4501201,4501330-4501924,
HDGFRP3	NM_016073	chr15	83808028-83819965,83820114-83826165,83826326-83826653,83826794-83832749,83832828-83876081,
HEATR2	NM_017802	chr7	766953-769298,769485-780454,780581-780982,781103-794224,794459-796417,796632-801388,801534-803441,803612-810106,810256-813683,813836-814641,814800-819588,819782-825152,
HEATR3	NM_182922	chr16	50100181-50100276,50100451-50102689,50102779-50104087,50104202-50106514,50106626-50109480,50109623-50112650,50112930-50117846,50117939-50118043,50118203-50118478,50118563-50120124,50120263-50128614,50128705-50134139,50134285-50136168,50136347-50138848,
HEATR6	NM_022070	chr17	58121496-58123384,58123591-58124668,58124767-58125623,58125750-58126939,58127064-58128202,58128339-58132874,58132963-58133474,58133599-58134407,58134765-58136781,58136883-58137249,58137458-58143568,58143748-58144793,58145094-58147070,58147210-58148065,58148169-58149574,58149691-58150523,58150641-58151105,58151248-58153489,58153599-58156055,
HEATR7A	NM_032450	chr8	145202980-145215871,145215993-145218672,145218752-145223196,145223344-145234356,145234490-145235079,145235244-145235326,145235427-145245685,145245839-145246616,145246759-145247210,145247305-145254023,145254104-145255329,145255445-145275501,145275577-145278009,145278134-145293657,145293767-145293936,145294083-145294224,145294267-145294515,145294659-145295002,145295057-145295471,145295581-145295893,145296015-145296296,145296421-145297270,145297419-145297503,145297532-145298395,145298520-145298764,145298846-145299123,145299240-145299345,145299443-145300057,145300164-145302202,145302340-145302468,145302583-145303778,145303933-145305113,145305270-145309714,145309882-145310410,145310609-145313678,145313818-145314141,145314258-145314812,145314961-145315087,145315278-145315578,145315736-145315808,145315945-145316015,145316120-

			145316185,145316253-145316556,
HEATR7A	NM_001099281	chr8	145202980-145218672,145218752-145223196,145223344-145234356,145234490-145235079,145235244-145235326,145235427-145245685,145245839-145246616,145246759-145247210,145247305-145254023,145254104-145255329,145255445-145267895,
HEATR7A	NM_001099280	chr8	145202980-145215871,145215993-145218672,145218752-145223196,145223344-145234356,145234490-145235079,145235244-145235326,145235427-145245685,145245839-145246616,145246759-145247210,145247305-145254023,145254104-145255329,145255445-145267895,
HEBP1	NM_015987	chr12	13128414-13140084,13140267-13142209,13142350-13152969,
HEBP2	NM_014320	chr6	138725735-138726280,138726418-138727106,138727289-138734015,
HERPUD1	NM_001010990	chr16	56966304-56969145,56969225-56970597,56970730-56973147,56973272-56973805,56974158-56976042,56976150-56977036,
HERPUD1	NM_001010989	chr16	56966304-56969145,56969225-56969314,56969388-56970597,56970730-56973147,56973272-56973805,56974158-56976042,56976150-56977036,
HERPUD1	NM_014685	chr16	56966304-56969145,56969225-56969311,56969388-56970597,56970730-56973147,56973272-56973805,56974158-56976042,56976150-56977036,
HERV-V2	NM_001191055	chr19	53548212-53552118,
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HHEX	NM_002729	chr10	94450105-94452123,94452304-94452457,94452510-94454302,
HHLA3	NM_001031693	chr1	70820795-70832125,70832221-70833298,
HHLA3	NM_001036645	chr1	70820892-70832125,70832221-70833298,
HHLA3	NM_001036646	chr1	70820791-70832125,70832221-70833298,
HHLA3	NR_027404	chr1	70820791-70832125,70832221-70832614,70832668-70833298,
HIBADH	NM_152740	chr7	27565992-27570809,27570968-27577958,27578037-27582584,27582720-27668988,27669112-27671953,27672065-27689090,27689253-27702315,
HIF1A	NM_001530	chr14	62162558-62187098,62187291-62188225,62188373-62188455,62188542-62193422,62193537-62194169,62194374-62199134,62199243-62200854,62201004-62203605,62203828-62204803,62205092-62207221,62207346-62207471,62207907-62211421,62211532-62212407,62212536-62213650,
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HINFP	NM_198971	chr11	118992350-118997643,118997836-119001433,119001665-119002243,119002357-119002538,119002693-119003204,119003284-119003369,119003492-119003572,119003713-119003803,119003930-119004792,
HINFP	NM_015517	chr11	118992350-118994276,118994395-118997643,118997836-119001433,119001665-119002243,119002357-119002538,119002693-119003204,119003284-119003369,119003492-119003572,119003713-119003803,119003930-119004792,
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HIST1H2BK	NM_080593	chr6	27106461-27114186,
HIVEP2	NM_006734	chr6	143075069-143080907,143081805-143082599,143082703-143085934,143086112-143089517,143089674-143090687,143096263-143097282,143097329-143104656,143104753-143158070,143158185-143266234,
HIVEP3	NM_024503	chr1	41976938-41978485,41979422-41984071,41984160-41990404,41990582-42041213,42041361-42045406,42050990-42094418,42094619-42166585,42166667-42384082,
HIVEP3	NM_001127714	chr1	41976935-41978485,41979422-41984071,41984160-41990404,41990582-42041213,42041361-42045406,42050990-42094418,42094619-42384082,

HJURP	NM_018410	chr2	234746299-234749253,234750852-234752849,234752930-234754372,234754467-234756041,234756108-234758407,234758506-234761209,234761267-234762488,234762557-234763028,
HLA-DQB2	NM_001198858	chr6	32724244-32725056,32725082-32726625,32726909-32729435,32729704-32731149,
HMGCL	NM_000191	chr1	24129055-24130888,24131016-24134623,24134814-24137224,24137290-24140678,24140829-24143163,24143261-24143964,24144074-24146998,24147084-24151844,
HMGCL	NM_001166059	chr1	24129055-24130888,24131016-24134623,24134814-24143163,24143261-24143964,24144074-24146998,24147084-24151844,
HMGCR	NM_000859	chr5	74633126-74638406,74638596-74639676,74639790-74640068,74640158-74641397,74641484-74643027,74643135-74645865,74645974-74646081,74646200-74646612,74646775-74646891,74647141-74647247,74647428-74650326,74650523-74650879,74651040-74651188,74651348-74652166,74652274-74654480,74654653-74654993,74655136-74655221,74655382-74655808,74655965-74656111,
HMGCR	NM_001130996	chr5	74633126-74638406,74638596-74639676,74639790-74640068,74640158-74641397,74641484-74643027,74643135-74645865,74645974-74646081,74646200-74646612,74646775-74646891,74647141-74647247,74647428-74650326,74650523-74651188,74651348-74652166,74652274-74654480,74654653-74654993,74655136-74655221,74655382-74655808,74655965-74656111,
HMGCS1	NM_002130	chr5	43291323-43292574,43292740-43292948,43293076-43294156,43294265-43294791,43294964-43295852,43296020-43297102,43297269-43298109,43298237-43298618,43299078-43313456,
HMGCS1	NM_001098272	chr5	43291323-43292574,43292740-43292948,43293076-43294156,43294265-43294791,43294964-43295852,43296020-43297102,43297269-43298109,43298237-43298618,43299078-43307866,43307927-43313456,
HMMR	NM_001142557	chr5	162887745-162896645,162896836-162898189,162898278-162898367,162898470-162900183,162900260-162900383,162900564-162901061,162901212-162902462,162902679-162905688,162905807-162909646,162909795-162910024,162910179-162910272,162910374-162911073,162911252-162917394,162917559-162918116,
HMMR	NM_012485	chr5	162887745-162890860,162890961-162891727,162891809-162896645,162896836-162898189,162898278-162898367,162898470-162900183,162900260-162900383,162900564-162901061,162901212-162902462,162902679-162905688,162905807-162909646,162909795-162910024,162910179-162910272,162910374-162911073,162911252-162917394,162917559-162918116,
HMMR	NM_012484	chr5	162887745-162890860,162890961-162891727,162891809-162894708,162894755-162896645,162896836-162898189,162898278-162898367,162898470-162900183,162900260-162900383,162900564-162901061,162901212-162902462,162902679-162905688,162905807-162909646,162909795-162910024,162910179-162910272,162910374-162911073,162911252-162917394,162917559-162918116,
HMMR	NM_001142556	chr5	162887745-162890860,162890961-162891727,162891809-162894705,162894755-162896645,162896836-162898189,162898278-162898367,162898470-162900183,162900260-162900383,162900564-162901061,162901212-162902462,162902679-162905688,162905807-162909646,162909795-162910024,162910179-162910272,162910374-162911073,162911252-162917394,162917559-162918116,
HMX2	NM_005519	chr10	124908163-124909084,
HN1	NM_001002032	chr17	73132346-73143649,73143749-73144622,73144767-73150435,
HN1	NM_001002033	chr17	73132346-73142759,73142780-73143649,73143749-73144622,73144767-73145184,73145281-73150435,
HN1	NM_016185	chr17	73132346-73142759,73142780-73143649,73143749-73144622,73144767-73150435,
HNRNPA2B1	NM_002137	chr7	26231959-26232113,26232198-26232869,26232994-26233193,26233315-26235465,26235530-26236019,26236102-26236175,26236279-26236425,26236638-26236933,26237082-26237240,26237353-26240190,
HNRNPA2B1	NM_031243	chr7	26231959-26232113,26232198-26232869,26232994-26233193,26233315-26235465,26235530-26236019,26236102-26236175,26236279-26236425,26236638-26236933,26237082-26237240,26237353-26237449,26237487-26240190,
HOMER1	NM_004272	chr5	78672021-78692644,78692727-78693348,78693461-78697720,78697879-78734831,78734973-78742874,78742969-78746811,78746945-78752683,78752842-78808591,
HOMEZ	NM_020834	chr14	23746397-23755120,
HOOK2	NM_013312	chr19	12874246-12874340,12874414-12874480,12874593-12875626,12875732-12875811,12875896-12876502,12876539-12876641,12876649-12876739,12876829-12876915,12877055-12878207,12878279-12878628,12878718-12878825,12878938-12880693,12880897-12881744,12881887-12881971,12882134-12882209,12882292-12883002,12883067-12883425,12883495-12883592,12883727-12883806,12883859-12885481,12885556-12885624,12885712-12886217,

HOOK2	NM_001100176	chr19	12874246-12874340,12874414-12874480,12874593-12875626,12875732-12875811,12875896-12876502,12876539-12876739,12876829-12876915,12877055-12878207,12878279-12878628,12878718-12878825,12878938-12880693,12880897-12881744,12881887-12881971,12882134-12882209,12882292-12883002,12883067-12883425,12883495-12883592,12883727-12883806,12883859-12885481,12885556-12885624,12885712-12886217,
HOXA11	NM_005523	chr7	27222648-27224053,
HOXB9	NM_024017	chr17	46700498-46703113,
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HRASLS5	NM_001146728	chr11	63231068-63233630,63233845-63235827,63235938-63256341,63256449-63257713,63257836-63258357,
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HSD11B1	NM_005525	chr1	209878376-209879154,209879287-209880052,209880166-209880286,209880474-209905779,209905925-209907647,
HSD11B1L	NM_181755	chr1	209859631-209878260,209878376-209879154,209879287-209880052,209880166-209880286,209880474-209905779,209905925-209907647,
HSPA12B	NM_001197327	chr20	3713442-3719303,3719365-3721460,3721560-3722929,3723056-3725547,3725736-3726138,3726245-3726563,3726679-3728862,3729039-3729877,3729966-3730395,3730502-3730614,3730875-3731449,3731555-3732156,
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HSPA1L	NM_005527	chr6	31779763-31782664,
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HSPG2	NM_005529	chr1	22149982-22150107,22150213-22150612,22150698-22150797,22150870-22151028,22151109-22151195,22151273-22154354,22154413-22154521,22154646-22154746,22154920-22155326,22155573-22155874,22156098-22156484,22156585-22157473,22157584-22157706,22157818-22157954,22158056-22158143,22158290-22158986,22159100-22159759,22159878-22159958,22160108-22160307,22160419-22161170,22161439-22162031,22162131-22163293,22163500-22165316,22165579-22165862,22166044-22166313,22166511-22167592,22167779-22168030,22168167-22168493,22168636-22168730,22168874-22169261,22169415-22169788,22169932-22170639,22170793-22172599,22172749-22172939,22173093-22173845,22173986-22174180,22174334-22174449,22174587-22175134,22175288-22175384,22175525-22176532,22176686-22176854,22176992-22178037,22178191-22178282,22178420-22178579,22178727-22179191,22179326-22179410,22179564-22180684,22180837-22181102,22181259-22181339,22181477-22181795,22181940-22182014,22182169-22182278,22182406-22183506,22183689-22183776,22183879-22186057,22186170-22186326,22186496-22186668,22186729-22188248,22188337-22188479,22188609-22190591,22190707-22191334,22191567-22191776,22191859-22192208,22192303-22198677,22198871-22199111,22199254-22199488,22199585-22199866,22199918-22200416,22200505-22200897,22201027-22201107,22201223-22201382,22201496-22202120,22202241-22202354,22202536-22202720,22202899-22203003,22203146-22204677,22204747-22204924,22204985-22205068,22205157-22205485,22205615-22206598,22206748-22206854,22207053-22207147,22207329-22207830,22207996-22211019,22211168-22211258,22211412-22211504,22211651-22211811,22211945-22213706,22213828-22213911,22214168-22214429,22214560-22216472,22216635-22216918,22216979-22217076,22217188-22222413,22222460-22222666,22222804-22263646,
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HYAL2	NM_033158	chr3	50355971-50356385,50356477-50356998,50357967-50358795,50359205-50360082,
HYAL2	NM_003773	chr3	50355971-50356385,50356477-50356998,50357967-50360082,
HYDIN	NM_032821	chr16	70841966-70843684,70843911-70852243,70852476-70861162,70861315-70862167,70862333-70863519,70863734-70866749,70866971-70867788,70868068-70869577,70869738-70871591,70871792-70873965,70874137-70883627,70883851-70884349,70884559-70889029,70889179-70891606,70891774-70893969,70894110-70894590,70894805-70895949,70896159-70896986,70897086-70900070,70900233-70902471,70902692-70905938,70906083-70908206,70908496-70908718,70908823-70913198,70913390-70913506,70913660-70916561,70916799-70917821,70918028-70923488,70923608-70925547,70925788-70926262,70926433-70928350,70928452-70929882,70929984-70934905,70935106-70937526,70937701-70937806,70937968-70941273,70941395-70942153,70942338-70942554,70942765-70952112,70952333-70954492,70955121-70969853,70970018-70972515,70972659-70975537,70975723-70977713,70977853-70986322,70986539-70989276,70989452-70993548,70993724-70995860,70996042-70998629,70998800-71004421,71004663-71007244,71007396-71007730,71007924-71008074,71008204-71008435,71008574-71009037,71009173-71012815,71012945-71015292,71015472-71019086,71019226-71021825,71022037-71022294,71022388-71025194,71025300-71025971,71026114-71052030,71052346-71054075,71054221-71059284,71059430-71061503,71061779-71065580,71065821-71094405,71094560-71096070,71096237-71098606,71098744-71101191,71101294-71103168,71103406-71113786,71113856-71122202,71122428-71127718,71127839-71149597,71149699-71163541,71163727-71171052,71171256-71186560,71186687-71196432,71196634-71209508,71209645-71212829,71212951-71218766,71218894-71220662,71220822-71264463,
HYDIN	NM_017558	chr16	71061779-71065580,71065821-71094405,71094560-71096070,71096237-71098606,71098744-71101191,71101294-71103168,71103406-71113786,71113856-71122202,71122428-71127718,71127839-71149597,71149699-71163541,71163727-71171052,71171256-71186560,71186687-71196432,71196634-71209508,71209645-71212829,71212951-71218766,71218894-71220662,71220822-71264463,
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IARS2	NM_018060	chr1	220267826-220269444,220269569-220273830,220273992-220275469,220275620-220275703,220275755-220275835,220275947-220276027,220276120-220276787,220276905-220279231,220279403-220280401,220280494-220284126,220284280-220287654,220287817-220298577,220298682-220300090,220300186-220307742,220307853-220310149,220310254-220311258,220311386-220312348,220312482-220313523,220313632-220315143,220315291-220316284,220316477-220318849,220318996-220320833,
IBSP	NM_004967	chr4	88720786-88723498,88723568-88723658,88723711-88723804,88723884-88727272,88727337-88731756,88731917-88732512,
ICA1L	NM_138468	chr2	203644372-203650639,203650731-203653551,203653811-203661611,203661688-203676467,203676513-203679423,203679508-203680632,203680733-203682139,203682267-203684422,203684623-203686079,203686205-203690416,203690491-203693569,203693740-203735251,203735380-203736340,
ICA1L	NM_178231	chr2	203690491-203693569,203693740-203734257,203734329-203735251,203735380-203735912,
IDH2	NM_002168	chr15	90627586-90628046,90628141-90628231,90628331-90628505,90628620-90630342,90630496-90630669,90630808-90631589,90631735-90631817,90631980-90633709,90633877-90634783,90634877-90645506,
IFRD1	NM_001550	chr7	112090838-112095816,112095923-112096055,112096142-112096967,112097094-112098914,112099074-112101919,112101972-

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IFRD1	NM_001007245	chr7	112063488-112090561,112090838-112095816,112095923-112096055,112096142-112096967,112097094-112098914,112099074-112101919,112101972-112102054,112102235-112102323,112102434-112108034,112108171-112112272,112112403-112112819,112112917-112115483,
IFRD1	NM_001197080	chr7	112063488-112095816,112095923-112096055,112096142-112096967,112097094-112098914,112099074-112101919,112101972-112102054,112102235-112102323,112102434-112108034,112108171-112112272,112112403-112112819,112112917-112115483,
IFRD1	NM_001197079	chr7	112092567-112095816,112095923-112096055,112096142-112096967,112097094-112098914,112099074-112101919,112101972-112102054,112102235-112102323,112102434-112108034,112108171-112112272,112112403-112112819,112112917-112115483,
IFRD2	NM_006764	chr3	50325703-50325838,50325936-50326012,50326143-50326229,50326369-50326684,50326792-50326876,50327060-50327141,50327194-50327358,50327518-50327599,50327726-50327817,50327904-50327989,50328111-50329646,
IFT27	NM_006860	chr22	37154454-37158946,37159058-37159961,37160081-37162180,37162242-37163348,37163410-37163825,37163904-37171716,
IFT27	NM_001177702	chr22	37154454-37158946,37159058-37159961,37160081-37162180,37162242-37163348,37163410-37163825,37163907-37164025,
IFT27	NM_001177701	chr22	37154454-37158946,37159058-37159961,37160081-37162180,37162242-37163348,37163410-37163825,37163907-37171716,
IFT27	NR_033531	chr22	37168766-37171716,
IFT74	NM_001099222	chr9	26947462-26961945,26962086-26978124,26978262-26980567,26980618-26984253,26984354-26984495,26984558-26988665,26988727-26990130,26990194-27009016,27009157-27011902,27011967-27016903,27017049-27018643,27018686-27029021,27029103-27044738,27044794-27047270,27047370-27048144,27048273-27055605,27055771-27056330,27056458-27060587,27060650-27062614,
IFT74	NM_025103	chr9	26956515-26961945,26962086-26978124,26978262-26980567,26980618-26984253,26984354-26984495,26984558-26988665,26988727-26990130,26990194-27009016,27009157-27011902,27011967-27016903,27017049-27018643,27018686-27029021,27029103-27044738,27044794-27047270,27047370-27048144,27048273-27055605,27055771-27056330,27056458-27060587,27060650-27062614,
IFT74	NM_001099224	chr9	26956515-26961945,26962086-26978124,26978262-26980567,26980618-26984253,26984354-26984495,26984558-26988665,26988727-26990130,26990194-27009016,27009157-27011902,27011967-27016903,27017049-27018643,27018686-27029021,27029103-27036446,
IFT74	NM_001099223	chr9	26947145-26961945,26962086-26978124,26978262-26980567,26980618-26984253,26984354-26984495,26984558-26988665,26988727-26990130,26990194-27009016,27009157-27011902,27011967-27016903,27017049-27018643,27018686-27029021,27029103-27044738,27044794-27047270,27047370-27048144,27048273-27055605,27055771-27056330,27056458-27060587,27060650-27062614,
IFT88	NM_175605	chr13	21141396-21141807,21141925-21142022,21142137-21148517,21148615-21157094,21157159-21163948,21164007-21165104,21165160-21165755,21165821-21166472,21166544-21170287,21170380-21171152,21171259-21172788,21172893-21173588,21173705-21175842,21176073-21179172,21179245-21189930,21190019-21199887,21199989-21205153,21205242-21212469,21212658-21215427,21215538-21217592,21217745-21218980,21219098-21228013,21228068-21230502,21230570-21237635,21237744-21245110,21245179-21264842,21264955-21265191,
IFT88	NM_006531	chr13	21141396-21148517,21148615-21157094,21157159-21163948,21164007-21165104,21165160-21165755,21165821-21166472,21166544-21170287,21170380-21171152,21171259-21172788,21172893-21173588,21173705-21175842,21176073-21179172,21179245-21189930,21190019-21199887,21199989-21205153,21205242-21212469,21212658-21215427,21215538-21217592,21217745-21218980,21219098-21228013,21228068-21230502,21230570-21237635,21237744-21245110,21245179-21264842,21264955-21265191,
IGF2BP1	NM_006546	chr17	47075283-47076469,47076532-47102978,47103029-47103826,47103880-47109270,47109336-47115528,47115812-47117317,47117454-47118738,47118863-47119602,47119740-47120788,47120913-47121327,47121449-47122351,47122428-47123250,47123384-47123620,47123736-47126712,
IGF2BP1	NM_001160423	chr17	47075283-47076469,47076532-47102978,47103029-47103826,47103880-47109270,47109336-47118738,47118863-47119602,47119740-47120788,47120913-47121327,47121449-47122351,47122428-47123250,47123384-47123620,47123736-47126712,
IGF2BP2	NM_001007225	chr3	185363412-185364811,185364927-185367189,185367323-185369880,185369957-185375072,185375191-185376127,185376198-185393082,185393220-185393577,185393702-185404843,185404980-185407141,185407416-185410485,185410551-185414398,185414452-185416085,185416136-185540939,185541002-185542569,
IGF2BP2	NM_006548	chr3	185363412-185364811,185364927-185367189,185367323-185369880,185369957-185375072,185375191-185376127,185376198-185390327,185390458-185393082,185393220-185393577,185393702-185404843,185404980-185407141,185407416-185410485,185410551-

			185414398,185414452-185416085,185416136-185540939,185541002-185542569,
IGF2R	NM_000876	chr6	160390428-160412214,160412356-160430040,160430167-160431717,160431818-160445602,160445737-160448215,160448347-160450580,160450688-160453581,160453746-160453972,160454140-160455449,160455555-160461590,160461757-160464178,160464321-160465544,160465690-160466775,160466915-160467528,160467678-160468189,160468369-160468822,160468940-160469405,160469576-160471503,160471685-160477454,160477558-160479053,160479157-160479936,160480131-160481577,160481750-160482533,160482679-160482783,160482961-160483562,160483652-160484445,160484663-160485431,160485564-160485834,160485934-160489279,160489418-160490898,160491091-160492940,160493069-160493795,160493917-160494243,160494502-160494787,160495008-160496877,160497029-160499231,160499395-160500610,160500820-160501159,160501308-160504980,160505217-160506025,160506164-160509063,160509180-160510137,160510286-160510946,160511136-160517469,160517658-160523549,160523704-160524776,160524848-160525704,
IGFBP3	NM_000598	chr7	45953434-45954402,45954545-45956145,45956267-45956810,45957039-45960335,
IGFBP3	NM_001013398	chr7	45953434-45954402,45954545-45956145,45956267-45956810,45957039-45960317,
IKBKAP	NM_003640	chr9	111631463-111637173,111637251-111640273,111640430-111640901,111641031-111641724,111641838-111642330,111642446-111643983,111644046-111644403,111644468-111651610,111651674-111653481,111653685-111655264,111655364-111656221,111656347-111658774,111658925-111659231,111659319-111659426,111659566-111660780,111660862-111660949,111661030-111662100,111662176-111662538,111662656-111663703,111663811-111663906,111663962-111665117,111665223-111665841,111665950-111668581,111668766-111670583,111670685-111673288,111673461-111674542,111674775-111678482,111678578-111679825,111679951-111681089,111681182-111681531,111681630-111685120,111685208-111688801,111688884-111689650,111689734-111692047,111692202-111693275,111693482-111696142,
IKBKB	NR_033819	chr8	42128988-42129599,42129724-42146150,42146247-42147672,42147792-42150959,42151031-42162703,42162794-42163859,42163951-42166417,42166544-42171838,42171948-42173726,42173858-42174226,42174423-42175173,42175290-42176068,42176194-42176786,42176940-42178251,42178363-42179412,42179464-42179570,42179672-42179863,42180013-42183486,42183616-42186640,42186733-42188430,
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IKBKB	NM_001556	chr8	42128988-42129599,42129724-42146150,42146247-42147672,42147792-42150959,42151031-42162703,42162794-42163859,42163951-42166417,42166544-42171838,42171948-42173726,42173858-42174226,42174423-42175173,42175290-42176068,42176194-42176786,42176940-42177101,42177165-42178251,42178363-42179412,42179464-42179570,42179672-42179863,42180013-42183486,42183616-42186640,42186733-42188430,
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IKBKB	NM_001190720	chr8	42128988-42146150,42146247-42147672,42147792-42150959,42151031-42162703,42162794-42163859,42163951-42166417,42166544-42171838,42171948-42173726,42173858-42174226,42174423-42175173,42175290-42176068,42176194-42176786,42176940-42177101,42177165-42178251,42178363-42179412,42179464-42179570,42179672-42179863,42180013-42183486,42183616-42186640,42186733-42188430,
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IL17C	NM_013278	chr16	88705056-88705387,88705718-88706220,
IL17F	NM_052872	chr6	52101967-52103526,52103749-52109193,
IL1A	NM_000575	chr2	113532845-113535562,113535689-113537071,113537244-113539179,113539404-113540291,113540342-113541299,113541356-113542018,

IL1F10	NM_032556	chr2	113830348-113831904,113831992-113832298,113832428-113832727,
IL1F10	NM_173161	chr2	113825594-113830286,113830348-113831904,113831992-113832298,113832428-113832727,
IL20RB	NM_144717	chr3	136677044-136699306,136699435-136701000,136701193-136708281,136708408-136710778,136710931-136714254,136714399-136728953,
IL6ST	NM_001190981	chr5	55237648-55238496,55238580-55243319,55243418-55247290,55247433-55247755,55247904-55248076,55248180-55251851,55252064-55253035,55253120-55256228,55256390-55259178,55259335-55259972,55260141-55264102,55264225-55265376,55265684-55272041,55272122-55278550,55278640-55290610,
IL6ST	NM_175767	chr5	55237648-55238496,55238580-55243319,55243418-55247290,55247433-55247755,55247904-55248076,55248180-55250636,55250821-55251851,55252064-55256228,55256390-55259178,55259335-55259972,55260141-55264102,55264225-55265376,55265684-55272041,55272122-55278550,55278640-55290610,
IL6ST	NM_002184	chr5	55237648-55238496,55238580-55243319,55243418-55247290,55247433-55247755,55247904-55248076,55248180-55250636,55250821-55251851,55252064-55253035,55253120-55256228,55256390-55259178,55259335-55259972,55260141-55264102,55264225-55265376,55265684-55272041,55272122-55278550,55278640-55290610,
ILF2	NM_004515	chr1	153635033-153635179,153635272-153635493,153635610-153635689,153635753-153636517,153636607-153636870,153636951-153637694,153637813-153638137,153638205-153640029,153640134-153640474,153640554-153640927,153641034-153642310,153642355-153642645,153642707-153643392,
INCA1	NM_001167987	chr17	4891850-4892072,4892240-4892721,4892920-4893183,4893225-4893445,4893561-4897687,4897771-4900296,4900425-4900789,
INCA1	NM_001167986	chr17	4891850-4892072,4892240-4892721,4892920-4893183,4893225-4893445,4893561-4897687,4897771-4899099,4899226-4900134,4900425-4900789,
INCA1	NM_001167985	chr17	4891850-4892072,4892240-4892721,4892875-4893183,4893225-4893445,4893561-4897687,4897771-4900296,4900425-4900789,
INCA1	NM_213726	chr17	4891850-4892072,4892240-4892721,4892875-4893183,4893225-4893445,4893561-4897687,4897771-4900134,4900425-4900789,
INCENP	NM_001040694	chr11	61891636-61895621,61895774-61896240,61896356-61897252,61898063-61905302,61905356-61906183,61906243-61906358,61906478-61907704,61907758-61908174,61908294-61908383,61908517-61908970,61908984-61912452,61912564-61912639,61912762-61913099,61913224-61914128,61914375-61915946,61916027-61916209,61916319-61917527,61917680-61919232,
INCENP	NM_020238	chr11	61891636-61895621,61895774-61896240,61896356-61897252,61898063-61905302,61905356-61906183,61906243-61906358,61906478-61907704,61907758-61908174,61908294-61908383,61908517-61912452,61912564-61912639,61912762-61913099,61913224-61914128,61914375-61915946,61916027-61916209,61916319-61917527,61917680-61919232,
INHBE	NM_031479	chr12	57849618-57849875,
INO80	NM_017553	chr15	41272639-41275058,41275276-41275958,41276120-41276393,41276551-41277534,41277625-41279287,41279392-41280012,41280173-41289725,41289800-41297789,41297886-41308284,41308414-41313096,41313324-41319792,41319935-41337100,41337274-41339604,41339700-41340408,41340475-41341483,41341619-41342131,41342301-41346125,41346213-41347443,41347563-41348818,41348905-41350835,41350980-41352063,41352125-41361766,41361864-41362663,41362746-41364045,41364257-41365624,41365694-41366566,41366764-41371897,41372103-41373216,41373272-41377565,41377782-41379758,41379881-41384223,41384381-41387797,41387867-41387955,41388127-41388364,41388552-41408169,
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INPP5K	NM_016532	chr17	1399174-1399352,1399459-1399611,1399697-1399958,1400098-1401228,1401417-1410272,1410384-1411407,1411521-1412470,1412648-1412975,1413094-1416745,1416856-1417164,1417274-1419748,
INSIG1	NM_005542	chr7	155089670-155089967,155090408-155093274,155093401-155093959,155094128-155094455,155094557-155099949,
INSIG1	NM_198337	chr7	155089670-155089967,155090408-155094455,155094557-155099949,
INSIG1	NM_198336	chr7	155089670-155089967,155090077-155093959,155094128-155094455,155094557-155095533,155095606-155099949,

INTS1	NM_001080453	chr7	1510329-1510480,1510592-1510767,1510861-1511205,1511278-1511907,1512023-1512706,1512821-1513200,1513330-1513802,1513997-1514339,1514475-1515582,1515708-1515863,1516092-1516204,1516294-1516428,1516555-1517184,1517310-1517387,1517573-1518000,1518143-1518360,1518522-1519064,1519321-1519951,1520078-1520469,1520570-1520976,1521125-1522180,1522344-1523376,1523490-1523637,1523807-1524732,1524839-1524924,1525106-1526259,1526411-1526556,1526738-1526954,1527086-1527394,1527594-1528978,1529041-1529225,1529319-1532644,1532743-1533388,1533548-1534450,1534530-1535067,1535190-1535790,1535901-1536772,1536951-1538046,1538190-1538341,1538489-1538609,1538798-1538889,1538997-1539107,1539269-1539518,1539658-1539804,1540003-1542535,1542828-1543537,1543638-1543957,
INTU	NM_015693	chr4	128554336-128564674,128565212-128577789,128577877-128584534,128584740-128590189,128590310-128595277,128595369-128605562,128605642-128608831,128609023-128621163,128621219-128625381,128625446-128626744,128626968-128627640,128628125-128629724,128629824-128632066,128632258-128635089,128635249-128637478,
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IQCC	NM_018134	chr1	32671325-32671753,32671899-32672108,32672363-32672601,32672722-32672839,
IQCC	NM_001160042	chr1	32671565-32671753,32671899-32672108,32672363-32672601,32672722-32672839,
IQCF5	NM_001145059	chr3	51908192-51909542,
IQCG	NM_032263	chr3	197616586-197618315,197618419-197619497,197619631-197639544,197639621-197640750,197640914-197652893,197652977-197659043,197659174-197665417,197665652-197670647,197670923-197672489,197672558-197686398,197686591-197686714,
IQCG	NM_001134435	chr3	197616586-197618315,197618419-197619497,197619631-197639544,197639621-197640750,197640914-197652893,197652977-197659043,197659174-197665417,197665652-197670647,197670923-197672489,197672558-197676708,
IQGAP3	NM_178229	chr1	156496392-156497742,156497853-156498299,156498403-156498706,156498875-156499895,156500110-156500950,156501040-156502770,156502899-156503563,156503668-156503799,156503934-156504291,156504526-156504953,156505040-156506971,156507114-156508599,156508826-156509164,156509330-156509628,156509783-156510498,156510709-156513771,156513843-156513942,156514016-156514179,156514265-156517863,156518036-156518138,156518280-156518371,156518541-156520051,156520144-156521495,156521661-156521764,156521888-156524025,156524185-156526323,156526486-156530724,156530814-156531628,156531794-156532377,156532458-156532924,156533105-156533343,156533459-156533547,156533617-156534405,156534484-156535817,156535897-156536180,156536339-156539166,156539256-156542283,
NRF2BP2	NM_001077397	chr1	234743599-234744239,
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ISOC2	NM_001136202	chr19	55964756-55966354,55966474-55966625,55966698-55967714,55967857-55972877,
ISOC2	NM_001136201	chr19	55964756-55966354,55966474-55966625,55966698-55967001,55967213-55967714,55967857-55972877,
ISOC2	NM_024710	chr19	55964756-55966354,55966474-55966625,55966746-55967001,55967213-55967714,55967857-55972877,
ITCH	NM_031483	chr20	32951156-32957198,32957277-32981595,32981688-32996455,32996599-33000319,33000446-33001546,33001686-33012284,33012332-33026277,33026437-33027958,33028150-33030011,33030109-33033090,33033267-33037214,33037286-33045193,33045280-33049896,33050027-33057851,33057926-33059247,33059321-33065575,33065666-33067433,33067595-33068402,33068538-33068869,33069012-33077069,33077192-33077625,33077732-33080304,33080403-33092134,33092209-33095498,
ITFG1	NM_030790	chr16	47189690-47192782,47192902-47195659,47195744-47196449,47196576-47252777,47252858-47271874,47271920-47292541,47292652-47294454,47294607-47345149,47345324-47347638,47347735-47399697,47399781-47409785,47409852-47462713,47462810-47485305,47485382-47486642,47486702-47487922,47488070-47493012,47493087-47494747,
ITLN2	NM_080878	chr1	160915083-160917717,160917823-160919834,160919957-160920341,160920502-160920831,160921081-160922408,160922524-160924175,160924241-160924515,
ITPRIP	NM_033397	chr10	106075823-106093094,106093257-106093383,
IVNS1ABP	NM_006469	chr1	185267421-185268840,185269016-185269129,185269263-185269347,185269476-185269567,185269691-185270102,185270329-185270564,185270696-185274666,185274776-185276144,185276272-185276619,185276795-185277930,185278008-185278133,185278305-185278513,185278644-185280225,185280455-185286083,

JHDM1D	NM_030647	chr7	139790989-139791602,139791878-139793854,139793939-139796353,139796564-139796697,139796848-139797343,139797443-139798677,139798834-139799697,139799824-139801749,139801961-139810893,139810985-139813289,139813383-139818911,139819020-139820240,139820330-139824419,139824584-139826435,139826624-139827240,139827384-139829291,139829454-139833337,139833457-139838903,139838991-139876542,
JKAMP	NM_001098625	chr14	59951312-59953447,59953523-59954390,59954547-59961734,59961943-59965443,59965627-59967907,59967986-59970570,
JKAMP	NM_016475	chr14	59951312-59953429,59953523-59954390,59954547-59961734,59961943-59965443,59965627-59967907,59967986-59970570,
KCMF1	NM_020122	chr2	85198591-85255010,85255180-85262137,85262279-85270685,85270789-85273225,85273402-85276487,85276772-85280269,
KCNA4	NM_002233	chr11	30035008-30038117,
KCNH7	NM_173162	chr2	163280046-163291706,163292108-163302526,163302954-163360951,163361168-163374238,163374669-163393433,163393591-163693045,163693278-163694951,
KCNH7	NM_033272	chr2	163228606-163229978,163230173-163236361,163236532-163241196,163241450-163250897,163250996-163253248,163253456-163256697,163256952-163279844,163280046-163291706,163292108-163302526,163302954-163360951,163361168-163369162,163369185-163374238,163374669-163393433,163393591-163693045,163693278-163694951,
KCNJ5	NM_000890	chr11	128761617-128781157,128782106-128786302,
KCNK13	NM_022054	chr14	90528884-90650453,
KCNK5	NM_003740	chr6	39159532-39161943,39162114-39162368,39162537-39163650,39163764-39196700,
KCNMB2	NM_005832	chr3	178276773-178512928,178513007-178525129,178525254-178543374,178543547-178545964,178546162-178560439,
KCNMB2	NM_181361	chr3	178254500-178525129,178525254-178543374,178543547-178545964,178546162-178560439,
KCNMB3	NM_171830	chr3	178961073-178962281,178962482-178968529,
KCNMB3	NM_014407	chr3	178961073-178962281,178962482-178968529,178968723-178968822,
KCNMB3	NM_171829	chr3	178961073-178962281,178962482-178968529,178968723-178976734,
KCNMB3	NM_171828	chr3	178961073-178962281,178962482-178968529,178968723-178984435,
KCNMB3	NM_001163677	chr3	178957853-178962281,178962482-178968529,178968723-178984435,
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KDELR2	NM_001100603	chr7	6502807-6509225,6509386-6513813,6513916-6523596,
KDELR2	NM_006854	chr7	6502807-6505700,6505955-6509225,6509386-6513813,6513916-6523596,
KDM4B	NM_015015	chr19	4969242-5016266,5016351-5032875,5033043-5039845,5040023-5041146,5041263-5047485,5047681-5071019,5071071-5077376,5077482-5082376,5082516-5110631,5110830-5119662,5119864-5131085,5131557-5131896,5132019-5133892,5134073-5135348,5135573-5137271,5137350-5137630,5137688-5137971,5138082-5143976,5144164-5144257,5144424-5144792,5144914-5150367,5150462-5151344,
KDM4D	NM_018039	chr11	94707233-94708816,94708913-94730186,
KIAA0174	NM_014761	chr16	71929493-71949527,71949632-71950363,71950546-71950948,71951038-71954640,71954726-71955244,71955357-71956375,71956584-71957189,71957284-71958674,71958721-71961515,
KIAA0182	NM_001134473	chr16	85645138-85682156,85682358-85687882,85688057-85688398,85688598-85689330,85689524-85689947,85690272-85690881,85691211-85694750,85695372-85696585,85696700-85696948,85697221-85698619,85698735-85699580,85699954-85701744,85702031-85704599,85704705-85706009,
KIAA0182	NM_014615	chr16	85647005-85667518,85667739-85682156,85682358-85687882,85688057-85688398,85688598-85689330,85689524-85689947,85690272-85690881,85691211-85694750,85695372-85696585,85696700-85696948,85697221-85698619,85698735-85699580,85699954-85701744,85702031-85704599,85704705-85706009,
KIAA0226	NM_014687	chr3	197402068-197402291,197402387-197403754,197403910-197404349,197404413-197407998,197408239-197408704,197408771-197409339,197409487-197410176,197410311-197411026,197411089-197420584,197420688-197421244,197421457-197422735,197422853-197423823,197423921-197427482,197428018-197428577,197428736-197430417,197430526-197431411,197431573-197431961,197432047-197444846,197445002-197463524,

KIAA0226	NM_001145642	chr3	197402068-197402291,197402387-197403754,197403910-197404349,197404413-197407998,197408239-197408704,197408771-197409339,197409487-197410176,197410311-197411026,197411089-197420584,197420688-197421244,197421457-197422735,197422853-197423823,197423921-197426056,197426103-197427482,197428018-197428577,197428736-197430417,197430526-197431411,197431573-197431961,197432047-197444846,197445002-197476138,
KIAA0528	NM_014802	chr12	22602826-22606828,22606977-22609903,22610096-22622641,22622730-22623756,22623846-22624331,22624423-22624899,22625000-22625218,22625282-22625676,22625742-22627683,22627826-22631245,22631412-22635489,22635678-22637629,22637823-22643055,22643153-22646155,22646272-22659643,22659754-22666226,22666314-22670918,22671072-22676358,22676559-22677404,22677562-22678542,22678640-22680653,22680827-22688190,22688279-22696993,22697114-22697252,
KIAA0649	NM_014811	chr9	138371869-138374527,138374662-138375794,138375929-138376293,
KIAA0753	NM_014804	chr17	6483185-6493097,6493324-6493828,6493951-6498290,6498374-6499476,6499664-6502555,6502641-6503698,6503779-6510191,6510283-6510499,6510591-6511666,6511785-6513312,6513481-6515237,6515469-6524106,6524319-6526200,6526418-6526827,6526892-6528073,6528182-6531435,6532062-6538329,6538492-6543955,
KIAA1024	NM_015206	chr15	79724883-79748438,79750788-79755407,79755664-79760527,
KIAA1274	NM_014431	chr10	72238816-72285677,72285893-72288983,72289088-72289643,72289825-72291044,72291211-72292375,72292538-72292749,72292827-72293676,72293830-72294179,72294281-72294493,72294600-72297565,72297663-72298034,72298165-72298646,72298765-72298846,72299004-72299334,72299519-72300856,72300999-72301217,72301291-72307060,72307203-72324118,72324276-72326335,
KIAA1324	NM_020775	chr1	109656959-109704514,109704637-109707119,109707314-109714486,109714636-109715108,109715191-109716094,109716202-109716308,109716460-109727665,109727756-109730797,109730977-109731686,109731817-109732212,109732305-109733986,109734094-109734346,109734486-109735231,109735497-109737041,109737217-109740094,109740277-109740599,109740698-109741193,109741297-109742474,109742603-109742679,109742860-109743355,109743523-109745564,
KIAA1524	NM_020890	chr3	108270167-108271079,108271221-108272493,108272578-108273221,108273337-108276063,108276262-108278602,108278715-108278799,108278876-108279494,108279689-108281971,108282092-108284200,108284302-108285342,108285486-108287000,108287162-108288234,108288455-108295116,108295194-108298126,108298274-108298411,108298536-108300260,108300359-108300953,108301050-108301822,108301931-108303910,108304060-108308119,
KIAA1609	NM_020947	chr16	84513633-84514133,84514315-84516196,84516317-84520235,84520666-84522882,84523029-84529287,84529520-84531538,84531718-84538205,
KIAA1644	NM_001099294	chr22	44645566-44681306,44681626-44692550,44692766-44696757,44696858-44708629,
KIAA1737	NM_033426	chr14	77564705-77571998,77572188-77576153,77576325-77579766,
KIF13B	NM_015254	chr8	28928284-28929135,28929834-28932796,28932861-28950260,28950396-28956648,28956759-28965654,28965710-28966949,28967029-28967433,28967588-28970978,28971073-28974346,28974525-28976383,28976510-28980106,28980164-28980881,28981010-28981539,28981641-28983997,28984029-28984637,28984786-28988048,28988183-28989823,28989983-28991555,28991728-28997578,28997709-28997983,28998135-28999672,28999821-29003893,29004058-29004907,29005120-29006092,29006285-29007812,29007901-29013241,29013374-29018248,29018385-29023177,29023290-29024888,29025103-29033583,29033697-29034981,29035096-29037619,29037756-29039434,29039524-29043807,29043990-29046030,29046125-29048512,29048575-29053702,29053717-29102861,29102957-29120495,
KIF14	NM_014875	chr1	200522896-200523594,200523735-200524506,200524583-200528456,200528581-200529848,200530009-200534195,200534382-200534571,200534798-200539037,200539134-200544717,200544820-200549380,200549512-200550327,200550423-200555227,200555356-200558343,200558498-200559251,200559401-200561206,200561369-200562793,200562898-200567363,200567550-200569176,200569242-200569482,200569632-200571022,200571197-200572352,200572470-200572965,200573084-200574409,200574519-200574990,200575023-200575872,200575927-200577956,200578057-200583444,200583534-200584481,200584738-200586738,200587967-200589537,
KIF15	NM_020242	chr3	44803377-44815885,44815930-44816744,44816930-44819605,44819684-44822375,44822415-44826335,44826435-44827885,44828067-44835707,44835919-44839041,44839169-44839324,44839449-44841804,44841930-44842940,44843019-44843255,44843467-44844304,44844484-44846517,44846661-44847335,44847479-44852336,44852536-44853672,44853782-44854565,44854673-44856401,44856569-44867529,44867682-44867865,44867953-44868949,44869021-44869704,44869793-44871461,44871568-44872386,44872511-44879765,44879914-44881845,44881949-44882564,44882731-44884615,44884727-44889475,44889550-44890011,44890051-44893277,44893445-44893698,44893832-44894163,

KIF18A	NM_031217	chr11	28042830-28045286,28045398-28056932,28057042-28057762,28058212-28080471,28080709-28083940,28084064-28090804,28090971-28098552,28098717-28104401,28104516-28104714,28104791-28106177,28106356-28110069,28110269-28112162,28112275-28112954,28113061-28116188,28116348-28119168,28119541-28129609,
KIF1B	NM_183416	chr1	10270937-10292306,10292493-10316303,10316382-10318549,10318731-10321961,10322029-10327436,10327617-10328208,10328322-10331558,10331638-10332297,10332365-10335484,10335562-10336377,10336458-10338042,10338187-10342456,10342592-10351138,10351220-10352103,10352181-10355142,10355224-10355716,10355825-10356638,10356724-10356953,10357136-10357230,10357305-10363219,
KIF1B	NM_015074	chr1	10270937-10292306,10292493-10316303,10316382-10318549,10318731-10321961,10322029-10327436,10327617-10328208,10328322-10331558,10331638-10332297,10332365-10335484,10335562-10336377,10336458-10338042,10338187-10342456,10342592-10351138,10351220-10352103,10352181-10355142,10355224-10355716,10355825-10356638,10356724-10356953,10357136-10357230,10357305-10380099,10380195-10381765,10381916-10383940,10384121-10384814,10384954-10386167,10386418-10394576,10394697-10396713,10396801-10397130,10397262-10397427,10397592-10399825,10399918-10402106,10402227-10403288,10403346-10405901,10406012-10407817,10407886-10408705,10408792-10412687,10412795-10420985,10421102-10421748,10421884-10423339,10423403-10425156,10425304-10425465,10425707-10428523,10428597-10431197,10431321-10434372,10434524-10434910,10435105-10435311,10435432-10436601,
KIF1C	NM_006612	chr17	4901452-4903143,4903266-4903513,4903648-4904065,4904144-4904515,4904697-4905352,4905420-4905757,4905938-4906024,4906138-4906905,4906985-4907144,4907212-4907291,4907369-4907860,4907941-4908148,4908296-4910208,4910380-4910556,4910638-4910760,4910838-4916946,4917028-4918036,4918133-4923289,4923375-4923785,4923974-4924099,4924174-4925385,4926005-4926761,
KIF20B	NM_016195	chr10	91461438-91465049,91465199-91468922,91469011-91469100,91469219-91469682,91469823-91470716,91470903-91473802,91473841-91474710,91474940-91476191,91476305-91477179,91477253-91477331,91477480-91478465,91478630-91479174,91479464-91483719,91483861-91484775,91484916-91486168,91486279-91487611,91487654-91488883,91489005-91492658,91492814-91497142,91498375-91498713,91498854-91503563,91503685-91505654,91505717-91511101,91511229-91512322,91512449-91514273,91514431-91518461,91518640-91520281,91520394-91522393,91522593-91528045,91528149-91528493,91528646-91532444,91532589-91533726,
KIF23	NM_138555	chr15	69706816-69708331,69708403-69709720,69709851-69713984,69714092-69714329,69714468-69714663,69714775-69715496,69715669-69718407,69718522-69718673,69718797-69721448,69721553-69727820,69727902-69727989,69728111-69728475,69728601-69728901,69729062-69730585,69730745-69732241,69732417-69732645,69732827-69733105,69733419-69737127,69737381-69738346,69738431-69738620,69738704-69739208,69739281-69740129,
KIF23	NM_004856	chr15	69706816-69708331,69708403-69709720,69709851-69713984,69714092-69714329,69714468-69714663,69714775-69715496,69715669-69718407,69718522-69718673,69718797-69721448,69721553-69727820,69727902-69727989,69728111-69728475,69728601-69728901,69729062-69730585,69730745-69732241,69732417-69732645,69732827-69733105,69733419-69737127,69737381-69738346,69738431-69738620,69738704-69739208,69739281-69740129,
KIF2C	NM_006845	chr1	45205675-45206583,45206680-45213054,45213158-45213322,45213373-45216112,45216237-45218802,45218927-45219403,45219506-45220420,45220518-45221599,45221656-45221745,45221910-45223226,45223319-45223578,45223644-45223719,45223813-45224876,45225021-45225950,45226157-45226262,45226375-45227586,45227656-45228016,45228124-45228215,45228331-45232496,45232622-45232767,
KIF4A	NM_012310	chrX	69510001-69510286,69510429-69510539,69510656-69516846,69517039-69518961,69519053-69521748,69521917-69522152,69522249-69549253,69549372-69550005,69550183-69553476,69553540-69561647,69561782-69563551,69563612-69563725,69563833-69572448,69572507-69573470,69573658-69593999,69594105-69595052,69595199-69595948,69596061-69606466,69606552-69607032,69607148-69615519,69615677-69615797,69615900-69622414,69622546-69623712,69623885-69624563,69624673-69625676,69625756-69626107,69626205-69626741,69626926-69637736,69637855-69639509,69639634-69639910,
KNR3DL1	NM_013289	chr19	55327990-55328987,55329025-55329768,55330055-55331166,55331468-55333018,55333314-55336481,55336534-55340814,55340921-55341381,55341436-55341552,
KITLG	NM_003994	chr12	88890959-88898934,88899013-88900086,88900156-88900803,88900915-88910109,88910268-88912472,88912645-88926216,88926281-88939527,88939643-88974039,
KITLG	NM_000899	chr12	88890959-88898934,88899013-88900086,88900156-88900803,88900915-88909309,88909395-88910109,88910268-88912472,88912645-88926216,88926281-88939527,88939643-88974039,
KLF3	NM_016531	chr4	38666083-38682206,38682304-38690204,38690693-38691348,38691501-38696365,38696528-38698701,

KLHDC1	NM_172193	chr14	50160009-50175875,50175948-50176425,50176545-50176979,50177100-50190590,50190671-50192402,50192488-50195642,50195728-50196206,50196267-50199420,50199535-50201305,50201380-50206814,50206901-50210469,50210524-50218302,
KLHL23	NM_144711	chr2	170590598-170591521,170592738-170597893,170598048-170605930,
KLHL23	NM_001199290	chr2	170551133-170551723,170551758-170553869,170554042-170591521,170592738-170597893,170598048-170605930,
KLHL28	NM_017658	chr14	45398395-45400534,45400745-45403316,45403762-45414231,45415132-45431047,
KLHL5	NM_015990	chr4	39064656-39077583,39077768-39082721,39082860-39083581,39083780-39088133,39088348-39098310,39098499-39104905,39105132-39109187,39109352-39114638,39114853-39116777,39116951-39122628,
KLHL5	NM_199039	chr4	39064656-39082721,39082860-39083581,39083780-39088133,39088348-39098310,39098499-39104905,39105132-39109187,39109352-39114638,39114853-39116777,39116951-39122628,
KLHL5	NM_001007075	chr4	39046717-39064177,39064656-39077583,39077768-39082721,39082860-39083581,39083780-39088133,39088348-39098310,39098499-39104905,39105132-39109187,39109352-39114638,39114853-39116777,39116951-39122628,
KLHL5	NM_001171654	chr4	39046717-39077583,39077768-39082721,39082860-39083581,39083780-39088133,39088348-39098310,39098499-39104905,39105132-39109187,39109352-39114638,39114853-39116777,39116951-39122628,
KMO	NM_003679	chr1	241695799-241712127,241712199-241712975,241713075-241714253,241714345-241718910,241718961-241723963,241724053-241725465,241725633-241728285,241728359-241729789,241729913-241731798,241731948-241749979,241750039-241752048,241752133-241753312,241753416-241753504,241753566-241755253,
KPNA2	NM_002266	chr17	66031957-66033224,66033324-66033472,66033612-66036792,66036883-66038199,66038470-66039019,66039116-66039214,66039480-66039952,66040188-66040435,66040620-66041886,66042038-66042618,
KRCC1	NM_016618	chr2	88328105-88333651,88333812-88336460,88336571-88355143,
KRT16	NM_005557	chr17	39766282-39766440,39766489-39766581,39766804-39767104,39767232-39767319,39767483-39767595,39767754-39767889,39767974-39768408,
KRT27	NM_181537	chr17	38933391-38933503,38933555-38933765,38933985-38935752,38935880-38935950,38936114-38936550,38936709-38937438,38937523-38938300,
KRT4	NM_002272	chr12	53201035-53201141,53201178-53201426,53201649-53202076,53202204-53202468,53202635-53203165,53203263-53204538,53204601-53205545,53205762-53207379,
KRT6C	NM_173086	chr12	52863082-52863193,52863230-52863452,52863675-52864287,52864415-52864914,52865081-52865203,52865301-52865454,52865517-52865848,52866065-52866980,
KRT81	NM_002281	chr12	52680278-52680573,52680607-52680884,52681107-52681378,52681506-52681766,52681933-52682143,52682241-52682997,52683060-52683860,52684071-52684879,
KRT84	NM_033045	chr12	52772165-52773658,52773692-52774145,52774368-52774862,52774990-52775143,52775310-52776219,52776317-52776787,52776850-52777372,52777583-52778822,
KRTCAP2	NM_173852	chr1	155142037-155142265,155142334-155145039,155145105-155145212,155145369-155145695,
KYNU	NM_001199241	chr2	143635306-143638912,143639000-143642916,143643106-143676176,143676299-143685226,143685311-143712377,143712441-143713770,143713844-143715208,143715285-143718191,143718340-143742651,143742752-143743515,143743591-143787194,143787249-143790803,143790891-143797995,143798228-143799614,
KYNU	NM_003937	chr2	143635306-143642916,143643106-143676176,143676299-143685226,143685311-143712377,143712441-143713770,143713844-143715208,143715285-143718191,143718340-143742651,143742752-143743515,143743591-143787194,143787249-143790803,143790891-143797995,143798228-143799614,
KYNU	NM_001032998	chr2	143635306-143642916,143643106-143676176,143676299-143685226,143685311-143712377,143712441-143713770,143713844-143715208,143715285-143718191,143718340-143742651,143742752-143743515,143743591-143746412,143746474-143746909,
LACTB	NM_032857	chr15	63414428-63414833,63414902-63419056,63419249-63419550,63419889-63421682,63421850-63433477,
LACTB	NM_171846	chr15	63414428-63414833,63414902-63419056,63419249-63419550,63419889-63421682,
LAG3	NM_002286	chr12	6882077-6882356,6882506-6882861,6883168-6883759,6884031-6884437,6884715-6886428,6886673-6886955,6887088-6887408,
LALBA	NM_002289	chr12	48961801-48962298,48962376-48962863,48963024-48963669,
LANCL1	NM_001136574	chr2	211299288-211300109,211300184-211300938,211301117-211302412,211302597-211305320,211305469-211306030,211306168-211319829,211320039-211336681,211336801-211341038,211341137-211341369,

LANCL1	NM_001136575	chr2	211299288-211300109,211300184-211300938,211301117-211302412,211302597-211305320,211305469-211306030,211306168-211319829,211320039-211336681,211336801-211341038,211341137-211341444,
LANCL1	NM_006055	chr2	211299288-211300109,211300184-211300938,211301117-211302412,211302597-211305320,211305469-211306030,211306168-211319829,211320039-211336681,211336801-211341038,211341137-211341342,
LCE1C	NM_178351	chr1	152777975-152779075,
LCE3E	NM_178435	chr1	152538706-152539212,
LCN2	NM_005564	chr9	130911943-130912515,130912654-130913915,130913997-130914183,130914305-130914460,130914564-130915377,130915406-130915588,
LDLR	NM_000527	chr19	11200292-11210897,11211022-11213338,11213463-11215894,11216277-11217239,11217364-11218066,11218191-11221326,11221448-11222188,11222316-11223952,11224126-11224209,11224439-11226768,11226889-11227533,11227675-11230766,11230910-11231044,11231199-11233848,11234021-11238682,11238762-11240187,11240347-11241955,
LDLR	NM_001195802	chr19	11200292-11210897,11210924-11216036,11216277-11217239,11217364-11218066,11218191-11221326,11221448-11222188,11222316-11223952,11224126-11224209,11224439-11226768,11226889-11227533,11227675-11230766,11230910-11231044,11231199-11233848,11234021-11238682,11238762-11240187,11240347-11241955,
LDLR	NM_001195800	chr19	11200292-11210897,11211022-11213338,11213463-11218066,11218191-11221326,11221448-11222188,11222316-11223952,11224126-11224209,11224439-11226768,11226889-11227533,11227675-11230766,11230910-11231044,11231199-11233848,11234021-11238682,11238762-11240187,11240347-11241955,
LDLR	NM_001195799	chr19	11200292-11210897,11211022-11215894,11216277-11217239,11217364-11218066,11218191-11221326,11221448-11222188,11222316-11223952,11224126-11224209,11224439-11226768,11226889-11227533,11227675-11230766,11230910-11231044,11231199-11233848,11234021-11238682,11238762-11240187,11240347-11241955,
LDLR	NM_001195798	chr19	11200292-11210897,11211022-11213338,11213463-11215894,11216277-11217239,11217364-11218066,11218191-11221326,11221448-11222188,11222316-11223952,11224126-11224209,11224439-11226768,11226889-11227533,11227675-11230766,11230910-11231044,11231199-11233848,11234021-11238682,11238762-11240187,11240347-11241961,
LDLR	NM_001195803	chr19	11200292-11210897,11211022-11213338,11213463-11217239,11217364-11218066,11218191-11221326,11221448-11222188,11222316-11223952,11224126-11224209,11224439-11226768,11226889-11227533,11227675-11230766,11230910-11233848,11234021-11238682,11238762-11240187,11240347-11241955,
LDLRAD3	NM_174902	chr11	35965695-36057651,36057800-36103201,36103329-36119875,36120012-36248633,36248981-36250708,
LEKR1	NM_001193283	chr3	156544899-156547073,156547167-156570555,156570772-156638362,156638484-156642282,
LEKR1	NM_001004316	chr3	156544166-156547073,156547167-156570555,156570772-156638362,156638484-156645216,156645394-156660316,156660504-156696981,156697065-156710440,156710520-156710861,156711067-156729200,156729296-156742547,156742714-156745890,156746192-156763127,
LGMN	NM_001008530	chr14	93170707-93170983,93171053-93172826,93172999-93176015,93176218-93178002,93178094-93178180,93178301-93179148,93179217-93180166,93180231-93180719,93180797-93182479,93182567-93183723,93183807-93185090,93185190-93198992,93199161-93207405,93207525-93214832,
LGMN	NM_005606	chr14	93170707-93170983,93171053-93172826,93172999-93176015,93176218-93178002,93178094-93178180,93178301-93179148,93179217-93180166,93180231-93180719,93180797-93182479,93182567-93183723,93183807-93185090,93185190-93198992,93199161-93214832,
LGSN	NM_001143940	chr6	63990506-63990925,63991126-63995490,63995659-64004816,64004951-64029817,
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LHX1	NM_005568	chr17	35295665-35297585,35297814-35297905,35298185-35299495,35299663-35300047,
LILRA2	NM_001130917	chr19	55085380-55085541,55085579-55085766,55086050-55086196,55086501-55086721,55087020-55087272,55087577-55098475,55098528-55098666,
LILRA2	NM_006866	chr19	55085380-55085541,55085579-55085766,55086050-55086196,55086501-55086721,55087020-55087272,55087577-55098666,
LIMA1	NM_001113546	chr12	50571853-50575685,50575821-50586233,50586348-50589611,50589671-50594558,50594668-50598333,50598484-50599765,50599852-50615802,50616269-50625446,50625494-50642414,50642558-50677201,
LIMA1	NM_016357	chr12	50571853-50575685,50575821-50586233,50586345-50589611,50589671-50594558,50594668-50598333,50598484-50599765,50599852-50615802,50616269-50625446,50625494-50642414,50642558-50677201,

LIMA1	NM_001113547	chr12	50571853-50575685,50575821-50586233,50586348-50589611,50589671-50594558,50594668-50598333,50598484-50599765,50599852-50615802,
LIN28A	NM_024674	chr1	26737414-26737875,26738074-26751792,26751979-26752731,
LIN9	NM_173083	chr1	226420308-226420795,226420895-226421043,226421225-226426670,226426798-226438538,226438621-226453232,226453336-226453912,226454034-226455656,226455792-226465474,226465634-226474032,226474160-226475363,226475499-226483541,226483648-226485418,226485515-226488872,226488907-226496808,
LIN9O1	NM_032808	chr15	77908243-77924650,
LIX1	NM_153234	chr5	96430740-96432512,96432592-96440892,96440990-96443062,96443205-96460168,96460334-96478197,
LMAN1L	NM_021819	chr15	75105371-75108496,75108653-75108766,75108876-75108971,75109032-75111057,75111159-75111491,75111614-75112383,75112441-75112974,75113109-75113414,75113568-75114168,75114242-75114981,75115051-75115898,75116024-75116690,75116820-75117815,
LMAN2L	NR_024520	chr2	97373136-97373449,97373571-97377391,97377508-97377599,97377763-97399254,97399339-97400144,97400264-97405589,
LMAN2L	NR_024521	chr2	97373136-97373449,97373571-97377391,97377508-97377599,97377763-97400144,97400264-97405589,
LMAN2L	NM_030805	chr2	97373136-97373449,97373571-97377391,97377508-97377599,97377763-97399254,97399339-97400144,97400264-97403684,97403805-97405589,
LMAN2L	NR_024519	chr2	97373136-97373449,97373571-97377391,97377508-97377599,97377763-97378842,97378877-97399254,97399339-97400144,97400264-97405589,
LMAN2L	NR_024518	chr2	97373136-97373449,97373571-97377391,97377508-97377599,97377763-97378842,97378877-97400144,97400264-97403684,97403805-97405589,
LMAN2L	NM_001142292	chr2	97373136-97373449,97373571-97377391,97377508-97377599,97377763-97378842,97378877-97399254,97399339-97400144,97400264-97403684,97403805-97405589,
LMO2	NM_001142316	chr11	33881122-33886146,33886364-33890890,
LMO2	NM_001142315	chr11	33881122-33886146,33886364-33890890,33891133-33891369,
LMO2	NM_005574	chr11	33881122-33886146,33886364-33890890,33891133-33891254,33891534-33903368,33903434-33913340,
LOC100128788	NR_027275	chr16	2787290-2787479,2787612-2788441,2788502-2793551,2793721-2799544,2799661-2802441,
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LOC100128881	NR_036480	chr16	89778631-89779095,89779227-89782877,89783313-89783750,
LOC100128977	NR_024559	chr17	43921528-43972844,
LOC100129046	NR_034091	chr1	94058066-94059928,94060007-94064472,94064548-94064716,
LOC100129518	NR_037166	chr6	160182669-160183024,
LOC100129636	NM_001195202	chr6	29004123-29007989,29008126-29012020,29012129-29031705,29031907-29032896,29032950-29044071,
LOC100129931	NR_033828	chr4	7035781-7036896,7037002-7046705,7046830-7047384,
LOC100130015	NR_027336	chr16	90110398-90110908,90111032-90113363,90113505-90114149,
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LOC100130581	NR_027413	chr17	41455182-41456489,41456631-41458639,41459029-41465655,
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LOC100130950	NR_034082	chr17	5095459-5113043,5113191-5117343,5117505-5118440,5118589-5126610,5126780-5137117,5137238-5137886,5138107-5138241,
LOC100131366	NR_033938	chr14	103654608-103654712,103654785-103654927,
LOC100132707	NR_024477	chr7	154720478-154720664,154720735-154735735,154736331-154738068,154738204-154738348,
LOC100132707	NR_024476	chr7	154720478-154720664,154720735-154735735,154736331-154738068,154738204-154738301,154738502-154739401,154739484-154739606,154739801-154741006,
LOC100188947	NR_024467	chr10	93067193-93110512,93110637-93284783,93284907-93299140,93299336-93371106,
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LOC100271722	NR_027036	chr22	46436933-46438452,46438521-46439441,46439580-46440487,
LOC100288730	NR_029383	chr13	28712543-28712682,
LOC100288842	NR_027442	chr9	123556201-123560851,
LOC100289187	NM_001195543	chr7	99195996-99197826,99197909-99202007,99202220-99204369,99204518-99205294,99205434-99208014,

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LOC100302640	NR_028303	chr3	106828852-106830905,106830994-106848733,106848840-106959288,
LOC100379224	NR_033341	chr19	44612491-44616973,
LOC144776	NR_027039	chr13	91544696-91545639,91545795-91553473,91553493-91555646,91555765-91563583,91563709-91578733,
LOC146880	NR_027487	chr17	62776324-62776459,62777158-62777511,
LOC146880	NR_026899	chr17	62746127-62746710,62746842-62747923,62748075-62750121,62750283-62750537,62750773-62754358,62754498-62754645,62754745-62758032,62758166-62758471,62758829-62760567,62760667-62776459,62777158-62777550,62777799-62778041,
LOC154860	NR_036484	chr7	121944323-121944625,121944798-121945340,121946317-121946568,121946715-121947355,121947543-121948539,121948612-121949636,
LOC283033	NR_033846	chr10	44404818-44404989,44405108-44438641,44438730-44439303,44439482-44441440,44441599-44460829,44461038-44462081,44462163-44465264,
LOC283038	NR_033848	chr10	127371901-127374844,127375017-127387691,127387757-127395149,127395253-127395522,
LOC283761	NR_027076	chr15	90048839-90053302,90053355-90066810,
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LOC284276	NR_015417	chr18	74240921-74242339,74242422-74269930,
LOC285629	NR_027111	chr5	160360815-160362995,160363117-160365459,
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LOC338799	NR_002809	chr12	122233633-122234095,122234149-122237751,122237863-122239476,122239515-122239611,122239715-122240535,122240691-122240783,
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LOC400043	NR_026656	chr12	54520397-54525772,
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LOC400657	NR_024484	chr18	72261076-72263662,
LOC401242	NR_033379	chr6	28829793-28831059,
LOC401431	NR_027040	chr7	149566948-149567329,149567441-149568729,149568886-149570311,
LOC440335	NR_029453	chr16	4838773-4844951,4845078-4845714,4845860-4845947,4846035-4846189,
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LOC494141	NR_026541	chr11	18230741-18231031,
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LOC57653	NR_036529	chr9	100000850-100008376,100008469-100013072,100013126-100013821,100013840-100038849,100038980-100039836,100039909-100041642,100041756-100043796,100043952-100049940,100050018-100052864,100052948-100053134,100053185-100053651,100053770-100070016,100070089-100070263,100070415-100071694,100071887-100074393,100074484-100075516,100075628-100076898,100077011-100077131,100077229-100079345,100079511-100080743,100080865-100082406,100082488-100085113,100085204-100086061,100086186-100087299,100087475-100088834,100088952-100090300,100090429-100092434,100092476-100092602,100093050-100105620,100105846-100116849,100116996-100117172,100117291-100119907,100120008-100122262,100122384-100124006,100124181-100124476,100124534-100124643,100124724-100127953,100128022-100128839,100128983-100132202,100132365-100132921,100133061-100133875,100133989-100136823,100136931-100137734,100137872-100139043,
LOC57653	NR_036528	chr9	100000850-100008376,100008469-100013072,100013126-100013821,100013840-100038849,100038980-100039836,100039909-100041642,100041756-100043796,100043952-100049940,100050018-100052864,100052948-100053134,100053185-100053651,100053770-100056227,100056393-100057125,100057274-100070016,100070089-100070263,100070415-100071694,100071887-100074393,100074484-100075516,100075628-100076673,100076804-100076898,100077011-100077131,100077229-100079345,100079511-100080743,100080865-100082406,100082488-100085113,100085204-100086061,100086186-100087299,100087475-100088834,100088952-100090300,100090429-100092434,100092476-100092602,100093050-100105620,100105846-100109594,100109772-100111391,100111574-100112689,100112838-100116849,100116996-100117172,100117291-100119907,100120008-100122262,100122384-100124006,100124181-100124476,100124724-100126331,100126411-100127953,100128022-100128839,100128983-100132202,100132365-100132921,100133061-100133875,100133989-100136823,100136931-100137734,100137872-100139043,
LOC595101	NR_002453	chr16	30278966-30279786,30279812-30280316,30280405-30281375,30281487-30284348,30284552-30284698,30284843-30287332,30287489-30288583,30288708-30288916,30289115-30289500,30289702-30290252,30290395-30291012,30291293-30291762,30291788-30292628,30292747-30292894,30293027-30296388,30296779-30297486,30297590-30299880,30300107-30302522,30302697-30304418,30304518-30305434,30305509-30305885,30306013-30309696,30309912-30311188,30311249-30312541,30312680-30316374,30316532-30317109,30317275-30346294,
LOC642345	NR_033829	chr13	88097386-88099349,88099489-88113177,88113225-88125693,88125809-88163619,88163726-88323089,
LOC643037	NM_001190462	chr11	94245840-94250747,94250854-94261248,94261376-94265060,
LOC728606	NR_024259	chr18	24269936-24283354,
LOC729375	NR_024252	chr3	129818202-129821605,129821757-129823007,129823141-129824371,129824475-129830120,
LOC729668	NR_003524	chr10	30653549-30653633,30653997-30654076,30654181-30654272,30654498-30658002,30658063-30658254,30658355-30658460,30658549-30662587,30662783-30663230,
LOC730441	NR_036483	chr7	141969705-141970965,141971121-141971770,
LOC91316	NR_024448	chr22	23981130-24002050,24002188-24025910,24026055-24032421,24032544-24036304,24037705-24042911,24043033-24047614,24047729-24051315,24051429-24051971,24052055-24056372,24056530-24057194,24057382-24059216,
LOX	NM_002317	chr5	121402445-121405746,121405864-121406187,121406285-121409706,121409865-121411097,121411237-121412586,121412697-121413048,
LOX	NM_001178102	chr5	121402445-121405746,121405864-121406187,121406285-121409706,121409865-121411097,121411237-121412586,
LOXL1	NM_005576	chr15	74220227-74235193,74235304-74238756,74238896-74239406,74239565-74240146,74240244-74241798,74241916-74244170,
LOXL3	NM_032603	chr2	74760807-74761007,74761121-74761225,74761364-74761441,74761559-74761656,74761902-74762417,74762582-74762713,74762883-74763121,74763278-74763416,74763599-74763834,74764056-74776494,74776711-74777310,74777476-74779447,74779774-74781001,
LPPR2	NM_022737	chr19	11466249-11467476,11467653-11468334,11468416-11470206,11470397-11470495,11470633-11471891,11472165-11473187,11473366-11474387,11474496-11474835,11474889-11475021,
LPPR2	NM_001170635	chr19	11466249-11467476,11467653-11468334,11468416-11470281,11470397-11470495,11470633-11471891,11472165-11473187,11473366-11474387,11474512-11474835,11474889-11475021,

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LRGUK	NM_144648	chr7	133812418-133821774,133821884-133824187,133824271-133827813,133827916-133832989,133833073-133842786,133842913-133848147,133848293-133859306,133859389-133861727,133861816-133863253,133863362-133868484,133868606-133876405,133876504-133881742,133881858-133883970,133884174-133886231,133886329-133906529,133906671-133932306,133932397-133933701,133933829-133943007,133943158-133948595,
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LRIT2	NM_001017924	chr10	85982437-85984087,85984871-85985165,
LRP11	NM_032832	chr6	150141840-150147398,150147496-150157219,150157434-150158472,150158600-150164117,150164261-150174137,150174297-150184542,
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LRPAP1	NM_002337	chr4	3514764-3516477,3516656-3517841,3517926-3519759,3519920-3520596,3520719-3521797,3521921-3526632,3526779-3533934,
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LRRC23	NM_006992	chr12	7014068-7014747,7014924-7015007,7015119-7015571,7015827-7016477,7016610-7019052,7019191-7023053,
LRRC23	NM_201650	chr12	7014068-7014747,7014924-7015007,7015119-7015571,7015827-7016477,7016610-7019052,7019191-7021892,7022192-7023053,
LRRC23	NM_001135217	chr12	7014240-7014747,7014924-7015007,7015119-7015571,7015827-7016477,7016610-7019052,7019191-7021892,7022192-7023053,
LRRC28	NM_144598	chr15	99791747-99796101,99796331-99816779,99816822-99827460,99827500-99828017,99828157-99874126,99874335-99892572,99892677-99901539,99901717-99903309,99903471-99926233,
LRRC42	NM_052940	chr1	54412223-54417657,54418146-54423820,54423954-54426027,54426148-54427705,54427796-54427967,54428083-54431967,54432054-54433336,
LRRC48	NM_031294	chr17	17876289-17877164,17877277-17880894,17881073-17887140,17887259-17891244,17891413-17896077,17896226-17897611,17897733-17898311,17898426-17900772,17900949-17907675,17907809-17909495,17909568-17910336,17910462-17919376,17919510-17919870,
LRRC48	NM_001130092	chr17	17876289-17877164,17877277-17880894,17881073-17887140,17887259-17891244,17891413-17896077,17896226-17897611,17897733-17898311,17898426-17900772,17900949-17907675,17907809-17909495,17909568-17910336,17910462-17910710,
LRRC48	NM_001130091	chr17	17876289-17876977,17877068-17877164,17877277-17880894,17881073-17887140,17887259-17891244,17891413-17896077,17896226-17897611,17897733-17898311,17898426-17900772,17900949-17907675,17907809-17909495,17909568-17910336,17910462-17910710,
LRRC48	NM_001130090	chr17	17876289-17876977,17877068-17877164,17877277-17880894,17881073-17887140,17887259-17891244,17891413-17896077,17896226-17897611,17897733-17898311,17898426-17900772,17900949-17907675,17907809-17909495,17909568-17910336,17910462-17919376,17919510-17919870,
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LRRC49	NM_001199017	chr15	71185282-71185921,71185995-71188186,71188276-71193259,71193364-71196889,71197095-71203869,71203938-71211387,71211533-71229098,71229162-71256122,71256272-71272438,71272524-71276431,71276597-71300716,71300956-71302144,71302332-71305141,71305253-71329516,71329672-71341746,
LRRC49	NM_001199018	chr15	71185282-71185921,71185980-71188186,71188276-71190704,71190795-71193259,71193364-71196889,71197095-71203869,71203938-71211387,71211533-71229098,71229162-71256122,71256272-71272438,71272524-71276431,71276597-71300716,71300956-71302144,71302332-71305141,71305253-71329516,71329672-71341746,
LRRC4C	NM_020929	chr11	40137885-40313741,
LRRC50	NM_178452	chr16	84179170-84182610,84182748-84183854,84183948-84188180,84188404-84189186,84189355-84193278,84193402-84199387,84199556-84203463,84203963-84205864,84205982-84208273,84208329-84209537,84209906-84211333,
LRRC56	NM_198075	chr11	537606-538596,538861-539578,539727-540672,540862-541535,541625-544718,544781-549900,549999-550070,550273-551129,551303-551649,551828-551901,551968-552088,552233-552567,552703-553961,
LRRC69	NM_001129890	chr8	92115073-92136719,92136848-92139314,92139389-92145336,92145534-92147894,92147968-92201748,92201852-92212839,92213021-92231116,
LRRC8A	NM_001127245	chr9	131644530-131669434,131671601-131678373,
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LRRC8A	NM_001127244	chr9	131645189-131648292,131648401-131669434,131671601-131678373,
LRTOMT	NM_001145307	chr11	71791932-71799341,71799427-71800073,71800212-71804540,71804748-71805992,71806143-71807767,
LRTOMT	NM_001145310	chr11	71791932-71799341,71799427-71800073,71800212-71804540,71804748-71805992,71806143-71816008,71816059-71817100,71817257-71818967,71819166-71819649,
LRTOMT	NM_001145309	chr11	71791932-71799341,71799427-71800073,71800212-71804540,71804748-71805992,71806143-71816008,71816059-71816980,71817257-

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LSS	NM_001145437	chr21	47611150-47611793,47611874-47614403,47614576-47615588,47615671-47616114,47616182-47625748,47625856-47626584,47626683-47627340,47627492-47628163,47628216-47629466,47629540-47630600,47630659-47632937,47632967-47633650,47633750-47635092,47635213-47635597,47635708-47636301,47636439-47639388,47639487-47641766,47641890-47642542,47642653-47647464,47647605-47648346,
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LSS	NM_002340	chr21	47611150-47611793,47611874-47614403,47614576-47615588,47615671-47616114,47616182-47625748,47625856-47626584,47626683-47627340,47627492-47628163,47628216-47629466,47629540-47630600,47630659-47632937,47632967-47633650,47633750-47635092,47635213-47635597,47635708-47636301,47636439-47639388,47639487-47641766,47641890-47642542,47642653-47647464,47647605-47648346,47648514-47648644,
LY6D	NM_003695	chr8	143866873-143867003,143867104-143867879,
LY6H	NM_002347	chr8	144239903-144240218,144240340-144240997,144241127-144241351,
LY6H	NM_001135655	chr8	144239903-144240218,144240340-144240997,144241127-144241613,
LY6H	NM_001130478	chr8	144239903-144240218,144240340-144240997,144241127-144241613,144241685-144241961,
LYL1	NM_005583	chr19	13210549-13211469,13211563-13211649,13212010-13213343,
LYPD1	NM_001077427	chr2	133403854-133425971,133426111-133428750,
LYPD1	NM_144586	chr2	133403854-133425971,133426111-133427452,
LYPD2	NM_205545	chr8	143831901-143832467,143832589-143833810,
LYPD6	NM_001195685	chr2	150186717-150294150,150294341-150305561,150305662-150325157,150325290-150327195,
LYPD6	NM_194317	chr2	150187237-150294150,150294341-150305561,150305662-150325157,150325290-150327195,
LYPD6B	NM_177964	chr2	149895316-149987395,149987468-150017276,150017350-150061765,150061919-150064826,150064927-150069504,150069637-150071058,
LYRM1	NM_020424	chr16	20911858-20926876,20927037-20931442,20931537-20935320,
LYRM1	NM_001128301	chr16	20912212-20913806,20914040-20926876,20927037-20931442,20931537-20935320,
LYRM1	NM_001128302	chr16	20912212-20926876,20927037-20931442,20931537-20935320,
LYZL6	NM_020426	chr17	34261870-34263757,34263838-34264760,34264921-34266220,
LYZL6	NM_001199951	chr17	34261870-34263757,34263838-34264760,34264921-34266220,34266449-34270569,
LZTFL1	NM_020347	chr3	45867825-45868846,45868952-45869929,45870108-45872403,45872483-45872563,45872631-45874540,45874614-45875728,45875791-45877080,45877277-45879417,45879544-45883479,
MAD1L1	NM_003550	chr7	1855865-1937834,1938027-1976321,1976534-1997262,1997355-2020086,2020177-2041698,2041757-2054135,2054278-2108827,2108974-2188785,2188874-2252845,2252909-2255518,2255635-2255790,2255923-2257595,2257679-2258965,2259092-2262208,2262390-2265043,2265186-2269617,2269779-2270182,2270400-2272505,
MAD1L1	NM_001013836	chr7	1855865-1937834,1938027-1976321,1976534-1997262,1997355-2020086,2020177-2041698,2041757-2054135,2054278-2108827,2108974-2188785,2188874-2252845,2252909-2255518,2255635-2255790,2255923-2257595,2257679-2258965,2259092-2262208,2262390-2265043,2265186-2269617,2269779-2270182,2270363-2272505,

MAD1L1	NM_001013837	chr7	1855865-1937834,1938027-1976321,1976534-1997262,1997355-2020086,2020177-2041698,2041757-2054135,2054278-2108827,2108974-2188785,2188874-2252845,2252909-2255518,2255635-2255790,2255923-2257595,2257679-2258965,2259092-2262208,2262390-2265043,2265186-2269617,2269779-2270182,2270360-2272505,
MAGEA10	NM_021048	chrX	151304158-151304231,151304307-151305341,151305442-151306945,
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MAGEA12	NM_005367	chrX	151900876-151903102,
MAGEA12	NM_001166387	chrX	151900876-151901707,151901815-151903102,
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MAGEA5	NM_021049	chrX	151284078-151284151,151284240-151286390,
MAML1	NM_014757	chr5	179160429-179192325,179193743-179195849,179196091-179198146,179198245-179200894,
MAN2B2	NM_015274	chr4	6577076-6578303,6578452-6580118,6580226-6588721,6588896-6590770,6590888-6594898,6595078-6596259,6596460-6598838,6599031-6599923,6600082-6602348,6602484-6606780,6607057-6610832,6611026-6611523,6611778-6612605,6612718-6612811,6613006-6615943,6616083-6619105,6619220-6621652,6621772-6622913,
MAP2K2	NM_030662	chr19	4090707-4094449,4094497-4095384,4095448-4097275,4097342-4099197,4099413-4101015,4101142-4101225,4101279-4102372,4102452-4110505,4110654-4117415,4117628-4123779,
MAP2K7	NM_145185	chr19	7968954-7974638,7974782-7974946,7975015-7975143,7975259-7975336,7975458-7975579,7975689-7975863,7976045-7976133,7976216-7976319,7976464-7977032,7977080-7977180,
MAP3K1	NM_005921	chr5	56111883-56152425,56152578-56155540,56155743-56160559,56160762-56161165,56161284-56161654,56161805-56167735,56167859-56168466,56168550-56168650,56168833-56170857,56171138-56174805,56174929-56176536,56176630-56176908,56177100-56177395,56178694-56179352,56179507-56180489,56180654-56181757,56181891-56183203,56183348-56184051,56184185-56189356,
MAP3K14	NM_003954	chr17	43342168-43342528,43342631-43343902,43344049-43344457,43344566-43344771,43345127-43347778,43347931-43348423,43348589-43350868,43350975-43351488,43351622-43351829,43351961-43362177,43362317-43363796,43364412-43364518,43364731-43366600,43366672-43367854,43368132-43394324,
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MAP3K4	NM_005922	chr6	161413116-161455289,161455482-161469646,161471012-161491638,161491883-161494496,161494645-161501911,161502071-161505531,161505650-161507409,161507511-161507614,161507700-161508718,161508987-161510352,161510504-161512409,161512573-161513040,161513176-161514008,161514089-161514803,161514884-161518110,161518209-161519308,161519460-161522922,161523025-161523729,161523812-161527544,161527738-161528929,161529002-161529773,161529892-161530785,161530947-161532866,161532991-161533698,161533807-161536153,161536335-161537880,
MAP7	NM_001198617	chr6	136665377-136666992,136667218-136677828,136677933-136680956,136681016-136681117,136681170-136681833,136681937-136682141,136682318-136683586,136683841-136686871,136687157-136687463,136687578-136693637,136693764-136698891,136699007-136704807,136704920-136732756,136732836-136742837,136742938-136871478,
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MAP7	NM_001198611	chr6	136665377-136666992,136667218-136677828,136677933-136680956,136681016-136681117,136681170-136681833,136681937-136682141,136682318-136683586,136683841-136686871,136687157-136687463,136687578-136693637,136693764-136698891,136699007-

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MAP7	NM_001198614	chr6	136665377-136666992,136667218-136677828,136677933-136680956,136681016-136681117,136681170-136681833,136681937-136682141,136682318-136683586,136683841-136686871,136687157-136687463,136687578-136693637,136693764-136698891,136699007-136704807,136704920-136709529,136709649-136710490,136710656-136732756,136732836-136742837,136742938-136846968,136847110-136847498,
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MAP7D1	NM_018067	chr1	36622065-36636570,36636917-36637112,36637183-36638063,36638229-36638963,36639080-36640497,36640610-36641798,36642183-36642296,36642444-36643472,36643803-36644018,36644198-36644284,36644425-36644520,36644627-36644861,36644917-36645111,36645159-36645265,36645358-36645473,36645669-36645847,
MAP7D2	NM_001168467	chrX	20026517-20028893,20029171-20030465,20030654-20031170,20031251-20031685,20031744-20033339,20033446-20034210,20034444-20043067,20043202-20043797,20044071-20060618,20060748-20062480,20062619-20070994,20071107-20074796,20074910-20081530,20081696-20082844,20082924-20134647,
MAP7D2	NM_001168466	chrX	20026517-20028893,20029171-20030465,20030654-20031170,20031251-20031685,20031744-20033339,20033446-20034210,20034444-20043067,20043202-20043797,20044071-20060618,20060748-20062480,20062619-20074796,20074910-20081530,20081696-20082844,20082924-20134866,
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MAP7D2	NM_152780	chrX	20026517-20028893,20029171-20030465,20030654-20031170,20031251-20031685,20031744-20033339,20033446-20034210,20034444-20043067,20043202-20043797,20044071-20060618,20060748-20062480,20062643-20070994,20071107-20074796,20074910-20081530,20081696-20082844,20082924-20134866,
MAPK13	NM_002754	chr6	36098479-36099046,36099178-36100396,36100457-36103528,36103639-36103794,36103826-36104259,36104309-36104431,36104548-36104654,36104728-36106140,36106222-36106477,36106558-36106654,36106833-36107069,
MAPK14	NM_001315	chr6	35996051-36020474,36020606-36027064,36027125-36040648,36040762-36041466,36041498-36041824,36041874-36043623,36043740-36044312,36044386-36067963,36068045-36070346,36070427-36075230,36075406-36076155,
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MAPK14	NM_139012	chr6	35996051-36020474,36020606-36027064,36027125-36040648,36040762-36041466,36041498-36041824,36041874-36043623,36043740-36044312,36044386-36063762,36063844-36070346,36070427-36075230,36075406-36076155,

MAPK14	NM_139014	chr6	35996051-36020474,36020606-36027064,36027125-36040648,36040762-36041466,36041498-36041824,36041874-36043623,36043740-36044312,36044386-36063762,36063844-36075230,36075406-36076155,
MAPK6	NM_002748	chr15	52311574-52338025,52339213-52342188,52342335-52350828,52350995-52353494,52353698-52356097,
MAPT	NM_001123066	chr17	43972053-44039685,44039837-44049223,44049312-44051749,44051838-44055739,44055807-44060542,44061297-44064404,44064462-44067242,44067442-44068824,44068953-44071288,44071344-44073763,44074031-44087674,44087769-44091607,44091691-44095982,44096097-44101320,
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MAPT	NM_016835	chr17	43972053-44039685,44039837-44049223,44049312-44051749,44051838-44055739,44055807-44060542,44061297-44064404,44064462-44067242,44067442-44068824,44068953-44073763,44074031-44087674,44087769-44091607,44091691-44095982,44096097-44101320,
MAPT	NM_005910	chr17	43972053-44039685,44039837-44049223,44049312-44051749,44051838-44055739,44055807-44064404,44064462-44068824,44068953-44073763,44074031-44087674,44087769-44091607,44091691-44095982,44096097-44101320,
MAPT	NM_016841	chr17	43972053-44039685,44039837-44055739,44055807-44064404,44064462-44068824,44068953-44073763,44074031-44091607,44091691-44095982,44096097-44101320,
MAPT	NM_016834	chr17	43972053-44039685,44039837-44055739,44055807-44064404,44064462-44068824,44068953-44073763,44074031-44087674,44087769-44091607,44091691-44095982,44096097-44101320,
MARCH6	NM_005885	chr5	10354030-10377908,10378007-10378869,10378945-10381910,10382056-10387104,10387179-10390442,10390613-10391652,10391844-10394192,10394256-10394863,10394898-10397403,10397457-10400894,10400955-10402169,10402252-10402494,10402565-10402643,10402720-10403517,10403654-10405668,10405790-10407212,10407315-10410249,10410389-10411443,10411650-10414543,10414615-10415598,10415782-10417380,10417517-10423845,10423937-10426500,10426635-10430003,10430141-10433704,
MAT2A	NM_005911	chr2	85766502-85768204,85768284-85768376,85768501-85768754,85768869-85768950,85769096-85769276,85769497-85769686,85769871-85770022,85770158-85770791,
MATN3	NM_002381	chr2	20192928-20194058,20194171-20196893,20197021-20200200,20200328-20201714,20201842-20202920,20203048-20205503,20206072-20212168,
MCART6	NM_001012755	chrX	103349972-103401557,
MCCC1	NM_020166	chr3	182733355-182735052,182735126-182737916,182738026-182740203,182740343-182743541,182743593-182751777,182751866-182755004,182755223-182756812,182756924-182759353,182759539-182763199,182763329-182769945,182770029-182775097,182775211-182788785,182788909-182788996,182789146-182790152,182790276-182804479,182804577-182810195,182810334-182812345,182812394-182817138,
MCF2	NM_001171879	chrX	138664663-138667223,138667338-138668535,138668647-138669873,138669948-138670517,138670598-138671992,138672087-138678706,138678930-138679617,138679745-138680563,138680658-138684563,138684658-138686838,138686910-138687026,138687144-138687870,138687939-138689848,138689939-138692458,138692498-138695373,138695423-138697038,138697212-138698439,138698633-138699670,138699864-138701744,138701866-138708350,138708467-138708780,138708916-138711852,138712004-138713552,138713671-138714492,138714614-138724625,
MCF2	NM_001171877	chrX	138664663-138669873,138669948-138670517,138670598-138671992,138672087-138678706,138678930-138679617,138679745-138680563,138680658-138684563,138684658-138686838,138686910-138687026,138687144-138687870,138687939-138689848,138689939-138692458,138692498-138697038,138697212-138698439,138698633-138699670,138699864-138701744,138701866-138708350,138708467-138708780,138708916-138711852,138712004-138714492,138714614-138724625,
MCF2	NM_001171878	chrX	138664663-138669873,138669948-138670517,138670598-138671992,138672087-138678706,138678930-138679617,138679745-138680563,138680658-138684563,138684658-138686838,138686910-138687026,138687144-138687870,138687939-138689848,138689939-138692458,138692498-138697038,138697212-138698439,138698633-138699670,138699864-138701744,138701866-138708350,138708467-138708780,138708916-138711852,138712004-138713552,138713671-138714492,138714614-138724625,
MCF2	NM_005369	chrX	138664663-138667223,138667338-138668535,138668647-138669873,138669948-138670517,138670598-138671992,138672087-138678706,138678930-138679617,138679745-138680563,138680658-138684563,138684658-138686838,138686910-138687026,138687144-138687870,138687939-138689848,138689939-138692458,138692498-138697038,138697212-138698439,138698633-138699670,138699864-

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MCF2	NM_001099855	chrX	138664663-138667223,138667338-138668535,138668647-138669873,138669948-138670517,138670598-138671992,138672087-138678706,138678930-138679617,138679745-138680563,138680658-138684563,138684658-138686838,138686910-138687026,138687144-138687870,138687939-138689848,138689939-138692458,138692498-138697038,138697212-138698439,138698633-138699670,138699864-138701744,138701866-138708350,138708467-138708780,138708916-138711852,138712004-138713552,138713671-138714492,138714614-138727725,138727818-138728946,138729063-138733877,138733948-138790263,
MCF2	NM_001171876	chrX	138664663-138667223,138667338-138668535,138668647-138669873,138669948-138670517,138670598-138671992,138672087-138678706,138678930-138679617,138679745-138680563,138680658-138684563,138684658-138686838,138686910-138687026,138687144-138687870,138687939-138689848,138689939-138692458,138692498-138695373,138695423-138697038,138697212-138698439,138698633-138699670,138699864-138701744,138701866-138708350,138708467-138708780,138708916-138711852,138712004-138713552,138713671-138714492,138714614-138727725,138727818-138728946,138729063-138733877,138733948-138790263,
MCM10	NM_182751	chr10	13203607-13206126,13206210-13212920,13213264-13214374,13214481-13214623,13214766-13217508,13217682-13222440,13222608-13224931,13225101-13228162,13228281-13230879,13231081-13233297,13233400-13234253,13234366-13234449,13234569-13237039,13237270-13239621,13239768-13240687,13240808-13243419,13243535-13246217,13246365-13251089,13251134-13251225,
MCM10	NM_018518	chr10	13203607-13206126,13206210-13212920,13213264-13214374,13214481-13214626,13214766-13217508,13217682-13222440,13222608-13224931,13225101-13228162,13228281-13230879,13231081-13233297,13233400-13234253,13234366-13234449,13234569-13237039,13237270-13239621,13239768-13240687,13240808-13243419,13243535-13246217,13246365-13251089,13251134-13251225,
MDGA2	NM_001113498	chr14	47311223-47314967,47315075-47324225,47324358-47342634,47342795-47343246,47343404-47346690,47346713-47351245,47351425-47389213,47389364-47426575,47426847-47504212,47504508-47530450,47530782-47566055,47566327-47600915,47601050-47613279,47613478-47687222,47687399-47770612,47770754-48143718,
MDGA2	NM_182830	chr14	47311223-47314967,47315075-47324225,47324358-47342634,47342795-47343246,47343404-47346690,47346713-47351245,47351425-47389213,47389364-47426575,47426847-47504212,47504508-47530450,47530782-47566055,47566327-47600915,47601050-47613279,47613478-47687222,47687394-47770612,47770754-47812299,
MDH1B	NM_001039845	chr2	207603236-207604315,207604386-207605776,207605829-207610344,207610398-207611009,207611151-207613742,207613908-207615656,207615800-207619731,207620230-207621620,207621765-207621959,207622096-207625623,207625738-207629972,
ME1	NM_002395	chr6	83921814-83926215,83926316-83933477,83933653-83937052,83937197-83938543,83938651-83947434,83947550-83949256,83949356-83963346,83963458-84025027,84025133-84055890,84056054-84061781,84061859-84108084,84108236-84117485,84117621-84140594,
ME3	NM_001161586	chr11	86152483-86153861,86153962-86157354,86157530-86158105,86158250-86159190,86159298-86160929,86161045-86161341,86161441-86176131,86176243-86198377,86198483-86209003,86209167-86219832,86219910-86267593,86267745-86270730,86270866-86382802,86383001-86383364,
ME3	NM_001014811	chr11	86152483-86153861,86153962-86157354,86157530-86158105,86158250-86159190,86159298-86160929,86161045-86161341,86161441-86176131,86176243-86198377,86198483-86209003,86209167-86219832,86219910-86267593,86267745-86270730,86270866-86382802,
ME3	NM_006680	chr11	86152483-86153861,86153962-86157354,86157530-86158105,86158250-86159190,86159298-86160929,86161045-86161341,86161441-86176131,86176243-86198377,86198483-86209003,86209167-86219832,86219910-86267593,86267745-86270730,86270866-86382802,86383001-86383338,
MED13	NM_005121	chr17	60023962-60024276,60024379-60028184,60028360-60030324,60030475-60032741,60032929-60033039,60033200-60033698,60033843-60038226,60038452-60038947,60039141-60040111,60040333-60042365,60042830-60043821,60044013-60045394,60045620-60050086,60050250-60059557,60060476-60061530,60061729-60062010,60062227-60062359,60062452-60064366,60064490-60069899,60069983-60072511,60072727-60087909,60088595-60106900,60107013-60107210,60107375-60108803,60109000-60111146,60111346-60112822,60112970-60129896,60130067-60140426,60140663-60142499,
MED16	NM_005481	chr19	868252-868414,868500-868861,868947-871035,871254-871924,872119-873447,873583-875242,875455-876972,877181-879935,880149-881557,881715-884901,885009-885768,886202-889636,889808-890135,890245-890961,891150-893084,

MED23	NM_004830	chr6	131908987-131910603,131910737-131911460,131911583-131912451,131912668-131913526,131913601-131914144,131914312-131915237,131915476-131917085,131917304-131917656,131917829-131919425,131919608-131919694,131919902-131921176,131921303-131923356,131923522-131924168,131924345-131925316,131925461-131926378,131926626-131927617,131927765-131929066,131929212-131931184,131931387-131937045,131937143-131939545,131939660-131940965,131941037-131941766,131941870-131943019,131943120-131944489,131944603-131946003,131946130-131948534,131948624-131948779,131948813-131949149,
MED23	NM_015979	chr6	131895436-131908847,131908987-131910603,131910737-131911460,131911583-131912451,131912668-131913526,131913601-131914144,131914312-131915237,131915476-131917085,131917304-131917656,131917829-131919425,131919608-131919694,131919902-131921176,131921303-131923356,131923522-131924168,131924345-131925316,131925461-131926378,131926626-131927617,131927765-131929066,131929212-131931184,131931387-131936462,131936482-131937045,131937143-131939545,131939660-131940965,131941037-131941766,131941870-131943019,131943120-131944489,131944603-131946003,131946130-131948534,131948624-131948779,131948813-131949149,
MEGF9	NM_001080497	chr9	123367920-123370017,123370289-123374672,123374818-123384892,123385034-123421650,123421854-123476034,
MEIS1	NM_002398	chr2	66663001-66664867,66665096-66666973,66667117-66667692,66667745-66668544,66668597-66670032,66670181-66691239,66691353-66739279,66739427-66775073,66775152-66794583,66794644-66795797,66795889-66796180,66796278-66798376,
MEIS3	NM_001009813	chr19	47906811-47909715,47909784-47910143,47910229-47910334,47910395-47910607,47910686-47912354,47912505-47912691,47912805-47917972,47918073-47918306,47918359-47919907,47919960-47920059,47920221-47920433,47920608-47922325,
MEIS3	NM_020160	chr19	47906811-47909715,47909784-47910143,47910229-47910334,47910395-47910607,47910824-47912354,47912505-47912691,47912805-47917972,47918124-47918306,47918359-47919907,47919960-47920059,47920221-47920433,47920608-47922325,
MELK	NM_014791	chr9	36573005-36581639,36581737-36583622,36583710-36589531,36589650-36594623,36594769-36597217,36597288-36599389,36599484-36607570,36607671-36630294,36630365-36633097,36633198-36642992,36643081-36651741,36651875-36657236,36657361-36665345,36665579-36669305,36669404-36670993,36671164-36674829,36674935-36677155,
MEMO1	NM_015955	chr2	32093562-32094915,32095022-32108453,32108532-32117059,32117204-32142993,32143107-32145865,32145980-32157134,32157205-32168369,32168453-32235254,
MEMO1	NM_001137602	chr2	32093562-32094915,32095022-32108453,32108532-32117059,32117204-32142993,32143107-32145865,32145980-32168369,32168453-32235254,
MGC3771	NR_024166	chr16	3160956-3164794,3164889-3164967,
MGC3771	NR_024167	chr16	3160956-3164794,3164884-3164967,
MGC87042	NM_207342	chr7	22459456-22532182,22532349-22532941,22533399-22534389,22534506-22539731,
MGC87042	NM_001164460	chr7	22478375-22532182,22532349-22532941,22533456-22534389,22534506-22539731,
MGRN1	NM_001142290	chr16	4675050-4700364,4700485-4701962,4702053-4702677,4702826-4707245,4707365-4714708,4714777-4715101,4715153-4718264,4718314-4721390,4721461-4723497,4723659-4727462,4727574-4730031,4730099-4731549,4731778-4732822,4732948-4733223,4733271-4733842,4733934-4736258,
MGRN1	NM_015246	chr16	4675050-4700364,4700485-4701962,4702053-4702677,4702826-4707245,4707365-4714708,4714777-4715101,4715153-4718264,4718314-4721390,4721461-4723497,4723659-4727462,4727574-4730031,4730099-4731549,4731778-4732822,4732948-4733223,4733271-4733842,4733934-4738795,
MGRN1	NM_001142289	chr16	4675050-4700364,4700485-4701962,4702053-4702677,4702826-4707245,4707365-4714708,4714777-4715098,4715153-4718264,4718314-4721390,4721461-4723497,4723659-4727462,4727574-4731549,4731778-4732822,4732948-4733223,4733271-4733842,4733934-4738795,
MGRN1	NM_001142291	chr16	4675050-4700364,4700485-4701962,4702053-4702677,4702826-4707245,4707365-4714708,4714777-4715098,4715153-4718264,4718314-4721390,4721461-4723497,4723659-4727462,4727574-4731549,4731778-4732822,4732948-4733223,4733271-4733842,4733934-4736258,
MICAL3	NM_001122731	chr22	18317316-18324586,18324784-18347663,18347753-18348688,18348779-18354601,18354790-18368642,18368818-18369934,18369999-18370087,18370202-18371798,18371997-18374249,18374399-18376572,18376671-18378048,18378177-18379010,18379128-18379488,18379748-18382212,18382315-18383606,18383764-18384642,18384746-18385395,18385514-18387396,18387606-18389313,18389653-18507045,
MICAL3	NM_001136004	chr22	18347753-18348688,18348779-18354601,18354790-18355511,18355621-18358211,18358321-18362110,18362169-18363969,18364070-18368642,18368818-18369934,18369999-18370087,18370202-18371798,18371997-18374249,18374399-18376572,18376671-18378048,18378177-18379010,18379128-18379488,18379748-18382212,18382315-18383606,18383764-18384642,18384746-18385395,18385514-18387396,18387606-

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MICAL3	NM_015241	chr22	18273683-18273762,18273838-18273966,18274068-18291608,18291704-18293467,18293580-18299454,18299551-18300075,18301896-18304191,18304276-18304794,18304937-18305711,18305827-18310408,18310548-18314618,18314874-18324586,18324784-18347663,18347753-18348688,18348779-18354601,18354790-18368642,18368818-18369934,18369999-18370087,18370202-18371798,18371997-18374249,18374399-18376572,18376671-18378048,18378177-18379010,18379128-18379488,18379748-18382212,18382315-18383606,18383764-18384642,18384746-18385395,18385514-18387396,18387606-18389313,18389653-18507045,
MINK1	NM_015716	chr17	4736936-4781610,4781678-4784277,4784336-4784425,4784553-4787656,4787769-4788205,4788298-4788776,4788909-4789204,4789261-4789413,4789494-4789744,4789922-4790403,4790475-4790873,4791086-4792940,4793059-4793810,4794031-4794244,4794420-4794749,4795012-4795442,4795530-4795949,4796064-4796272,4796363-4796727,4796893-4797281,4797389-4797467,4797607-4797818,4797929-4798368,4798538-4798643,4798789-4798991,4799128-4799296,4799399-4799486,4799638-4799722,4799884-4799967,4800109-4800497,
MINK1	NM_153827	chr17	4736936-4781610,4781678-4784277,4784336-4784425,4784553-4787656,4787769-4788205,4788298-4788776,4788909-4789204,4789261-4789413,4789494-4789744,4789922-4790403,4790475-4790873,4791086-4792940,4793059-4793810,4794031-4794244,4794420-4794749,4795012-4795442,4795530-4795695,4795808-4795949,4796064-4796272,4796363-4796727,4796893-4797281,4797389-4797467,4797607-4797818,4797929-4798368,4798538-4798643,4798789-4798991,4799128-4799296,4799399-4799486,4799638-4799722,4799884-4799967,4800109-4800497,
MINK1	NM_170663	chr17	4736936-4781610,4781678-4784277,4784336-4784425,4784553-4787656,4787769-4788205,4788298-4788776,4788909-4789204,4789261-4789413,4789494-4789744,4789922-4790403,4790475-4790873,4791086-4792940,4793059-4793810,4794031-4794244,4794420-4794749,4795012-4795442,4795530-4795949,4796064-4796272,4796363-4796579,4796605-4796727,4796893-4797281,4797389-4797467,4797607-4797818,4797929-4798368,4798538-4798643,4798789-4798991,4799128-4799296,4799399-4799486,4799638-4799722,4799884-4799967,4800109-4800497,
MINK1	NM_001024937	chr17	4736936-4781610,4781678-4784277,4784336-4784425,4784553-4787656,4787769-4788205,4788298-4788776,4788909-4789204,4789261-4789413,4789494-4789744,4789922-4790403,4790475-4790873,4791086-4792940,4793059-4793810,4794031-4794244,4794420-4794809,4795012-4795442,4795530-4795695,4795808-4795949,4796064-4796272,4796363-4796727,4796893-4797281,4797389-4797467,4797607-4797818,4797929-4798368,4798538-4798643,4798789-4798991,4799128-4799296,4799399-4799486,4799638-4799722,4799884-4799967,4800109-4800497,
MIP	NM_012064	chr12	56845250-56846854,56846937-56847373,56847540-56848036,
MKI67	NM_002417	chr10	129897520-129899520,129899966-129900841,129907688-129908640,129908798-129909907,129910081-129910189,129910310-129910395,129910710-129911689,129911867-129913190,129914272-129914753,129914801-129917515,129917584-129921143,129921261-129921353,129921434-129923838,129924021-129924361,
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MKL2	NM_014048	chr16	14165223-14173145,14173212-14234399,14234618-14304098,14304166-14306209,14306267-14307400,14307478-14310981,14311145-14312675,14312856-14328001,14328141-14334092,14334342-14339383,14339518-14340328,14341215-14342781,14342939-14345717,14345881-14346220,14346360-14351956,14352019-14354764,
MLF1IP	NM_024629	chr4	185616556-185618799,185618958-185621972,185622036-185623241,185623291-185623515,185623596-185631224,185631335-185634096,185634168-185637549,185637788-185638288,185638351-185646109,185646217-185650070,185650190-185652072,185652123-185655168,
MLLT1	NM_005934	chr19	6213182-6213346,6213420-6213735,6213809-6213948,6214050-6216414,6216525-6217963,6218053-6222130,6222696-6226986,6227114-6230579,6230725-6262237,6262322-6270588,6270771-6279782,
MMP15	NM_002428	chr16	58060417-58071374,58071525-58072168,58072299-58073777,58074087-58074439,58074603-58075519,58075775-58076133,58076274-58077112,58077265-58077414,58077532-58078909,
MORC2	NM_014941	chr22	31322859-31324004,31324195-31328344,31328440-31328530,31328757-31328874,31329018-31329451,31329508-31330045,31330179-31330766,31331149-31331233,31331310-31332496,31332631-31332917,31333025-31333568,31333699-31333800,31333957-31334050,31334193-31335606,31335694-31335944,31336029-31336743,31336825-31337418,31337546-31337876,31337990-31338097,31338259-31342326,31342437-

			31345736,31345829-31346361,31346432-31352747,31352784-31354625,31354681-31359209,31359321-31363050,
MORN1	NM_024848	chr1	2253019-2255534,2255583-2267906,2267988-2268154,2268290-2288869,2289038-2290029,2290155-2303918,2304031-2305898,2305997-2316415,2316505-2317244,2317337-2318856,2318969-2319676,2319777-2321362,2321436-2322895,
MOV10	NM_001130079	chr1	113217253-113217468,113217672-113231555,113231761-113232035,113232273-113232460,113232721-113234285,113234422-113235381,113235552-113236638,113236795-113237073,113237252-113237369,113237519-113238036,113238197-113238768,113238874-113239057,113239157-113239250,113239469-113240614,113240734-113240907,113241101-113241335,113241412-113242305,113242433-113242514,113242605-113242839,113242963-113243036,
MOV10	NM_020963	chr1	113217352-113217452,113217672-113231555,113231761-113232035,113232273-113232460,113232721-113234285,113234422-113235381,113235552-113236638,113236795-113237073,113237252-113237369,113237519-113238036,113238197-113238768,113238874-113239057,113239157-113239250,113239469-113240614,113240734-113240907,113241101-113241335,113241412-113242305,113242433-113242514,113242605-113242839,113242963-113243036,
MPHOSPH6	NM_005792	chr16	82182469-82182912,82183009-82185027,82185120-82197685,82197800-82203728,
MPHOSPH9	NM_022782	chr12	123641456-123645326,123645397-123645681,123645931-123646660,123646766-123647559,123647682-123648495,123648638-123649847,123650025-123651200,123651337-123661233,123661337-123664471,123664538-123665708,123665758-123678931,123679149-123682792,123682882-123686709,123686867-123687169,123687632-123687795,123687923-123694601,123694710-123699289,123699382-123702921,123703047-123705917,
MPP6	NM_016447	chr7	24613213-24659669,24659840-24663283,24663404-24681333,24681488-24689229,24689384-24690102,24690332-24703207,24703341-24705205,24705307-24705638,24705709-24708116,24708280-24718748,24718953-24720009,24720140-24727055,
MPZL1	NM_003953	chr1	167691480-167734818,167734987-167741510,167741726-167742471,167742606-167745299,167745404-167757055,
MPZL1	NM_024569	chr1	167691480-167734818,167734987-167741510,167741726-167742471,167742606-167757055,
MPZL1	NM_001146191	chr1	167691480-167734818,167734987-167757055,
MR1	NM_001194999	chr1	181002601-181003021,181003211-181018186,181018449-181019280,181019423-181021369,181021647-181022707,181022814-181024359,
MR1	NM_001531	chr1	181002601-181003021,181003211-181018186,181018449-181019145,181019423-181021369,181021647-181022707,181022814-181024359,
MR1	NM_001195035	chr1	181002601-181003021,181003211-181018186,181018449-181019145,181019423-181024359,
MR1	NM_001195000	chr1	181002601-181003021,181003211-181018186,181018449-181019145,181019423-181022707,181022814-181024359,
MRPL33	NM_145330	chr2	27994667-27995539,27995560-28002298,
MRPL33	NM_004891	chr2	27994667-27995539,27995560-27997289,27997398-28002298,
MRPL34	NM_023937	chr19	17416767-17416973,
MRPL39	NM_017446	chr21	26958067-26961145,26961195-26965122,26965278-26966203,26966271-26969612,26969727-26972109,26972179-26973678,26973780-26976106,26976248-26978759,26978968-26979713,
MRPL39	NM_080794	chr21	26958067-26960011,26960102-26961145,26961195-26965122,26965278-26966203,26966271-26969612,26969727-26972109,26972179-26973678,26973780-26976106,26976248-26978759,26978968-26979713,
MRPL54	NM_172251	chr19	3762817-3765162,3765330-3767257,
MRPS25	NM_022497	chr3	15094141-15094885,15094975-15100874,15100983-15106566,
MRPS26	NM_030811	chr20	3026927-3027017,3027166-3027258,3027384-3028379,
MSL3L2	NR_024322	chr2	234775997-234776971,
MSRA	NM_001135671	chr8	9953554-10065341,10065412-10102612,10102734-10159042,10159149-10177391,10177500-10285656,
MSRA	NM_001135670	chr8	9912169-10065341,10065412-10159042,10159149-10177391,10177500-10285656,
MSRA	NM_012331	chr8	9912169-10065341,10065412-10102612,10102734-10159042,10159149-10177391,10177500-10285656,
MSRA	NM_001199729	chr8	9953554-9953752,9953829-10065341,10065412-10102612,10102734-10159042,10159149-10177391,10177500-10285656,
MST4	NM_001042452	chrX	131157688-131188657,131188890-131197459,131197518-131202241,131202352-131202438,131202598-131205095,131205246-131206294,131206390-131206839,131206904-131206983,131207122-131208161,

MST4	NM_016542	chrX	131157436-131157534,131157688-131188657,131188890-131197459,131197518-131202241,131202352-131202438,131202598-131203504,131203692-131205095,131205246-131206294,131206390-131206839,131206904-131206983,131207122-131208161,
MST4	NM_001042453	chrX	131157436-131157534,131157688-131197459,131197518-131202241,131202352-131202438,131202598-131203504,131203692-131205095,131205246-131206294,131206390-131206839,131206904-131206983,131207122-131208161,
MSTO1	NM_018116	chr1	155580124-155580214,155580352-155580828,155580900-155581005,155581083-155581338,155581395-155581478,155581619-155581772,155581892-155581971,155582108-155582207,155582362-155582633,155582767-155582838,155583025-155583251,155583358-155583446,155583558-155583848,
MT1G	NM_005950	chr16	56700883-56701222,56701290-56701876,
MT4	NM_032935	chr16	56599072-56601661,56601729-56602751,
MTBP	NM_022045	chr8	121457829-121458671,121458754-121463241,121463317-121463409,121463563-121466085,121466146-121467673,121467820-121468791,121468911-121471453,121471590-121473399,121473496-121475930,121476002-121483058,121483178-121500397,121500573-121502701,121502811-121509631,121509795-121514730,121514850-121518944,121519102-121522172,121522270-121528163,121528432-121530089,121530341-121530942,121531058-121534892,121534960-121535536,
MTCH1	NM_014341	chr6	36936751-36937813,36937891-36938180,36938250-36938421,36938471-36940477,36940573-36943432,36943494-36944973,36945027-36945408,36945468-36945852,36945932-36946279,36946388-36949362,36949449-36953627,
MTFR1	NM_014637	chr8	66557020-66582106,66582254-66594586,66594687-66605877,66605995-66616927,66617165-66619243,66619492-66620076,66620247-66621209,
MTFR1	NM_001145839	chr8	66557020-66582106,66582254-66594586,66594687-66605877,66605995-66616927,66617165-66619243,66619492-66620076,
MTFR1	NM_001145838	chr8	66582254-66605877,66605995-66616927,66617165-66619243,66619492-66620076,66620247-66621209,
MTIF3	NM_152912	chr13	28010031-28011251,28011411-28014124,28014587-28019223,28019294-28024644,
MTIF3	NM_001166263	chr13	28010031-28011251,28011411-28014124,28014587-28015152,28015215-28019223,28019294-28024644,
MTIF3	NM_001166262	chr13	28010031-28011251,28011411-28014124,28014587-28019223,28019294-28024199,
MTIF3	NM_001166261	chr13	28010031-28011251,28011411-28014124,28014587-28019223,28019294-28024277,
MTMR9LP	NR_026850	chr1	32697571-32697641,32697786-32700303,32700416-32700551,32700812-32704894,32705027-32705468,32706266-32706736,
MTNR1A	NM_005958	chr4	187455712-187476334,
MTRF1	NM_004294	chr13	41791365-41797390,41797491-41800566,41800705-41808024,41808144-41814395,41814570-41826779,41826889-41827083,41827167-41828663,41828757-41834627,41835052-41837619,
MTRR	NM_024010	chr5	7869303-7870881,7871037-7873484,7873640-7875369,7875489-7878055,7878436-7883266,7883391-7885812,7885968-7886726,7886817-7889206,7889389-7891483,7891528-7892838,7893027-7895845,7895966-7896975,7897070-7897176,7897361-7900025,
MTRR	NM_002454	chr5	7869329-7870881,7871037-7873484,7873640-7875369,7875489-7878055,7878436-7883266,7883391-7885812,7885968-7886726,7886817-7889206,7889389-7891483,7891528-7892838,7893027-7895845,7895966-7896975,7897070-7897176,7897361-7900025,
MTSS1L	NM_138383	chr16	70698353-70698499,70698667-70698821,70699000-70699367,70699444-70708207,70708432-70710782,70710882-70711693,70711803-70712153,70712313-70713216,70713227-70713531,70713608-70713687,70713781-70713872,70713959-70714695,70714771-70714865,70714929-70719624,
MUM1L1	NM_152423	chrX	105412419-105415003,105415133-105421215,105421353-105447976,105448164-105449210,
MUM1L1	NM_001171020	chrX	105412419-105415003,105415133-105447976,105448164-105449210,
MVD	NM_002461	chr16	88719014-88719706,88719817-88721098,88721216-88721605,88721826-88722062,88722139-88722511,88722713-88723842,88723991-88724321,88724438-88725056,88725129-88729417,
MVP	NM_005115	chr16	29831832-29841834,29841996-29842197,29842395-29845052,29845178-29845254,29845388-29847023,29847120-29848041,29848280-29851497,29851781-29852915,29853162-29853234,29853434-29855812,29856201-29857182,29857301-29857477,29857606-29858516,29858707-29859081,
MVP	NM_017458	chr16	29831832-29841793,29841996-29842197,29842395-29845052,29845178-29845254,29845388-29847023,29847120-29848041,29848280-29851497,29851781-29852915,29853162-29853234,29853434-29855812,29856201-29857182,29857301-29857477,29857606-29858516,29858707-29859081,

MYBL2	NM_002466	chr20	42295944-42302444,42302540-42310422,42310496-42311432,42311527-42315490,42315713-42320795,42320960-42328395,42328685-42331128,42331544-42333857,42333999-42338601,42338703-42340126,42340242-42341640,42341747-42343772,42343924-42344597,
MYBPHL	NM_001010985	chr1	109835211-109836826,109836872-109837731,109837920-109838854,109838993-109839403,109839565-109839670,109839812-109840042,109840240-109840789,109840880-109849467,
MYF5	NM_005593	chr12	81111344-81112135,81112213-81112638,
MYH2	NM_001100112	chr17	10424750-10426405,10426503-10426623,10426730-10426811,10426984-10427074,10427202-10427781,10427987-10428072,10428383-10428539,10428666-10428766,10428934-10429008,10429194-10429914,10430113-10430253,10430374-10431063,10431192-10432005,10432397-10432477,10432570-10432651,10432799-10432879,10433058-10433147,10433392-10434948,10435206-10436600,10436739-10436824,10436950-10438388,10438508-10438593,10438683-10439845,10439924-10440548,10440860-10440980,10441153-10442520,10442672-10442759,10442880-10443243,10443384-10443909,10444015-10446190,10446291-10446413,10446479-10447026,10447121-10447217,10447334-10447415,10447445-10448661,10448820-10450790,10450936-10451032,10451258-10452690,10452735-10452874,
MYH2	NM_017534	chr17	10424750-10426405,10426503-10426623,10426730-10426811,10426984-10427074,10427202-10427781,10427987-10428072,10428383-10428539,10428666-10428766,10428934-10429008,10429194-10429914,10430113-10430253,10430374-10431063,10431192-10432005,10432397-10432477,10432570-10432651,10432799-10432879,10433058-10433147,10433392-10434948,10435206-10436600,10436739-10436824,10436950-10438388,10438508-10438593,10438683-10439845,10439924-10440548,10440860-10440980,10441153-10442520,10442672-10442759,10442880-10443243,10443384-10443909,10444015-10446190,10446291-10446413,10446479-10447026,10447121-10447217,10447334-10447415,10447445-10448661,10448820-10450790,10450936-10451032,10451258-10452690,10452735-10452951,
MYH3	NM_002470	chr17	10531997-10532912,10533052-10533157,10533255-10533407,10533514-10533603,10533776-10534926,10535054-10535128,10535334-10535791,10536102-10536906,10537033-10537332,10537500-10538155,10538341-10538682,10538881-10539050,10539171-10541124,10541253-10541358,10541750-10542188,10542281-10542359,10542507-10542613,10542792-10542875,10543120-10543311,10543569-10543648,10543787-10543878,10544004-10544400,10544520-10544600,10544690-10545555,10545628-10545732,10546041-10546141,10546314-10547666,10547818-10547899,10548020-10549022,10549163-10549244,10549350-10550497,10550598-10550678,10550744-10551872,10551967-10552892,10553003-10553689,10553719-10554827,10554986-10555735,10555881-10558176,10558390-10559405,
MYLK2	NM_033118	chr20	30407232-30407334,30407436-30407927,30408350-30409240,30409541-30411278,30411386-30412060,30412156-30414406,30414518-30414598,30414742-30418620,30418693-30418814,30418945-30419504,30419659-30419805,30419940-30421518,
MYO1C	NM_033375	chr17	1369047-1370534,1370636-1370772,1370872-1371132,1371205-1371280,1371418-1371545,1371603-1371695,1371791-1372823,1372909-1373467,1373629-1373727,1373814-1373913,1373984-1374363,1374442-1374515,1374631-1375199,1375319-1375415,1375523-1377902,1377985-1378104,1378153-1378230,1378327-1380797,1380891-1381183,1381266-1381379,1381487-1381702,1381787-1381908,1382030-1382723,1382797-1382884,1383000-1383819,1383920-1383998,1384180-1385770,1385853-1386153,1386354-1386902,1387020-1387440,1387598-1394892,
MYO1C	NM_001080950	chr17	1369047-1370534,1370636-1370772,1370872-1371132,1371205-1371280,1371418-1371545,1371603-1371695,1371791-1372823,1372909-1373467,1373629-1373727,1373814-1373913,1373984-1374363,1374442-1374515,1374631-1375199,1375319-1375415,1375523-1377902,1377985-1378104,1378153-1378230,1378327-1380797,1380891-1381183,1381266-1381379,1381487-1381702,1381787-1381908,1382030-1382723,1382797-1382884,1383000-1383819,1383920-1383998,1384180-1385770,1385853-1386153,1386354-1386902,1387020-1387440,1387598-1388986,
MYO1C	NM_001080779	chr17	1369047-1370534,1370636-1370772,1370872-1371132,1371205-1371280,1371418-1371545,1371603-1371695,1371791-1372823,1372909-1373467,1373629-1373727,1373814-1373913,1373984-1374363,1374442-1374515,1374631-1375199,1375319-1375415,1375523-1377902,1377985-1378104,1378153-1378230,1378327-1380797,1380891-1381183,1381266-1381379,1381487-1381702,1381787-1381908,1382030-1382723,1382797-1382884,1383000-1383819,1383920-1383998,1384180-1385770,1385853-1386153,1386354-1386902,1387020-1387440,1387598-1395705,
MYO1F	NM_012335	chr19	8586489-8587259,8587431-8587516,8587714-8590361,8590447-8591335,8591486-8591671,8591820-8592220,8592368-8595078,8595250-8595341,8595458-8601134,8601281-8601381,8601482-8601831,8601940-8604829,8604913-8606788,8606876-8609179,8609349-8610532,8610621-8612918,8613007-8613119,8613202-8615042,8615241-8615444,8615579-8616622,8616759-8616915,8617049-8618021,8618113-8618232,8618322-8619359,8619456-8619536,8619628-8620541,8620681-8642189,

MYO7A	NM_000260	chr11	76839536-76841633,76841699-76853753,76853869-76858842,76858997-76866951,76867138-76867704,76867828-76867906,76868051-76868323,76868439-76869321,76869477-76870491,76870570-76871207,76871329-76872017,76872162-76873164,76873377-76873897,76874035-76877100,76877209-76883792,76883932-76885800,76885961-76886416,76886511-76888593,76888690-76890089,76890176-76890779,76891000-76891418,76891528-76892424,76892636-76892995,76893201-76893467,76893646-76894111,76894203-76895631,76895761-76900387,76900516-76901063,76901185-76901740,76901916-76903094,76903324-76905397,76905570-76908524,76908644-76909538,76909667-76910578,76910864-76912491,76912684-76913343,76913470-76914103,76914263-76915119,76915275-76916505,76916663-76917140,76917248-76918332,76918448-76919473,76919563-76919740,76919849-76922195,76922383-76922864,76922983-76923995,76924081-76924903,76925025-76925650,
MYO7A	NM_001127179	chr11	76839536-76841633,76841699-76853753,76853869-76858842,76858997-76866951,76867138-76867704,76867828-76867906,76868051-76868323,76868439-76869321,76869477-76870491,76870570-76871207,76871329-76872017,76872162-76873164,76873377-76873897,76874035-76877100,76877209-76883792,76883932-76885800,76885961-76886416,76886511-76888593,76888690-76890089,76890176-76890779,76891000-76891418,76891528-76892424,76892636-76892995,76893201-76893467,76893646-76894111,76894203-76895631,
MYO7A	NM_001127180	chr11	76839536-76841633,76841699-76853753,76853869-76858842,76858997-76866951,76867138-76867704,76867828-76867906,76868051-76868323,76868439-76869321,76869477-76870491,76870570-76871207,76871329-76872017,76872162-76873164,76873377-76873897,76874035-76877100,76877209-76883792,76883932-76885800,76885961-76886416,76886511-76888593,76888690-76890089,76890176-76890779,76891000-76891418,76891528-76892424,76892636-76892995,76893201-76893467,76893646-76894111,76894203-76895631,76895761-76900387,76900516-76901063,76901185-76901740,76901916-76903094,76903324-76905397,76905570-76908524,76908644-76909538,76909667-76910692,76910864-76912491,76912684-76913343,76913470-76914103,76914263-76915119,76915275-76916505,76916663-76917140,76917248-76918332,76918448-76919473,76919563-76919740,76919849-76922195,76922383-76922864,76922977-76923995,76924081-76924903,76925025-76925650,
MYOF	NM_133337	chr10	95066759-95069775,95069925-95070289,95070401-95072775,95072968-95076469,95076571-95079627,95079771-95082833,95082931-95083025,95083116-95085581,95085723-95088518,95088669-95089419,95089592-95092976,95093070-95093513,95093671-95095676,95095804-95097570,95097671-95099908,95099922-95103611,95103690-95107372,95107540-95109563,95109727-95110952,95111053-95111168,95111329-95111420,95111604-95113566,95113646-95115383,95115494-95116430,95116606-95119588,95119736-95121207,95121315-95123716,95123833-95126147,95126313-95129400,95129534-95132685,95132843-95134518,95134713-95137078,95137187-95139618,95139745-95140974,95141154-95147552,95147671-95148785,95148912-95155897,95155982-95157002,95157048-95157143,95157214-95159147,95159253-95161173,95161302-95161987,95162105-95162615,95162648-95163778,95163831-95163912,95163977-95168542,95168673-95169328,95169497-95185826,95185916-95191163,95191274-95211805,95211899-95216637,95216695-95241862,
MYOF	NM_013451	chr10	95066759-95069775,95069925-95070289,95070401-95072775,95072968-95076469,95076571-95079627,95079771-95082833,95082931-95083025,95083116-95085581,95085723-95088518,95088669-95089419,95089592-95092976,95093070-95093513,95093671-95095676,95095804-95097570,95097671-95099908,95099922-95103611,95103690-95107372,95107540-95109563,95109727-95110952,95111053-95111168,95111329-95111420,95111604-95113566,95113646-95115383,95115494-95116430,95116606-95119588,95119736-95121207,95121315-95123716,95123833-95126147,95126313-95129400,95129534-95132685,95132843-95134518,95134713-95137078,95137187-95139618,95139745-95140974,95141154-95147552,95147671-95148785,95148912-95152672,95152713-95155897,95155982-95157002,95157048-95157143,95157214-95159147,95159253-95161173,95161302-95161987,95162105-95162615,95162648-95163778,95163831-95163912,95163977-95168542,95168673-95169328,95169497-95185826,95185916-95191163,95191274-95211805,95211899-95216637,95216695-95241862,
MYOG	NM_002479	chr1	203053160-203053773,203053857-203054617,
MYOM3	NM_152372	chr1	24384118-24385412,24385470-24387548,24387573-24387761,24387800-24388434,24388600-24389614,24389725-24389980,24390021-24390560,24390650-24392379,24392492-24393509,24393579-24394458,24394520-24394711,24394858-24397605,24397744-24398457,24398504-24400648,24400760-24401807,24401966-24402647,24402764-24406504,24406685-24407818,24407947-24408489,24408679-24409081,24409205-24410956,24411130-24413132,24413318-24416026,24416156-24416553,24416609-24417285,24417487-24418662,24418806-24419435,24419599-24421341,24421481-24421930,24421977-24424411,24424502-24426168,24426266-24432408,24432568-24433561,24433723-24434481,24434564-24434964,24435145-24438519,
MZT2B	NM_025029	chr2	130940026-130940198,130940349-130948040,

NAA15	NM_057175	chr4	140222986-140255326,140255413-140258000,140258107-140262064,140262224-140263978,140264115-140265338,140265494-140270614,140270736-140272343,140272441-140272657,140272766-140275178,140275253-140278538,140278710-140280895,140281050-140281652,140281783-140282876,140283092-140291363,140291559-140297517,140297628-140299908,140300009-140305984,140306133-140307285,140307385-140309036,
NAA35	NM_024635	chr9	88556189-88557068,88557199-88571273,88571309-88573385,88573502-88574706,88574783-88576926,88577096-88589880,88589949-88590027,88590073-88591598,88591651-88592276,88592362-88593180,88593297-88611312,88611493-88618498,88618560-88622271,88622380-88624778,88624847-88627959,88628060-88628632,88628813-88631452,88631591-88632411,88632481-88633168,88633311-88633612,88633737-88635802,88635885-88636814,
NAALADL1	NM_005468	chr11	64812930-64813292,64813387-64813497,64813587-64813659,64813835-64813915,64813999-64814945,64815038-64815117,64815211-64815451,64815521-64815622,64815688-64815770,64815858-64820688,64820810-64820961,64821049-64821720,64821827-64821925,64822211-64824841,64824966-64825345,64825469-64825548,64825723-64825807,
NAGPA	NM_016256	chr16	5075687-5077134,5077200-5077277,5077381-5077845,5077895-5077979,5078187-5078879,5079010-5080384,5080495-5081744,5081886-5083272,5083730-5083828,
NAGS	NM_153006	chr17	42082458-42083003,42083280-42083390,42083606-42083895,42084078-42084689,42084863-42084957,42085142-42085814,
NAT15	NM_001083601	chr16	3493838-3498469,3498541-3526220,3526338-3529469,3529601-3532500,3532599-3533361,3533598-3534697,3535062-3535465,
NAT15	NM_024845	chr16	3508182-3526220,3526338-3529469,3529601-3532500,3532599-3533361,3533598-3534697,3535084-3535465,
NAT15	NM_001083600	chr16	3508182-3526220,3526338-3529469,3529601-3532500,3532599-3533361,3533598-3534697,3535062-3535465,
NBAS	NM_015909	chr2	15307448-15319110,15319241-15326864,15327005-15330386,15330528-15358895,15359093-15372544,15372636-15374667,15374872-15378590,15378811-15415606,15415943-15416973,15417226-15427195,15427308-15432659,15432891-15448338,15448478-15449293,15449372-15467872,15467995-15468321,15468437-15470720,15470890-15492114,15492206-15493675,15493835-15496425,15496541-15506702,15506818-15514730,15514845-15519724,15519956-15523337,15523442-15534349,15534474-15536535,15536600-15542290,15542426-15555668,15555844-15557649,15557837-15564437,15564593-15567833,15567919-15601323,15601462-15601809,15601916-15607451,15607532-15607786,15607929-15608504,15608658-15613344,15613472-15614189,15614449-15615809,15616005-15618348,15618414-15629016,15629147-15644267,15644338-15651334,15651475-15674665,15674766-15676540,15676676-15679345,15679481-15691615,15691661-15693548,15693598-15694183,15694263-15696905,15696944-15698702,15698759-15701310,
NBPF1	NM_017940	chr1	16890682-16891300,16891414-16892126,16892305-16892900,16892955-16893672,16893847-16894472,16894526-16895566,16895732-16899635,16899689-16900980,16901188-16901650,16901725-16902760,16902977-16903810,16903915-16905686,16905898-16907238,16907452-16907913,16907988-16909037,16909254-16910087,16910192-16911982,16912194-16913543,16913757-16914218,16914293-16915342,16915559-16916392,16916497-16918340,16918552-16918652,16918809-16919934,16920063-16921085,16921157-16921424,16921505-16935001,16935275-16939831,
NBPF3	NM_032264	chr1	21766842-21771439,21771713-21795179,21795391-21797123,21797228-21798060,21798277-21799334,21799409-21799871,21800079-21801391,21801445-21804635,21804801-21805840,21805894-21806542,21806717-21807421,21807475-21808088,21808263-21808975,21809029-21809634,
NCALD	NM_001040629	chr8	102701635-102705017,102705125-102731478,102731877-102792150,102792208-102928035,102928087-103032463,103032518-103136463,
NCALD	NM_001040630	chr8	102701635-102705017,102705125-102731478,102731877-102928035,102928087-103032463,103032518-103136796,
NCALD	NM_001040627	chr8	102701635-102705017,102705125-102731478,102731877-102928035,102928087-103032463,103032518-103136463,
NCALD	NM_032041	chr8	102701635-102705017,102705125-102731478,102731877-102803088,
NCALD	NM_001040628	chr8	102701635-102705017,102705125-102731478,102731877-102792150,102792208-102928035,102928087-103032463,103032518-103041236,103041325-103136463,
NCALD	NM_001040626	chr8	102701635-102705017,102705125-102731478,102731877-102899367,102899456-102928035,102928087-103032463,103032518-103136463,
NCALD	NM_001040625	chr8	102701635-102705017,102705125-102731478,102731877-102928035,102928087-103032463,103032518-103041236,103041325-103136463,
NCALD	NM_001040624	chr8	102701635-102705017,102705125-102731478,102731877-102899367,102899456-102928035,102928087-103032463,103032518-103041236,103041325-103136463,

NCAPH	NM_015341	chr2	97001587-97007378,97007633-97007786,97007879-97008492,97008587-97008902,97009043-97009841,97009968-97017567,97017759-97019042,97019136-97019919,97020127-97024781,97024932-97025879,97025988-97026324,97026449-97030217,97030330-97031612,97031797-97032993,97033112-97034708,97034802-97035161,97035239-97039028,
NCBP1	NM_002486	chr9	100396198-100403074,100403165-100403842,100403945-100405484,100405643-100407397,100407507-100407891,100408015-100409772,100409844-100410288,100410506-100412783,100412883-100413590,100413656-100416078,100416191-100417160,100417227-100417982,100418047-100418291,100418368-100420920,100421026-100423226,100423351-100424322,100424427-100425234,100425330-100426620,100426726-100429043,100429160-100431126,100431257-100431873,100431989-100433366,
NCCRP1	NM_001001414	chr19	39687960-39688691,39688756-39688840,39688894-39689808,39689906-39690984,39691125-39691254,
NCOA2	NM_006540	chr8	71025879-71033535,71033627-71036117,71036318-71036921,71037101-71039046,71039283-71040666,71040746-71040935,71041216-71044070,71044238-71050436,71050568-71053417,71053635-71056875,71057084-71060506,71060719-71068204,71069476-71071738,71071888-71074944,71075090-71075698,71075802-71078799,71078990-71082435,71082615-71086989,71087095-71126136,71126311-71128893,71129000-71208977,71209036-71315933,
NCOA3	NM_001174088	chr20	46130764-46211925,46212006-46250971,46251075-46252653,46252828-46254123,46254226-46255744,46255921-46256303,46256494-46256664,46256768-46262238,46262381-46262760,46262940-46264064,46264458-46264633,46265507-46266390,46266528-46267750,46267947-46268364,46268567-46268667,46268796-46270955,46271129-46275815,46276111-46277747,46277842-46279724,46280021-46281148,46281325-46281673,46281817-46282148,
NCOA3	NM_001174087	chr20	46130764-46211925,46212006-46250971,46251075-46252653,46252828-46254123,46254226-46255744,46255921-46256303,46256494-46256664,46256768-46262238,46262381-46262790,46262940-46264064,46264458-46264633,46265507-46266390,46266528-46267750,46267947-46268319,46268567-46268667,46268796-46270955,46271129-46275815,46276111-46277747,46277854-46279727,46280021-46281148,46281325-46281673,46281817-46282148,
NCOA3	NM_181659	chr20	46130764-46211925,46212006-46250971,46251075-46252653,46252828-46254123,46254226-46255744,46255921-46256303,46256494-46256664,46256768-46262238,46262381-46262790,46262940-46264064,46264458-46264633,46265507-46266390,46266528-46267750,46267947-46268319,46268567-46268667,46268796-46270955,46271129-46275815,46276111-46277747,46277854-46279724,46280021-46281148,46281325-46281673,46281817-46282148,
NCOA3	NM_006534	chr20	46130764-46211925,46212006-46250971,46251075-46252653,46252828-46254123,46254226-46255744,46255921-46256303,46256494-46256664,46256768-46262238,46262381-46262790,46262940-46264064,46264458-46264633,46265507-46266390,46266528-46267750,46267947-46268319,46268567-46268667,46268796-46270955,46271129-46275815,46276111-46277747,46277842-46279724,46280021-46281148,46281325-46281673,46281817-46282148,
NCOA5	NM_020967	chr20	44691529-44691997,44692320-44693666,44693868-44695692,44695821-44697139,44697278-44698847,44699176-44708024,44708093-44718454,
NCRNA00094	NR_015427	chr9	136890659-136890965,136891213-136891328,
NCRNA00160	NR_024351	chr21	36096252-36096342,36096495-36105205,36105378-36106256,36106339-36106981,36107054-36109405,
NCRNA00200	NR_015376	chr10	1205931-1206491,1206578-1208485,
NCRNA00221	NR_027457	chr14	106938645-106944773,106944969-106950169,
NCRNA00263	NR_026762	chr10	102133770-102140971,102141206-102147792,
NDC80	NM_006101	chr18	2571683-2572974,2573086-2574986,2575066-2577743,2577869-2577966,2578141-2578924,2579029-2585110,2585202-2587827,2587923-2589201,2589310-2590015,2590162-2595413,2595621-2599016,2599171-2601393,2601485-2606412,2606507-2608697,2608830-2610756,2610861-2616434,
NDRG1	NM_006096	chr8	134251363-134254264,134254318-134256596,134256634-134258857,134258907-134260116,134260170-134260956,134261015-134262681,134262787-134266780,134266839-134269018,134269107-134270607,134270670-134271409,134271474-134274288,134274411-134276788,134276896-134292473,134292511-134296490,134296573-134309375,
NDRG1	NM_001135242	chr8	134251363-134254264,134254318-134256596,134256634-134258857,134258907-134260116,134260170-134260956,134261015-134262681,134262787-134266780,134266839-134269018,134269107-134270607,134270670-134271409,134271474-134274288,134274411-134276788,134276896-134292473,134292511-134296490,134296573-134308978,
NDUFA12	NM_018838	chr12	95365397-95387944,95388034-95396513,95396598-95397369,

NDUFB10	NM_004548	chr16	2009756-2011152,2011293-2011496,2011638-2011796,
NDUFB6	NM_001199987	chr9	32553943-32558906,32558953-32572877,
NDUFB6	NM_002493	chr9	32553943-32558906,32558953-32570956,32571051-32572877,
NDUFB6	NM_182739	chr9	32553943-32570956,32571051-32572877,
NDUFS6	NM_004553	chr5	1801664-1802433,1802489-1814451,1814576-1815963,
NECAP1	NM_015509	chr12	8234980-8242530,8242633-8242789,8242896-8244363,8244447-8245270,8245381-8245466,8245652-8248195,8248300-8248636,
NECAP1	NR_024260	chr12	8234980-8242530,8242633-8242789,8242896-8245270,8245381-8245466,8245652-8248195,8248300-8248636,
NEGR1	NM_173808	chr1	71873254-72058498,72058652-72076707,72076830-72163689,72163823-72241853,72241981-72400760,72400995-72748000,
NEIL3	NM_018248	chr4	178231264-178243611,178243735-178256840,178256977-178257260,178257476-178260935,178261012-178262628,178262797-178272532,178272704-178274460,178274883-178281655,178281832-178283441,
NEK10	NM_199347	chr3	27257372-27297785,27297863-27326091,27326196-27326329,27326453-27329187,27329235-27332106,27332246-27332751,27332882-27332973,27333078-27335077,27335144-27337102,27337182-27338668,27338732-27343185,27343327-27346236,27346463-27349348,27349437-27350415,27350497-27352438,27352508-27353588,27353669-27355786,27355830-27363666,27363753-27385761,27385862-27387575,27387708-27393954,27394017-27394301,27394411-27409012,27409054-27410714,
NEK2	NM_002497	chr1	211836995-211840446,211840574-211842453,211842675-211843621,211843750-211844542,211844627-211846823,211847066-211847636,211847856-211848724,
NEURL4	NM_032442	chr17	7219647-7220522,7220690-7220778,7220893-7221105,7221252-7221382,7221492-7221586,7221676-7221812,7221994-7222367,7222528-7224076,7224243-7224429,7224593-7224678,7224779-7224877,7225107-7225182,7225330-7226052,7226186-7226265,7226443-7226802,7226883-7226964,7227043-7227131,7227332-7227425,7227590-7227712,7227800-7228116,7228300-7228526,7228793-7228958,7229033-7229572,7229663-7229754,7229868-7230028,7230329-7230482,7230550-7230757,7231204-7232348,
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NEUROD2	NM_006160	chr17	37762858-37763979,
NFE2L1	NM_003204	chr17	46125825-46127967,46128991-46133746,46133961-46134392,46134484-46134704,46134865-46135655,
NFIB	NM_001190738	chr9	14088326-14120437,14120624-14125629,14125766-14146686,14146807-14150142,14150265-14155822,14155893-14179724,14179780-14306986,14307520-14398521,
NFIB	NM_001190737	chr9	14088326-14112996,14113081-14116205,14116346-14120437,14120624-14125629,14125766-14146686,14146807-14150142,14150265-14155822,14155893-14179724,14179780-14306986,14307520-14313479,
NFIB	NM_005596	chr9	14088326-14120437,14120624-14125629,14125766-14146686,14146807-14150142,14150265-14155822,14155893-14179724,14179780-14306986,14307520-14313479,
NFXL1	NM_152995	chr4	47850354-47853110,47853166-47853871,47853960-47857074,47857181-47864861,47864933-47877142,47877311-47880540,47880683-47881111,47881135-47886361,47886455-47887513,47887675-47887894,47888017-47892628,47892721-47896195,47896320-47898538,47898665-47899982,47900099-47900772,47900875-47900974,47901138-47901385,47901566-47905208,47905341-47907252,47907364-47912839,47913012-47915984,47916223-47916565,
NGRN	NM_001033088	chr15	90809109-90809518,90809631-90814418,
NGRN	NR_028052	chr15	90809631-90814418,
NHSL1	NM_020464	chr6	138745954-138750846,138750981-138751528,138754818-138768136,138768331-138794441,138794571-138817354,138817509-138892845,
NHSL1	NM_001144060	chr6	138745954-138750846,138750981-138751528,138754818-138763118,138763252-138768136,138768331-138794441,138794571-138817354,138817509-138820368,
NINJ1	NM_004148	chr9	95884513-95887179,95887345-95888690,95888921-95896423,

NIPBL	NM_133433	chr5	36877281-36953718,36953863-36955572,36955740-36958204,36958334-36961584,36961686-36962223,36962377-36970976,36971139-36972045,36972144-36975876,36976505-36984776,36986404-36995722,36995907-37000473,37000673-37000917,37000991-37001089,37001181-37002762,37002868-37003361,37003450-37006457,37006691-37007423,37007577-37008108,37008191-37008723,37008826-37010187,37010328-37014783,37014868-37016138,37016273-37017119,37017265-37019411,37019503-37020559,37020776-37020875,37020980-37022151,37022252-37022344,37022493-37024685,37024822-37026329,37026430-37027459,37027515-37036479,37036590-37038702,37038841-37044447,37044590-37044736,37044832-37045543,37045700-37046209,37046302-37048602,37048778-37049211,37049404-37051879,37051989-37052466,37052669-37057286,37057435-37058991,37059268-37060944,37061121-37063890,37064081-37064627,
NIPBL	NM_015384	chr5	36877281-36953718,36953863-36955572,36955740-36958204,36958334-36961584,36961686-36962223,36962377-36970976,36971139-36972045,36972144-36975876,36976505-36984776,36986404-36995722,36995907-37000473,37000673-37000917,37000991-37001089,37001181-37002762,37002868-37003361,37003450-37006457,37006691-37007423,37007577-37008108,37008191-37008723,37008826-37010187,37010328-37014783,37014868-37016138,37016273-37017119,37017265-37019411,37019503-37020559,37020776-37020875,37020980-37022151,37022252-37022344,37022493-37024685,37024822-37026329,37026430-37027459,37027515-37036479,37036590-37038702,37038841-37044447,37044590-37044736,37044832-37045543,37045700-37046209,37046302-37048602,37048778-37049211,37049404-37051879,37051989-37052466,37052669-37057286,37057435-37058991,37059268-37060944,37061121-37063890,
NKG7	NM_005601	chr19	51875090-51875192,51875329-51875413,51875562-51875631,
NKX2-3	NM_145285	chr10	101293247-101294740,
NLGN2	NM_020795	chr17	7312032-7315474,7315527-7317661,7317813-7317980,7318168-7318273,7318468-7318828,7319427-7320243,
NLRP8	NM_176811	chr19	56459636-56463902,56463979-56465865,56467467-56473431,56473604-56477577,56477747-56481908,56482063-56485016,56485189-56487497,56487670-56490758,56490931-56499178,
NME1-NME2	NM_001018136	chr17	49231024-49233010,49233142-49237339,49237443-49238519,49238634-49244186,49244318-49245601,49245705-49247296,49247411-49248846,
NME1-NME2	NR_037149	chr17	49231024-49231584,49231806-49233010,49233142-49237339,49237443-49238519,49238634-49244186,49244318-49245601,49245705-49247296,49247411-49248846,
NME2	NM_001018137	chr17	49243043-49244186,49244318-49245601,49245705-49247296,49247411-49248846,
NME2	NM_001018139	chr17	49243925-49244186,49244318-49245601,49245705-49247296,49247411-49248846,
NME2	NM_001018138	chr17	49244318-49245601,49245705-49247296,49247411-49248846,
NME2	NM_002512	chr17	49243859-49244186,49244318-49245601,49245705-49247296,49247411-49248846,
NME2	NM_001198682	chr17	49243859-49244186,49244318-49245601,49245705-49248846,
NMNAT3	NM_178177	chr3	139280235-139292438,139292523-139297712,139297898-139356803,139356905-139396545,
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NOL10	NM_024894	chr2	10712317-10717760,10717865-10729167,10729417-10729702,10729878-10740977,10741069-10742900,10743001-10743202,10743284-10747309,10747438-10784444,10784499-10794605,10794674-10797866,10798018-10799296,10799377-10803083,10803171-10807342,10807405-10808782,10808850-10811678,10811817-10813644,10813684-10815918,10815998-10822095,10822196-10824691,10824739-10829920,
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NOL8	NM_017948	chr9	95060169-95060537,95060619-95061164,95061237-95062170,95062299-95063831,95064105-95068033,95068113-95069166,95069307-95072451,95072544-95072833,95072958-95073426,95073542-95076547,95078419-95080896,95080969-95081501,95081639-95083948,95084029-95085721,95085786-95086303,95086492-95087586,
NOL8	NR_024020	chr9	95060169-95060537,95060619-95061164,95061237-95062170,95062299-95063831,95064105-95068033,95068113-95069166,95069307-95072451,95072544-95072833,95072958-95073426,95073542-95076547,95078419-95080896,95080969-95081501,95081639-95083948,95084029-95085516,95085634-95085721,95085786-95086303,95086492-95087598,

NOMO2	NM_001004060	chr16	18511367-18511696,18511826-18512247,18512342-18518129,18518251-18520485,18520589-18522865,18522978-18524670,18524756-18525662,18525806-18527203,18527333-18528509,18528625-18530549,18530678-18530821,18530983-18531917,18532002-18532085,18532306-18535164,18535262-18535809,18535875-18538857,18538947-18540821,18540960-18542357,18542491-18542786,18542930-18544325,18544502-18549846,18549999-18550179,18550287-18553492,18553584-18553914,18554054-18554937,18555092-18558548,18558623-18560841,18560950-18562759,18562862-18566127,18566175-18569022,18569114-18573196,
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NOSTRIN	NM_001171631	chr2	169643147-169644369,169644559-169654663,169654733-169657574,169657714-169658889,169659184-169668075,169668163-169681142,169681228-169684666,169684731-169684928,169685012-169687980,169688045-169690735,169690836-169699500,169699628-169707344,169707517-169707592,169707693-169707787,169707915-169711860,169711971-169713198,169713289-169716020,169716148-169717303,169717420-169718468,169718560-169721342,
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NOSTRIN	NM_001039724	chr2	169659184-169668075,169668163-169681142,169681228-169684666,169684731-169684928,169685012-169687980,169688045-169690735,169690836-169699500,169699628-169707592,169707693-169707787,169707915-169711860,169711971-169713198,169713289-169716020,169716148-169717303,169717420-169718468,169718560-169721342,
NOSTRIN	NM_001171632	chr2	169659184-169668075,169668163-169684666,169684731-169684928,169685012-169687980,169688045-169690735,169690836-169699500,169699628-169707592,169707693-169707787,169707915-169711860,169711971-169713198,169713289-169716020,169716148-169717303,169717420-169718468,169718560-169721342,
NPHP1	NM_000272	chr2	110881641-110883212,110883259-110886761,110886837-110889254,110889369-110901117,110901219-110902068,110902147-110904328,110904413-110905491,110905604-110907757,110907834-110917702,110917833-110919178,110919275-110920623,110920713-110922095,110922308-110922627,110922733-110926027,110926131-110927381,110927576-110935998,110936125-110937199,110937262-110958996,110959072-110962475,
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NPHP1	NM_001128179	chr2	110881641-110883212,110883259-110886761,110886837-110889254,110889369-110901117,110901219-110902068,110902147-110904328,110904413-110905491,110905604-110907757,110907834-110917702,110917833-110919178,110919275-110920623,110920710-110922263,110922308-110922627,110922733-110926027,110926131-110927381,110927576-110958996,110959072-110962475,
NPHP1	NM_001128178	chr2	110881641-110883212,110883259-110886761,110886837-110889254,110889369-110901117,110901219-110902068,110902147-110904328,110904413-110905491,110905604-110907757,110907834-110917702,110917833-110919178,110919275-110920623,110920713-110922263,110922308-110922627,110922733-110926027,110926131-110927381,110927576-110935998,110936125-110937199,110937262-110958996,110959072-110962475,
NPHS2	NM_014625	chr1	179520587-179521736,179521817-179523609,179523667-179526160,179526366-179528812,179528897-179530422,179530497-179533823,179533929-179544724,
NPLOC4	NM_017921	chr17	79526443-79532529,79532634-79534441,79534560-79536040,79536138-79539041,79539115-79555968,79556131-79563140,79563269-79564269,79564343-79567365,79567454-79571572,79571754-79573715,79573841-79575752,79575849-79577234,79577285-79580342,79580521-79589190,79589305-79596749,79596832-79603940,

NPM1	NM_199185	chr5	170815011-170817053,170817135-170818307,170818429-170818708,170818804-170819712,170819821-170819916,170819983-170827155,170827215-170832304,170832408-170834702,170834779-170837529,
NPM1	NM_002520	chr5	170815011-170817053,170817135-170818307,170818429-170818708,170818804-170819712,170819821-170819916,170819983-170827155,170827215-170827841,170827930-170832304,170832408-170834702,170834779-170837529,
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NPRL2	NM_006545	chr3	50385105-50385188,50385333-50385553,50385673-50385746,50385842-50385956,50385995-50386114,50386214-50386303,50386442-50386815,50386926-50387094,50387265-50387360,50387454-50388004,
NPY	NM_000905	chr7	24323895-24324858,24325048-24329116,24329199-24331280,
NPY1R	NM_000909	chr4	164246911-164247006,164247858-164253632,
NPY5R	NM_006174	chr4	164265153-164266864,164266906-164268602,164268675-164271415,
NR1I2	NM_022002	chr3	119501700-119526074,119526295-119528906,119529042-119530384,119530574-119531531,119531808-119533824,119533969-119534168,119534287-119534571,119534679-119535913,
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NRG2	NM_013982	chr5	139228283-139231187,139231417-139232015,139232145-139232487,139232613-139235259,139235364-139239472,139239498-139245132,139245211-139251304,139251427-139260439,139260560-139266923,139267097-139421953,
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NRIP3	NM_020645	chr11	9005108-9005420,9005517-9005617,9005672-9007256,9007398-9009093,9009178-9009663,9009830-9025307,
NRM	NM_007243	chr6	30656720-30657051,30657230-30657822,30658021-30658617,
NSD1	NM_022455	chr5	176560954-176562086,176563032-176618883,176619021-176631119,176631294-176636635,176639197-176662820,176662947-176665236,176665509-176666755,176666867-176671194,176671272-176673677,176673798-176675180,176675326-176678729,176678855-176683950,176684153-176686988,176687170-176694561,176694720-176696601,176696809-176700671,176700786-176707564,176707836-176709464,176709583-176710786,176710930-176715818,176715927-176718953,176719160-176720831,
NSD1	NM_172349	chr5	176560156-176562086,176562202-176562940,176563032-176618883,176619021-176631119,176631294-176636635,176639197-176662820,176662947-176665236,176665509-176666755,176666867-176671194,176671272-176673677,176673798-176675180,176675326-176678729,176678855-176683950,176684153-176686988,176687170-176694561,176694720-176696601,176696809-176700671,176700786-176707564,176707836-176709464,176709583-176710786,176710930-176715818,176715927-176718953,176719160-176720831,
NSMCE1	NM_145080	chr16	27236558-27237045,27237168-27238039,27238158-27244320,27244469-27245507,27245587-27246497,27246621-27268754,27268903-27280025,
NT5C2	NM_012229	chr10	104849666-104850366,104850545-104850691,104850754-104851319,104851373-104852894,104853067-104853727,104853796-104854103,104854213-104855694,104855738-104857046,104857132-104858686,104858742-104859681,104859777-104860800,104860860-104860990,104861084-104865461,104865559-104866344,104866464-104899161,104899237-104934613,104934740-104940986,104941086-104952991,
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NUDT16P1	NR_027766	chr3	131081286-131082198,
NUDT16P1	NR_002949	chr3	131080913-131081014,131081286-131082198,
NUDT19	NM_001105570	chr19	33183581-33200089,33200299-33202656,
NUDT21	NM_007006	chr16	56466646-56468241,56468358-56468664,56468742-56473567,56473659-56480536,56480602-56481699,56481902-56484997,
NUF2	NM_145697	chr1	163292003-163295820,163295965-163297276,163297353-163298016,163298095-163298634,163298698-163306539,163306639-163307808,163307884-163309169,163309268-163310152,163310217-163313521,163313661-163315466,163315609-163317551,163317729-163318733,163318871-163325123,
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NUP155	NM_004298	chr5	37292141-37292979,37293088-37294429,37294568-37298968,37299081-37299548,37299671-37301537,37301653-37302879,37303011-37303360,37303517-37304839,37304946-37305157,37305313-37307397,37307535-37309229,37309370-37310652,37310846-37314298,37314431-37318088,37318188-37324092,37324210-37326001,37326070-37327729,37327879-37328458,37328523-37329290,37329381-37330138,37330235-37331785,37331898-37333563,37333736-37337918,37338021-37341190,37341345-37342649,37342749-37348605,37348699-37349272,37349348-37350260,37350368-37351290,37351459-37352837,37352932-37358181,37358254-37363988,37364087-37364347,37364487-37370766,
NUP155	NM_153485	chr5	37292141-37292979,37293088-37294429,37294568-37298968,37299081-37299548,37299671-37301537,37301653-37302879,37303011-37303360,37303517-37304839,37304946-37305157,37305313-37307397,37307535-37309229,37309370-37310652,37310846-37314298,37314431-37318088,37318188-37324092,37324210-37326001,37326070-37327729,37327879-37328458,37328523-37329290,37329381-37330138,37330235-37331785,37331898-37333563,37333736-37337918,37338021-37341190,37341345-37342649,37342749-37348605,37348699-37349272,37349348-37350260,37350368-37351290,37351459-37352837,37352932-37358181,37358254-37363988,37364087-37364347,37364487-37370921,
NUP188	NM_015354	chr9	131710031-131711466,131711523-131715050,131715126-131718627,131718714-131719229,131719312-131720287,131720334-131721079,131721174-131721292,131721414-131730783,131730997-131731677,131731794-131733035,131733238-131735437,131735529-131741539,131741607-131742883,131743005-131743541,131743670-131744826,131744981-131745179,131745308-131745570,131745660-131745751,131745830-131747177,131747294-131748835,131748958-131749086,131749155-131749866,131749997-131750324,131750466-131752397,131752506-131755474,131755683-131755802,131755974-131756650,131756722-131757133,131757203-131757596,131757794-131760428,131760508-131760815,131760903-131761449,131761597-131761901,131762085-131763806,131764009-131764161,131764256-131765094,131765255-131765594,131765734-131767424,131767501-131767580,131767810-131767922,131768056-131768327,131768403-131768516,131768648-131768779,
NUP205	NM_015135	chr7	135242721-135255851,135255996-135258400,135258574-135261016,135261163-135261715,135261877-135262542,135262773-135263497,135263664-135269578,135269756-135272321,135272440-135272601,135272741-135276196,135276349-135277733,135277941-135279293,135279478-135282114,135282167-135282744,135282956-135285616,135285718-135286116,135286256-135287551,135287743-135289086,135289209-135290891,135290975-135291497,135291664-135291993,135292120-135298905,135299022-135300662,135300814-135301401,135301475-135301836,135301996-135302348,135302431-135303158,135303352-135304169,135304439-135304536,135304637-135307523,135307674-135309910,135310104-135310986,135311110-135312719,135312860-135315090,135315219-135320327,135320406-135322677,135322808-135323303,135323432-135327938,135328107-135329641,135329767-135330214,135330345-135330904,135330980-135333150,
NUP54	NM_017426	chr4	77036648-77038815,77038928-77039226,77039348-77045800,77045910-77051807,77051903-77052381,77052438-77053674,77053873-77055326,77055516-77057337,77057566-77065300,77065446-77065541,77065627-77069459,
NUP93	NM_014669	chr16	56764124-56782144,56782339-56792448,56792568-56832386,56832451-56839414,56839545-56852574,56852651-56855414,56855506-56857617,56857759-56862887,56863022-56864438,56864598-56865752,56865920-56866205,56866301-56867125,56867319-56868038,56868167-

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NUSAP1	NM_001129897	chr15	41625249-41634582,41634653-41641294,41641440-41643184,41643328-41648235,41648339-41650345,41650457-41657598,41657788-41663723,41663883-41669392,41669503-41672289,
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NUSAP1	NM_016359	chr15	41625249-41634582,41634653-41641294,41641440-41643184,41643328-41648235,41648339-41650345,41650457-41657598,41657788-41663723,41663883-41667908,41668027-41669392,41669503-41672289,
NUTF2	NM_005796	chr16	67880889-67899003,67899133-67902241,67902315-67902402,67902503-67904701,
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NXF5	NM_032946	chrX	101087256-101092462,101092627-101092752,101092813-101093170,101093228-101093312,101093383-101093760,101093799-101095469,101095581-101095758,101095868-101095986,101096077-101096231,101096303-101096448,101096531-101096644,101096751-101096860,101096946-101097712,101097868-101098092,101098278-101112475,
NXNL2	NM_001161625	chr9	91150652-91159292,
NXNL2	NM_145283	chr9	91150652-91186000,91186124-91190000,
NXPH4	NM_007224	chr12	57610810-57618659,
OGDHL	NM_001143997	chr10	50943398-50944067,50944224-50944401,50944567-50945830,50945905-50945991,50946119-50946235,50946309-50947705,50947886-50948754,50948884-50950872,50951025-50952038,50952169-50952694,50952799-50953388,50953543-50953842,50954024-50954794,50954925-50955073,50955255-50957770,50957863-50958883,50959032-50959871,50960028-50960177,50960295-50960682,50960787-50970283,
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OGDHL	NM_018245	chr10	50943398-50944067,50944224-50944401,50944567-50945830,50945905-50945991,50946119-50946235,50946309-50947705,50947886-50948754,50948884-50950872,50951025-50952038,50952169-50952694,50952799-50953388,50953543-50953842,50954024-50954794,50954925-50955073,50955255-50957770,50957863-50958883,50959032-50959871,50960028-50960177,50960295-50960682,50960787-50964820,50964993-50966433,50966640-50970283,
OIP5	NM_007280	chr15	41602048-41605469,41605553-41611854,41611979-41624111,41624180-41624436,
OLIG2	NM_005806	chr21	34398335-34399107,
OMA1	NM_145243	chr1	58946847-58971730,58971882-58992931,58993008-58996271,58996402-58999623,58999733-58999828,59000004-59002183,59002414-59004465,59004983-59012373,
ONECUT2	NM_004852	chr18	55104177-55143667,
OPN3	NM_014322	chr1	241757994-241761046,241761300-241767560,241767882-241803182,
ORC6	NM_014321	chr16	46723683-46724901,46725033-46726292,46726458-46727003,46727095-46729472,46729587-46729927,46729998-46731368,
OSBP2	NM_030758	chr22	31091541-31137146,31137357-31266414,31266670-31283411,31283606-31284208,31284328-31285162,31285222-31285475,31285624-31286713,31286961-31289107,31289230-31289448,31289554-31289623,31289721-31289802,31289989-31301822,31302057-31302182,
OSCP1	NM_145047	chr1	36883857-36884590,36884656-36886075,36886217-36887749,36887821-36888367,36888498-36888962,36889068-36897401,36897484-36898021,36898191-36904355,36904512-36915857,
OSCP1	NM_206837	chr1	36894077-36897401,36897484-36898021,36898191-36904355,36904512-36915857,
OTOL1	NM_001080440	chr3	161214960-161216957,161217049-161220093,161220158-161220812,

OTP	NM_032109	chr5	76926620-76932644,76933056-76934336,
OXR1	NM_001198533	chr8	107282596-107371702,107371865-107531169,107531368-107691436,107691521-107695425,107695535-107696472,107696588-107704954,107705106-107715132,107715319-107718608,107719374-107722848,107723019-107726049,107726214-107749746,107749829-107751684,107751812-107752569,107752724-107754448,107754546-107758015,107758091-107763032,
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OXR1	NM_001198535	chr8	107738538-107751684,107751812-107752569,107752724-107754448,107754546-107758015,107758091-107763032,
P2RX4	NM_002560	chr12	121648102-121654935,121655085-121659714,121659788-121659895,121659970-121660748,121660847-121666334,121666417-121666526,121666670-121666764,121666903-121670215,121670311-121670412,121670480-121670798,121670896-121671324,
P4HA1	NM_001017962	chr10	74768051-74769563,74769662-74770725,74770796-74773980,74774048-74776602,74776654-74790023,74790129-74804737,74804810-74806681,74806860-74810809,74811008-74813107,74813349-74828602,74828742-74831785,74831939-74833487,74833586-74834564,74834674-74856522,
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P4HA1	NM_000917	chr10	74768051-74769563,74769662-74770725,74770796-74773980,74774048-74776602,74776654-74790023,74790129-74803643,74803716-74806681,74806860-74810809,74811008-74813107,74813349-74828602,74828742-74831785,74831939-74833487,74833586-74834564,74834674-74856522,
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PABPN1L	NM_001080487	chr16	88930204-88930643,88930788-88931259,88931349-88931428,88931537-88931969,88932039-88932212,88932350-88932758,
PACRGL	NM_001130727	chr4	20702411-20706087,20706157-20706281,20706438-20715053,20715163-20728906,
PACRGL	NM_145048	chr4	20702411-20706087,20706157-20706281,20706438-20709424,20709494-20711304,20711397-20714409,20714546-20715053,20715163-20728906,
PACSIN2	NM_001184970	chr22	43267476-43272141,43272340-43272892,43273017-43275052,43275176-43278188,43278311-43280390,43280568-43284647,43284805-43286951,43287189-43289461,43289620-43308025,43308164-43411025,
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PAIP1	NM_182789	chr5	43527572-43529886,43529982-43533838,43533895-43534953,43535073-43535634,43535743-43536919,43537047-43539024,43539138-43543104,43543219-43547828,43548016-43555930,43556102-43556919,
PAIP1	NM_183323	chr5	43527572-43529886,43529982-43533838,43533895-43534953,43535073-43535634,43535743-43536919,43537047-43539024,43539138-43543104,43543219-43547828,43548016-43555930,43556102-43557440,
PAIP1	NM_006451	chr5	43527572-43529886,43529982-43533838,43533895-43534953,43535073-43535634,43535743-43536919,43537047-43539024,43539138-43543104,43543219-43547828,43548016-43555930,43556102-43556682,
PALM	NM_002579	chr19	709152-726136,726190-727006,727089-727562,727695-731093,731246-734171,734195-736017,736079-740350,740484-746283,
PALM	NM_001040134	chr19	709152-726136,726190-727006,727089-727562,727695-731093,731246-734171,734195-736017,736079-746283,
PAPD7	NM_006999	chr5	6714813-6737621,6737747-6738794,6738843-6739843,6739966-6742601,6742711-6743823,6743954-6746325,6746541-6748575,6748704-6749668,6749771-6750442,6750617-6751150,6751311-6752984,6753151-6754862,
PAPD7	NM_001171806	chr5	6746541-6748575,6748704-6749668,6749771-6750442,6750617-6751150,6751311-6752984,6753151-6754862,
PAPD7	NM_001171805	chr5	6714813-6737621,6737747-6738794,6738843-6739843,6739966-6742601,6742711-6743823,6743954-6746325,6746541-6748575,6748704-6749668,6749771-6750442,6750617-6751150,6751311-6752984,6753151-6754865,
PAQR7	NM_178422	chr1	26190353-26197098,
PARD3	NM_001184786	chr10	34400491-34408539,34408669-34420389,34420512-34558583,34558828-34573061,34573174-34606033,34606267-34620043,34620273-34625125,34625172-34626201,34626355-34630553,34630745-34636891,34637044-34648073,34648246-34648997,34649188-34663800,34663931-34666893,34667035-34671466,34671851-34673055,34673183-34688256,34688342-34690752,34690846-34739243,34739377-34759011,34759192-34805905,34806088-34985244,34985348-35103802,
PARD3	NM_019619	chr10	34400491-34408539,34408669-34420389,34420512-34558583,34558828-34573061,34573174-34606033,34606267-34620043,34620273-34625125,34625172-34626201,34626355-34630553,34630745-34636882,34637044-34648073,34648246-34648997,34649188-34661424,34661465-34663800,34663931-34666893,34667035-34671466,34671851-34673055,34673183-34688256,34688342-34690752,34690846-34739243,34739377-34759011,34759192-34805905,34806088-34985244,34985348-35103802,
PARD3	NM_001184790	chr10	34400491-34408539,34408669-34420389,34420512-34558583,34558828-34573061,34573174-34606033,34606267-34620043,34620273-34625125,34625172-34626291,34626355-34630553,34630745-34636891,34637044-34648073,34648246-34648997,34649188-34663800,34663931-34666893,34667035-34671466,34671851-34673055,34673183-34688256,34688342-34690752,34690846-34759011,34759192-34805905,34806088-34985244,34985348-35103802,
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PARD3	NM_001184794	chr10	34601311-34606033,34606267-34620043,34620273-34625125,34625172-34626291,34626355-34630553,34630745-34636891,34637044-34648073,34648246-34648997,34649188-34663800,34663931-34666893,34667035-34671466,34671851-34673055,34673183-34688256,34688342-34690752,34690846-34739243,34739377-34759011,34759192-34805905,34806088-34985244,34985348-35103802,
PARD3	NM_001184791	chr10	34400491-34408539,34408669-34420389,34420512-34558583,34558828-34606033,34606267-34620043,34620273-34626201,34626355-34630553,34630745-34636891,34637044-34648073,34648246-34648997,34649188-34663800,34663931-34666893,34667035-34671466,34671851-34673055,34673183-34688256,34688342-34690752,34690846-34759011,34759192-34805905,34806088-34985244,34985348-35103802,
PARD3	NM_001184792	chr10	34601311-34606033,34606267-34620043,34620273-34625125,34625172-34626201,34626355-34630553,34630745-34636891,34637044-34648073,34648246-34648997,34649188-34661424,34661465-34663800,34663931-34666893,34667035-34671466,34671851-34673055,34673183-34688256,34688342-34690752,34690846-34739243,34739377-34759011,34759192-34805905,34806088-34985244,34985348-35103802,

PARD3	NM_001184787	chr10	34400491-34408539,34408669-34420389,34420512-34558583,34558828-34606033,34606267-34620043,34620273-34625125,34625172-34626201,34626355-34630553,34630745-34636882,34637044-34648073,34648246-34648997,34649188-34661424,34661465-34663800,34663931-34666893,34667035-34671466,34671851-34673055,34673183-34688256,34688342-34690752,34690846-34739243,34739377-34759011,34759192-34805905,34806088-34985244,34985348-35103802,
PARD3	NM_001184789	chr10	34400491-34408539,34408669-34420389,34420512-34558583,34558828-34606033,34606267-34620043,34620273-34625125,34625172-34626291,34626355-34630553,34630745-34636891,34637044-34648073,34648246-34648997,34649188-34663800,34663931-34666893,34667035-34671466,34671851-34673055,34673183-34688256,34688342-34690752,34690846-34739243,34739377-34759011,34759192-34805905,34806088-34985244,34985348-35103802,
PARD3	NM_001184793	chr10	34601311-34606033,34606267-34620043,34620273-34625125,34625169-34626291,34626355-34630553,34630745-34636891,34637044-34648073,34648246-34648997,34649188-34661424,34661465-34663800,34663931-34666893,34667035-34671466,34671851-34673055,34673183-34688256,34688342-34690752,34690846-34739243,34739377-34759011,34759192-34805905,34806088-34985244,34985348-35103802,
PARP11	NM_020367	chr12	3921606-3923201,3923355-3931037,3931170-3931249,3931324-3935322,3935400-3938074,3938197-3939054,3939185-3982376,
PARP3	NM_001003931	chr3	51976725-51977368,51977555-51978103,51978234-51978404,51978595-51978792,51978927-51979012,51979241-51979509,51979661-51979867,51979956-51980180,51980360-51981754,51981912-51982325,
PARP3	NM_005485	chr3	51976725-51977363,51977555-51978103,51978234-51978404,51978595-51978792,51978927-51979012,51979241-51979509,51979661-51979867,51979956-51980180,51980360-51981754,51981912-51982325,
PCDH11X	NM_032968	chrX	91091044-91131778,91134273-91456372,91456455-91518111,91518143-91642732,91642933-91723296,91723322-91873261,
PCDH11X	NM_001168360	chrX	91091044-91131778,91134273-91456372,91456455-91518111,91518143-91642732,91642933-91873261,
PCDH11X	NM_032969	chrX	91091044-91131778,91134273-91456372,91456455-91642732,91642933-91723296,91723322-91873261,
PCDH11X	NM_032967	chrX	91034684-91065470,91065578-91066234,91066295-91090458,91091044-91131778,91134273-91137904,
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PCDH11X	NM_001168362	chrX	91091044-91131778,91134273-91642732,91642933-91723296,91723322-91873261,
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PCDH12	NM_016580	chr5	141325371-141328995,141329149-141331056,141331156-141334535,
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PCDHGA7	NM_018920	chr5	140764891-140874372,140874433-140884958,140885049-140890512,
PCDHGB4	NM_003736	chr5	140769849-140874372,140874433-140884958,140885049-140890512,
PCGF3	NM_006315	chr4	699760-724417,724458-724757,724900-727459,727579-728718,728817-731253,731311-737260,737373-738386,738477-755065,755205-758770,758853-759818,
PCOLCE	NM_002593	chr7	100200175-100201051,100201162-100201580,100201841-100202712,100202839-100203297,100203436-100204037,100204254-100205073,100205147-100205258,100205431-100205558,
PDE11A	NM_001077197	chr2	178494291-178528592,178528678-178534219,178534296-178540181,178540247-178545552,178545632-178562058,178562161-178565847,178565940-178576495,178576607-178592384,178592494-178592752,178592901-178634049,178634102-178681554,178681649-178682583,178682653-178684945,178685023-178704976,178705111-178740584,178740651-178762783,178762926-178769823,178769915-178879027,178879188-178969027,178969204-178972979,
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PDE11A	NM_001077196	chr2	178494291-178528592,178528678-178534219,178534296-178540181,178540247-178545552,178545632-178562058,178562161-178565847,178565940-178576495,178576607-178592384,178592494-178592752,178592901-178634049,178634102-178681554,178681649-178682583,178682653-178684945,178685023-178704976,178705111-178740584,178740651-178753344,
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PDE4A	NM_001111308	chr19	10541763-10556892,10557086-10559591,10559630-10559754,10559827-10561277,10561329-10561503,10561618-10565503,10565599-10568553,10568779-10570074,10570175-10570269,10570436-10571678,10571780-10572200,10572357-10572551,10572676-10574467,10574652-10577561,
PDE4A	NM_001111307	chr19	10531761-10556892,10557086-10559591,10559630-10559754,10559827-10561277,10561329-10561503,10561618-10565503,10565599-10568553,10568779-10570074,10570175-10570269,10570436-10571678,10571780-10572200,10572357-10572551,10572676-10574467,10574652-10577561,
PDE4A	NM_006202	chr19	10564006-10565503,10565599-10568553,10568779-10570074,10570175-10570269,10570436-10571678,10571780-10572200,10572357-10572551,10572676-10574467,10574652-10577561,
PDE4A	NM_001111309	chr19	10543248-10556892,10557086-10559591,10559630-10559754,10559827-10561277,10561329-10561503,10561618-10565503,10565599-10568553,10568779-10570074,10570175-10570269,10570436-10571678,10571780-10572200,10572357-10572551,10572676-10574467,10574652-10577561,
PDE6B	NM_001145291	chr4	619884-628464,628619-629667,629759-647639,647782-647867,647944-648611,648678-649727,649796-650032,650082-650661,650813-651138,651284-652739,652807-654254,654403-655921,656031-656296,656408-656887,656977-657557,657660-657901,658011-658668,658734-659042,659119-660318,660404-661643,661796-663836,
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PDE6B	NM_000283	chr4	619884-628464,628619-629667,629759-647639,647782-647867,647944-648611,648678-649727,649796-650032,650082-650661,650813-651138,651284-652739,652807-654254,654403-655921,656031-656296,656408-656887,656977-657557,657660-657901,658011-658668,658734-659042,659119-660318,660404-661643,661796-663833,
PDE8A	NM_173454	chr15	85525580-85607599,85607658-85610243,85610436-85619091,85619150-85619962,85620019-85626785,85626876-85632567,85632648-85641177,85641268-85643244,85643298-85643385,85643430-85652282,85652362-85656606,85656679-85657102,85657269-85658668,85658719-85659213,85659351-85660870,85661071-85664026,85664246-85666290,85666425-85669436,85669606-85679763,85679895-85681026,
PDE8A	NM_002605	chr15	85525580-85607599,85607658-85610243,85610436-85619091,85619150-85619962,85620019-85626785,85626876-85632567,85632648-85634273,85634413-85641177,85641268-85643244,85643298-85643385,85643430-85652282,85652362-85656606,85656679-85657102,85657269-85658668,85658719-85659213,85659351-85660870,85661071-85664026,85664246-85666290,85666425-85669436,85669606-85679763,85679895-85681026,
PDIA5	NM_006810	chr3	122786054-122808013,122808142-122811200,122811290-122821256,122821342-122821596,122821644-122825594,122825689-122829789,122829852-122835076,122835146-122842911,122843005-122843117,122843191-122849325,122849464-122864367,122864440-122864944,122865107-122869079,122869212-122873816,122873889-122880166,122880303-122880725,
PDIA5	NR_028444	chr3	122786054-122808013,122808142-122811200,122811290-122821256,122821342-122821596,122821644-122825594,122825689-122829789,122829852-122835076,122835146-122842911,122843005-122843117,122843191-122864367,122864440-122864963,122865107-122869079,122869212-122873816,122873889-122880166,122880303-122880725,
PDIA6	NM_005742	chr2	10924453-10925058,10925157-10927405,10927566-10928821,10928896-10929021,10929108-10929873,10930016-10930843,10930960-10931919,10932052-10933220,10933329-10937205,10937334-10937824,10937884-10942623,10942767-10952802,
PDSS2	NM_020381	chr6	107475982-107515024,107515059-107531641,107531775-107533311,107533487-107566750,107566824-107595231,107595432-107655400,107655537-107780192,
PDXDC2P	NR_003610	chr16	70010636-70010712,70011907-70011978,70012016-70016251,70016398-70016559,70016661-70020282,70020413-70023857,70024112-70024498,70024587-70029970,70030130-70030291,70030372-70044652,70044760-70045742,70045833-70048005,70048071-70051948,70052001-70055725,70055853-70057280,70057381-70057531,70057582-70058487,70058574-70064889,70064970-70065801,70065872-70068072,70068264-70070333,70070482-70072806,70072889-70076252,70076320-70076831,70076907-70099657,
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PDZD3	NR_033122	chr11	119056220-119056632,119056662-119056799,119056951-119057186,119057400-119057977,119058169-119058271,119058410-119058647,119058854-119059062,119059261-119059347,119059577-119059712,119059915-119060170,
PDZD3	NM_024791	chr11	119056220-119056632,119056662-119056799,119056875-119057186,119057400-119057977,119058169-119058271,119058368-119058647,119058854-119059062,119059261-119059347,119059577-119059712,119059915-119060170,
PECI	NM_006117	chr6	4116264-4117540,4117686-4119418,4119510-4125482,4125605-4126367,4126472-4127994,4128066-4130604,4130795-4130999,4131100-4133781,4133936-4135743,
PECI	NM_001166010	chr6	4116264-4117540,4117686-4119418,4119510-4125482,4125605-4126367,4126472-4127994,4128066-4130604,4130795-4130999,4131100-4133781,4133936-4135602,
PECI	NR_028588	chr6	4116264-4117540,4117686-4119418,4119510-4125482,4125605-4126367,4126472-4127994,4128066-4130411,4130484-4130604,4130795-4130999,4131100-4133781,4133936-4135743,
PECI	NM_206836	chr6	4116264-4117540,4117686-4119418,4119510-4125482,4125605-4126367,4126472-4127994,4128066-4130604,4130795-4130999,4131100-4133781,4133946-4135743,
PERP	NM_022121	chr6	138413406-138417489,138417632-138428262,
PGA3	NM_001079807	chr11	60971093-60971577,60971742-60973980,60974100-60974967,60975088-60975761,60975963-60977312,60977431-60978560,60978707-60978807,60978908-60980023,
PGK1	NM_000291	chrX	77359903-77365362,77365415-77369239,77369397-77369511,77369658-77372807,77372913-77373546,77373668-77378330,77378447-77378690,77378872-77380369,77380549-77380822,77380923-77381285,
PGR	NM_000926	chr11	100910003-100912674,100912834-100920658,100920791-100922153,100922300-100933176,100933484-100962489,100962608-

			100996736,100996890-100998163,
PHACTR2	NM_001100166	chr6	143929460-144033151,144033321-144070120,144070203-144074889,144075050-144086396,144086936-144093393,144093595-144095194,144095353-144098463,144098521-144104354,144104418-144109908,144110048-144128192,144128271-144144809,
PHACTR2	NM_014721	chr6	143929460-144033151,144033321-144070120,144070203-144074889,144075050-144081536,144081778-144086396,144086936-144093393,144093595-144095194,144095353-144098463,144098521-144104354,144104418-144109908,144110048-144128192,144128271-144144809,
PHACTR2	NM_001100165	chr6	143999347-144033151,144033321-144070120,144070203-144074889,144075050-144086396,144086936-144093393,144093595-144095194,144095353-144098463,144098521-144104354,144104418-144109908,144110048-144128192,144128271-144144809,
PHACTR2	NM_001100164	chr6	143999347-144033151,144033321-144070120,144070203-144074889,144075050-144081536,144081778-144086396,144086936-144093393,144093595-144095194,144095353-144098463,144098521-144104354,144104418-144109908,144110048-144128192,144128271-144144809,
PHF11	NM_001040443	chr13	50070232-50080769,50080893-50087193,50087303-50092152,50092288-50095028,50095077-50096177,50096244-50097309,50097378-50098219,50098353-50100521,50100595-50102645,
PHF11	NM_001040444	chr13	50070619-50071190,50071354-50080769,50080893-50087193,50087303-50092152,50092288-50095028,50095077-50096177,50096244-50097309,50097378-50098219,50098353-50100521,50100595-50102645,
PHF2	NM_005392	chr9	96339154-96392250,96392338-96398691,96398808-96407909,96408072-96411351,96411495-96415459,96415648-96416693,96416858-96418214,96418304-96418769,96418878-96420425,96420519-96421791,96421883-96422472,96422843-96425187,96425309-96425797,96425918-96427966,96428147-96428270,96428343-96429360,96429523-96435865,96436145-96437207,96437305-96437960,96438072-96438874,96439246-96439868,
PHGR1	NM_001145643	chr15	40643264-40645431,40645469-40648264,
PHIP	NM_017934	chr6	79651048-79655015,79655215-79655716,79655978-79656426,79656592-79657338,79657493-79664529,79664681-79664947,79665000-79665328,79665400-79668190,79668318-79671405,79671528-79672812,79672970-79675418,79675482-79675660,79675774-79679550,79679635-79679764,79679891-79680496,79680606-79688307,79688429-79692601,79692835-79695067,79695146-79697924,79698067-79700583,79700703-79707129,79707315-79707969,79708109-79711614,79711842-79713445,79713576-79724797,79724934-79725345,79725501-79726259,79726360-79727061,79727104-79727198,79727301-79728804,79728877-79735234,79735337-79735658,79735882-79752558,79752721-79770193,79770294-79770383,79770536-79787163,79787225-79787415,79787447-79787570,79787631-79787744,
PHKB	NM_000293	chr16	47495338-47531308,47531400-47533665,47533806-47536900,47537002-47545574,47545684-47549430,47549513-47581342,47581460-47614204,47614270-47621577,47621675-47622814,47623014-47627409,47627469-47628046,47628126-47630282,47630443-47644735,47644832-47674944,47675002-47675508,47675604-47682442,47682528-47683009,47683116-47684453,47684538-47684740,47684833-47694415,47694479-47694566,47694731-47695628,47695712-47697586,47697646-47698794,47698887-47703124,47703329-47722950,47723087-47727287,47727419-47730290,47730400-47732357,47732500-47733138,
PHKB	NM_001031835	chr16	47495338-47497791,47497905-47531308,47531400-47533665,47533806-47536900,47537002-47545574,47545684-47549430,47549513-47581342,47581460-47614204,47614270-47621577,47621675-47622814,47623014-47627409,47627469-47628046,47628126-47630282,47630443-47644735,47644832-47674944,47675002-47675508,47675604-47682442,47682528-47683009,47683116-47684453,47684538-47684740,47684833-47694415,47694479-47694566,47694731-47695628,47695712-47697586,47697646-47699851,47699944-47703124,47703329-47722950,47723087-47727287,47727419-47730290,47730400-47732357,47732500-47733138,
PHKG2	NM_001172432	chr16	30759812-30760122,30760237-30762425,30762603-30762868,30762925-30764551,30764619-30764713,30764879-30767501,30767594-30767686,30767842-30767909,30768037-30768123,30768281-30771438,
PHKG2	NM_000294	chr16	30759812-30760122,30760237-30762425,30762603-30762868,30762925-30764551,30764619-30764713,30764879-30767501,30767594-30767686,30767842-30767909,30768037-30768123,
PHLDB1	NM_001144759	chr11	118478415-118484529,118484612-118485272,118485398-118486754,118486927-118495648,118495776-118498019,118499367-118501922,118502197-118502628,118502771-118502874,118503014-118506109,118506267-118509607,118509720-118509878,118509970-118514516,118514659-118514788,118514893-118516072,118516369-118516451,118516544-118518644,118518793-118520780,118520899-118521148,118521253-118526313,118526401-118527391,

PHLDB1	NM_001144758	chr11	118478415-118484529,118484612-118485272,118485398-118486754,118486927-118495648,118495776-118498019,118499367-118501922,118502197-118502628,118502771-118502874,118503014-118506109,118506267-118509607,118509720-118509878,118509970-118512970,118513113-118514516,118514659-118514788,118514893-118516072,118516369-118516451,118516544-118518644,118518793-118520780,118520899-118521148,118521253-118526313,118526401-118526568,118526603-118527391,
PHLDB1	NM_015157	chr11	118477388-118484007,118484166-118484529,118484612-118485272,118485398-118486754,118486927-118495648,118495776-118498019,118499367-118501922,118502197-118502628,118502771-118502874,118503014-118506109,118506267-118509607,118509720-118509878,118509970-118512970,118513113-118514516,118514659-118514788,118514893-118516072,118516369-118516451,118516544-118518644,118518793-118520780,118520899-118521148,118521253-118526313,118526401-118526568,118526603-118527391,
PHTF1	NM_006608	chr1	114240348-114240882,114241010-114242324,114242422-114243414,114243572-114246701,114246790-114247286,114247420-114248510,114248785-114249214,114249345-114252874,114253098-114254366,114254458-114254560,114254736-114255899,114256061-114267379,114267516-114269038,114269197-114280730,114280891-114281350,114281422-114300319,114300378-114301279,
PHYHD1	NM_001100877	chr9	131684636-131689315,131689476-131696059,131696137-131696288,131696338-131698725,131698783-131700034,131700058-131702646,131702777-131702876,131702995-131703722,131703851-131703945,
PHYHD1	NM_001100876	chr9	131683948-131684207,131684327-131684560,131684636-131689315,131689476-131696059,131696137-131696288,131696338-131698725,131698783-131698860,131698925-131700034,131700058-131702646,131702777-131702876,131702995-131703722,131703851-131703945,
PHYHD1	NM_174933	chr9	131683948-131684207,131684327-131684560,131684636-131689315,131689476-131696059,131696137-131696288,131696338-131698725,131698783-131698860,131698925-131702646,131702777-131702876,131702995-131703722,131703851-131703945,
PI3	NM_002638	chr20	43803643-43804500,43804778-43805009,
PIAS1	NM_016166	chr15	68346689-68378642,68379089-68434282,68434369-68434626,68434676-68438152,68438245-68438902,68439039-68445926,68446034-68457067,68457143-68466068,68466231-68467973,68468106-68468810,68468993-68473548,68473693-68475966,68476006-68479878,
PIAS4	NM_015897	chr19	4007786-4012919,4013348-4024032,4024119-4028142,4028186-4028506,4028599-4028716,4028847-4028927,4029035-4033096,4033172-4033416,4033579-4037370,4037503-4037612,
PIF1	NM_025049	chr15	65108557-65108771,65108965-65110143,65110291-65110454,65110544-65111314,65111423-65112044,65112186-65113179,65113288-65113364,65113481-65113564,65113720-65114463,65114591-65114675,65114810-65115975,65116554-65117790,
PIGA	NM_002641	chrX	15339895-15342785,15342994-15343140,15343275-15344034,15344169-15349336,15350115-15353621,
PIGA	NM_020473	chrX	15339895-15342785,15342994-15343140,15343275-15344034,15344169-15353621,
PIGA	NR_033835	chrX	15339895-15342785,15342994-15343140,15343275-15344034,15344169-15349710,15350115-15353621,
PIGA	NR_033836	chrX	15339895-15342785,15342994-15343140,15343275-15344034,15344169-15349994,15350115-15353621,
PIGG	NM_001127178	chr4	493279-494183,494391-499505,499717-501192,501383-502616,502760-509760,509975-514843,515063-515447,515731-517246,517703-520826,521020-524223,524535-527605,527771-532940,
PIGG	NM_017733	chr4	493279-494183,494391-499505,499717-501192,501383-502616,502760-509760,509975-514843,515039-515447,515731-517246,517703-520826,521020-524223,524535-527605,527771-532940,
PIGL	NM_004278	chr17	16120776-16137283,16137385-16203200,16203293-16216859,16216929-16219993,16220027-16221087,16221223-16229112,
PIH1D2	NM_001082619	chr11	111934946-111941158,111941426-111941760,111942008-111942357,111942483-111943720,111943930-111944702,
PIH1D2	NM_138789	chr11	111938730-111941158,111941426-111941760,111942008-111942357,111942483-111943720,111943930-111944702,
PINK1	NM_032409	chr1	20960429-20964333,20964623-20966383,20966486-20970981,20971166-20972051,20972217-20974996,20975126-20975486,20975725-20976925,
PNR	NM_003662	chrX	15403239-15408305,15408374-15415569,15415654-15425626,15425673-15444027,15444114-15473969,15474178-15477778,15477864-15497850,15497945-15509283,15509433-15511277,
PNR	NM_001018109	chrX	15403239-15408305,15408374-15415569,15415654-15425626,15425673-15444027,15444114-15473969,15474178-15477778,15477864-15497850,15497945-15509283,15509433-15511311,
PITX3	NM_005029	chr10	103990859-103991343,103991548-103991718,103991850-104001088,
PLA2G16	NM_001128203	chr11	63342519-63357570,63357841-63365531,63365636-63381470,63381541-63381855,
PLA2G16	NM_007069	chr11	63342519-63357570,63357841-63365531,63365636-63381470,

PLA2G2E	NM_014589	chr1	20246943-20248789,20248898-20249108,20249249-20250011,
PLA2G7	NM_005084	chr6	46672434-46672888,46673039-46675726,46675899-46677062,46677156-46678280,46678396-46679231,46679357-46680004,46680075-46682195,46682291-46684119,46684266-46684710,46684834-46690518,46690663-46702915,
PLA2G7	NM_001168357	chr6	46672434-46672888,46673039-46675726,46675899-46677062,46677156-46678280,46678396-46679231,46679357-46680004,46680075-46682195,46682291-46684119,46684266-46684710,46684834-46690518,46690663-46703285,
PLA2R1	NM_001007267	chr2	160803429-160803928,160804071-160806117,160806288-160807849,160808090-160811708,160811858-160812207,160812340-160813019,160813139-160824048,160824190-160825765,160825871-160826657,160826724-160832577,160832737-160833194,160833232-160833793,160833928-160836339,160836426-160840437,160840585-160843665,160843870-160862161,160862333-160869772,160869887-160873123,160873224-160876615,160876775-160879174,160879371-160884727,160884873-160885359,160885475-160889468,160889644-160898534,160898710-160901283,160901669-160918804,
PLA2R1	NM_001195641	chr2	160798504-160798636,160798671-160801415,160801594-160803316,160803429-160803928,160804071-160806117,160806288-160807849,160808090-160811708,160811858-160812207,160812340-160813019,160813139-160824048,160824190-160825765,160825871-160826657,160826724-160832577,160832737-160833194,160833232-160833793,160833928-160836339,160836426-160840437,160840585-160843665,160843870-160862161,160862333-160869772,160869887-160873123,160873224-160876615,160876775-160879174,160879371-160884727,160884873-160885359,160885475-160889468,160889644-160898534,160898710-160901283,160901669-160918804,
PLA2R1	NM_007366	chr2	160798504-160798636,160798671-160801415,160801594-160803310,160803429-160803928,160804071-160806117,160806288-160807849,160808090-160811708,160811858-160812207,160812340-160813019,160813139-160824048,160824190-160825765,160825871-160826657,160826724-160832577,160832737-160833194,160833232-160833793,160833928-160836339,160836426-160840437,160840585-160843665,160843870-160862161,160862333-160869772,160869887-160873123,160873224-160876615,160876775-160879174,160879371-160884727,160884873-160885359,160885475-160889468,160889644-160898534,160898710-160901283,160901669-160918804,
PLCD3	NM_133373	chr17	43190073-43190229,43190381-43190488,43190626-43190805,43190974-43191616,43191735-43192460,43192612-43192709,43192858-43193997,43194152-43195359,43195506-43195656,43195860-43196180,43196411-43197690,43197822-43198267,43198498-43198576,43198740-43209613,
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PLD1	NM_002662	chr3	171321093-171323087,171323207-171330067,171330223-171338174,171338311-171360628,171360680-171362698,171362814-171377001,171377092-171379848,171379961-171392288,171392404-171394503,171394624-171395354,171395485-171404473,171404589-171405159,171405375-171406464,171406667-171410120,171410233-171417533,171417617-171426543,171426629-171427348,171427500-171431681,171431836-171442484,171442579-171443806,171443867-171451232,171451300-171452653,171452761-171453280,171453428-171455320,171455450-171455680,171455873-171528187,
PLD1	NM_001130081	chr3	171321093-171323087,171323207-171330067,171330223-171338174,171338311-171360628,171360680-171362698,171362814-171377001,171377092-171379848,171379961-171392288,171392404-171394503,171394624-171395354,171395485-171405159,171405375-171406464,171406667-171410120,171410233-171417533,171417617-171426543,171426629-171427348,171427500-171431681,171431836-171442484,171442579-171443806,171443867-171451232,171451300-171452653,171452761-171453280,171453428-171455320,171455450-171455680,171455873-171528187,
PLD2	NM_002663	chr17	4710521-4711065,4711177-4711277,4711410-4711567,4711712-4712393,4712501-4712591,4712659-4712786,4712847-4712984,4713079-4713170,4713325-4714095,4714247-4717711,4717797-4717926,4718007-4718769,4718882-4719057,4719230-4719913,4720042-4720230,4720351-4720439,4720555-4721295,4721402-4721590,4721681-4721787,4721903-4722067,4722119-4722377,4722514-4722722,4722878-4725086,4725203-4725933,
PLEKHA8	NM_001197026	chr7	30068419-30084699,30084818-30085824,30085982-30087446,30087573-30088838,30088999-30090048,30090091-30092323,30092483-30094323,30094482-30094871,30094959-30100498,30100559-30101511,30101644-30102286,30102359-30113685,30113749-30118204,
PLEKHA8	NM_032639	chr7	30068419-30084699,30084818-30085824,30085982-30087446,30087573-30088838,30088999-30090048,30090091-30092323,30092483-30094323,30094482-30094871,30094959-30100498,30100559-30101511,30101644-30102286,30102359-30129767,

PLEKHA8	NM_001197027	chr7	30068419-30084699,30084818-30085824,30085982-30087446,30087573-30088838,30088999-30090048,30090091-30092323,30092483-30094323,30094482-30094871,30094959-30100498,30100559-30101511,30101644-30102286,30102359-30113685,30113749-30157584,
PLEKHG1	NM_001029884	chr6	150921154-150971862,150971923-151054718,151055229-151089772,151089875-151107524,151107596-151116990,151117039-151121853,151122006-151125744,151125878-151130239,151130424-151130515,151130613-151130782,151130871-151139317,151139353-151140813,151140911-151142329,151142370-151144788,151144813-151151716,151153342-151160967,
PLEKHM1P	NR_024386	chr17	62781486-62782683,62782843-62783364,62783430-62788465,62788661-62793380,62793528-62796116,62797036-62800946,62801219-62817883,62818171-62818370,62818512-62825277,62825368-62833172,
PLEKHM2	NM_015164	chr1	16011114-16042730,16042839-16043200,16043312-16044386,16044488-16045031,16045121-16046227,16046416-16047822,16047884-16051810,16052041-16053507,16054328-16054572,16054644-16054760,16054853-16055162,16055229-16055595,16055686-16056290,16056425-16057025,16057218-16057685,16057753-16058382,16058544-16058843,16059025-16059105,16059224-16060290,
PMAIP1	NM_021127	chr18	57567468-57569877,
PNKP	NM_007254	chr19	50364623-50364704,50364768-50364863,50364953-50365027,50365139-50365299,50365363-50365440,50365539-50365626,50365721-50365793,50365866-50365945,50365996-50366944,50367018-50367219,50367329-50367434,50367494-50367579,50367661-50368382,50368684-50369654,50369703-50370309,50370475-50370724,
PNMA2	NM_007257	chr8	26366760-26367062,26367194-26371330,
PNPLA4	NM_004650	chrX	7868859-7870028,7870183-7880067,7880135-7889752,7889890-7890043,7890140-7893979,7894174-7895325,
PNPLA4	NM_001142389	chrX	7868859-7870028,7870183-7880067,7880135-7889752,7889890-7890043,7890140-7893979,7894174-7895725,
PNPLA4	NM_001172672	chrX	7868859-7870028,7870183-7880067,7880135-7889752,7889890-7890043,7890140-7895725,
POC1A	NM_001161581	chr3	52110002-52130583,52130729-52156393,52156494-52159127,52159198-52172183,52172319-52179860,52179978-52181002,52181112-52183224,52183406-52183830,52184004-52185030,52185188-52188369,
POC1A	NM_001161580	chr3	52110002-52156393,52156494-52159127,52159198-52172183,52172319-52179860,52179978-52181002,52181112-52183224,52183406-52183830,52184004-52185030,52185117-52188369,
POC1A	NM_015426	chr3	52110002-52130583,52130729-52156393,52156494-52159127,52159198-52172183,52172319-52179860,52179978-52181002,52181112-52183224,52183406-52183830,52184004-52185030,52185117-52188369,
PODXL2	NM_015720	chr3	127348133-127358086,127358367-127379219,127380003-127381078,127381155-127387282,127387441-127387982,127388046-127390275,127390457-127391109,
POLDIP3	NM_178136	chr22	42981975-42983510,42983579-42987959,42988091-42991541,42991621-42992190,42992372-42995702,42995800-42998774,42999167-43010803,
POLDIP3	NM_032311	chr22	42981975-42983510,42983579-42987959,42988091-42991541,42991621-42992190,42992372-42995702,42995800-42997974,42998063-42998774,42999167-43010803,
POLG2	NM_007215	chr17	62474106-62476404,62476507-62479034,62479117-62481843,62481986-62486911,62487087-62488782,62488890-62489010,62489139-62492523,
POLQ	NM_199420	chr3	121151265-121151763,121151881-121154967,121155123-121158837,121158964-121168160,121168274-121178895,121179082-121186364,121186488-121187150,121187279-121190835,121191012-121192195,121192335-121195385,121195581-121200417,121200660-121202231,121202430-121203886,121204032-121206147,121209256-121212323,121212569-121215653,121215780-121217322,121217518-121228406,121228551-121228884,121229091-121230732,121230877-121238716,121238931-121240848,121240997-121248490,121248640-121251835,121252057-121255945,121256056-121258278,121258437-121260194,121260327-121263572,121263754-121264560,
POLR2D	NM_004805	chr2	128605760-128608162,128608260-128610497,128610580-128615600,
POLR3K	NM_016310	chr16	97558-101556,101646-103474,
POMT2	NM_013382	chr14	77743825-77744735,77744852-77745070,77745213-77746164,77746272-77746362,77746424-77746733,77746807-77750138,77750217-77751291,77751385-77751822,77751976-77753085,77753166-77755103,77755175-77757655,77757724-77762505,77762617-77765030,77765115-77765796,77765905-77767431,77767593-77769176,77769287-77771033,77771144-77772678,77772785-77778290,77778377-77786775,
POPDC2	NM_022135	chr3	119361409-119367105,119367516-119373350,119373461-119378778,
POU4F3	NM_002700	chr5	145718796-145719109,
POU6F1	NM_002702	chr12	51584376-51585377,51585548-51586111,51586255-51589751,51589957-51590580,51590711-51591551,

POU6F1	NR_026893	chr12	51584376-51585377,51585548-51586111,51586255-51589751,51589957-51590580,51590711-51591551,51591807-51592331,51592470-51593528,51593652-51597954,51598152-51600571,51600668-51611424,
PPIA	NM_021130	chr7	44836393-44838844,44838877-44838989,44839080-44839299,44839474-44840884,
PPIL6	NM_173672	chr6	109714141-109721236,109721374-109740388,109740447-109748048,109748198-109748295,109748360-109752358,109752549-109757305,109757403-109761657,
PPIL6	NM_001111298	chr6	109714141-109721236,109721374-109724232,109724312-109740388,109740447-109748048,109748198-109748295,109748360-109752358,109752549-109757305,109757403-109761657,
PPM1B	NM_177969	chr2	44396414-44436347,44436467-44445104,44445218-44445617,44445677-44457550,
PPM1B	NM_001033556	chr2	44396414-44428323,44429185-44436347,
PPM1B	NM_177968	chr2	44396414-44428323,44429185-44436347,44436467-44445104,44445218-44445617,44445677-44459453,
PPM1B	NM_002706	chr2	44396414-44428323,44429185-44436347,44436467-44445104,44445218-44445617,44445677-44457550,
PPM1B	NM_001033557	chr2	44396414-44428323,44429185-44436347,44436467-44445104,44445218-44445617,44445677-44457130,
PPM1M	NM_001122870	chr3	52280331-52280709,52280829-52281696,52281811-52282167,52282254-52282349,52282470-52282651,52282717-52282970,52283080-52283188,52283339-52283684,
PPM1M	NM_144641	chr3	52280331-52280709,52280829-52280988,52281245-52281696,52281811-52282167,52282254-52282349,52282470-52282651,52282717-52282970,52283080-52283188,52283339-52283684,
PPP1CB	NM_002709	chr2	28975043-28999715,28999849-29001673,29001906-29004602,29004709-29006771,29006845-29011522,29011676-29016727,29016864-29022063,
PPP1CB	NM_206876	chr2	28974687-28974902,28975043-28999715,28999849-29001673,29001906-29004602,29004709-29006771,29006845-29011522,29011676-29016727,29016864-29022063,
PPP1R14C	NM_030949	chr6	150464635-150535878,150535964-150537958,150537993-150569880,
PPP3R1	NM_000945	chr2	68408143-68413598,68413785-68414385,68414447-68415644,68415823-68444222,68444264-68479255,
PPP6R2	NM_014678	chr22	50781980-50810447,50810580-50832320,50832565-50845116,50845305-50852979,50853119-50854519,50854587-50857294,50857409-50857776,50857892-50860681,50860810-50861889,50862044-50869600,50869812-50870692,50870759-50873393,50873511-50874794,50874882-50875933,50876033-50876270,50876330-50876601,50876728-50877026,50877192-50878128,50878287-50878388,50878479-50879249,50879456-50882293,50882547-50882626,
PPP6R3	NM_001164164	chr11	68228296-68272611,68272718-68286967,68287120-68305125,68305360-68312304,68312493-68315533,68315673-68318587,68318655-68321611,68321726-68326032,68326148-68331769,68331901-68337214,68337366-68338506,68338573-68341575,68341693-68343424,68343512-68355393,68355493-68358126,68358183-68359042,68359175-68363563,68363687-68367807,68367963-68369329,68369438-68370808,68370961-68377370,68377492-68382098,
PPP6R3	NM_018312	chr11	68228296-68272611,68272718-68286967,68287120-68305125,68305360-68312304,68312493-68315533,68315673-68318587,68318655-68321611,68321726-68326032,68326148-68331769,68331901-68337214,68337366-68338506,68338573-68341575,68341693-68343424,68343512-68355393,68355493-68358126,68358183-68359042,68359175-68363563,68363687-68367807,68367963-68369329,68369438-68370808,68370961-68377370,68377492-68380532,
PPP6R3	NM_001164163	chr11	68228296-68286967,68287120-68305125,68305360-68312304,68312493-68315533,68315673-68318587,68318655-68321611,68321726-68326032,68326148-68331769,68331901-68334480,68334635-68337214,68337366-68338506,68338573-68341575,68341693-68343424,68343512-68355393,68355493-68358126,68358183-68359042,68359175-68363563,68363687-68367807,68367963-68369329,68369438-68370808,68370961-68377370,68377492-68380532,
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PPP6R3	NM_001164160	chr11	68228296-68286967,68287120-68305125,68305360-68312304,68312493-68315533,68315673-68318587,68318655-68321611,68321726-68326032,68326148-68331769,68331901-68334480,68334635-68337214,68337366-68338506,68338573-68341575,68341693-68343424,68343512-68350509,68350598-68355393,68355493-68358126,68358183-68359042,68359175-68363563,68363687-68367807,68367963-68369329,68369438-68370808,68370961-68377077,68377097-68377370,68377492-68380532,
PPPDE1	NM_016076	chr1	244816658-244849897,244849972-244852549,244852645-244855179,244855323-244868856,
PRAM1	NM_032152	chr19	8555111-8555220,8555257-8555358,8555394-8555476,8555641-8555769,8555880-8555982,8556042-8562646,8562725-8563105,8563174-8563258,8564665-8567447,
PRAME	NM_206954	chr22	22891066-22892146,22892757-22893187,22893512-22899230,22899330-22899963,22900001-22901580,
PRAME	NM_206953	chr22	22891066-22892146,22892757-22893187,22893512-22899230,22900001-22901580,
PRAME	NM_006115	chr22	22891066-22892146,22892757-22893187,22893512-22899230,22899351-22899963,22900001-22901580,
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PRAME	NM_206955	chr22	22891066-22892146,22892757-22893187,22893512-22899230,22899351-22899963,22900001-22901376,
PRAMEF11	NM_001146344	chr1	12885362-12887106,12887690-12888355,12888665-12891208,
PRC1	NM_003981	chr15	91510433-91512307,91512351-91512675,91512854-91513632,91513745-91517364,91517477-91517813,91517962-91519904,91520002-91522386,91522525-91523470,91523620-91524112,91524264-91524727,91524900-91524976,91525212-91527246,91527371-91527921,91528056-91537635,
PRC1	NM_199414	chr15	91510433-91512752,91512854-91513632,91513745-91517364,91517477-91517813,91517962-91519904,91520002-91522386,91522525-91523470,91523620-91524112,91524264-91524727,91524900-91524976,91525212-91527246,91527371-91527921,91528056-91537635,
PRC1	NM_199413	chr15	91510433-91512675,91512854-91513632,91513745-91517364,91517477-91517813,91517962-91519904,91520002-91522386,91522525-91523470,91523620-91524112,91524264-91524727,91524900-91524976,91525212-91527246,91527371-91527921,91528056-91537635,
PRDM1	NM_182907	chr6	106546970-106547173,106547428-106552698,106553809-106554244,106554375-106554784,
PRDM1	NM_001198	chr6	106534471-106536074,106536325-106543488,106543610-106547173,106547428-106552698,106553809-106554244,106554375-106554784,
PRDM4	NM_012406	chr12	108128300-108133158,108133329-108134721,108135038-108135996,108136126-108136972,108137060-108138318,108138439-108140050,108140202-108145190,108145987-108147699,108147887-108150607,108150743-108154280,108154549-108154732,
PRDX4	NM_006406	chrX	23685929-23689644,23689764-23693105,23693224-23697280,23697405-23700511,23700644-23701786,23701823-23704400,
PRDX6	NM_004905	chr1	173446632-173450463,173450622-173454498,173454647-173455392,173455541-173456872,
PRELID2	NM_138492	chr5	145140089-145144492,145144564-145176003,145176111-145197455,145197618-145199506,145199582-145202638,145202698-145205559,145205764-145214738,
PRELID2	NM_205846	chr5	145140089-145144492,145144564-145176003,145176111-145197455,145197618-145199506,145199582-145202638,145202698-145214738,
PRELID2	NM_182960	chr5	145140089-145144492,145144564-145176003,145176111-145197455,145197618-145198940,145198978-145199506,145199582-145202638,145202698-145214738,
PRICKLE4	NM_013397	chr6	41748565-41749086,41749259-41751198,41751344-41751867,41751977-41752671,41752811-41753073,41753279-41753864,41754071-41754498,
PRIM2	NM_000947	chr6	57182500-57183233,57183398-57185253,57185359-57188997,57189079-57190721,57190844-57244697,57244795-57246827,57246967-57372286,57372356-57393110,57393185-57398130,57398318-57467078,57467207-57472357,57472442-57498965,57499036-57512470,57512788-57512795,
PRKAG2	NM_001040633	chr7	151254319-151257608,151257704-151261162,151261311-151262430,151262470-151262804,151262972-151265800,151265929-151267255,151267312-151269748,151269796-151271975,151272036-151273455,151273539-151292429,151292541-151329153,151329225-151372504,151372724-151478236,151478518-151483554,151483628-151511500,
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PRKAG2	NM_016203	chr7	151254319-151257608,151257704-151261162,151261311-151262430,151262470-151262804,151262972-151265800,151265929-

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PRKD1	NM_002742	chr14	30046663-30047479,30047567-30066695,30066965-30068231,30068332-30068860,30069024-30093356,30093465-30095688,30095763-30098245,30098300-30099946,30100228-30102073,30102153-30103622,30103748-30105494,30105701-30107693,30107773-30107898,30108111-30132903,30133066-30135281,30135415-30194740,30194881-30396453,
PRPF31	NM_015629	chr19	54619178-54621649,54621836-54621951,54622014-54625237,54625323-54625874,54625974-54626831,54626940-54627126,54627298-54627876,54628036-54629901,54629993-54631446,54631576-54631678,54631753-54632430,54632561-54632645,54632746-54634736,
PRPF8	NM_006445	chr17	1554251-1554400,1554605-1554706,1554848-1554940,1555083-1556834,1556978-1557069,1557311-1558642,1558838-1559684,1559860-1559940,1560056-1561545,1561676-1561818,1562058-1562649,1562843-1563133,1563296-1563724,1563873-1563990,1564122-1564285,1564457-1564563,1564701-1564903,1565085-1565198,1565448-1576373,1576492-1576649,1576862-1577038,1577187-1577734,1577975-1578444,1578634-1578912,1579107-1579220,1579349-1579499,1579665-1579797,1580006-1580268,1580467-1580857,1580989-1581810,1581947-1582054,1582176-1582309,1582501-1582583,1582705-1582901,1583094-1584018,1584126-1584221,1584349-1584770,1584985-1585112,1585333-1585421,1585588-1586825,1586996-1587764,1587877-1588072,
PRR11	NM_018304	chr17	57233167-57247107,57247242-57262413,57262566-57262799,57262924-57270851,57271096-57272116,57272217-57272690,57272805-57274903,57274965-57275052,57275151-57278922,
PRR25	NM_001013638	chr16	855911-857470,857647-863294,
PRR7	NM_030567	chr5	176873962-176880955,176881042-176881828,176882496-176882723,
PRR7	NM_001174101	chr5	176873962-176881828,176882496-176882723,
PRR7	NM_001174102	chr5	176875409-176881828,176882496-176882723,
PRRC1	NM_130809	chr5	126853469-126859150,126859275-126860221,126860613-126862308,126862471-126865984,126866089-126869313,126869479-126874730,126874836-126883509,126883614-126887397,
PRRG1	NM_001173490	chrX	37208723-37265460,37265513-37285091,37285254-37312387,
PRRG1	NM_000950	chrX	37208649-37245850,37245943-37265460,37265513-37285091,37285254-37312387,
PRRG1	NM_001142395	chrX	37208649-37265460,37265513-37285091,37285254-37312387,
PRRG1	NM_001173489	chrX	37208723-37245850,37245943-37265460,37265513-37285091,37285254-37312387,
PRRG1	NM_001173486	chrX	37208649-37265460,37265513-37285091,37285254-37300042,
PRSS23	NM_007173	chr11	86511694-86518671,
PRSS41	NM_001135086	chr16	2848616-2848958,2849126-2849285,2849571-2854388,2854548-2854913,
PSMA1	NM_001143937	chr11	14536038-14539186,14539292-14539424,14539528-14540541,14540588-14541841,
PSMA1	NM_002786	chr11	14526795-14529200,14529313-14532416,14532498-14535114,14535246-14535361,14535434-14535947,14536038-14539186,14539292-14539424,14539528-14540541,14540588-14541841,
PSMA1	NM_148976	chr11	14526795-14529200,14529313-14532416,14532498-14535114,14535246-14535361,14535434-14535947,14536038-14539186,14539292-14539424,14539528-14540541,14540588-14632510,14632698-14664999,
PSMC6	NM_002806	chr14	53174023-53175025,53175107-53175199,53175241-53175480,53175535-53177817,53177887-53178126,53178243-53180597,53180687-53184797,53184861-53184945,53185071-53185693,53185757-53187577,53187700-53187826,53187909-53190681,53190755-53194215,
PSMD11	NM_002815	chr17	30771633-30773961,30774065-30781511,30781638-30791065,30791139-30791537,30791597-30796015,30796212-30800817,30800964-30801780,30801843-30804537,30804602-30806267,30806395-30806867,30806905-30807162,30807216-30807505,30807650-30807769,
PSMD7	NM_002811	chr16	74330887-74334011,74334105-74334948,74335043-74335451,74335551-74336108,74336191-74338199,74338293-74339185,
PSME4	NM_014614	chr2	54092711-54093220,54093361-54093882,54094018-54096511,54096676-54101474,54101632-54102762,54102893-54112825,54112913-54114394,54114605-54114993,54115127-54115856,54115950-54117239,54117346-54119943,54120098-54120809,54120937-54122142,54122214-54122718,54122874-54123939,54124023-54125005,54125137-54125436,54125492-54127016,54127155-54128485,54128697-54131160,54131294-54133733,54133831-54133941,54134006-54135455,54135556-54135645,54135703-54135919,54135978-54137210,54137268-54146286,54146384-54147328,54147488-54148024,54148242-54149652,54149722-54150184,54150256-54150456,54150557-54152674,54152827-54153094,54153161-54154529,54154621-54155252,54155441-54158970,54159238-54159803,54159898-54161740,54161865-54163222,54163299-54163899,54163965-

54164526,54164678-54167091,54167138-54175556,54175675-54176278,54176421-54197678,

PSMG3	NM_001134340	chr7	1607487-1608758,1608997-1609643,
PSMG3	NM_032302	chr7	1607487-1608758,
PTCD3	NM_017952	chr2	86333475-86335471,86335526-86335621,86335660-86338234,86338282-86343651,86343722-86344176,86344283-86346042,86346168-86348600,86348718-86350822,86350886-86352116,86352206-86352576,86352639-86352916,86353004-86354282,86354429-86355062,86355115-86357769,86357861-86358199,86358230-86359439,86359548-86360299,86360380-86360467,86360560-86361413,86361501-86361960,86362111-86363642,86363686-86364103,86364264-86364590,
PTDSS1	NM_014754	chr8	97274448-97285525,97285619-97296335,97296382-97299248,97299375-97307324,97307485-97311920,97312074-97316266,97316410-97318670,97318785-97321783,97321851-97332472,97332574-97342439,97342510-97343252,97343324-97345683,
PTGER3	NM_001126044	chr1	71418743-71419444,71419473-71439978,71440072-71477986,71478168-71512362,
PTGER3	NM_198716	chr1	71318543-71419444,71419473-71477986,71478168-71512362,
PTGER3	NM_198718	chr1	71418743-71419444,71419473-71477986,71478168-71512362,
PTGER3	NM_198715	chr1	71478168-71512362,
PTGER3	NM_198719	chr1	71437417-71439978,71440072-71477986,71478168-71512362,
PTGER3	NM_198714	chr1	71318543-71419444,71419473-71439978,71440072-71477986,71478168-71512362,
PTGER3	NR_028292	chr1	71318543-71327986,71328081-71334925,71335003-71419444,71419473-71477986,71478168-71512362,
PTGER3	NR_028293	chr1	71318543-71327986,71328081-71334925,71335003-71477986,71478168-71512362,
PTGER3	NM_198717	chr1	71318543-71477986,71478168-71512362,
PTGER3	NR_028294	chr1	71318543-71327986,71328081-71331370,71331517-71419444,71419473-71477986,71478168-71512362,
PTGR1	NM_001146108	chr9	114325512-114332369,114332490-114337012,114337123-114341074,114341232-114345750,114345870-114348276,114348446-114355204,114355263-114356500,114356548-114359595,114359713-114361881,
PTGR1	NM_012212	chr9	114325512-114332369,114332490-114337012,114337123-114341074,114341232-114345750,114345870-114348276,114348446-114355204,114355263-114356500,114356548-114359595,114359713-114361617,
PTGR1	NM_001146109	chr9	114312080-114332369,114332490-114337012,114337123-114341074,114341232-114345750,114345870-114348276,114348446-114355204,114355263-114356500,114356548-114359595,114359713-114361881,
PTK2	NM_005607	chr8	141669778-141675014,141675097-141678366,141678524-141684395,141684504-141685557,141685599-141696729,141696794-141710988,141711122-141712667,141712807-141716216,141716305-141727695,141727809-141745348,141745555-141749115,141749207-141753327,141753430-141754749,141754867-141756857,141756960-141762329,141762416-141771262,141771362-141774331,141774390-141799571,141799626-141803451,141803484-141810556,141810676-141813640,141813750-141828374,141828454-141828977,141829120-141840569,141840626-141856357,141856422-141856696,141856778-141874409,141874499-141889568,141889737-141900640,141900869-141994175,141994255-142011222,
PTK2	NM_153831	chr8	141669778-141675014,141675097-141678366,141678524-141684395,141684504-141685557,141685599-141696729,141696794-141710988,141711122-141712667,141712807-141716216,141716305-141727695,141727809-141745348,141745555-141749115,141749207-141753327,141753430-141754749,141754867-141756857,141756960-141762329,141762416-141771262,141771362-141774331,141774390-141799571,141799626-141803451,141803484-141810556,141810676-141813640,141813750-141828374,141828454-141828977,141829120-141840569,141840626-141856357,141856422-141856696,141856778-141874409,141874499-141889568,141889737-141900640,141900869-141935758,141935849-142011222,
PTK2	NM_001199649	chr8	141669778-141675014,141675097-141678366,141678524-141679824,141679835-141684395,141684504-141685527,141685599-141696729,141696794-141710988,141711122-141712667,141712807-141716216,141716305-141727695,141727809-141745348,141745555-141749115,141749207-141753327,141753430-141754749,141754867-141756857,141756960-141762329,141762416-141771262,141771362-141774331,141774390-141799571,141799626-141803451,141803484-141810556,141810676-141813640,141813750-141828374,141828454-

			141828977,141829120-141840569,141840626-141856357,141856422-141856696,141856778-141874409,141874499-141889568,141889737-141900640,141900869-141935758,141935849-142011222,
PTPLB	NM_198402	chr3	123213818-123219360,123219541-123221405,123221529-123247231,123247322-123286607,123286628-123301057,123301177-123303718,
PTPRK	NM_002844	chr6	128291426-128294165,128294303-128294807,128294973-128297800,128297928-128298066,128298200-128302259,128302435-128303974,128304126-128304385,128304523-128306864,128307021-128311912,128312031-128312437,128312537-128313816,128313855-128316605,128316684-128318044,128318134-128319863,128320050-128326227,128326390-128330273,128330414-128385901,128385940-128388662,128388938-128399956,128400064-128403580,128403784-128404858,128404970-128410833,128411138-128505575,128505871-128540065,128540242-128561178,128561296-128563664,128563748-128643182,128643456-128718709,128718834-128841402,
PTPRK	NM_001135648	chr6	128291426-128294165,128294303-128294807,128294973-128297800,128297928-128298066,128298200-128302259,128302435-128303974,128304126-128304385,128304523-128306864,128307021-128311912,128312031-128312437,128312537-128313816,128313855-128316392,128316412-128316605,128316684-128318044,128318134-128319863,128320050-128326227,128326390-128330273,128330414-128385901,128385940-128388662,128388938-128399956,128400064-128403580,128403784-128404858,128404970-128410833,128411138-128505575,128505871-128540065,128540242-128561178,128561296-128563664,128563748-128643182,128643456-128718709,128718834-128841402,
PTPRT	NM_007050	chr20	40709573-40710520,40710658-40713320,40713486-40714366,40714494-40727059,40727193-40730762,40730938-40733207,40733359-40735424,40735562-40738971,40739128-40743837,40743956-40747041,40747141-40748573,40748612-40757392,40757471-40770553,40770643-40789990,40790183-40827878,40828029-40864867,40864899-40877325,40877463-40911127,40911166-40944361,40944637-40979266,40979371-40980722,40980926-41076858,41076970-41100904,41101203-41306504,41306800-41385100,41385277-41400073,41400191-41408856,41408940-41419833,41420107-41514445,41514573-41818284,
PTPRT	NM_133170	chr20	40709573-40710520,40710658-40713320,40713486-40714366,40714494-40727059,40727193-40730762,40730938-40733207,40733359-40735424,40735562-40738971,40739128-40743837,40743956-40747041,40747141-40748573,40748612-40757392,40757471-40770553,40770643-40789990,40790183-40827878,40828029-40864867,40864899-40877325,40877463-40899035,40899094-40911127,40911166-40944361,40944637-40979266,40979371-40980722,40980926-41076858,41076970-41100904,41101203-41306504,41306800-41385100,41385277-41400073,41400191-41408856,41408940-41419833,41420107-41514445,41514573-41818284,
PTRH2	NM_016077	chr17	57775340-57784730,
PVRL4	NM_030916	chr1	161042676-161043013,161043090-161043508,161043586-161044005,161044164-161044399,161044550-161046143,161046266-161047241,161047534-161049378,161049740-161059006,
PYGO1	NM_015617	chr15	55839346-55841106,55841194-55881000,
PYGO2	NM_138300	chr1	154932323-154933451,154933503-154933948,
PYY	NM_004160	chr17	42030349-42030475,42030558-42030662,42030852-42031216,42031344-42035304,42035397-42043654,42043901-42081757,
QPRT	NM_014298	chr16	29690532-29705983,29706521-29708315,29708449-29708518,
RAB11B	NM_004218	chr19	8455341-8464745,8464943-8466968,8467164-8467367,8467450-8468295,
RAB14	NM_016322	chr9	123943852-123945206,123945239-123945587,123945677-123949229,123949298-123952830,123953010-123954447,123954503-123955637,123955698-123963915,
RAB1A	NM_004161	chr2	65315825-65316071,65316205-65318115,65318213-65325103,65325201-65331866,65331941-65357025,
RAB1A	NM_015543	chr2	65315825-65325103,65325201-65331866,65331941-65357025,
RAB32	NM_006834	chr6	146865258-146870598,146870878-146875590,
RAB3GAP2	NM_012414	chr1	220324749-220324946,220325107-220326525,220326749-220327308,220327400-220330610,220330831-220331142,220331219-220332726,220332764-220335538,220335611-220338073,220338142-220340633,220340742-220340842,220341018-220344232,220344463-220345229,220345392-220345977,220346085-220355597,220355693-220356054,220356274-220357376,220357506-220358991,220359084-220363043,220363110-220363404,220363489-220363717,220363863-220364408,220364627-220366580,220366722-220368418,220368510-220368638,220368720-220369590,220369741-220375616,220375717-220379247,220379349-220383728,220383832-220384141,220384219-220384295,220384345-220386227,220386311-220387196,220387322-220406139,220406206-220445563,

RABEP1	NM_001083585	chr17	5185816-5211987,5212118-5235242,5235448-5238477,5238640-5241312,5241434-5250083,5250221-5253744,5253925-5257652,5257786-5264501,5264971-5266205,5266312-5268415,5268534-5271663,5271764-5276607,5276750-5280409,5280601-5281470,5281528-5284682,5284801-5286415,5286864-5286887,
RABEP1	NM_004703	chr17	5185816-5211987,5212118-5235242,5235448-5238477,5238640-5241312,5241434-5250083,5250221-5253744,5253925-5257652,5257786-5264501,5264971-5266205,5266312-5268415,5268534-5271663,5271764-5276607,5276750-5280409,5280601-5281470,5281528-5283657,5283758-5284682,5284801-5286415,5286864-5286887,
RABGAP1L	NM_014857	chr1	174128796-174188261,174188434-174190108,174190303-174200281,174200494-174210619,174210796-174219611,174219771-174221616,174221729-174241550,174241619-174244969,174245074-174247749,174247918-174274122,174274266-174340115,174340211-174363131,174363284-174606511,174606627-174652658,174652735-174668661,174668789-174671249,174671395-174721449,174721493-174780968,174781099-174926592,174926687-174927026,
RABGAP1L	NM_001035230	chr1	174844852-174846528,174846744-174926592,174926687-174927026,
RACGAP1	NM_001126104	chr12	50384127-50384465,50384576-50385779,50385917-50386026,50386161-50386331,50386439-50387912,50388113-50388195,50388293-50390821,50390988-50392922,50393055-50393397,50393517-50394953,50395036-50396028,50396084-50398016,50398088-50399037,50399176-50400215,50400420-50410412,50410503-50419109,
RACGAP1	NM_001126103	chr12	50384127-50384465,50384576-50385779,50385917-50386026,50386161-50386331,50386439-50387912,50388113-50388195,50388293-50390821,50390988-50392922,50393055-50393397,50393517-50394953,50395036-50396028,50396084-50398016,50398088-50399037,50399176-50400215,50400420-50410412,50410503-50412297,50412373-50414843,50414961-50419179,
RACGAP1	NM_013277	chr12	50384127-50384465,50384576-50385779,50385917-50386026,50386161-50386331,50386439-50387912,50388113-50388195,50388293-50390821,50390988-50392922,50393055-50393397,50393517-50394953,50395036-50396028,50396084-50398016,50398088-50399037,50399176-50400215,50400420-50410412,50410503-50413525,50413590-50414843,50414961-50419179,
RAD51	NM_002875	chr15	40987624-40990953,40991044-40993260,40993400-40998373,40998493-41001221,41001315-41011001,41011098-41020907,41021023-41021701,41021833-41022049,41022173-41023251,
RAD51	NM_133487	chr15	40987624-40990953,40991044-40993260,40993400-40994002,40994125-41001221,41001315-41011001,41011098-41020907,41021023-41021701,41021833-41022049,41022173-41023251,
RAD51	NM_001164270	chr15	40987624-40990953,40991044-40993260,40993400-40998373,40998493-41001221,41001315-41011001,41011098-41020907,41021023-41021701,41021833-41023251,
RAD51	NM_001164269	chr15	40987520-40990953,40991044-40993260,40993400-40994002,40994125-41001221,41001315-41011001,41011098-41020907,41021023-41021701,41021833-41022049,41022173-41023251,
RAD52	NM_134424	chr12	1022619-1023058,1023288-1023595,1023699-1025508,1025650-1025803,1025987-1034614,1034692-1036309,1036430-1038983,1039053-1039215,1039311-1040384,1040488-1042139,1042243-1058766,
RAD54B	NM_012415	chr8	95384616-95390406,95390609-95390794,95390863-95392371,95392635-95399210,95399388-95403835,95404128-95405969,95406111-95411640,95411850-95412464,95412692-95416303,95416468-95419665,95419949-95423347,95423544-95470494,95470665-95479631,95479784-95487227,
RAD9A	NM_004584	chr11	67159550-67159630,67159703-67160123,67160254-67160965,67161082-67161160,67161262-67163185,67163297-67163381,67163493-67163580,67163647-67163732,67163872-67164648,67164858-67164933,
RAD9B	NM_152442	chr12	110940189-110941609,110941682-110943420,110943578-110944382,110944499-110950582,110950684-110952853,110952962-110956479,110956588-110956677,110956744-110957597,110957722-110959980,110960217-110968328,110968439-110969377,
RAGE	NM_014226	chr14	102695704-102695792,102695995-102698042,102698159-102698870,102699046-102700023,102700127-102717147,102717328-102718091,102718142-102718252,102718333-102729881,102729954-102732158,102732250-102749813,102749930-102771297,
RAI2	NM_021785	chrX	17820155-17879216,
RAI2	NR_033348	chrX	17820155-17855655,17855851-17878627,
RAI2	NR_033349	chrX	17820155-17878627,
RAI2	NM_001172732	chrX	17819846-17819994,17820155-17879216,
RAI2	NM_001172739	chrX	17820155-17855655,17855851-17879216,

RAI2	NM_001172743	chrX	17820155-17855655,17855854-17879216,
RALGPS1	NM_014636	chr9	129677255-129724502,129724626-129728121,129728231-129739972,129740025-129796708,129796794-129812320,129812412-129815124,129815219-129831507,129831636-129928346,129928486-129930956,129931052-129936992,129937062-129957368,129957497-129958751,129958911-129961292,129961346-129974408,129974516-129974904,129974999-129975221,129975329-129977028,129977122-129981017,
RALGPS1	NM_001190728	chr9	129724626-129728121,129728231-129739972,129740025-129796708,129796794-129812320,129812412-129815124,129815219-129831507,129831636-129928346,129928486-129930956,129931052-129936992,129937062-129957368,129957497-129972972,129973058-129974408,129974516-129974904,129974999-129975245,129975329-129977028,129977122-129979183,
RALGPS1	NM_001190729	chr9	129677292-129724502,129724626-129728121,129728231-129739972,129740025-129796708,129796794-129812320,129812412-129815124,129815219-129831507,129831636-129928346,129928486-129930956,129931052-129936992,129937062-129957368,129957497-129972972,129973058-129974408,129974516-129974904,129974999-129975221,129975329-129977028,129977122-129979183,
RALGPS1	NM_001190730	chr9	129677292-129724502,129724626-129728121,129728231-129739972,129740025-129796708,129796794-129812320,129812412-129815124,129815219-129831507,129831636-129928346,129928486-129930956,129931052-129936992,129937062-129940174,
RAMP2	NM_005854	chr17	40913377-40913850,40913918-40914371,40914482-40914613,
RAPGEF2	NM_014247	chr4	160189368-160225492,160225626-160235741,160235921-160243497,160243636-160244609,160244770-160251008,160251163-160251484,160251651-160252581,160252691-160252780,160252986-160253076,160253187-160253601,160253850-160259461,160259621-160260264,160260507-160262714,160263100-160264129,160264343-160264431,160264557-160265186,160265212-160266256,160266482-160267939,160268151-160271287,160271442-160273835,160274063-160274637,160275199-160277003,160277311-160279264,
RAPGEF5	NM_012294	chr7	22162140-22165220,22165277-22170653,22170720-22175654,22175744-22176549,22176602-22179641,22179734-22184660,22184841-22186513,22186638-22190023,22190123-22194071,22194223-22196426,22196507-22197471,22197504-22200134,22200234-22202013,22202160-22206686,22206767-22232983,22233074-22233531,22233652-22259483,22259611-22270463,22270539-22306581,22306632-22330792,22330861-22347956,22348127-22349586,22349710-22354987,22355096-22357604,22357657-22396447,
RARRES3	NM_004585	chr11	63304350-63306986,63307097-63312091,63312362-63313619,
RASAL1	NM_001193520	chr12	113537874-113538431,113538486-113539692,113539815-113541749,113541887-113541964,113542104-113543517,113543692-113544900,113545047-113545888,113546031-113549889,113550084-113552603,113552718-113553003,113553070-113553438,113553594-113553737,113553857-113554876,113554967-113556931,113557065-113557165,113557249-113559312,113559444-113565615,113565679-113565868,113565984-113568688,113568747-113573201,113573405-113573879,
RASAL1	NM_001193521	chr12	113537874-113538431,113538486-113539692,113539815-113541749,113541887-113541964,113542020-113543517,113543689-113544900,113545047-113545888,113546028-113549889,113550084-113552603,113552718-113553003,113553070-113553438,113553594-113553737,113553857-113554876,113554967-113556931,113557065-113557165,113557249-113559312,113559444-113565615,113565679-113565868,113565984-113568688,113568747-113573201,
RASAL1	NM_004658	chr12	113537874-113538431,113538486-113539692,113539815-113541749,113541887-113541964,113542104-113543517,113543689-113544900,113545047-113545888,113546028-113549889,113550084-113552603,113552718-113553003,113553070-113553438,113553594-113553737,113553857-113554876,113554967-113556931,113557065-113557165,113557249-113559312,113559444-113565615,113565679-113565868,113565984-113568688,113568747-113573201,113573405-113573864,
RASGEF1B	NM_152545	chr4	82348947-82353451,82353526-82354992,82355118-82355791,82355889-82361986,82362084-82363449,82363531-82366678,82366783-82366895,82366993-82368656,82368733-82369221,82369439-82377803,82377943-82378651,82378776-82380484,82380669-82392922,
RASGEF1C	NM_175062	chr5	179528526-179529069,179529144-179538455,179538581-179541444,179541542-179545607,179545705-179545785,179545867-179546344,179546449-179548058,179548150-179554607,179554684-179555408,179555611-179563376,179563516-179564588,179564713-179564874,179565059-179636026,
RASGRF1	NM_153815	chr15	79254579-79264206,79264277-79265643,79265763-79272960,79273042-79277347,79277547-79282529,79282616-79284031,79284137-79288080,79288143-79290436,79290551-79291059,79291168-79292083,79292256-79294002,79294130-79296142,79296518-79297057,

RASGRF1	NM_002891	chr15	79254579-79264206,79264277-79265643,79265763-79272960,79273042-79277347,79277547-79282529,79282616-79284031,79284137-79288080,79288143-79290436,79290551-79291059,79291168-79292083,79292256-79294002,79294130-79296142,79296518-79298517,79298777-79304829,79304870-79307667,79307752-79310110,79310249-79312381,79312447-79317654,79317817-79320081,79320202-79323740,79323852-79324463,79324659-79327471,79327553-79339086,79339342-79341836,79341931-79350674,79350824-79356760,79356869-79382563,
RASGRF1	NM_001145648	chr15	79254579-79264206,79264277-79265643,79265763-79272960,79273042-79277347,79277547-79282529,79282616-79284031,79284137-79288080,79288143-79290436,79290551-79291059,79291168-79292083,79292256-79294002,79294130-79296142,79296518-79298526,79298777-79307667,79307752-79310110,79310249-79312381,79312447-79317654,79317817-79320081,79320202-79323740,79323852-79324463,79324659-79327471,79327553-79339086,79339342-79341836,79341931-79350674,79350824-79356760,79356869-79382563,
RAX	NM_013435	chr18	56936734-56939591,56939847-56940148,
RBBP6	NM_006910	chr16	24552114-24557482,24557584-24560264,24560303-24564832,24564879-24566934,24567025-24567140,24567239-24567627,24567769-24570824,24570999-24572931,24573037-24573143,24573483-24574518,24574617-24574742,24574823-24574929,24574986-24576116,24576187-24578462,24578827-24579111,24579215-24580064,24581821-24582195,
RBBP6	NM_032626	chr16	24552114-24557482,24557584-24560264,
RBBP6	NM_018703	chr16	24552114-24557482,24557584-24560264,24560303-24564832,24564879-24566934,24567025-24567140,24567239-24567627,24567769-24570824,24570999-24572931,24573037-24573143,24573483-24574518,24574617-24574742,24574823-24574929,24574986-24576116,24576187-24578462,24578827-24580064,24581821-24582195,
RBKS	NM_022128	chr2	28004656-28050432,28050623-28055551,28055645-28065932,28066099-28069907,28069972-28070899,28070965-28081304,28081439-28113122,
RBM19	NM_016196	chr12	114261127-114282471,114282594-114296594,114296702-114352772,114352891-114356195,114356253-114358414,114358496-114362500,114362563-114364857,114365035-114374810,114374942-114377763,114377966-114380127,114380240-114383631,114383730-114384157,114384281-114385137,114385270-114386636,114386842-114387886,114387960-114390315,114390396-114392934,114393017-114395585,114395856-114397015,114397210-114397668,114397709-114397862,114397984-114400035,114400220-114403995,
RBM19	NM_001146699	chr12	114255992-114261012,114261127-114282471,114282594-114296594,114296702-114352772,114352891-114356195,114356253-114358414,114358496-114362500,114362563-114364857,114365035-114374810,114374942-114377763,114377966-114380127,114380240-114383631,114383730-114384157,114384281-114385137,114385270-114386636,114386842-114387886,114387960-114390315,114390396-114392934,114393017-114395585,114395856-114397015,114397210-114397668,114397709-114397862,114397984-114400035,114400220-114403995,
RBM19	NM_001146698	chr12	114260452-114261012,114261127-114282471,114282594-114296594,114296702-114352772,114352891-114356195,114356253-114358414,114358496-114362500,114362563-114364857,114365035-114374810,114374942-114377763,114377966-114380127,114380240-114383631,114383730-114384157,114384281-114385137,114385270-114386636,114386842-114387886,114387960-114390315,114390396-114392934,114393017-114395585,114395856-114397015,114397210-114397668,114397709-114397862,114397984-114400035,114400220-114403995,
RBM24	NM_001143941	chr6	17282451-17283034,17283160-17284886,17284943-17291985,
RBM24	NM_153020	chr6	17283160-17284886,17284943-17291985,
RBM24	NM_001143942	chr6	17281981-17283034,17283160-17284886,17284943-17291985,
RBM34	NM_001161533	chr1	235316081-235318194,235318428-235323824,235323963-235324206,235324383-235324487,
RBM34	NM_015014	chr1	235295313-235298965,235299086-235299347,235299389-235301190,235301256-235301404,235301490-235311717,235311763-235316019,235316081-235318194,235318428-235323824,235323963-235324206,235324383-235324487,
RBM34	NR_027762	chr1	235295313-235298965,235299086-235299347,235299389-235301190,235301256-235301404,235301490-235311717,235311763-235316019,235316081-235318194,235318428-235324206,235324383-235324487,
RBM45	NM_152945	chr2	178977574-178980987,178981112-178982780,178982909-178985012,178985137-178985905,178986087-178988247,178988379-178988553,178988640-178988852,178989018-178990709,178990912-178994122,
RCBTB1	NM_018191	chr13	50108399-50115010,50115143-50115810,50115964-50118871,50119000-50123592,50123785-50125460,50125605-50126312,50126422-50129649,50129810-50134052,50134221-50140752,50140905-50141288,50141457-50154639,50154721-50159578,
RCHY1	NM_001009922	chr4	76407877-76415789,76415912-76416932,76416993-76417097,76417144-76419309,76419390-76434028,76434146-76434385,76434507-76439405,

RCHY1	NM_015436	chr4	76407877-76415789,76415912-76416819,76416848-76416932,76416993-76417097,76417144-76419309,76419390-76434028,76434146-76434385,76434507-76439405,
RCHY1	NM_001008925	chr4	76407877-76415789,76415910-76416819,76416848-76416932,76416993-76417097,76417144-76419309,76419390-76434028,76434146-76434385,76434507-76439405,
RDH10	NM_172037	chr8	74207814-74209427,74209665-74231329,74231430-74233165,74233313-74234912,74235046-74235146,
REM2	NM_173527	chr14	23352600-23353881,23354225-23354473,23354549-23355231,23355441-23355821,
REPS1	NM_001128617	chr6	139226270-139228630,139228738-139229803,139229954-139232411,139232509-139233900,139234088-139235832,139235899-139236993,139237114-139238690,139238765-139241350,139241454-139242172,139242262-139251112,139251236-139262470,139262627-139264648,139264714-139264988,139265153-139265633,139265760-139266354,139266510-139266636,139266835-139268925,139269051-139308665,
REPS1	NM_031922	chr6	139226270-139228630,139228738-139229803,139229954-139232411,139232509-139233900,139234088-139235832,139235899-139236993,139237114-139238690,139238762-139241350,139241454-139242172,139242262-139247536,139247619-139251112,139251236-139262470,139262627-139264648,139264714-139264988,139265153-139265633,139265760-139266354,139266510-139266636,139266835-139268925,139269051-139308665,
RERG	NM_032918	chr12	15262452-15264276,15264352-15273995,15274054-15370361,15370538-15374127,
RERG	NM_001190726	chr12	15262452-15264276,15264352-15370361,15370538-15374127,
RESP18	NM_001007089	chr2	220192286-220193644,220193731-220193883,220193975-220194357,220194487-220195491,220195598-220197244,220197461-220197881,
RETNLB	NM_032579	chr3	108474753-108475353,108475436-108475904,
RFC4	NM_002916	chr3	186507854-186507929,186508045-186508113,186508196-186509512,186509640-186510277,186510400-186510591,186510737-186512445,186512567-186515322,186515404-186518904,186518985-186522370,186522514-186524077,
RFC4	NM_181573	chr3	186507854-186507929,186508045-186508113,186508196-186509512,186509640-186510277,186510400-186510591,186510737-186512445,186512567-186515322,186515404-186518904,186518985-186522370,186522514-186524212,
RFWD3	NM_018124	chr16	74657970-74660239,74660453-74662348,74662565-74664677,74664856-74666419,74666572-74670242,74670476-74671752,74671869-74678258,74678352-74678437,74678634-74683028,74683101-74685816,74686021-74694828,74695350-74700682,
RG9MTD2	NM_152292	chr4	100470514-100472040,100472148-100474940,100475092-100477301,100477378-100478500,100478574-100479204,100479369-100480309,100480508-100484523,
RG9MTD2	NM_001134665	chr4	100470514-100472040,100472148-100474940,100475092-100477301,100477378-100478500,100478574-100479204,100479369-100480309,100480519-100485068,
RG9MTD2	NM_001134666	chr4	100470514-100472040,100472148-100474940,100475092-100477301,100477378-100478500,100478574-100479204,100479369-100480309,100480508-100485068,
RG9MTD3	NM_144964	chr9	37753850-37761898,37762115-37762572,37762683-37763624,37763751-37768071,37768226-37769936,37770017-37770667,37770737-37776277,37776403-37777596,
RGPD2	NM_001078170	chr2	88056946-88071686,88071884-88074461,88074603-88081641,88083867-88084592,88084689-88088239,88088359-88091507,88091593-88091679,88091861-88092739,88092888-88093148,88093288-88093552,88093713-88094634,88094760-88094925,88095103-88095184,88095368-88097482,88097694-88100122,88100212-88106213,88106411-88111002,88111150-88111493,88111726-88115786,88115941-88116383,88116497-88118076,88118143-88125175,
RGPD2	NM_001078170	chr2	87141045-87178417,87178484-87180063,87180177-87180619,87180774-87184827,87185060-87185403,87185551-87190150,87190348-87196349,87196439-87198868,87199080-87201194,87201378-87201459,87201637-87201802,87201928-87202849,87203010-87203274,87203414-87203674,87203823-87204701,87204883-87204969,87205055-87208204,87208324-87211875,87211972-87212697,87214923-87221962,87222104-87224684,87224882-87239634,
RGR	NM_002921	chr10	86004926-86007345,86007504-86008664,86008800-86012611,86012767-86014080,86014200-86017647,86017763-86018262,
RGR	NM_001012722	chr10	86004926-86007345,86007504-86008676,86008800-86012611,86012767-86014080,86014200-86018262,
RGR	NM_001012720	chr10	86004926-86007345,86007504-86008676,86008800-86012611,86012767-86014080,86014200-86017647,86017763-86018262,

RGS12	NM_002926	chr4	3316677-3317795,3319779-3344662,3344781-3388141,3388165-3415797,3415969-3416477,3416572-3417703,3417849-3418638,3418820-3419113,3419269-3422367,3422446-3424101,3424298-3424630,3424706-3425240,3425369-3427189,3427288-3429815,3429897-3430283,3430439-3432132,
RGS12	NM_198229	chr4	3316677-3317795,3319779-3344662,3344781-3388141,3388165-3415797,3415969-3416477,3416572-3417703,3417849-3418638,3418820-3419113,3419269-3422367,3422446-3424101,3424298-3424630,3424706-3425240,3425369-3427189,3427288-3429815,3429897-3430283,3430439-3432132,3432683-3441180,
RGS12	NM_198227	chr4	3372049-3388141,3388165-3415797,3415969-3416477,3416572-3417703,3417849-3418638,3418820-3419113,3419269-3422367,3422446-3424101,3424298-3424630,3424706-3425240,3425369-3427189,3427288-3429815,3429897-3430283,3430439-3432132,3432683-3441180,
RGS14	NM_006480	chr5	176785071-176792962,176792986-176793176,176793357-176793707,176793802-176793890,176794036-176794413,176794559-176794713,176794827-176795156,176795268-176795716,176795922-176797590,176797666-176797904,176798033-176798164,176798248-176798349,176798398-176798474,176798591-176798872,
RHBDD3	NM_012265	chr22	29656227-29656313,29656603-29656689,29656854-29659822,29660208-29661466,29661658-29663413,29663567-29663735,
RHCG	NM_016321	chr15	90015087-90015940,90016095-90019984,90020060-90020311,90020438-90020746,90020885-90021066,90021206-90022551,90022720-90023490,90023640-90026296,90026449-90030028,90030217-90039590,
RHOV	NM_133639	chr15	41165700-41165880,41165941-41166128,
RHOXF1	NM_139282	chrX	119243261-119246777,119246825-119249373,
RIBC1	NM_001031745	chrX	53449954-53450261,53450352-53453223,53453342-53454949,53455033-53455229,53455576-53456800,53456921-53457342,53457739-53457853,
RIBC1	NM_144968	chrX	53449954-53450261,53450352-53453223,53453342-53454949,53455033-53455229,
RILPL2	NM_145058	chr12	123900469-123907589,123907705-123915053,123915207-123920627,
RIPK2	NM_003821	chr8	90770462-90775055,90775211-90777567,90777725-90781998,90782158-90783967,90784019-90784893,90785057-90792301,90792389-90796276,90796368-90798819,90798915-90801547,90801711-90802305,
RIPK3	NM_006871	chr14	24805602-24806089,24806152-24806290,24806667-24806899,24806969-24807077,24807247-24807453,24807502-24807626,24807774-24808219,24808531-24808661,24808804-24809011,
RIPK4	NM_020639	chr21	43162158-43164040,43164301-43165917,43166023-43166771,43166932-43169312,43169364-43171255,43171406-43176683,43176977-43187018,
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RIPPLY1	NM_001171706	chrX	106144139-106146361,
RIPPLY2	NM_001009994	chr6	84563231-84563412,84563493-84563814,84563881-84566959,
RNASE11	NM_145250	chr14	21052656-21055720,21055785-21058317,
RNASE2	NM_002934	chr14	21423696-21423924,
RNF125	NM_017831	chr18	29598991-29617077,29617233-29622140,29622237-29625603,29625695-29645863,29645973-29648259,
RNF126	NM_194460	chr19	648278-648370,648488-648880,648976-649677,649749-650232,650297-651609,651856-652231,652297-652824,652885-663045,
RNF145	NM_001199383	chr5	158586044-158588272,158588631-158589938,158590088-158595879,158596064-158596685,158596828-158600989,158601167-158603638,158603876-158608966,158609060-158621722,158621833-158630440,158630665-158636237,
RNF145	NM_001199382	chr5	158586044-158588272,158588631-158589938,158590088-158595879,158596064-158596685,158596828-158600989,158601167-158603638,158603876-158608966,158609060-158621722,158621833-158630440,158630665-158634481,
RNF145	NM_144726	chr5	158586044-158588272,158588631-158589938,158590088-158595879,158596064-158596685,158596828-158600989,158601167-158603638,158603876-158608966,158609060-158621722,158621833-158630440,158630665-158634761,
RNF145	NM_001199381	chr5	158586044-158588272,158588631-158589938,158590088-158595879,158596064-158596685,158596828-158600989,158601167-158603638,158603876-158608966,158609060-158621722,158621833-158630440,158630665-158634891,
RNF145	NM_001199380	chr5	158586044-158588272,158588631-158589938,158590088-158595879,158596064-158596685,158596828-158600989,158601167-158603638,158603876-158608966,158609060-158621722,158621833-158630440,158630665-158636859,
RNF168	NM_152617	chr3	196199644-196202100,196202184-196210639,196210763-196214268,196214450-196215476,196215555-196229742,
RNF180	NM_001113561	chr5	63461781-63496633,63496770-63507890,63507988-63509383,63510345-63513186,63513224-63621011,63621239-63626106,63626234-63665440,
RNF180	NM_178532	chr5	63461781-63496633,63496770-63507890,63507988-63509383,63510345-63513186,

RNF19A	NM_015435	chr8	101271475-101272080,101272226-101273768,101273984-101276260,101276424-101276897,101277014-101281011,101281176-101282095,101282242-101287179,101287390-101299727,101300496-101312754,101312880-101315386,
RNF19A	NM_183419	chr8	101271475-101272080,101272226-101273768,101273984-101276260,101276424-101276897,101277014-101281011,101281176-101282095,101282242-101287179,101287390-101299727,101300496-101322093,
RNF214	NM_207343	chr11	117103443-117104981,117105096-117109315,117109828-117110515,117110577-117115159,117115302-117117523,117117665-117150622,117150721-117150885,117150976-117152028,117152121-117152314,117152415-117152608,117152987-117153118,117153253-117153460,117153567-117153829,117153927-117155800,
RNF214	NM_001077239	chr11	117103492-117104981,117105096-117109315,117109828-117110515,117110577-117115159,117115302-117117523,117117665-117150622,117150721-117150885,117150976-117152028,117152121-117152314,117152415-117152608,117152987-117153118,117153253-117153460,117153567-117153829,117153927-117155800,
RNF215	NM_001017981	chr22	30775612-30775698,30775803-30776049,30776195-30776269,30776391-30780326,30780485-30781891,30781979-30782057,30782131-30782603,30782749-30783016,
RNF216L	NR_023384	chr7	5013793-5015930,5016068-5023300,5023405-5024539,5024707-5026196,5026263-5028692,5028809-5035104,5035214-5036239,
RNF216L	NR_015449	chr7	5013793-5015930,5016068-5023300,5023405-5024539,5024707-5028692,5028809-5036239,
RNF216L	NR_023385	chr7	5013793-5015930,5016068-5023300,5023405-5024539,5024707-5036239,
RNMTL1	NM_018146	chr17	685933-686321,686568-691203,691373-694772,
ROBO1	NM_002941	chr3	78648078-78649261,78649460-78655881,78656192-78663796,78663951-78666783,78667192-78676469,78676720-78680309,78680456-78683083,78683193-78684921,78685259-78688892,78689049-78695296,78695341-78696777,78696806-78700880,78701080-78706246,78706420-78708834,78708958-78710178,78710412-78711141,78711265-78717031,78717200-78717282,78717453-78717632,78717716-78719244,78719452-78734894,78735068-78737796,78737923-78763545,78763675-78766423,78766564-78766911,78767034-78795891,78796051-78987749,78988078-79174604,79174690-79638972,79639112-79816900,
ROBO1	NM_001145845	chr3	78648078-78649261,78649460-78655881,78656192-78663796,78663951-78666783,78667192-78676469,78676720-78680309,78680456-78683083,78683193-78684921,78685094-78688892,78689049-78695296,78695341-78700880,78701080-78706246,78706420-78708834,78708958-78710178,78710412-78711141,78711265-78717031,78717200-78717282,78717453-78717632,78717716-78719244,78719452-78734894,78735068-78737796,78737923-78742496,78742507-78763545,78763675-78766423,78766564-78766911,78767034-78795891,78796051-78987749,78988078-79067555,
ROBO1	NM_133631	chr3	78648078-78649261,78649460-78655881,78656192-78663796,78663951-78666783,78667192-78676469,78676720-78680309,78680456-78683083,78683193-78684921,78685259-78688892,78689049-78695296,78695341-78700880,78701080-78706246,78706420-78708834,78708958-78710178,78710412-78711141,78711265-78717031,78717200-78717282,78717453-78717632,78717716-78719244,78719452-78734894,78735068-78737796,78737923-78742496,78742507-78763545,78763675-78766423,78766564-78766911,78767034-78795891,78796051-78987749,78988078-79067555,
RORB	NM_006914	chr9	77112900-77245196,77245284-77249545,77249689-77257328,77257732-77275531,77275655-77277388,77277523-77280402,77280512-77282705,77282818-77286703,77286818-77300377,
RP1-177G6-2	NR_028345	chrX	139791971-139793784,
RP1-177G6-2	NR_028344	chrX	139791971-139793784,139793822-139795680,
RPF1	NM_025065	chr1	84945193-84946637,84946696-84948596,84948679-84955314,84955412-84956000,84956156-84961054,84961139-84961563,84961747-84961925,84962054-84963110,
RPGR	NM_000328	chrX	38129086-38132637,38132731-38134340,38134400-38135838,38136026-38146345,38146499-38147112,38147295-38150210,38150278-38150644,38150738-38156535,38156706-38158207,38158395-38160498,38160625-38163886,38164044-38169866,38170027-38176567,38176719-38178080,38178241-38180278,38180343-38182104,38182199-38182650,38182778-38186591,
RPGR	NM_001034853	chrX	38146499-38147112,38147295-38150210,38150278-38150644,38150738-38156535,38156706-38158207,38158395-38160498,38160625-38163886,38164044-38169866,38170027-38176567,38176719-38178080,38178241-38180278,38180343-38182104,38182199-38182650,38182778-38186591,

RPGRIP1	NM_020366	chr14	21756221-21762834,21762969-21769123,21769397-21770645,21770744-21771488,21771703-21775888,21775996-21778741,21778767-21779981,21780130-21780590,21780666-21785853,21786010-21788174,21788337-21789416,21789562-21790011,21790164-21792775,21793230-21793389,21793543-21793988,21794333-21795780,21795967-21796581,21796787-21798406,21798547-21802762,21802865-21811193,21811388-21813270,21813357-21816329,21816462-21819261,
RPH3A	NM_014954	chr12	113229818-113229946,113230069-113266104,113266195-113285499,113285648-113303217,113303349-113304560,113304646-113306233,113306401-113307562,113307603-113307696,113307845-113312887,113312976-113313482,113313547-113314445,113314672-113316922,113317004-113319575,113319652-113321096,113321208-113325600,113325729-113327827,113327886-113328652,113328809-113332381,113332465-113333580,113333679-113334453,
RPH3A	NM_001143854	chr12	113229818-113229946,113230069-113266104,113266195-113274294,113274308-113285499,113285648-113303217,113303349-113304560,113304646-113306233,113306401-113307562,113307603-113307696,113307845-113312887,113312976-113313482,113313547-113314445,113314672-113316922,113317004-113319575,113319652-113321096,113321208-113325600,113325729-113327827,113327886-113328652,113328809-113332381,113332465-113333580,113333679-113334453,
RPL17-C18ORF32	NM_001199355	chr18	47008781-47009952,47010142-47015727,47015921-47016822,47016923-47017161,47017298-47017773,47017816-47017900,
RPL17-C18ORF32	NM_001199356	chr18	47008781-47009952,47010142-47015727,47015921-47016822,47016923-47017161,47017298-47017900,47017955-47018826,
RPL23AP82	NR_026982	chr22	51222501-51223599,51223722-51237081,
RPL23AP82	NR_026981	chr22	51195755-51221546,51221723-51223599,51223722-51237081,
RPL37	NM_000997	chr5	40832676-40834281,40834368-40834571,40834709-40835283,
RPL3L	NM_005061	chr16	1994895-1995498,1995620-1995834,1995932-1996624,1996728-1996937,1997100-1997193,1997382-2000843,2000981-2002873,2003044-2003955,2004150-2004628,
RPS27L	NM_015920	chr15	63446260-63447818,63447931-63448610,63448721-63449597,
RP53	NM_001005	chr11	75110622-75111736,75111869-75112682,75112778-75113394,75113491-75115062,75115252-75115714,75115913-75116656,
RPS8	NM_001012	chr1	45241273-45241704,45241813-45242345,45242447-45243284,45243462-45243670,45243802-45244246,
RPUSD3	NM_173659	chr3	9879892-9880714,9880856-9881866,9881992-9882214,9882301-9882380,9882490-9883665,9883767-9883881,9883928-9885147,9885286-9885572,
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RRM2	NM_001034	chr2	10263025-10263108,10263185-10263512,10263658-10263861,10263980-10264842,10264978-10267000,10267097-10267212,10267348-10268973,10269080-10269166,10269282-10269359,
RRM2	NM_001165931	chr2	10263025-10263108,10263185-10263512,10263658-10263861,10263980-10264842,10264978-10267000,10267097-10267212,10267348-10268973,10269080-10269166,10269282-10269359,
RRP8	NM_015324	chr11	6621496-6621714,6621813-6621897,6622006-6622154,6622286-6622377,6622833-6623080,6623446-6624632,
RSPH1	NM_080860	chr21	43892981-43896006,43896158-43897399,43897555-43902745,43902819-43905777,43905915-43906479,43906572-43912866,43912974-43913074,43913190-43916241,
RSPO1	NM_001038633	chr1	38077350-38077419,38078594-38079374,38079565-38079854,38080006-38082154,38082348-38095238,38095622-38097514,38097695-38097957,38098026-38100236,
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RTN1	NM_206857	chr14	60063506-60069781,60069842-60069928,60069977-60070568,60070640-60072084,60072225-60074001,60074211-60193635,
RTN4RL1	NM_178568	chr17	1841103-1928145,
RUSC2	NM_001135999	chr9	35539106-35546425,35548533-35555055,35555699-35555947,35556135-35556303,35556446-35557909,35557988-35558192,35558369-35558457,35558565-35559221,35559270-35560024,35560849-35560955,35561095-35561176,
RUSC2	NM_014806	chr9	35490170-35546425,35548533-35555055,35555699-35555947,35556135-35556303,35556446-35557909,35557988-35558192,35558369-35558457,35558565-35559221,35559270-35560024,35560849-35560955,35561095-35561176,

S100A8	NM_002964	chr1	153362720-153362869,153363034-153363515,
SAMD14	NM_174920	chr17	48190413-48191286,48191444-48191549,48191671-48191719,48191805-48192926,48193088-48193192,48193269-48193365,48193455-48194769,48195060-48195523,48195692-48202279,48202336-48206879,
SARNP	NR_026722	chr12	56146625-56151165,56151338-56154333,56154425-56182857,56182928-56184349,56184377-56188141,56188172-56188589,56188665-56189807,56189861-56194344,56194414-56197411,56197513-56211448,
SARNP	NM_033082	chr12	56151338-56154333,56154425-56182857,56182928-56184349,56184377-56188141,56188172-56188589,56188665-56189807,56189861-56194344,56194414-56194636,56194685-56197411,56197513-56211448,
SARNP	NR_026723	chr12	56146625-56151165,56151338-56154333,56154425-56182857,56182928-56184349,56184377-56188141,56188172-56188589,56188665-56189807,56189861-56194344,56194414-56194636,56194685-56197411,56197513-56211448,
SARS	NR_034073	chr1	109779996-109780351,
SARS	NR_034072	chr1	109756751-109757167,
SARS	NM_006513	chr1	109756751-109766598,109766671-109770972,109771055-109772034,109772195-109773498,109773644-109774251,109774409-109777830,109778054-109778597,109778729-109779011,109779171-109779864,109779996-109780351,
SAT1	NR_027783	chrX	23801535-23801773,23801827-23801915,23802001-23802409,23802521-23803443,23803547-23803635,23803678-23803801,
SAT1	NM_002970	chrX	23801535-23801773,23801827-23801915,23802001-23803443,23803547-23803635,23803678-23803801,
SATB2	NM_001172509	chr2	200137396-200173481,200173681-200188524,200188682-200193419,200193634-200213422,200213897-200233326,200233431-200245085,200245211-200246415,200246544-200298059,200298238-200320590,200320820-200322060,
SATB2	NM_015265	chr2	200137396-200173481,200173681-200188524,200188682-200193419,200193634-200213422,200213897-200233326,200233431-200245085,200245211-200246415,200246544-200298059,200298238-200320590,200320820-200325173,200325256-200335735,
SATB2	NM_001172517	chr2	200137396-200173481,200173681-200188524,200188682-200193419,200193634-200213422,200213897-200233326,200233431-200245085,200245211-200246415,200246544-200298059,200298238-200320590,200320820-200325173,200325256-200329557,
SC4MOL	NM_006745	chr4	166248917-166254490,166254778-166258939,166259090-166259802,166259931-166261371,166261528-166262901,
SC4MOL	NM_001017369	chr4	166248917-166258939,166259090-166259802,166259931-166261371,166261528-166262901,
SCAPER	NM_020843	chr15	76641078-76643576,76643630-76646288,76646482-76668501,76668653-76673717,76673957-76696863,76697021-76726417,76726652-76763551,76763677-76797198,76797316-76866497,76866626-76914103,76914171-76957992,76958131-76994097,76994207-76995189,76995344-76998242,76998326-77020934,77021079-77025568,77025726-77046147,77046290-77057300,77057414-77057676,77057796-77057902,77057980-77059257,77059430-77064081,77064296-77067194,77067459-77087619,77087782-77092587,77092706-77096872,77096975-77134073,77134273-77150148,77150221-77154755,77154875-77176151,
SCAPER	NM_001145923	chr15	76641078-76643576,76643630-76646288,76646482-76668501,76668653-76673717,76673957-76696863,76697021-76726417,76726652-76763551,76763677-76797198,76797316-76866497,76866626-76914103,76914171-76957992,76958131-76994097,76994207-76995189,76995344-76998242,76998326-77020934,77021079-77025568,77025726-77046147,77046290-77057300,77057414-77057676,77057796-77057902,77057980-77059257,77059430-77064081,77064296-77067194,77067459-77085572,77085733-77087619,77087782-77092587,77092706-77096872,77096975-77134073,77134273-77148149,77148218-77150148,77150221-77154184,
SCARB2	NM_005506	chr4	77082905-77084376,77084537-77087401,77087455-77089554,77089630-77091018,77091139-77095295,77095467-77096942,77097064-77097588,77097682-77100668,77100859-77102105,77102255-77116858,77117018-77134578,
SCARF1	NM_145352	chr17	1538912-1540001,1540150-1540233,1540357-1542098,1542221-1543765,1543961-1546734,1547262-1548126,1548230-1548470,1548534-1548889,
SCARF1	NM_145350	chr17	1538912-1540001,1540113-1540233,1540357-1542098,1542221-1542931,1543037-1543204,1543335-1543740,1543961-1546734,1547262-1548126,1548230-1548470,1548534-1548889,
SCARF1	NM_003693	chr17	1538912-1540001,1540150-1540233,1540357-1542098,1542221-1542931,1543037-1543204,1543335-1543740,1543961-1546734,1547262-1548126,1548230-1548470,1548534-1548889,
SCARF1	NR_028076	chr17	1538912-1540001,1540150-1540233,1540357-1542098,1542221-1542931,1543037-1543204,1543961-1546734,1547262-1548126,1548230-1548470,1548534-1548889,
SCARF1	NR_028075	chr17	1538912-1540001,1540150-1540233,1540357-1542098,1542221-1542931,1543037-1543204,1543265-1543740,1543961-1546734,1547262-1548126,1548230-1548470,1548534-1548889,

SCD	NM_005063	chr10	102107289-102107819,102108104-102112121,102112254-102114182,102114390-102116287,102116522-102120489,
SCFD1	NM_182835	chr14	31091606-31099681,31099772-31103151,31103244-31107329,31107454-31108981,31109071-31112520,31112612-31118732,31118790-31119769,31119857-31122693,31122795-31139460,31139602-31142461,31142554-31143128,31143204-31144188,31144272-31163977,31164076-31169392,31169465-31171500,31171582-31175027,31175092-31177194,31177272-31185128,31185184-31188529,31188584-31191088,31191124-31191698,31191766-31203994,31204065-31204790,
SCFD1	NM_016106	chr14	31091606-31097413,31097486-31099681,31099772-31103151,31103244-31107329,31107454-31108981,31109071-31112520,31112612-31118732,31118790-31119769,31119857-31122693,31122795-31139460,31139602-31142461,31142554-31143128,31143204-31144188,31144272-31163977,31164076-31169392,31169465-31171500,31171582-31175027,31175092-31177194,31177272-31185128,31185184-31188529,31188584-31191088,31191124-31191698,31191766-31203994,31204065-31204790,
SCFD2	NM_152540	chr4	53740229-53751912,53752034-53773622,53773759-53786890,53787038-54011498,54011750-54139991,54140169-54179801,54179931-54218763,54218934-54231269,
SCN1B	NM_199037	chr19	35521765-35523430,35523599-35524401,
SCN1B	NM_001037	chr19	35521765-35523430,35523599-35524401,35524644-35530019,35530163-35530537,35530611-35530699,
SCUBE2	NM_001170690	chr11	9042745-9043421,9043503-9047247,9047402-9051429,9051593-9052303,9052473-9055171,9055344-9068901,9069110-9075182,9075307-9077338,9077457-9080848,9080973-9081953,9082072-9087436,9087528-9088242,9088361-9090915,9091043-9096026,9096163-9100929,9101057-9111252,9111377-9112941,
SCUBE2	NM_020974	chr11	9042745-9043421,9043503-9047247,9047402-9048909,9049109-9051429,9051593-9052303,9052473-9068901,9069110-9069488,9069646-9072151,9072258-9074291,9074380-9074644,9074763-9075182,9075307-9077338,9077457-9080848,9080973-9081953,9082072-9087436,9087528-9088242,9088361-9090915,9091043-9096026,9096163-9100929,9101057-9111252,9111377-9112941,
SCUBE3	NM_152753	chr6	35182281-35195355,35195480-35196389,35196517-35199500,35199637-35200625,35200753-35200960,35201079-35205677,35205796-35207527,35207652-35208149,35208268-35208916,35209044-35209318,35209437-35209581,35209688-35209979,35210098-35210397,35210558-35210796,35211014-35211369,35211533-35211738,35211908-35212425,35212589-35213003,35213203-35213719,35213874-35213981,35214063-35216331,
SEC14L3	NM_174975	chr22	30856130-30857295,30857467-30857540,30857682-30858071,30858180-30860805,30860891-30862319,30862382-30862967,30863065-30864493,30864684-30866004,30866066-30866197,30866243-30866492,30866570-30867890,
SEC24A	NM_021982	chr5	133984864-133996807,133997277-134002511,134002687-134007497,134007577-134010303,134010466-134010733,134010908-134011711,134011816-134015290,134015419-134018061,134018173-134022478,134022593-134023869,134023990-134028290,134028348-134029415,134029624-134032814,134032937-134033587,134033748-134039447,134039623-134041015,134041128-134044401,134044579-134050712,134050852-134053757,134053864-134056686,134056781-134059255,134059361-134060668,
SEC24D	NM_014822	chr4	119644811-119649714,119649806-119652469,119652663-119653886,119654068-119659414,119659535-119660302,119660443-119661816,119661964-119662094,119662193-119665141,119665314-119666097,119666216-119673149,119673245-119673850,119674044-119678874,119679001-119685955,119686073-119689326,119689467-119718836,119718966-119726996,119727110-119736181,119736311-119736604,119736882-119738417,119738568-119745773,119745905-119754732,119754893-119757094,
SEC31A	NM_014933	chr4	83740407-83742188,83742262-83745706,83745828-83748520,83748786-83750151,83750212-83763291,83763635-83765537,83765663-83769955,83770131-83772582,83772758-83774721,83774869-83776054,83776183-83778103,83778284-83778840,83778918-83782782,83782862-83783685,83783726-83784469,83784546-83785513,83785752-83787959,83788114-83788306,83788470-83791476,83791578-83793095,83793240-83795762,83795905-83796878,83796976-83799881,83800082-83801950,83802076-83803009,83803091-83812239,
SEC31A	NM_001077208	chr4	83740407-83742188,83742262-83745706,83745828-83748520,83748786-83750151,83750212-83763336,83763635-83765537,83765663-83769955,83770131-83772582,83772758-83774721,83774869-83776054,83776183-83778103,83778284-83778840,83778918-83782782,83782862-83783685,83783726-83784469,83784546-83785513,83785752-83787959,83788114-83788306,83788470-83791476,83791578-83793095,83793240-83795762,83795905-83796878,83796976-83799881,83800082-83801950,83802076-83803009,83803094-83812239,
SEC31A	NM_001077206	chr4	83740407-83742188,83742262-83745706,83745828-83748520,83748786-83750151,83750212-83765537,83765663-83769955,83770131-83772582,83772758-83774721,83774869-83776054,83776183-83778103,83778284-83778840,83778918-83782782,83782862-83783685,83783726-83784469,83784546-83785513,83785752-83787959,83788114-83788306,83788470-83791476,83791578-83793095,83793240-83795762,83795905-

			83796878,83796976-83799881,83800082-83801950,83802076-83803009,83803094-83812239,
SEC31A	NM_001077207	chr4	83740407-83742188,83742262-83745706,83745828-83748520,83748786-83750151,83750212-83763291,83763635-83765537,83765663-83769955,83770131-83772582,83772758-83774721,83774869-83776054,83776183-83778103,83778284-83778840,83778918-83782782,83782862-83783685,83783726-83784469,83784546-83785513,83785752-83787959,83788114-83788306,83788470-83791476,83791578-83793095,83793240-83795762,83795905-83796878,83796976-83799881,83800082-83801950,83802076-83803009,83803094-83812239,
SEC31A	NM_001191049	chr4	83740407-83742188,83742262-83745706,83745828-83748520,83748786-83750151,83750212-83763336,83763635-83765537,83765663-83769955,83770131-83772582,83772758-83774721,83774869-83776054,83776183-83778103,83778284-83778840,83778918-83782782,83782862-83783685,83783726-83784469,83784546-83785513,83785752-83787959,83788114-83788306,83788470-83791476,83791578-83793095,83793240-83795762,83795905-83796878,83796976-83799881,83800082-83801950,83802076-83812239,
SEC31A	NM_016211	chr4	83740407-83742188,83742262-83745706,83745828-83748520,83748786-83750151,83750212-83763291,83763635-83765537,83765663-83769955,83770131-83772582,83772758-83774721,83774869-83776054,83776183-83778103,83778284-83778840,83778918-83784469,83784546-83785513,83785752-83787959,83788114-83788306,83788470-83791476,83791578-83793095,83793240-83795762,83795905-83796878,83796976-83799881,83800082-83801950,83802076-83803009,83803094-83812239,
SECISBP2	NM_024077	chr9	91933528-91934565,91934713-91940340,91940592-91940810,91940954-91943573,91943802-91947821,91947902-91949435,91949646-91953371,91953496-91954777,91954869-91956260,91956395-91961795,91961964-91962992,91963130-91964689,91964845-91965545,91965768-91972324,91972481-91972912,91973107-91973634,
SECISBP2L	NM_014701	chr15	49285124-49288562,49288784-49292028,49292185-49293072,49293295-49301411,49301576-49303926,49304061-49304843,49305015-49308755,49308899-49309043,49309213-49309743,49309826-49319560,49319678-49320339,49320366-49320648,49320880-49325160,49325298-49327529,49327856-49329786,49329967-49338471,
SECISBP2L	NM_001193489	chr15	49285124-49288562,49288784-49292028,49292185-49293072,49293295-49301411,49301576-49303926,49304061-49304843,49305015-49308755,49308899-49309043,49309213-49309743,49309826-49311613,49311750-49319560,49319678-49320339,49320366-49320648,49320880-49325160,49325298-49327529,49327856-49329786,49329967-49338471,
SELO	NM_031454	chr22	50640020-50644744,50644950-50646963,50647146-50648608,50648741-50649058,50649341-50654144,50654297-50655118,50655306-50655399,50655558-50655632,
SEMA4B	NM_198925	chr15	90744968-90760669,90760835-90760997,90761062-90763023,90763124-90764212,90764326-90764597,90764713-90764844,90764998-90766789,90766973-90767068,90767221-90768198,90768411-90768512,90768630-90768891,90769060-90770787,90770875-90771134,
SEMA4B	NM_020210	chr15	90728314-90744688,90744968-90760669,90760835-90760997,90761062-90763023,90763124-90764212,90764326-90764597,90764713-90764844,90764998-90766789,90766973-90767068,90767221-90768198,90768411-90768512,90768630-90768891,90769060-90770787,90770875-90771134,
SENP5	NM_152699	chr3	196594945-196612020,196613566-196626535,196626643-196626793,196626934-196627234,196627284-196630402,196630482-196650283,196650423-196654665,196654751-196656502,196656555-196657682,
SEPSECS	NM_016955	chr4	25125848-25127314,25127407-25128884,25128980-25146394,25146488-25146624,25146756-25153580,25153685-25156618,25156774-25157657,25157818-25158476,25158597-25160573,25160730-25161876,
SEPT1	NM_052838	chr16	30389842-30389929,30390022-30390337,30390505-30390754,30390856-30391251,30391355-30392446,30392566-30392658,30392795-30393079,30393205-30393412,30393501-30393594,30393687-30393844,30393920-30394054,
SEPT7	NM_001011553	chr7	35840883-35872406,35872511-35903160,35903269-35912274,35912377-35913249,35913386-35919431,35919551-35922092,35922187-35923499,35923598-35925436,35925490-35930276,35930404-35937856,35937994-35942684,35942826-35943862,
SEPT7	NM_001788	chr7	35840884-35872406,35872511-35903160,35903269-35912274,35912377-35913249,35913386-35919431,35919551-35922092,35922187-35923499,35923598-35925436,35925490-35930276,35930404-35937856,35937994-35942684,35942826-35943862,
SERPINB3	NM_006919	chr18	61323296-61324063,61324221-61324502,61324647-61325745,61325865-61326631,61326762-61328032,61328091-61328284,61328477-61329078,
SERPINF1	NM_002615	chr17	1665408-1670195,1670289-1673144,1673345-1674321,1674479-1675164,1675370-1678350,1678495-1679824,1680037-1680479,
SERPINI1	NM_005025	chr3	167453924-167506897,167507167-167508158,167508391-167510376,167510573-167512406,167512613-167525030,167525130-

			167540772,167540861-167542259,167542351-167543033,
SERPINI1	NM_001122752	chr3	167453612-167506897,167507167-167508158,167508391-167510376,167510573-167512406,167512613-167525030,167525130-167540772,167540861-167542259,167542351-167543033,
SET	NM_003011	chr9	131451935-131453447,131453507-131454135,131454280-131454939,131455045-131455145,131455261-131455915,131456088-131456173,131456322-131456918,
SET	NM_001122821	chr9	131446287-131453447,131453507-131454135,131454280-131454939,131455045-131455145,131455261-131455915,131456088-131456173,131456322-131456918,
SETBP1	NM_015559	chr18	42260987-42281138,42281798-42449193,42449249-42529844,42533306-42618448,42618621-42643042,
SETBP1	NM_001130110	chr18	42260361-42281138,42281798-42449193,42449249-42456528,
SEZ6L	NM_001184776	chr22	26565730-26688370,26689113-26690256,26690392-26692852,26693047-26694948,26695136-26701943,26702111-26706634,26706803-26707732,26707929-26709728,26709869-26736400,26736599-26743683,26743880-26761336,26761533-26771539,26771656-26773637,26773742-26776230,
SEZ6L	NM_021115	chr22	26565730-26688370,26689113-26690256,26690392-26692852,26693047-26694948,26695136-26701943,26702111-26706634,26706803-26707732,26707929-26709728,26709869-26736400,26736599-26743683,26743880-26747016,26747210-26761336,26761533-26769415,26769450-26771539,26771656-26773637,26773742-26776230,
SEZ6L	NM_001184777	chr22	26565730-26688370,26689113-26690256,26690392-26692852,26693047-26694948,26695136-26701943,26702111-26706634,26706803-26707732,26707929-26709728,26709869-26736400,26736599-26743683,26743880-26747016,26747210-26771539,26771656-26773637,26773742-26776230,
SEZ6L	NM_001184775	chr22	26565730-26688370,26689113-26690256,26690392-26692852,26693047-26694948,26695136-26701943,26702111-26706634,26706803-26707732,26707929-26709728,26709869-26736400,26736599-26743683,26743880-26747016,26747210-26761336,26761533-26771545,26771656-26773637,26773742-26776230,
SEZ6L	NM_001184774	chr22	26565730-26688370,26689113-26690256,26690392-26692852,26693047-26694948,26695136-26701943,26702111-26706634,26706803-26707732,26707929-26709728,26709869-26736400,26736599-26743683,26743880-26747016,26747210-26761336,26761533-26771539,26771656-26773637,26773742-26776230,
SEZ6L	NM_001184773	chr22	26565730-26688370,26689113-26690256,26690392-26692852,26693047-26694948,26695136-26701943,26702111-26706634,26706803-26707732,26707929-26709728,26709869-26736400,26736599-26743683,26743880-26747016,26747210-26761336,26761533-26769415,26769450-26771542,26771656-26773637,26773742-26776230,
SF3B3	NM_012426	chr16	70557832-70560488,70560630-70562774,70563103-70564646,70564821-70566380,70566524-70569209,70569324-70572224,70572364-70573005,70573111-70575570,70575738-70578339,70578437-70582271,70582346-70588347,70588501-70588952,70589110-70590080,70590238-70590787,70590933-70594370,70594495-70595531,70595688-70597777,70597954-70598966,70599174-70599269,70599428-70601312,70601440-70602184,70602399-70602944,70603045-70603907,70604053-70604996,70605103-70605574,
SGOL1	NM_001012411	chr3	20212308-20212533,20212725-20216495,20216548-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227549,
SGOL1	NM_001199253	chr3	20212308-20212533,20212725-20216495,20216548-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227438,
SGOL1	NM_001199252	chr3	20202719-20212214,20212308-20212533,20212725-20215739,20216548-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227438,
SGOL1	NM_001199251	chr3	20212308-20212533,20212725-20215739,20216548-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227438,
SGOL1	NM_001012412	chr3	20202719-20212214,20212308-20212533,20212725-20216495,20216548-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227549,
SGOL1	NM_001012409	chr3	20212308-20212533,20212725-20215739,20216548-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227549,
SGOL1	NM_001199254	chr3	20202719-20212214,20212308-20212533,20212725-20216495,20216548-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227438,
SGOL1	NM_001012410	chr3	20202719-20212214,20212308-20212533,20212725-20215739,20216548-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227549,
SGOL1	NM_138484	chr3	20202719-20212214,20212308-20212533,20212725-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227549,

SGOL1	NM_001199256	chr3	20202719-20212214,20212308-20212533,20212725-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227438,
SGOL1	NM_001199257	chr3	20202719-20216495,20216548-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227438,
SGOL1	NM_001012413	chr3	20212308-20212533,20212725-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227549,
SGOL1	NM_001199255	chr3	20212308-20212533,20212725-20218091,20218152-20219761,20219840-20225098,20225297-20225376,20225527-20227438,
SGOL2	NM_001160046	chr2	201390976-201397695,201397832-201399717,201399895-201400786,201400866-201407300,201407388-201434384,201434616-201435771,201438701-201440032,201440185-201445256,
SGOL2	NM_001160033	chr2	201390976-201397695,201397832-201399717,201399895-201400786,201400866-201407300,201407388-201434384,201434616-201435771,201438701-201440039,201440185-201448170,
SGOL2	NM_152524	chr2	201390976-201397695,201397832-201399717,201399895-201400786,201400866-201407300,201407388-201434384,201434616-201435771,201438701-201440032,201440185-201448170,
SGSM2	NM_014853	chr17	2241040-2246837,2246915-2264929,2265094-2265401,2265565-2266130,2266200-2266281,2266429-2266757,2266894-2267351,2267478-2267888,2267958-2268189,2268352-2268507,2268636-2270563,2270700-2274554,2274710-2275482,2275549-2275635,2275783-2276245,2276376-2276623,2276808-2278784,2279170-2279429,2279556-2280025,2280110-2280251,2280363-2281149,2281248-2282328,2282498-2282724,
SGSM2	NM_001098509	chr17	2241040-2246837,2246915-2264929,2265094-2265401,2265565-2266130,2266200-2266281,2266429-2266757,2266894-2267351,2267478-2267888,2267958-2268189,2268352-2268507,2268636-2274554,2274710-2275482,2275549-2275635,2275783-2276245,2276376-2276623,2276808-2278784,2279170-2279429,2279556-2280025,2280110-2280251,2280363-2281149,2281248-2282328,2282498-2282724,
SH2B1	NM_015503	chr16	28878355-28878650,28878754-28880325,28880419-28880527,28880705-28883099,28883305-28883509,28883723-28883853,28884027-28884489,28884591-28884766,
SH2B1	NM_001145812	chr16	28875584-28877331,28878355-28878650,28878754-28880325,28880419-28880527,28880705-28883099,28883305-28883509,28883723-28883853,28884027-28884489,28884591-28884766,
SH2B1	NM_001145796	chr16	28875267-28877331,28878355-28878650,28878754-28880325,28880419-28880527,28880705-28883099,28883305-28883509,28883723-28883853,28884027-28884489,28884591-28884766,
SH2B1	NM_001145795	chr16	28875267-28877331,28878355-28878650,28878754-28880325,28880419-28880527,28880705-28883099,28883305-28883509,28883723-28883853,28884027-28884766,
SH2B1	NM_001145797	chr16	28875267-28877331,28878355-28878650,28878754-28880325,28880419-28880527,28880705-28883099,28883305-28883509,28883723-28883853,28884080-28884489,28884591-28884766,
SH2D6	NM_198482	chr2	85662247-85662534,85662620-85662787,85662948-85663587,85663718-85663958,
SH3GL82	NM_020145	chr9	131771071-131771383,131771626-131772048,131772151-131772397,131772489-131772947,131772973-131774513,131774578-131776688,131776783-131777048,131777184-131783368,131783499-131784559,131784703-131790369,
SH3RF2	NM_152550	chr5	145316258-145317384,145317870-145379619,145379891-145383619,145383717-145393308,145393625-145427333,145427427-145428636,145428809-145435542,145435777-145439427,145439788-145441987,
SHCBP1	NM_024745	chr16	46615967-46617426,46617570-46617913,46618002-46629462,46629583-46633741,46633875-46637449,46637572-46637885,46638056-46638138,46638374-46642207,46642302-46649856,46650067-46651544,46651662-46652115,46652285-46655167,
SHF	NM_138356	chr15	45460332-45464079,45464201-45464343,45464517-45465772,45465915-45467415,45467624-45470361,45470505-45490968,45491319-45492923,
SI	NM_001041	chr3	164697219-164700029,164700199-164700788,164700840-164704924,164705015-164709139,164709266-164709963,164710022-164710099,164710186-164712043,164712194-164714321,164714440-164714524,164714561-164716326,164716462-164724602,164724743-164725697,164725787-164727065,164727184-164730766,164730831-164732909,164733022-164733738,164733869-164735334,164735462-164735547,164735662-164735756,164735855-164737388,164737559-164739015,164739172-164741356,164741565-164748498,164748656-164750308,164750481-164751181,164751233-164754175,164754266-164755686,164755813-164756864,164756923-164757673,164757760-164758726,164758883-164760845,164760964-164764627,164764801-164766913,164767033-164767577,164767664-164772980,164773096-164776749,164776871-164776954,164777088-164777688,164777816-164780157,164780272-164781228,164781330-164783047,164783221-164785126,164785280-164786508,164786620-164786864,164786984-164792317,164792456-164793681,164793801-164796219,

SIPA1L2	NM_020808	chr1	232535020-232538136,232538220-232539192,232539318-232539869,232539925-232551238,232551372-232561333,232561555-232564155,232564311-232567991,232568218-232574852,232575243-232577035,232577141-232577512,232577615-232579346,232579432-232581273,232581533-232596631,232596908-232600584,232601163-232607115,232607275-232615371,232615477-232619536,232619713-232626618,232626809-232629271,232629407-232649601,
SNRT3	NM_012239	chr11	216719-218830,219042-224076,224240-230450,230553-232981,233216-233341,233535-236046,
SNRT3	NM_001017524	chr11	216719-218830,219042-224076,224240-230450,230553-232981,233216-233341,233535-236192,
SNRT6	NM_016539	chr19	4174944-4175023,4175149-4175675,4175758-4175837,4175935-4177074,4177136-4179099,4179284-4180777,4180907-4182469,
SNRT6	NM_001193285	chr19	4174944-4175023,4175149-4175837,4175935-4177074,4177136-4179099,4179284-4180777,4180907-4182469,
SIX2	NM_016932	chr2	45233625-45235688,
SIX5	NM_175875	chr19	46269370-46269606,46270414-46271298,
SLC10A7	NM_001029998	chr4	147177673-147179842,147179990-147204342,147204418-147214079,147214133-147215080,147215248-147227076,147227162-147247111,147247149-147363933,147363974-147424999,147425077-147431063,147431202-147438188,147438273-147442768,
SLC10A7	NM_032128	chr4	147363974-147424999,147425077-147431063,147431202-147438188,147438273-147442768,
SLC12A1	NM_000338	chr15	48498528-48499729,48500337-48512829,48512963-48513116,48513194-48518671,48518769-48521384,48521526-48522588,48522701-48524922,48525036-48527072,48527202-48533710,48533797-48536948,48537102-48539104,48539214-48539532,48539658-48541770,48541874-48543810,48543968-48548006,48548108-48551395,48551509-48559756,48559899-48561853,48561962-48566766,48566851-48577301,48577447-48580238,48580372-48580600,48580714-48583973,48584062-48591335,48591473-48593510,48593580-48594945,
SLC12A1	NM_001184832	chr15	48498528-48499729,48500337-48512829,48512963-48513116,48513194-48519274,48519372-48521384,48521526-48522588,48522701-48524922,48525036-48527072,48527202-48533710,48533797-48536948,48537102-48539104,48539214-48539532,48539658-48541770,48541874-48543810,48543968-48548006,48548108-48551395,48551509-48559756,48559899-48561853,48561962-48566766,48566851-48577301,48577447-48580238,48580372-48580600,48580714-48583973,48584062-48591335,48591473-48593510,48593580-48594945,
SLC14A2	NM_007163	chr18	43195548-43204594,43204780-43205646,43205829-43206921,43207113-43212313,43212444-43216953,43217148-43219709,43219859-43221172,43221309-43223095,43223147-43223949,43224126-43243748,43243873-43246100,43246185-43246898,43247060-43247796,43247988-43248312,43248443-43249269,43249464-43252863,43253013-43253646,43253783-43258938,43258990-43262282,
SLC15A1	NM_005073	chr13	99337170-99338442,99338552-99339833,99339979-99340500,99340611-99340722,99340832-99354732,99354784-99356541,99356690-99358386,99358508-99360938,99361022-99361824,99361915-99361994,99362029-99362119,99362166-99364106,99364198-99364750,99364839-99368130,99368215-99371489,99371575-99373747,99373840-99374056,99374158-99376164,99376286-99378375,99378519-99378620,99378704-99379095,99379114-99404847,
SLC22A6	NM_004790	chr11	62744354-62744615,62744860-62746958,62747069-62747204,62747421-62748455,62748573-62748730,62748856-62749312,62749483-62751007,62751164-62751414,62751520-62751792,
SLC22A6	NM_153276	chr11	62744354-62744654,62744860-62746958,62747069-62747204,62747421-62748455,62748573-62748730,62748856-62749312,62749483-62751007,62751164-62751414,62751520-62751792,
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SLC25A12	NM_003705	chr2	172641986-172644079,172644172-172644297,172644458-172647959,172648100-172650135,172650278-172666114,172666197-172666732,172666787-172669847,172670008-172671629,172671713-172683306,172683393-172690471,172690567-172691235,172691376-172693629,172693778-172700877,172701019-172712342,172712460-172725189,172725334-172749713,172749769-172750711,
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SLC25A24	NM_013386	chr1	108679460-108681678,108681831-108686163,108686333-108690899,108691009-108697603,108697758-108700082,108700243-108703802,108703916-108724561,108724651-108728448,108728577-108742576,
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SLC26A6	NM_022911	chr3	48663434-48663649,48663788-48664062,48664119-48664307,48664489-48665377,48665472-48665865,48665975-48666053,48666148-48667073,48667145-48667303,48667412-48667493,48667591-48667869,48667949-48668038,48668154-48668424,48668574-48668655,48668740-48669080,48669235-48669311,48669478-48669676,48669830-48670405,48670518-48670682,48670824-48670908,48671069-48672802,
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SLC30A3	NM_003459	chr2	27478329-27479252,27479389-27479654,27479762-27480020,27480221-27480771,27480927-27481027,27481176-27481619,27481803-27485678,
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SLC35D1	NM_015139	chr1	67470132-67474766,67474851-67486050,67486131-67487216,67487286-67507917,67508012-67512946,67513051-67515463,67515534-67516114,67516188-67517693,67517763-67518452,67518541-67518637,67518673-67519492,
SLC35D2	NM_007001	chr9	99083624-99084278,99084363-99086371,99086452-99098997,99099067-99106184,99106279-99107579,99107684-99113383,99113454-99114318,99114392-99122434,99122504-99126744,99126833-99130552,99130588-99145757,
SLC3A2	NM_002394	chr11	62623854-62638215,62638310-62639047,62639142-62648489,62648920-62649363,62649539-62650378,62650472-62651927,62651998-62652102,62652163-62652647,62652830-62652935,62653081-62655605,62655691-62655801,

SLC3A2	NM_001012662	chr11	62623854-62639047,62639142-62644254,62644352-62648489,62648920-62649363,62649539-62650378,62650472-62651927,62651998-62652102,62652163-62652647,62652830-62652935,62653081-62655605,62655691-62655801,
SLC3A2	NM_001012664	chr11	62623854-62648489,62648920-62649363,62649539-62650378,62650472-62651927,62651998-62652102,62652163-62652647,62652830-62652935,62653081-62655605,62655691-62655801,
SLC3A2	NM_001012663	chr11	62623854-62639047,62639142-62648489,62648920-62649363,62649539-62650378,62650472-62651927,62651998-62652102,62652163-62652647,62652830-62652935,62653081-62655605,62655691-62655801,
SLC3A2	NM_001013251	chr11	62648920-62649363,62649539-62650378,62650472-62651927,62651998-62652102,62652163-62652647,62652830-62652935,62653081-62655605,62655691-62655801,
SLC3A2	NM_001012661	chr11	62623854-62638215,62638310-62639047,62639142-62644257,62644352-62648489,62648920-62649363,62649539-62650378,62650472-62651927,62651998-62652102,62652163-62652647,62652830-62652935,62653081-62655605,62655691-62655801,
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SLC40A1	NM_014585	chr2	190426918-190428308,190428952-190430078,190430326-190436439,190436568-190437570,190437688-190439885,190440047-190444537,190444607-190445142,
SLC43A1	NM_001198810	chr11	57252716-57254566,57254692-57256387,57256463-57256722,57256866-57258695,57258836-57259062,57259100-57259187,57259336-57261464,57261645-57263502,57263638-57265224,57265319-57268250,57268329-57268459,57268517-57268623,57268803-57281429,57281598-57282252,
SLC43A1	NM_003627	chr11	57252716-57254566,57254692-57256387,57256463-57256722,57256866-57258695,57258836-57259062,57259100-57259187,57259336-57261464,57261645-57263502,57263638-57265224,57265319-57268250,57268329-57268459,57268517-57268623,57268803-57281429,57281598-57282915,
SLC6A10P	NR_003083	chr16	32889164-32890144,32890318-32890497,32890670-32890750,32890853-32890937,32891042-32891797,32891923-32892012,32893409-32893850,32895025-32896229,
SLC6A15	NM_018057	chr12	85277820-85279212,85279341-85279688,85279848-85285609,85286088-85306300,
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SLC6A15	NM_182767	chr12	85255786-85257216,85257381-85260811,85260973-85264255,85264450-85266379,85266574-85266864,85267108-85270274,85270387-85277636,85277820-85279212,85279341-85279688,85279848-85285609,85286088-85306300,
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SLC7A5	NM_003486	chr16	87866632-87868018,87868198-87870102,87870254-87871449,87871548-87872318,87872424-87873306,87873432-87874033,87874080-87874654,87874762-87885328,87885456-87902489,
SLC7A8	NM_182728	chr14	23596553-23597226,23597406-23598857,23599009-23600668,23600767-23607128,23607234-23608631,23608757-23609678,23609834-23612286,23612414-23623466,
SLC7A8	NM_012244	chr14	23596553-23597226,23597406-23598857,23599009-23600668,23600767-23607128,23607234-23608631,23608757-23609678,23609834-23612286,23612414-23634492,23634646-23635543,23635750-23651971,
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SLC9A6	NM_001042537	chrX	135067987-135076943,135077145-135080265,135080345-135080639,135080718-135081013,135081128-135084265,135084373-135092599,135092743-135095106,135095214-135095506,135095597-135098802,135098918-135104743,135104857-135106487,135106643-

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SLITRK2	NM_001144009	chrX	144903403-144903899,
SLITRK2	NM_001144005	chrX	144899545-144901990,144902055-144903347,144903403-144903521,144903682-144903899,
SLITRK2	NM_001144008	chrX	144903403-144903521,144903682-144903899,
SLITRK2	NM_001144010	chrX	144903403-144903521,144903672-144903911,
SLITRK2	NM_001144006	chrX	144903403-144903521,144903682-144903911,
SLITRK2	NM_001144003	chrX	144899545-144901990,144902055-144903347,144903403-144903521,144903672-144903899,
SLITRK2	NM_001144004	chrX	144899545-144901990,144902055-144903347,144903403-144903521,144903672-144903911,
SLITRK2	NM_032539	chrX	144899545-144901990,144902055-144902864,144903403-144903521,144903672-144903899,
SLITRK5	NM_015567	chr13	88325081-88327634,
SLURP1	NM_020427	chr8	143822695-143823219,143823341-143823744,
SMARCC1	NM_003074	chr3	47629797-47632149,47632328-47651554,47651818-47663695,47663832-47676678,47676835-47677510,47677627-47680213,47680271-47702782,47702946-47703822,47704083-47712146,47712208-47716963,47717079-47718117,47718273-47719686,47719802-47721925,47721999-47727537,47727661-47730875,47730915-47734729,47734791-47742766,47742893-47747897,47748021-47752171,47752299-47755903,47755981-47762154,47762226-47770513,47770585-47777522,47777617-47779517,47779601-47787396,47787484-47814305,47814427-47823091,
SMARCD2	NM_001098426	chr17	61910352-61910427,61910531-61910656,61910781-61910945,61911083-61911267,61911367-61911525,61911689-61911832,61911936-61912063,61912161-61912770,61912928-61914280,61914405-61914553,61914598-61914799,61914986-61919817,
SMG6	NM_017575	chr17	1964917-1968365,1968449-1968760,1968974-1972070,1972226-1985102,1985251-1989017,1989196-2075950,2076154-2089955,2090126-2091691,2091810-2139784,2139932-2147950,2148014-2185939,2186154-2186917,2187030-2195844,2195925-2196163,2196272-2200535,2200648-2201155,2201350-2202198,2203959-2206925,
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SNHG9	NR_003142	chr16	2015131-2015405,
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SNRPN	NM_022806	chr15	25068971-25131661,25131737-25165156,25165272-25207259,25207357-25213077,25213230-25219456,25219604-25220503,25220657-25221450,25221564-25222022,25222177-25222923,25223064-25223338,25223466-25223552,
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SOCS4	NM_080867	chr14	55494190-55509668,
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SOCS6	NM_004232	chr18	67956327-67991777,
SORBS3	NM_001018003	chr8	22423386-22423856,22423998-22424172,22424227-22424333,22424382-22424572,22424689-22426659,22426787-22428421,22428735-22429229,22429335-22429851,22429960-22432178,
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SPATA4	NM_144644	chr4	177106044-177109268,177109387-177113776,177113999-177114107,177114228-177114602,177114734-177116494,
SPATA5L1	NM_024063	chr15	45695717-45697516,45697704-45702568,45702729-45706767,45706979-45707783,45707978-45709465,45709598-45710753,45710881-45713239,
SPATA5L1	NR_027635	chr15	45695717-45697516,45697704-45702568,45702729-45706767,45706979-45707783,45708008-45709465,45709598-45710753,45710881-45713239,
SPATC1	NM_198572	chr8	145086895-145094808,145095365-145095467,145096009-145096131,145096273-145101526,
SPATC1	NM_001134374	chr8	145086895-145094808,145095365-145095467,145096009-145101526,
SPIN1	NM_006717	chr9	91003454-91041295,91041507-91063854,91063905-91077409,91077665-91083285,91083521-91089991,

SPINK5	NM_006846	chr5	147443663-147444908,147444936-147449884,147450014-147451709,147451784-147465966,147466096-147468103,147468169-147469055,147469185-147470726,147470792-147473915,147474045-147475379,147475469-147477428,147477558-147478795,147478879-147480015,147480145-147480916,147481000-147481342,147481472-147484513,147484564-147486598,147486728-147488314,147488401-147491329,147491459-147492429,147492498-147493923,147494053-147495931,147496030-147497998,147498128-147498547,147498622-147499570,147499700-147499856,147499955-147503394,147503524-147504326,147504401-147505284,147505414-147506544,147506643-147510820,147510953-147513358,147513451-147516544,
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SPINK8	NM_001080525	chr3	48348494-48351392,48351437-48360985,48361109-48362513,48362565-48369763,
SPPL2A	NM_032802	chr15	51000072-51012135,51012298-51014319,51014399-51017416,51017521-51018516,51018575-51023160,51023237-51024798,51024882-51028296,51028400-51028839,51028938-51031875,51032026-51039690,51039826-51040308,51040400-51040883,51041068-51041831,51041944-51057663,
SPRR1B	NM_003125	chr1	153003724-153004801,
SPTAN1	NM_003127	chr9	131314976-131329015,131329257-131331049,131331177-131336952,131337095-131337476,131337625-131339100,131339236-131339406,131339553-131339629,131339786-131340387,131340525-131341914,131342018-131343199,131343339-131344059,131344172-131344756,131344836-131344971,131345129-131345354,131345561-131346065,131346249-131346559,131346805-131346998,131347123-131348025,131348245-131349883,131349978-131351086,131351223-131353754,131353905-131355260,131355322-131356452,131356653-131360677,131360784-131361240,131361266-131362357,131362395-131365820,131365870-131366603,131366697-131367311,131367458-131367573,131367757-131369881,131369983-131370129,131370329-131370407,131370556-131371151,131371257-131371399,131371564-131373991,131374125-131374386,131374526-131375658,131375765-131377909,131378120-131379917,131380040-131380264,131380388-131381148,131381283-131383435,131383536-131386605,131386767-131387380,131387459-131388046,131388258-131388668,131388967-131389663,131389778-131390202,131390222-131392598,131392655-131394404,131394603-131394708,131394764-131394849,131394998-131395085,131395235-131395486,
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SPTAN1	NM_001195532	chr9	131314976-131329015,131329257-131331049,131331177-131336952,131337095-131337476,131337625-131339100,131339236-131339406,131339553-131339629,131339786-131340387,131340525-131341914,131342018-131343199,131343339-131344059,131344172-131344756,131344836-131344971,131345129-131345354,131345561-131346065,131346249-131346559,131346805-131346998,131347123-131348025,131348245-131349883,131349978-131351086,131351223-131353754,131353905-131356452,131356653-131360677,131360784-131361240,131361266-131362357,131362395-131365820,131365870-131366603,131366697-131367311,131367458-131367573,131367757-131369881,131369983-131370129,131370329-131370407,131370556-131371151,131371257-131371399,131371564-131373991,131374125-131374386,131374526-131375658,131375765-131377909,131378120-131379917,131380040-131380264,131380388-131381148,131381283-131383435,131383536-131386605,131386767-131387380,131387459-131388046,131388258-131388668,131388967-131389663,131389778-131390202,131390222-131392598,131392655-131394404,131394603-131394708,131394764-131394849,131394998-131395085,131395235-131395486,
SQSTM1	NM_003900	chr5	179248142-179249956,179250054-179250856,179251088-179251180,179251324-179252144,179252227-179260030,179260247-179260585,179260783-179263434,
SQSTM1	NM_001142299	chr5	179234124-179238572,179238683-179249956,179250054-179250856,179251088-179251180,179251324-179252144,179252227-179260030,179260247-179260585,179260783-179263434,
SQSTM1	NM_001142298	chr5	179233592-179238572,179238683-179249956,179250054-179250856,179251088-179251180,179251324-179252144,179252227-179260030,179260247-179260585,179260783-179263434,
SRBD1	NM_018079	chr2	45616739-45620082,45620269-45640251,45640433-45645502,45645681-45646925,45647034-45704130,45704215-45715377,45715471-45773869,45773979-45774659,45774752-45778262,45778422-45780760,45780870-45789790,45789896-45800344,45800482-45801764,45801863-45807012,45807153-45808830,45808950-45812745,45812914-45826586,45826975-45829040,45829223-45832499,45832581-45838356,
SRD5A1	NM_001047	chr5	6633983-6651953,6652122-6656189,6656293-6662927,6663080-6668313,
SREBF2	NM_004599	chr22	42229363-42262833,42263285-42264613,42264797-42266891,42267040-42269800,42270024-42271339,42271456-42271545,42271729-42273231,42273426-42273944,42274128-42276718,42276997-42280844,42281016-42289119,42289290-42290822,42290942-42293054,42293166-42294651,42294786-42296332,42296503-42298972,42299160-42300865,42300979-42301442,
SREK1IP1	NM_173829	chr5	64020401-64023932,64024007-64036882,64037028-64050140,64050190-64064330,
SRP72	NM_006947	chr4	57333911-57335817,57335940-57337884,57338010-57340218,57340364-57340444,57340558-57342835,57342869-57344543,57344670-57344756,57344816-57349303,57349437-57350900,57351031-57352489,57352564-57354113,57354180-57355552,57355650-57356497,57356603-57356732,57356812-57357595,57357735-57361521,57361561-57366700,57366862-57367848,
SRP9	NM_001130440	chr1	225965715-225971000,225971071-225974562,225974688-225976940,
SRP9	NM_003133	chr1	225965715-225971000,225971071-225976940,
SRPRB	NM_021203	chr3	133502989-133524518,133524847-133525451,133525548-133526588,133526668-133529959,133530044-133534432,133534571-133535720,133535777-133538395,
SSBP1	NM_003143	chr7	141438211-141438922,141438991-141441967,141442030-141443359,141443502-141443700,141443790-141445294,141445385-141450109,
ST8SIA3	NM_015879	chr18	55020257-55021631,55021756-55024142,55024702-55027224,
STAM2	NM_005843	chr2	152977317-152980278,152980450-152982738,152982894-152988626,152988683-152989685,152989775-152989914,152989999-152992021,152992118-153000339,153000528-153001400,153001472-153003674,153003823-153004536,153004637-153004737,153004815-153006657,153006744-153032115,
STARD13	NM_178007	chr13	33679848-33680893,33681072-33684008,33684228-33684821,33685045-33685913,33686030-33686856,33687069-33692200,33692401-33700216,33700378-33701508,33701684-33703064,33704427-33716445,33716511-33739472,33739556-33741686,33741760-33760013,
STARD13	NM_178006	chr13	33679848-33680893,33681072-33684008,33684228-33684821,33685045-33685913,33686030-33686856,33687069-33692200,33692401-33700216,33700378-33701508,33701684-33703064,33704427-33716445,33716511-33739472,33739556-33741686,33741760-33859605,
STARD13	NM_052851	chr13	33679848-33680893,33681072-33684008,33684228-33684821,33685045-33685913,33686030-33686856,33687069-33692200,33692401-33700216,33700378-33701508,33701684-33703064,33704427-33716445,33716511-33739472,33739556-33741686,33741760-33779954,
STC2	NM_003714	chr5	172745253-172750220,172750434-172752869,172753014-172755044,

STIL	NM_003035	chr1	47717595-47725959,47726212-47728573,47728786-47735305,47735539-47737746,47737914-47745911,47746882-47748015,47748132-47753221,47753333-47755105,47755258-47759128,47759217-47761435,47761521-47765575,47765825-47767231,47767421-47767904,47768019-47770559,47770669-47775946,47776035-47779706,
STIL	NM_001048166	chr1	47717595-47725959,47726212-47728573,47728789-47735305,47735539-47737746,47737914-47745911,47746882-47748015,47748132-47753221,47753333-47755105,47755258-47759128,47759217-47761435,47761521-47765575,47765825-47767231,47767421-47767904,47768019-47770559,47770669-47775946,47776035-47779706,
STK11	NM_000455	chr19	1207203-1218414,1218500-1219321,1219413-1220370,1220505-1220578,1220717-1221210,1221340-1221946,1222006-1222982,1223172-1226451,1226663-1227590,
STK3	NM_006281	chr8	99468229-99538968,99539146-99560195,99560390-99591890,99592018-99608258,99608398-99718693,99718863-99719373,99719540-99761502,99761619-99779469,99779600-99786965,99787048-99837741,
STK32B	NM_018401	chr4	5053643-5141630,5141688-5170024,5170178-5332945,5333121-5399932,5399972-5418570,5418662-5448398,5448504-5458532,5458651-5461828,5461956-5468428,5468562-5469731,5469798-5500670,
STON2	NM_033104	chr14	81737217-81743243,81745084-81837330,81837530-81862236,81862523-81864637,
STOX1	NM_001130162	chr10	70587691-70641712,70641867-70644014,70646375-70652343,
STOX1	NM_152709	chr10	70587691-70641712,70641867-70644014,70646375-70652343,
STOX1	NM_001130160	chr10	70587691-70641712,70641867-70652343,
STOX1	NM_001130159	chr10	70587691-70641712,70641867-70644014,70644216-70652343,
STOX1	NM_001130161	chr10	70587691-70641712,70641867-70644014,70646375-70652343,70652530-70654996,
STRADA	NM_001003786	chr17	61781112-61781363,61781408-61781699,61781943-61783993,61784100-61784605,61784779-61787849,61787975-61788086,61788197-61790764,61790888-61791364,61791469-61805716,61805774-61819099,
STRADA	NM_001003787	chr17	61781112-61781363,61781408-61781699,61781943-61783993,61784100-61784605,61784779-61787849,61787975-61788086,61788197-61790764,61790888-61791364,61791469-61800656,61800687-61803996,61804056-61805692,61805774-61819099,
STRADA	NM_001165969	chr17	61781112-61781363,61781408-61781790,61781943-61783993,61784100-61784605,61784779-61787849,61787975-61788086,61788197-61790764,61790888-61791364,61791469-61805692,61805774-61819099,
STRADA	NM_153335	chr17	61781943-61783993,61784100-61784605,61784779-61787849,61787975-61788086,61788197-61790764,61790888-61791364,61791469-61805716,61805774-61819099,
STRADA	NM_001165970	chr17	61781112-61781363,61781408-61781790,61781943-61783993,61784100-61784605,61784779-61787849,61787975-61788086,61788197-61790764,61790888-61803996,61804056-61805692,61805774-61819099,
STRADA	NM_001003788	chr17	61781112-61781363,61781408-61781699,61781943-61783993,61784100-61784605,61784779-61787849,61787975-61788086,61788197-61790764,61790888-61791364,61791469-61803996,61804056-61805692,61805774-61819099,
STX18	NM_052874	chr16	31004223-31004449,31004562-31004666,31004806-31008002,31008078-31008270,31008381-31008821,31008897-31012247,31012324-31012413,31012515-31012848,31012925-31021686,
SUN1	NM_001171945	chr7	856311-856915,857137-872140,872239-878433,878624-881581,881768-882841,882870-882976,
SUN1	NM_001171946	chr7	855241-872140,872239-878433,878624-881581,881768-882841,882870-882976,
SUN1	NM_001171944	chr7	856311-872140,872239-878433,878624-881581,881768-891585,891681-892244,892305-892448,892590-893044,893256-894555,894644-895993,896039-897463,897595-899763,900020-901015,901102-905587,905705-908984,909154-912105,912200-912850,
SUN1	NM_025154	chr7	856311-878433,878624-881581,881768-882841,882870-882976,883158-891585,891681-892244,892305-892445,892590-893044,893256-894555,894644-895993,896039-897463,897595-899763,900020-901015,901102-905587,905705-908984,909154-912105,912200-912850,
SUN1	NM_001130965	chr7	872239-878433,878624-881581,881768-882841,882870-882976,883158-891019,891120-891585,891681-892244,892305-892445,892590-893044,893256-894555,894644-895993,896039-897463,897595-899763,900020-901015,901102-905587,905705-908984,909154-912105,912200-912850,
SURF1	NM_003172	chr9	136218838-136218914,136218998-136219299,136219464-136219547,136219622-136220602,136220796-136221512,136221597-136221677,136221813-136223122,136223176-136223274,
SURF2	NM_017503	chr9	136223547-136223788,136223945-136224585,136224691-136226824,136227006-136227139,136227311-136227930,

SUSD3	NM_145006	chr9	95821113-95838064,95838255-95840126,95840276-95841751,95841885-95846817,
SVIP	NM_148893	chr11	22844680-22848751,22848867-22849368,22849421-22851239,
SYCN	NM_001080468	chr19	39693637-39694498,
SYNPO2L	NM_024875	chr10	75408638-75410664,
SYNPO2L	NM_001114133	chr10	75408638-75412895,75413412-75413885,75414039-75415574,
SYT6	NM_205848	chr1	114634705-114636355,114636426-114640347,114640500-114641714,114641888-114646221,114646344-114680115,114680676-114682235,114682503-114696230,
SYT9	NM_175733	chr11	7273563-7324268,7324622-7334624,7335173-7437271,7437394-7439186,7439360-7441735,7441867-7488021,
TAF2	NM_003184	chr8	120744427-120754772,120754897-120756526,120756634-120758943,120759175-120768244,120768356-120770311,120770383-120772837,120772979-120774653,120774849-120790257,120790370-120793291,120793434-120795619,120795874-120797439,120797507-120800576,120800688-120801028,120801145-120801830,120801987-120803562,120803700-120805604,120805692-120807770,120807872-120809228,120809344-120809900,120810087-120814032,120814266-120816116,120816260-120818521,120818642-120831584,120831747-120843915,120843972-120844720,
TAF9B	NM_015975	chrX	77387271-77388833,77388946-77392410,77392488-77393244,77393381-77393457,77393596-77394338,77394422-77395056,
TALDO1	NM_006755	chr11	747579-755877,756003-758948,759058-760120,760254-763342,763520-763745,763945-764286,764434-764811,
TARBP2	NM_134323	chr12	53895246-53895797,53895969-53896809,53896914-53897495,53897593-53898179,53898254-53898480,53898600-53898917,53899047-53899431,53899635-53899773,
TARBP2	NM_004178	chr12	53894786-53895802,53895969-53896809,53896914-53897495,53897593-53898179,53898254-53898480,53898600-53898917,53899047-53899431,53899635-53899773,
TARBP2	NM_134324	chr12	53895493-53895797,53895969-53896809,53896914-53897495,53897593-53898179,53898254-53898480,53898600-53898917,53899047-53899431,53899635-53899773,
TARS	NM_152295	chr5	33441250-33445428,33445511-33448645,33448838-33453392,33453518-33455048,33455172-33455690,33455810-33456105,33456172-33456252,33456333-33457360,33457509-33458669,33458770-33459798,33459967-33461005,33461170-33461261,33461401-33461770,33461850-33462009,33462112-33462202,33462309-33463856,33463931-33466974,33467091-33467663,
TAX1BP1	NM_006024	chr7	27779889-27788135,27788306-27797648,27797753-27805451,27805641-27809293,27809454-27824780,27824931-27825016,27825109-27827035,27827223-27831623,27831850-27832683,27832832-27833940,27834066-27835733,27835839-27839582,27839710-27855966,27856140-27856507,27856658-27867355,27867440-27868245,
TAX1BP1	NM_001079864	chr7	27779889-27788135,27788306-27797648,27797753-27805451,27805641-27809293,27809454-27824780,27824931-27825016,27825109-27827035,27827223-27831623,27831850-27832683,27832832-27833940,27834066-27835733,27835839-27839582,27839710-27855966,27856014-27856507,27856658-27867355,27867440-27868245,
TBC1D10B	NM_015527	chr16	30369895-30369982,30370139-30370491,30370683-30370857,30370925-30371046,30371163-30376219,30376328-30376424,30376534-30376814,30376916-30380547,
TBC1D19	NM_018317	chr4	26585915-26614789,26614864-26616028,26616076-26622233,26622311-26638831,26638908-26640391,26640457-26641761,26641810-26661217,26661330-26667953,26668028-26673769,26673810-26675396,26675511-26685295,26685372-26689965,26690030-26719553,26719640-26721701,26721748-26737075,26737110-26741484,26741596-26744128,26744222-26750031,26750149-26755440,26755513-26756493,
TBCEL	NM_152715	chr11	120895001-120916381,120916533-120918235,120918377-120924258,120924442-120925759,120926018-120929052,120929181-120930676,120930795-120957485,
TBCEL	NM_001130047	chr11	120894864-120916381,120916533-120918235,120918377-120924258,120924442-120925759,120926018-120929052,120929181-120930676,120930795-120957485,
TBRG4	NM_004749	chr7	45140026-45140855,45140972-45141100,45141214-45141422,45141670-45141944,45142091-45142930,45143043-45143696,45143856-45144135,45144309-45145038,45145364-45148424,45148887-45151240,
TBRG4	NM_199122	chr7	45140026-45140855,45140972-45141100,45141214-45141422,45141670-45141944,45142091-45142930,45143043-45145038,45145364-45148424,45148887-45151261,
TBRG4	NM_030900	chr7	45140026-45140855,45140972-45141100,45141214-45141422,45141670-45141944,45142091-45142930,45143043-45145038,45145364-

			45148424,45148887-45151240,
TBX10	NM_005995	chr11	67399366-67399787,67399884-67400072,67400142-67400417,67400575-67401658,67401832-67402285,67402389-67402465,67402735-67406935,
TBX19	NM_005149	chr1	168250532-168260396,168260663-168262380,168262517-168266960,168267024-168269658,168269722-168274244,168274435-168277978,168278116-168281944,
TBX3	NM_005996	chr12	115110108-115111968,115112641-115114116,115114276-115115383,115115462-115117308,115117457-115118682,115118952-115120615,
TBX3	NM_016569	chr12	115110108-115111968,115112641-115114116,115114276-115115383,115115462-115117308,115117457-115117716,115117778-115118682,115118952-115120615,
TBX4	NM_018488	chr17	59534038-59534896,59534993-59543178,59543300-59544869,59545019-59555986,59556141-59557240,59557331-59557449,59557681-59560259,
TCAM1P	NR_002947	chr17	61934784-61936662,61936985-61937232,61937657-61938046,61938315-61939647,61939892-61940083,61940491-61940515,
TCEA3	NM_003196	chr1	23707968-23710837,23710911-23713764,23713913-23720370,23720525-23724034,23724095-23724283,23724449-23735155,23735220-23743740,23743884-23744395,23744503-23745568,23745633-23751056,
TCERG1	NM_001040006	chr5	145826972-145834617,145834845-145836744,145836899-145838445,145838901-145843112,145843357-145849105,145849308-145850197,145850312-145851049,145851140-145858054,145858217-145859416,145859475-145859589,145859658-145862153,145862291-145863101,145863193-145872481,145872602-145878097,145878250-145882936,145883103-145883385,145883570-145886589,145886771-145887434,145887520-145888706,145888809-145890002,
TCERG1	NM_006706	chr5	145826972-145834617,145834845-145836744,145836899-145838445,145838901-145843112,145843357-145847902,145847967-145849105,145849308-145850197,145850312-145851049,145851140-145858054,145858217-145859416,145859475-145859589,145859658-145862153,145862291-145863101,145863193-145872481,145872602-145878097,145878250-145882936,145883103-145883385,145883570-145886589,145886771-145887434,145887520-145888706,145888809-145890002,
TCTN1	NM_001082538	chr12	111052208-111057639,111057762-111064165,111064298-111066570,111066724-111070275,111070365-111072473,111072585-111074284,111074307-111078186,111078323-111078827,111078955-111079345,111079433-111080052,111080195-111082770,111082935-111084999,111085142-111085552,111085699-111086846,
TCTN1	NM_001173976	chr12	111052208-111054080,111054158-111057639,111057762-111064165,111064298-111066570,111066724-111070275,111070365-111072473,111072585-111074284,111074307-111078186,111078323-111078827,111078955-111079345,111079433-111082776,111082935-111084999,111085142-111085552,111085699-111086846,
TCTN1	NM_024549	chr12	111052208-111057639,111057762-111064165,111064298-111066570,111066724-111070275,111070365-111072199,111072269-111074284,111074307-111078186,111078323-111078827,111078955-111079345,111079433-111080052,111080195-111082770,111082935-111085014,111085142-111085552,111085699-111086846,
TCTN1	NM_001173975	chr12	111052269-111057639,111057762-111064165,111064298-111066570,111066724-111070275,111070365-111072473,111072585-111074284,111074307-111078186,111078323-111078827,111078955-111079345,111079433-111080052,111080195-111082770,111082935-111085014,111085142-111085552,111085699-111086846,
TCTN1	NM_001082537	chr12	111052208-111057639,111057762-111064165,111064298-111066570,111066724-111070275,111070365-111072473,111072585-111074284,111074307-111078186,111078323-111078827,111078955-111079345,111079433-111080052,111080195-111082770,111082935-111085014,111085142-111085552,111085699-111086846,
TCTN2	NM_024809	chr12	124155870-124156052,124156162-124156601,124156680-124158160,124158358-124163734,124163837-124171381,124171583-124172596,124172725-124175078,124175222-124177203,124177271-124179387,124179524-124179765,124179845-124180960,124181043-124181632,124181746-124184249,124184358-124189077,124189236-124191271,124191399-124191530,124191621-124192149,
TCTN2	NM_001143850	chr12	124155870-124156052,124156162-124156601,124156680-124158163,124158358-124163734,124163837-124171381,124171583-124172596,124172725-124175078,124175222-124177203,124177271-124179387,124179524-124179765,124179845-124180960,124181043-124181632,124181746-124184249,124184358-124189077,124189236-124191271,124191399-124191530,124191621-124192149,
TDO2	NM_005651	chr4	156824946-156825168,156825276-156826217,156826310-156828872,156828945-156830037,156830167-156831175,156831364-156832647,156832757-156835473,156835587-156837005,156837065-156838545,156838627-156839299,156839392-156840987,

TECTA	NM_005422	chr11	120973439-120976538,120976674-120979918,120980208-120983779,120983919-120984260,120984428-120989013,120989428-120996009,120996582-120998459,120999054-121000345,121000921-121008128,121008732-121016262,121016826-121023588,121023790-121028548,121028934-121030842,121031131-121032782,121033080-121035980,121036093-121037285,121037490-121038761,121038927-121039384,121039635-121058539,121058704-121059787,121059877-121060471,121060590-121061413,
TEKT2	NM_014466	chr1	36549751-36550469,36550679-36550762,36550890-36551435,36551643-36552303,36552449-36552530,36552647-36552803,36552913-36553038,36553184-36553327,36553409-36553572,
TEKT3	NM_031898	chr17	15207470-15211979,15212136-15215574,15215799-15217402,15217548-15222392,15222465-15231307,15231393-15234322,15234932-15243343,15243379-15244833,
TEX101	NM_001130011	chr19	43919191-43920031,43920136-43920249,43920395-43920523,43920708-43922028,43922159-43922318,
TEX101	NM_031451	chr19	43892882-43905646,43905714-43906916,43907012-43910373,43910672-43920031,43920136-43920249,43920395-43920523,43920708-43922028,43922159-43922318,
TEX2	NM_018469	chr17	62226452-62228199,62228322-62230303,62230515-62232200,62232328-62238159,62238294-62248458,62248560-62254683,62254832-62265526,62265797-62270917,62271250-62272253,62272456-62289932,62291603-62340526,
TEX9	NM_198524	chr15	56657676-56657775,56657869-56665637,56665703-56676148,56676230-56680668,56680719-56681514,56681599-56683439,56683617-56686361,56686446-56686857,56687033-56704498,56704635-56719801,56719938-56720563,56720672-56737867,
TFF2	NM_005423	chr21	43766656-43767593,43767742-43769988,43770140-43770986,
TFG	NM_006070	chr3	100428566-100432485,100432714-100438817,100438903-100447554,100447703-100451350,100451517-100455418,100455561-100463675,100463776-100466991,
TFG	NM_001007565	chr3	100428276-100432485,100432714-100438817,100438903-100447554,100447703-100451350,100451517-100455418,100455561-100463675,100463776-100466991,
TFG	NM_001195479	chr3	100428566-100432485,100432714-100438817,100438903-100447554,100447703-100451350,100451517-100455418,100455549-100463675,100463776-100466991,
TFG	NM_001195478	chr3	100428433-100432485,100432714-100438817,100438903-100447554,100447703-100451350,100451517-100455418,100455561-100463675,100463776-100466991,
TFRC	NM_003234	chr3	195779056-195780287,195780430-195781949,195782173-195785153,195785237-195785443,195785504-195787049,195787119-195789451,195789517-195789723,195789811-195791178,195791300-195792312,195792472-195794387,195794529-195794901,195795002-195796324,195796440-195798265,195798370-195798872,195799024-195800799,195800997-195802028,195802232-195803933,195803994-195808700,
TFRC	NM_001128148	chr3	195779056-195780287,195780430-195781949,195782173-195785153,195785237-195785443,195785504-195787049,195787119-195789451,195789517-195789723,195789811-195791178,195791300-195792312,195792472-195794387,195794529-195794901,195795002-195796324,195796440-195798265,195798370-195798872,195799024-195800799,195800997-195802028,195802232-195803933,195803994-195808912,
TGFBR3	NM_001195684	chr1	92149415-92161227,92161337-92163644,92163688-92174218,92174341-92177798,92178100-92181791,92181952-92182123,92182266-92184867,92185022-92185448,92185785-92187510,92187702-92193214,92193364-92195360,92195531-92200331,92200517-92224168,92224308-92262842,92263029-92327026,92327202-92365192,92365255-92371381,
TGFBR3	NM_001195683	chr1	92149415-92161227,92161337-92163644,92163688-92174218,92174341-92177798,92178100-92181791,92181952-92182123,92182266-92184867,92185022-92185448,92185785-92187510,92187702-92193214,92193364-92195360,92195531-92200331,92200517-92224168,92224308-92262842,92263029-92327026,92327202-92351433,
TGFBR3	NM_003243	chr1	92149415-92161227,92161337-92163644,92163688-92174218,92174341-92177798,92178100-92181791,92181952-92182123,92182266-92184867,92185022-92185448,92185788-92187510,92187702-92193214,92193364-92195360,92195531-92200331,92200517-92224168,92224308-92262842,92263029-92327026,92327202-92351433,
TGFBR3	NR_036634	chr1	92149415-92161227,92161337-92163644,92163688-92174218,92174341-92177798,92178100-92181791,92181952-92182123,92182266-92184867,92185022-92185448,92185788-92187510,92187702-92193214,92193364-92195360,92195531-92200331,92200517-92224168,92224308-92262842,92263029-92266514,92266613-92327026,92327202-92351433,

THAP4	NM_015963	chr2	242524141-242541309,242541415-242542383,242542495-242545727,242545889-242572330,242573495-242576354,
THAP4	NM_001164356	chr2	242524141-242541309,242541415-242542383,242542495-242545727,242545889-242556825,
TIGD7	NM_033208	chr16	3352010-3355210,
TJP1	NM_003257	chr15	29993894-29996424,29996510-29997730,29997950-30000761,30001241-30003033,30003205-30008813,30009043-30010223,30010323-30010468,30011343-30011979,30012221-30012560,30012913-30018581,30018684-30018983,30019196-30020139,30020224-30024635,30024733-30024833,30025020-30025296,30025518-30026476,30026587-30029466,30029619-30033533,30033641-30034844,30034986-30053340,30053490-30053802,30053973-30054536,30054642-30058467,30058746-30064265,30064370-30065434,30065561-30092847,30092906-30114203,
TJP1	NM_175610	chr15	29993894-29996424,29996510-29997730,29997950-30000761,30001241-30003033,30003205-30008813,30009043-30010223,30010323-30010468,30011343-30012560,30012913-30018581,30018684-30018983,30019196-30020139,30020224-30024635,30024733-30024833,30025020-30025296,30025518-30026476,30026587-30029466,30029619-30033533,30033641-30034844,30034986-30053340,30053490-30053802,30053973-30054536,30054642-30058467,30058746-30064265,30064370-30065434,30065561-30092847,30092906-30114203,
TKT	NM_001135055	chr3	53259626-53259765,53259948-53260770,53260895-53262070,53262166-53262290,53262376-53263021,53263154-53263294,53263453-53264471,53264638-53265371,53265567-53267170,53267291-53268997,53269191-53274265,53274365-53275146,53275262-53276139,53276259-53289850,
TKT	NM_001064	chr3	53259948-53260770,53260895-53262070,53262166-53262290,53262376-53263021,53263154-53263294,53263453-53264471,53264638-53265371,53265567-53267170,53267291-53268997,53269191-53274265,53274365-53275146,53275262-53276139,53276259-53289850,
TLE1	NM_005077	chr9	84199221-84199361,84199440-84200418,84200571-84202594,84202744-84205718,84205968-84207938,84208190-84225133,84225212-84226682,84226875-84228290,84228437-84230895,84231050-84231559,84231615-84235354,84235473-84248261,84248280-84249010,84249217-84267127,84267204-84268887,84268952-84300589,84300636-84300746,84300812-84302247,84302350-84303130,
TLR3	NM_003265	chr4	186990403-186997765,186998215-186999992,187000186-187003472,187005327-187005797,
TLR7	NM_016562	chrX	12885243-12885598,12885701-12903629,
TLX3	NM_021025	chr5	170736791-170737152,170737398-170738391,
TM4SF20	NM_024795	chr2	228228729-228230807,228230961-228235629,228235697-228243800,
TM6SF1	NM_001144903	chr15	83776525-83781547,83781653-83784595,83784695-83788328,83788434-83790671,83790756-83791507,83791631-83793422,83793529-83796108,83796230-83805231,
TM6SF1	NM_023003	chr15	83776525-83781547,83781653-83784595,83784695-83788328,83788434-83790671,83790756-83791507,83791631-83793422,83793529-83795505,83795600-83796108,83796230-83805231,
TMBIM1	NM_022152	chr2	219140345-219140747,219140803-219141725,219141823-219142087,219142177-219142354,219142394-219142656,219142698-219143236,219143289-219143759,219143815-219144010,219144077-219144747,219144850-219146661,219146905-219157187,
TMC6	NM_007267	chr17	76109293-76109627,76109706-76113348,76113429-76113547,76113726-76113881,76114017-76115050,76115128-76115376,76115474-76116732,76116914-76117092,76117246-76117635,76117793-76118684,76118831-76120068,76120261-76120603,76120863-76120968,76121067-76121237,76121345-76121805,76121966-76122356,76122448-76122603,76122730-76122856,76122988-76128420,
TMC6	NM_001127198	chr17	76109293-76109627,76109706-76113348,76113429-76113547,76113726-76113881,76114017-76115050,76115128-76115376,76115474-76116732,76116914-76117092,76117246-76117635,76117793-76118684,76118831-76120068,76120261-76120603,76120863-76120968,76121067-76121237,76121345-76121805,76121966-76122356,76122448-76122603,76122730-76122856,76122988-76124691,
TMEM101	NM_032376	chr17	42089605-42090375,42090524-42091723,42091906-42092182,
TMEM106A	NM_145041	chr17	41363942-41364244,41364414-41365038,41365272-41365845,41365911-41367805,41367961-41368466,41368609-41368714,41368760-41369276,41369332-41369698,
TMEM108	NM_023943	chr3	132757280-132764744,132764865-132948108,132948196-133098594,133100006-133109022,133109179-133114706,
TMEM108	NM_001136469	chr3	132757280-132764744,132764865-132948112,132948196-133098594,133100006-133109022,133109179-133114706,
TMEM127	NM_017849	chr2	96919854-96920569,96920736-96930874,96931251-96931605,
TMEM127	NM_001193304	chr2	96919854-96920569,96920736-96930874,96931228-96931605,
TMEM132A	NM_178031	chr11	60692206-60694674,60694891-60695111,60695332-60696099,60696433-60697980,60698132-60699159,60699357-60699454,60699600-60701012,60701217-60701958,60702237-60702722,60702916-60703334,

TMEM132A	NM_017870	chr11	60692206-60694674,60694891-60695111,60695332-60696099,60696433-60697980,60698132-60699156,60699357-60699454,60699600-60701012,60701217-60701958,60702237-60702722,60702916-60703334,
TMEM132B	NM_052907	chr12	125811222-125833996,125834890-125900075,125900224-126003983,126004172-126068395,126068541-126128620,126128828-126135227,126135500-126136985,126137179-126138109,
TMEM140	NM_018295	chr7	134833023-134849168,
TMEM164	NM_017698	chrX	109246001-109310573,109310625-109352306,109352375-109388024,109388105-109414646,109414749-109416471,
TMEM164	NM_032227	chrX	109246407-109246727,109247393-109310573,109310625-109352306,109352375-109388024,109388105-109414646,109414749-109416471,
TMEM165	NM_018475	chr4	56262564-56277779,56278007-56283237,56283415-56283968,56284153-56290703,56290811-56291541,
TMEM167B	NM_020141	chr1	109633505-109635510,109635644-109637037,
TMEM221	NM_001190844	chr19	17547737-17556006,17556094-17558950,
TMEM229B	NM_182526	chr14	67940659-67953715,67953890-67981801,
TMEM26	NM_178505	chr10	63170505-63173215,63173294-63188682,63188905-63190975,63191091-63195926,63196007-63212647,
TMEM39A	NM_018266	chr3	119151062-119153607,119153730-119155636,119155826-119156600,119156951-119165863,119166020-119171292,119171378-119176863,119177088-119180807,119180996-119182181,
TMEM49	NM_030938	chr17	57785110-57808780,57808884-57812697,57812835-57814812,57814905-57816196,57816309-57842330,57842500-57851113,57851247-57886155,57886238-57889029,57889148-57895071,57895135-57915654,57915759-57917127,
TMEM5	NM_014254	chr12	64173910-64174797,64174955-64178748,64178853-64195869,64196186-64199012,64199185-64202453,
TMEM8B	NM_001042590	chr9	35829953-35834456,35834648-35835006,35835216-35841129,35841265-35841521,35841792-35842387,35842715-35845970,35846066-35846253,35846379-35846464,35846609-35846812,35846993-35852822,35852971-35853136,35853255-35853500,
TMEM8B	NM_001042589	chr9	35829317-35829872,35829953-35834456,35834648-35835006,35835216-35841129,35841265-35841521,35841792-35842387,35842715-35845970,35846066-35846253,35846379-35846464,35846609-35846812,35846993-35852822,35852971-35853136,35853255-35853500,
TMEM8B	NM_016446	chr9	35829389-35829872,35829953-35834456,35834648-35835006,35835216-35841129,35841265-35841521,35841792-35842387,35842715-35845970,35846066-35846253,35846379-35846464,35846609-35846812,
TMEM91	NM_001098823	chr19	41882760-41884184,41884425-41888675,41888827-41889777,
TMEM91	NM_001042595	chr19	41883229-41884184,41884425-41888675,41888827-41889464,
TMEM91	NM_001098821	chr19	41882760-41884184,41884425-41888675,41888827-41889618,
TMEM91	NM_001098822	chr19	41882760-41884184,41884425-41888675,41888827-41889766,
TMEM91	NM_001098825	chr19	41870001-41884184,41884425-41888675,41888827-41889766,
TMEM91	NM_001098824	chr19	41882760-41884184,41884425-41888675,41888827-41889789,
TMOD2	NM_014548	chr15	52043910-52058568,52058765-52060457,52060616-52065907,52066032-52069127,52069216-52073239,52073372-52074916,52075026-52090392,52090538-52098572,52098719-52100615,
TMOD2	NM_001142885	chr15	52043910-52058568,52058765-52060457,52060616-52065907,52066032-52069127,52069216-52073239,52073372-52090392,52090538-52098572,52098719-52100615,
TMOD3	NM_014547	chr15	52122034-52155006,52155208-52161412,52161571-52179784,52179909-52181251,52181343-52186010,52186143-52188614,52188724-52192350,52192496-52194087,52194234-52200971,
TMOD4	NM_013353	chr1	151142580-151142993,151143140-151143394,151143540-151143907,151144017-151144107,151144240-151144742,151144834-151145973,151146092-151146865,151147024-151147227,151147394-151148398,
TMPRSS11E	NM_014058	chr4	69313242-69327537,69327664-69332347,69332471-69334595,69334665-69337176,69337342-69340439,69340480-69341977,69342157-69343085,69343347-69344565,69344710-69362359,
TMPRSS13	NM_001077263	chr11	117772981-117774368,117774523-117774672,117774817-117776351,117776452-117779325,117779500-117780519,117780684-117781420,117781466-117782481,117782576-117784490,117784622-117785105,117785230-117787883,117787990-117789122,117789554-117800000,
TMUB2	NM_001076674	chr17	42264478-42265042,42265112-42266388,42266957-42267867,
TMUB2	NM_024107	chr17	42264478-42266388,42266957-42267867,

TMUB2	NM_177441	chr17	42265112-42266301,42266957-42267867,
TNFAIP8L2	NM_024575	chr1	151129199-151131140,
TNFAIP8L3	NM_207381	chr15	51350641-51386739,51386885-51397200,
TNFRSF14	NM_003820	chr1	2488173-2489163,2489274-2489780,2489908-2491260,2491418-2492061,2492154-2493110,2493255-2494302,2494336-2494585,
TNFRSF21	NM_014452	chr6	47200731-47202404,47202635-47220990,47221258-47251672,47252169-47253678,47254332-47277150,
TNFSF12-TNFSF13	NM_172089	chr17	7452630-7452789,7452839-7453435,7453513-7454114,7454170-7454258,7454296-7460093,7460220-7462939,7463020-7463161,7463211-7463364,7463485-7463665,7463806-7464039,
TNIP2	NM_024309	chr4	2744248-2746112,2746234-2746422,2746673-2747171,2747263-2749380,2749673-2757739,
TNIP2	NM_001161527	chr4	2744248-2746112,2746234-2746422,2746673-2747171,2747263-2749380,2749673-2757674,
TOMM20L	NM_207377	chr14	58862812-58863014,58863060-58869396,58869480-58874042,58874187-58875245,
TOMM7	NM_019059	chr7	22852805-22857617,22857668-22862294,
TOPORS	NM_005802	chr9	32544325-32550770,32550967-32552430,
TOPORS	NM_001195622	chr9	32544325-32552430,
TOR1A	NM_000113	chr9	132576502-132580797,132580927-132581022,132581200-132584858,132585126-132586185,
TP53I3	NM_004881	chr2	24300632-24302312,24302511-24303687,24303902-24305753,24306023-24307057,
TP53I3	NM_147184	chr2	24300632-24302312,24302511-24303687,24303902-24305753,24306023-24307057,24307202-24307599,
TPH1	NM_004179	chr11	18042713-18044343,18044479-18045433,18045531-18047120,18047249-18048035,18048173-18050710,18050909-18051057,18051127-18054819,18054922-18057504,18057690-18062191,
TPPP	NM_007030	chr5	665412-666083,666239-677863,678180-693391,
TPPP2	NM_173846	chr14	21498464-21498670,21498914-21499169,21499325-21500049,
TPRG1	NM_198485	chr3	188889921-188925163,188925384-188933079,188933173-188956520,188956699-189028173,189028329-189038413,
TPTE	NM_199259	chr21	10907041-10908823,10908896-10910305,10910400-10914361,10914443-10916368,10916476-10920082,10920165-10921932,10921996-10933850,10933941-10934037,10934121-10934935,10934998-10941906,10941973-10942709,10942775-10942919,10943021-10944566,10944788-10951264,10951428-10952911,10952964-10959739,10959801-10970007,10970063-10971290,10971346-10973721,10973777-10985043,10985103-10987767,10987878-10990761,
TPTE	NM_199261	chr21	10907041-10908823,10908896-10910305,10910400-10914361,10914443-10916368,10916476-10920082,10920165-10921932,10921996-10933850,10933941-10934037,10934121-10934935,10934998-10941906,10941973-10942709,10942775-10942919,10943021-10944566,10944788-10951264,10951428-10952911,10952964-10959739,10959801-10969073,10969129-10970007,10970063-10971290,10971346-10973721,10973777-10985043,10985103-10987767,10987878-10990761,
TPTE	NM_199260	chr21	10907041-10908823,10908896-10910305,10910400-10914361,10914443-10916368,10916476-10920082,10920165-10921932,10921996-10933850,10933941-10934037,10934121-10934935,10934998-10941906,10941973-10942709,10942775-10942919,10943021-10944666,10944788-10951264,10951428-10952911,10952964-10970007,10970063-10971290,10971346-10973721,10973777-10985043,10985103-10987767,10987878-10990761,
TPX2	NM_012112	chr20	30327425-30330342,30330451-30345208,30345386-30347858,30347983-30354357,30354486-30358144,30358275-30359361,30359486-30363668,30363792-30365288,30365442-30366614,30366788-30370050,30370194-30371506,30371725-30380536,30380634-30381649,30381828-30382203,30382352-30385205,30385319-30386166,30386356-30388771,
TRABD	NM_025204	chr22	50624431-50631454,50631523-50632003,50632084-50632767,50632936-50633327,50633470-50635668,50635781-50635876,50636018-50636250,50636425-50636502,50636616-50636772,
TRAF3IP1	NM_015650	chr2	239229427-239233945,239234016-239234448,239234612-239237325,239237471-239237565,239237984-239241463,239241537-239242599,239242677-239247001,239247099-239253136,239253240-239256094,239256117-239257403,239257490-239257964,239258050-239261466,239261592-239261812,239261851-239264643,239264722-239306098,239306321-239307393,
TRAF3IP1	NM_001139490	chr2	239229427-239233945,239234016-239234448,239234612-239237325,239237471-239237565,239237984-239241463,239241537-239242599,239242677-239256094,239256117-239257403,239257490-239257964,239258050-239261466,239261592-239261812,239261851-239264643,239264722-239306098,239306321-239307393,

TRAIP	NM_005879	chr3	49866659-49866889,49866942-49867048,49867200-49867451,49867502-49869347,49869502-49877203,49877294-49877715,49877807-49878416,49878506-49879257,49879373-49879884,49879981-49881232,49881362-49881972,49882014-49884956,49885042-49885574,49885634-49893787,
TRAK1	NM_001042646	chr3	42133053-42166910,42167107-42218304,42218383-42226175,42226294-42229535,42229638-42230506,42230617-42233048,42233129-42234565,42234698-42235314,42235391-42236294,42236434-42240667,42240746-42242308,42242547-42243926,42244245-42251257,42251478-42260984,42261089-42264432,
TRAK1	NM_014965	chr3	42201966-42218304,42218383-42226175,42226294-42229535,42229638-42230506,42230617-42233048,42233129-42234565,42234698-42235314,42235391-42236294,42236434-42240667,42240746-42242308,42242547-42243926,42244245-42251257,
TRAM1	NM_014294	chr8	71487241-71495397,71495560-71495883,71496029-71499128,71499235-71499339,71499412-71506739,71506826-71508496,71508557-71510128,71510247-71510367,71510491-71512252,71512318-71520310,
TRAPPC6A	NM_024108	chr19	45666482-45667172,45667268-45667420,45667506-45668109,45668229-45668383,45668453-45681349,
TRIM10	NM_052828	chr6	30121549-30122086,30122264-30123502,30123537-30124714,30124832-30125144,30125169-30126174,30126407-30126925,30127023-30128205,
TRIM10	NM_006778	chr6	30122264-30123502,30123537-30124714,30124832-30125144,30125169-30126174,30126407-30126925,30127023-30128205,
TRIM15	NM_033229	chr6	30131843-30134951,30135049-30136075,30136308-30137016,30137041-30138276,30138394-30138751,30138786-30139607,
TRIM32	NM_001099679	chr9	119449661-119459942,
TRIM32	NM_012210	chr9	119449661-119459939,
TRIM35	NM_171982	chr8	27145645-27146677,27146798-27147671,27147696-27151595,27151828-27155979,27156077-27168316,
TRIM45	NM_001145635	chr1	117655076-117655979,117656108-117658195,117658312-117659236,117659368-117660708,117661390-117663334,
TRIM45	NM_025188	chr1	117655076-117655979,117656108-117658195,117658312-117659236,117659368-117660654,117661390-117663334,
TRIM66	NM_014818	chr11	8639551-8640295,8640516-8640928,8641083-8641595,8641672-8641991,8642120-8642577,8642869-8643190,8643367-8644361,8644424-8645904,8646002-8646254,8646776-8660199,8660363-8661772,8662700-8664554,8664674-8667286,8667435-8667992,8668109-8669515,8669634-8669961,8670096-8671285,8671435-8673345,8673451-8680282,
TRIM8	NM_030912	chr10	104404945-104414408,104414506-104414835,104415071-104415861,104415895-104416025,104416143-104416502,
TRIP10	NM_004240	chr19	6739797-6741019,6741137-6741234,6741293-6742976,6743126-6743203,6743268-6743503,6743610-6743717,6743848-6744563,6744712-6744809,6745006-6746461,6746573-6749943,6750078-6750301,6750443-6750521,6750645-6751072,
TRIP13	NM_004237	chr5	893206-894900,895068-896778,896910-900607,900665-901454,901547-904261,904336-907243,907309-908101,908190-908468,908577-911956,912112-914578,914693-916017,916089-917121,
TRIP13	NM_001166260	chr5	893206-894900,895068-896778,896910-900607,900665-901454,901547-904261,904336-907243,907309-908101,908190-908468,
TRNP1	NM_001013642	chr1	27321104-27326336,
TROAP	NM_005480	chr12	49717133-49717385,49717536-49717626,49717821-49719282,49719442-49719528,49719668-49719857,49719942-49720449,49720504-49720990,49721114-49722708,49722839-49722942,49723028-49723176,49723238-49723638,49723775-49723926,49724727-49724935,49725191-49725354,
TROAP	NM_001100620	chr12	49717133-49717385,49717536-49717626,49717821-49717936,
TRPC4AP	NM_199368	chr20	33591087-33591211,33591420-33592259,33592374-33593496,33593607-33594236,33594379-33595351,33595444-33596465,33596551-33597988,33598092-33600809,33600870-33603809,33603943-33608991,33609136-33622924,33623112-33632306,33632516-33637667,33637798-33642777,33642835-33645315,33645375-33657097,33657216-33665847,33665978-33680415,
TRPC4AP	NM_015638	chr20	33591087-33591211,33591420-33592259,33592374-33593496,33593607-33594236,33594379-33595351,33595444-33596465,33596551-33597988,33598092-33600809,33600870-33603809,33603943-33608991,33609160-33622924,33623112-33632306,33632516-33637667,33637798-33642777,33642835-33645315,33645375-33657097,33657216-33665847,33665978-33680415,
TRPC6	NM_004621	chr11	101323838-101324379,101324457-101325747,101325833-101340156,101340233-101341912,101342118-101342866,101343064-101344238,101344505-101347030,101347266-101353678,101353897-101359666,101359833-101362285,101362470-101374753,101375530-101454063,
TRPC7	NM_001167577	chr5	135549293-135551886,135551964-135560960,135561043-135561720,135561944-135567040,135567238-135583157,135583424-135587335,135587571-135601906,135602125-135610359,135610526-135692294,135693074-135700939,

TRPC7	NM_020389	chr5	135549293-135551886,135551964-135560960,135561043-135561720,135561944-135567040,135567238-135583157,135583424-135587335,135587571-135601906,135602125-135610359,135610526-135651283,135651468-135692294,135693074-135700939,
TRPC7	NM_001167576	chr5	135549293-135551886,135551964-135560960,135561043-135561720,135561944-135567040,135567238-135583157,135583424-135587335,135587571-135601906,135602125-135692294,135693074-135700939,
TRPM7	NM_017672	chr15	50854006-50862082,50862191-50862299,50862353-50866469,50866677-50866832,50866917-50867047,50867333-50867919,50867987-50868064,50868117-50870834,50870862-50873069,50873106-50875284,50875357-50878587,50878686-50881787,50881854-50884106,50884824-50885812,50885947-50886624,50886811-50888450,50888579-50891317,50891494-50897061,50897342-50899395,50899526-50901776,50901922-50902001,50902159-50903288,50903519-50904744,50905027-50905902,50906039-50906318,50906461-50911940,50911996-50916361,50916498-50920344,50920447-50923612,50923687-50925064,50925190-50926577,50926754-50929617,50929791-50931619,50931746-50935535,50935751-50940882,50941083-50949976,50950017-50955162,50955244-50978726,
TRPM8	NM_024080	chr2	234826078-234835176,234835300-234839311,234839387-234845995,234846154-234847640,234847820-234851218,234851393-234854498,234854675-234855730,234855800-234858591,234858791-234862559,234862664-234863774,234863895-234869418,234869711-234871924,234872022-234873270,234873402-234875252,234875400-234878337,234878452-234878852,234879071-234888830,234888924-234890416,234890560-234891695,234891869-234894330,234894510-234904968,234905161-234915495,234915597-234916712,234916748-234923204,234923299-234925941,
TRPV1	NM_080706	chr17	3470282-3474816,3474934-3475414,3475544-3476925,3477250-3480418,3480487-3480890,3481058-3483749,3483822-3486630,3486725-3489060,3489221-3491480,3491662-3493099,3493400-3493544,3493687-3494256,3494411-3494479,3494648-3495359,
TRPV1	NM_080705	chr17	3470282-3474816,3474934-3475414,3475544-3476925,3477250-3480418,3480487-3480890,3481058-3483749,3483822-3486630,3486725-3489060,3489221-3491480,3491662-3493099,3493400-3493544,3493687-3494256,3494411-3494479,3494648-3495359,3495678-3498956,
TRPV1	NM_018727	chr17	3470282-3474816,3474934-3475414,3475544-3476925,3477250-3480418,3480487-3480890,3481058-3483749,3483822-3486630,3486725-3489060,3489221-3491480,3491662-3493099,3493400-3493544,3493687-3494256,3494411-3494479,3494648-3495359,3495678-3500210,
TRPV1	NM_080704	chr17	3470282-3474816,3474934-3475414,3475544-3476925,3477250-3480418,3480487-3480890,3481058-3483749,3483822-3486630,3486725-3489060,3489221-3491480,3491662-3493099,3493400-3493544,3493687-3494256,3494411-3494479,3494648-3495359,3495678-3511719,3511860-3512601,
TRYX3	NM_001001317	chr7	141952191-141952290,141952432-141954873,141955132-141955353,141955494-141957486,141957569-141957809,
TSC1	NM_001162427	chr9	135772142-135772569,135772733-135772808,135772998-135776100,135776225-135776974,135777087-135777990,135778175-135779036,135779205-135779796,135779842-135780966,135781527-135782116,135782223-135782686,135782758-135785956,135786080-135786387,135786501-135786838,135786956-135787667,135787845-135796748,135796824-135797204,135797361-135798733,135798880-135802586,135802692-135804152,135804340-135810418,135810483-135819928,
TSC1	NM_000368	chr9	135772142-135772569,135772733-135772808,135772998-135776100,135776225-135776974,135777087-135777990,135778175-135779036,135779205-135779796,135779842-135780966,135781527-135782116,135782223-135782686,135782758-135785956,135786080-135786387,135786501-135786838,135786956-135787667,135787845-135796748,135796824-135797204,135797361-135798733,135798880-135800972,135801127-135802586,135802692-135804152,135804340-135810418,135810483-135819928,
TSC1	NM_001162426	chr9	135772142-135772569,135772733-135772808,135772998-135776100,135776225-135776974,135777087-135777990,135778175-135779036,135779205-135779796,135779842-135780966,135781527-135782116,135782223-135782686,135782758-135785956,135786077-135786387,135786501-135786838,135786956-135787667,135787845-135796748,135796824-135797204,135797361-135798733,135798880-135800972,135801127-135802586,135802692-135804152,135804340-135810418,135810483-135819928,
TSC22D1	NM_006022	chr13	45009020-45010178,45010232-45010638,
TSC22D1	NM_183422	chr13	45009020-45010178,45010232-45147297,
TSGA10	NM_025244	chr2	99614685-99634661,99634813-99634997,99635104-99636741,99636946-99651691,99651903-99681400,99681588-99685349,99685462-99688167,99688338-99689479,99689537-99695120,99695277-99697743,99697861-99720428,99720582-99721820,99721900-99721988,99722161-99725294,99725455-99725850,99725976-99727311,99727379-99734005,99734223-99735012,99735150-99743509,99743640-99771154,
TSGA10	NM_182911	chr2	99614685-99634661,99634813-99634997,99635104-99636741,99636946-99651691,99651903-99681400,99681588-99685349,99685462-99688167,99688338-99689479,99689537-99695120,99695277-99697743,99697861-99720428,99720582-99721820,99721900-99721968,99722161-

			99725294,99725455-99725850,99725976-99727311,99727379-99734005,99734223-99743509,99743640-99757889,
TSPYL2	NM_022117	chrX	53112488-53113725,53113805-53113935,53114049-53114134,53114282-53114407,53114504-53114811,53115493-53116956,
TSTD2	NM_139246	chr9	100365050-100367007,100367148-100367763,100367924-100368423,100368544-100372626,100372734-100373854,100373982-100380037,100380160-100387961,100388280-100389678,100389895-100395523,
TTC12	NM_017868	chr11	113185341-113186963,113187038-113194008,113194174-113194714,113194738-113195325,113195405-113196244,113196368-113200640,113200702-113205686,113205760-113209494,113209557-113210006,113210197-113211384,113211456-113212557,113212648-113214992,113215163-113220793,113220888-113221959,113222022-113222790,113222930-113230083,113230184-113230660,113230731-113233121,113233225-113234548,113234650-113235555,113235783-113236945,
TTC13	NM_001122835	chr1	231042766-231044456,231044538-231044686,231044767-231047214,231047296-231048367,231048505-231051937,231052046-231056254,231056341-231057165,231057251-231059585,231059680-231060585,231060720-231061261,231061394-231064681,231064840-231067042,231067219-231067480,231067624-231069523,231069608-231075130,231075243-231076184,231076303-231090077,231090150-231093968,231094046-231096953,231097050-231114304,
TTC13	NM_024525	chr1	231042766-231044456,231044538-231044686,231044767-231047214,231047296-231048367,231048505-231051937,231052049-231056254,231056341-231057165,231057251-231059585,231059680-231060585,231060720-231061261,231061394-231064681,231064840-231067042,231067219-231067480,231067624-231069523,231069608-231075130,231075243-231076184,231076303-231079550,231079645-231081133,231081201-231090077,231090150-231093968,231094046-231096953,231097050-231114304,
TTC23L	NM_144725	chr5	34839365-34840768,34840845-34845590,34845779-34850288,34850414-34863001,34863160-34864540,34864668-34866995,34867175-34869008,34869119-34880284,34880414-34896873,34896981-34899493,
TTC26	NM_024926	chr7	138818607-138819399,138819539-138822591,138822686-138824634,138824751-138827000,138827052-138831889,138832037-138832950,138833124-138845692,138845769-138849876,138849981-138851584,138851642-138853088,138853144-138854033,138854099-138862958,138863049-138863259,138863345-138864318,138864390-138865836,138865945-138872150,138872286-138874065,
TTC26	NM_001144923	chr7	138818607-138819399,138819539-138824634,138824751-138827000,138827052-138831889,138832037-138832950,138833124-138845692,138845769-138849876,138849981-138851584,138851642-138853088,138853144-138854033,138854099-138862958,138863049-138863259,138863345-138864318,138864390-138865836,138865945-138872150,138872286-138874065,
TTC26	NM_001144920	chr7	138818607-138819399,138819539-138822591,138822686-138824634,138824751-138827000,138827052-138831889,138832037-138832950,138833124-138845692,138845769-138849876,138849981-138851584,138851642-138853088,138853144-138854033,138854099-138862958,138863049-138863259,138863345-138864318,138864390-138865836,138865945-138874065,
TTC31	NM_022492	chr2	74710263-74710447,74710538-74717150,74717255-74717369,74717601-74717781,74717867-74718253,74718312-74718420,74718503-74718606,74718800-74719129,74719183-74719264,74719357-74719429,74719573-74719771,74719875-74720047,
TTC31	NR_027749	chr2	74710263-74710447,74710538-74717369,74717601-74717781,74717867-74718253,74718312-74718420,74718503-74718606,74718794-74719129,74719183-74719264,74719357-74719429,74719573-74719771,74719875-74720047,
TTC8	NM_198309	chr14	89291166-89305794,89305917-89307207,89307273-89307379,89307541-89307767,89307859-89310148,89310195-89319313,89319401-89323532,89323622-89327564,89327677-89336401,89336543-89337891,89338068-89338672,89338797-89341368,89341454-89343636,
TTC8	NM_198310	chr14	89291166-89305794,89305917-89307207,89307273-89307379,89307541-89310148,89310195-89319313,89319401-89323532,89323622-89327564,89327677-89336401,89336543-89337891,89338068-89338672,89338797-89341368,89341454-89343636,
TTC8	NM_144596	chr14	89291166-89300035,89300067-89305794,89305917-89307207,89307273-89307379,89307541-89307767,89307859-89310148,89310195-89319313,89319401-89323532,89323622-89327564,89327677-89336401,89336543-89337891,89338068-89338672,89338797-89341368,89341454-89343636,
TTF1	NM_007344	chr9	135251556-135254444,135254532-135261941,135262009-135263524,135263616-135265982,135266219-135267461,135267594-135271818,135271899-135273526,135273714-135275420,135275646-135276840,135278216-135282175,
TTK	NM_001166691	chr6	80714431-80715545,80715700-80717524,80717749-80718101,80718210-80720529,80720675-80721149,80721266-80721444,80721519-80721601,80721698-80722994,80723084-80724178,80724304-80732039,80732190-80736096,80736232-80737600,80737729-80741182,80741277-80744700,80744860-80744981,80745135-80746190,80746317-80747682,80747765-80749411,80749590-80749911,80749998-80750321,80750421-

			80751834,
TTK	NM_003318	chr6	80714431-80715557,80715700-80717524,80717749-80718101,80718210-80720529,80720675-80721149,80721266-80721444,80721519-80721601,80721698-80722994,80723084-80724178,80724304-80732039,80732190-80736093,80736232-80737600,80737729-80741182,80741277-80744700,80744860-80744981,80745135-80746190,80746317-80747682,80747765-80749411,80749590-80749911,80749998-80750321,80750421-80751834,
TTLL2	NM_031949	chr6	167738709-167752133,167752292-167753591,
TTLL3	NM_001025930	chr3	9852079-9852303,9852394-9854625,9854796-9854930,9855030-9859327,9859444-9860504,9860605-9862228,9862426-9867482,9867633-9868679,9868925-9870642,9871080-9874786,9874930-9876363,9876592-9876776,
TTLL3	NR_037162	chr3	9852394-9854625,9854796-9854930,9855030-9857756,9857887-9859327,9859444-9860237,9860605-9862228,9862426-9867482,9867633-9868679,9868757-9870642,9871080-9876363,
TTLL9	NM_001008409	chr20	30458753-30458923,30458999-30474997,30475043-30486274,30486369-30496392,30496506-30497538,30497726-30507665,30507736-30510764,30510857-30512810,30512853-30513850,30513895-30521601,30521662-30522493,30522692-30525197,30525313-30526943,30527070-30530746,
TUG1	NR_002323	chr22	31367766-31368839,31369588-31371154,
TXNRD1	NM_182742	chr12	104681125-104705066,104705191-104707021,104707096-104709553,104709675-104712689,104712834-104713246,104713364-104714867,104715095-104719113,104719208-104720123,104720202-104721291,104721450-104725310,104725420-104728013,104728111-104732915,104733052-104742129,
TXNRD1	NM_003330	chr12	104681125-104682707,104682819-104705066,104705191-104707021,104707096-104709553,104709675-104712689,104712834-104713246,104713364-104714867,104715095-104719113,104719208-104720123,104720202-104721291,104721450-104725310,104725420-104728013,104728111-104732915,104733052-104742129,
TXNRD1	NM_001093771	chr12	104609672-104645303,104645457-104651795,104651858-104682707,104682819-104705066,104705191-104707021,104707096-104709553,104709675-104712689,104712834-104713246,104713364-104714867,104715095-104719113,104719208-104720123,104720202-104721291,104721450-104725310,104725420-104728013,104728111-104732915,104733052-104742129,
TXNRD1	NM_182743	chr12	104680888-104705066,104705191-104707021,104707096-104709553,104709675-104712689,104712834-104713246,104713364-104714867,104715095-104719113,104719208-104720123,104720202-104721291,104721450-104725310,104725420-104728013,104728111-104732915,104733052-104742129,
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TYW3	NM_001162916	chr1	75199103-75202224,75202307-75214433,75214507-75217974,75218110-75229576,
TYW3	NM_138467	chr1	75199103-75202224,75202307-75204372,75204473-75214433,75214507-75217974,75218110-75229576,
TYW3	NR_027962	chr1	75199216-75202224,75202307-75204372,75204473-75214433,75214507-75217974,75218110-75229576,
UBA6	NM_018227	chr4	68484851-68488547,68488644-68488851,68488941-68489842,68489972-68490710,68490906-68492076,68492196-68494787,68494861-68496182,68496254-68497424,68497490-68497573,68497627-68499061,68499192-68499958,68500041-68500145,68500237-68501169,68501277-68504659,68504843-68506867,68506947-68510414,68510497-68511654,68511735-68512440,68512510-68514784,68514930-68527905,68527974-68528855,68528934-68529601,68529666-68530905,68531011-68534267,68534393-68536186,68536311-68539413,68539496-68543327,68543441-68544155,68544252-68547279,68547310-68547835,68547932-68562361,68562426-68566765,
UBA7	NM_003335	chr3	49842871-49843328,49843431-49843504,49843599-49845167,49845361-49845451,49845546-49845817,49845902-49846407,49846593-49846821,49846898-49846973,49847159-49847246,49847313-49847409,49847617-49847694,49847862-49847948,49848106-49848183,49848266-49848415,49848525-49848704,49848889-49849301,49849450-49849540,49849640-49849839,49849977-49850079,49850172-49850493,49850602-49850680,49850817-49850910,49851081-49851163,
UBE2E2	NM_152653	chr3	23244956-23250181,23250367-23258751,23258804-23541097,23541232-23574043,23574193-23631223,

UBLCP1	NM_145049	chr5	158690369-158695876,158696078-158696914,158697008-158697366,158697454-158697534,158697652-158699029,158699130-158701591,158701631-158702154,158702255-158705244,158705363-158710218,158710348-158711910,
UBR1	NM_174916	chr15	43237669-43242458,43242562-43244474,43244647-43250209,43250289-43252841,43252900-43256131,43256242-43258349,43258485-*43262716,43262806-43268913,43269066-43270076,43270146-43276093,43276192-43277083,43277141-43281015,43281166-43282226,43282319-*43290364,43290464-43294751,43294903-43296033,43296129-43299275,43299483-43307884,43308068-43309291,43309380-43313471,43313574-43314898,43315000-43317025,43317182-43317577,43317628-43318757,43318862-43319972,43320027-43322140,43322267-43324764,43324830-43328374,43328478-43328724,43328792-43329969,43330082-43330367,43330431-43335411,43335594-43339357,43339488-43340588,43340690-43346938,43347098-43348540,43348641-43350537,43350628-43351281,43351391-43351898,43352024-43352248,43352313-43360094,43360235-43362991,43363124-43367175,43367288-43374834,43374915-43378180,43378439-43398138,
UBTF	NM_014233	chr17	42284736-42284820,42284966-42285065,42285139-42285230,42285280-42286718,42286910-42287011,42287102-42287490,42287603-42287684,42287842-42288158,42288316-42288405,42288521-42288656,42288700-42288972,42289116-42289239,42289375-42289710,42289823-42290185,42290308-42290584,42290651-42293020,42293178-42293272,42293358-42293895,42294073-42295538,
UBTF	NM_001076684	chr17	42284736-42284820,42284966-42285065,42285139-42285230,42285280-42286718,42286910-42287011,42287102-42287490,42287603-42287684,42287842-42288158,42288316-42288405,42288521-42288656,42288700-42288972,42289116-42289239,42289375-42290185,42290308-42290584,42290651-42293020,42293178-42293272,42293358-42293895,42294073-42295538,42295665-42296811,
UBTF	NM_001076683	chr17	42284736-42284820,42284966-42285065,42285139-42285230,42285280-42286718,42286910-42287011,42287102-42287490,42287603-42287684,42287842-42288158,42288316-42288405,42288521-42288656,42288700-42288972,42289116-42289239,42289375-42290185,42290308-42290584,42290651-42293020,42293178-42293272,42293358-42293895,42294073-42295538,42295665-42298106,
UBXN11	NM_183008	chr1	26609061-26609138,26609281-26609353,26609429-26610631,26610737-26610851,26610974-26611953,26612033-26612312,26612529-26620694,26620823-26623408,26623487-26623916,26623973-26624451,26624554-26627415,26627516-26628183,26628214-26629302,26629410-26629532,26629659-26633081,
UBXN11	NM_145345	chr1	26609061-26609138,26609281-26609353,26609429-26610631,26610737-26610851,26610974-26611953,26612033-26612312,26612529-26620694,26620823-26623408,26623487-26623916,26623973-26624451,26624554-26628183,26628214-26629302,26629410-26633081,26633196-26644536,
UBXN11	NM_001077262	chr1	26609061-26609138,26609281-26609353,26609429-26610631,26610737-26610851,26610974-26611953,26612033-26612312,26612529-26627415,26627516-26628183,26628214-26629302,26629410-26633081,
UCA1	NR_015379	chr19	15940149-15942063,15942167-15945310,
UCHL5	NM_015984	chr1	192985526-192990225,192990326-192992054,192992170-192992972,192993077-192997213,192997279-192998307,192998440-192998516,192998580-192998660,192998788-193018874,193018982-193020882,193020948-193028313,
UCHL5	NM_001199261	chr1	192985526-192990225,192990326-192992054,192992167-192992972,192993077-192997213,192997279-192998307,192998440-192998516,192998580-192998660,192998788-193018874,193018982-193020882,193020948-193028313,
UCHL5	NM_001199262	chr1	192987951-192989435,192989512-192990225,192990326-192992054,192992167-192992972,192993077-192997213,192997279-192998307,192998440-192998516,192998580-192998660,192998788-193018874,193018982-193020882,193020948-193028313,
UCHL5	NM_001199263	chr1	192987951-192990225,192990326-192992054,192992167-192992972,192993077-192997213,192997279-192998307,192998440-192998516,192998580-192998660,192998788-193018874,193018982-193020882,193020948-193028313,
UFD1L	NM_001035247	chr22	19438268-19442323,19442354-19443201,19443292-19444108,19444158-19444374,19444442-19445592,19445663-19452723,19452798-19455394,19455527-19459208,19459332-19462589,19462624-19462991,19463126-19466604,
UFD1L	NM_005659	chr22	19438268-19442270,19442354-19443201,19443292-19444108,19444158-19444374,19444442-19445592,19445663-19452723,19452798-19455394,19455527-19459208,19459332-19462589,19462624-19462991,19463126-19466604,
UGT2A1	NM_006798	chr4	70455370-70460193,70460415-70460878,70460968-70461966,70462100-70464962,70465113-70512646,
UGT2B10	NM_001075	chr4	69870854-69874573,69874795-69875632,69875722-69879739,69879872-69883954,69884106-69885380,69886058-69886075,
UGT2B10	NM_001075	chr4	69682456-69683745,69683896-69687987,69688121-69692126,69692216-69693045,69693267-69696316,
UGT2B10	NM_001144767	chr4	69682204-69683745,69683896-69687987,69688121-69692126,69692216-69693045,69693267-69696316,
UGT2B10	NM_001144767	chr4	69870854-69874573,69874795-69875632,69875722-69879739,69879872-69883954,69884106-69885632,69886058-69886075,

UGT2B7	NM_001074	chr4	69962960-69964256,69964407-69968523,69968657-69972891,69972981-69973819,69974041-69978173,
UIMC1	NM_016290	chr5	176332494-176333010,176333049-176334113,176334179-176335522,176335696-176338310,176338391-176370334,176370490-176378473,176378579-176382958,176383037-176385092,176385156-176395554,176396289-176396596,176396708-176397741,176397868-176402395,176402482-176409468,176409625-176433283,
UIMC1	NM_001199298	chr5	176332494-176333010,176333049-176334113,176334179-176335522,176335696-176338310,176338391-176370334,176370490-176378473,176378579-176382958,176383037-176385092,176385156-176395554,176396289-176396596,176396708-176397741,,176397868-176402395,176402482-176409468,176409625-176433649,
UIMC1	NM_001199297	chr5	176332494-176333010,176333049-176334113,176334179-176335522,176335696-176338310,176338391-176370334,176370490-176378473,176378579-176382958,176383037-176385092,176385156-176395554,176396289-176396596,176396708-176397741,176397868-176402395,176402482-176409468,176409625-176428997,176429113-176433538,
ULBP1	NM_025218	chr6	150285271-150289741,150290007-150290219,150290497-150291150,150291284-150292503,
ULBP3	NM_024518	chr6	150385850-150386532,150386810-150387033,150387299-150390113,
UNC5B	NM_170744	chr10	72972822-73039576,73039803-73044475,73044621-73045081,73045187-73046444,73046627-73047353,73047523-73048323,73048490-73048713,73048748-73050670,73050867-73051187,73051579-73052222,73052312-73053160,73053331-73053455,73053691-73055566,73055718-73056333,73056500-73057664,73057848-73058867,
UQCRB	NM_006294	chr8	97243361-97244000,97244169-97245382,97245456-97247738,
UQCRB	NM_001199975	chr8	97243361-97244000,97244169-97245382,97245456-97246649,97246765-97247738,
USH1G	NM_173477	chr17	72914172-72915547,72916767-72919003,
USO1	NM_003715	chr4	76650070-76678647,76678727-76691590,76691693-76691973,76692078-76692233,76692291-76695827,76695950-76703831,76704012-76708213,76708356-76711301,76711392-76711794,76711951-76714841,76715055-76720773,76720886-76721502,76721623-76721769,76721953-76722230,76722354-76725285,76725426-76726291,76726457-76727637,76727726-76730104,76730205-76731583,76731693-76733311,76733529-76734357,
USP10	NM_005153	chr16	84733718-84767039,84767110-84773913,84773976-84778237,84779280-84792320,84792414-84792967,84793079-84793495,84793553-84793776,84793882-84796593,84796695-84797690,84797870-84801797,84801965-84806145,84806292-84808764,84808832-84812499,
USP20	NM_001110303	chr9	132597779-132612090,132612204-132614817,132614916-132618584,132618640-132620327,132620392-132620744,132620878-132623214,132623313-132623820,132623892-132625463,132625579-132627580,132627661-132630282,132630729-132631139,132631282-132631587,132631705-132631949,132632124-132632730,132632827-132635759,132635795-132635976,132636024-132636853,132637036-132637106,132637235-132637587,132637759-132637837,132637921-132638407,132638518-132640615,132640720-132641850,132641924-132642390,132642569-132642744,
USP20	NM_006676	chr9	132597779-132612090,132612204-132614817,132614916-132618584,132618640-132620327,132620392-132620744,132620878-132623214,132623313-132623820,132623892-132625463,132625579-132627580,132627661-132630282,132630729-132631139,132631282-132631587,132631705-132631949,132632124-132632730,132632827-132635759,132635795-132635976,132636024-132636853,132637036-132637106,132637235-132637587,132637759-132637837,132637921-132638407,132638518-132640615,132640720-132641850,132641924-132642390,
USP20	NM_001008563	chr9	132597877-132612090,132612204-132614817,132614916-132618584,132618640-132620327,132620392-132620744,132620878-132623214,132623313-132623820,132623892-132625463,132625579-132627580,132627661-132630282,132630729-132631139,132631282-132631587,132631705-132631949,132632124-132632730,132632827-132635759,132635795-132635976,132636024-132636853,132637036-132637106,132637235-132637587,132637759-132637837,132637921-132638407,132638518-132640615,132640720-132641850,132641924-132642390,132642569-132642744,
USP28	NM_020886	chr11	113670138-113672203,113672401-113673878,113674004-113674518,113674600-113675393,113675474-113675588,113675769-113677209,113677307-113679018,113679160-113679783,113679977-113682996,113683227-113684605,113684678-113685894,113686105-113688378,113688560-113694325,113694423-113697953,113698083-113699917,113700068-113701587,113701666-113702640,113702716-113704140,113704280-113704969,113705058-113711318,113711480-113712383,113712491-113723221,113723356-113724978,113725058-113746165,

USP39	NM_006590	chr2	85843587-85846341,85846413-85848606,85848703-85850767,85850906-85852660,85852815-85857842,85858070-85863174,85863254-85864490,85864560-85866324,85866515-85868097,85868242-85872069,85872207-85875051,85875140-85875882,
USP6NL	NM_001080491	chr10	11505849-11523767,11523922-11526968,11527070-11527166,11527234-11527814,11527911-11531099,11531222-11532829,11532880-11535116,11535228-11543098,11543208-11551592,11551675-11560532,11560574-11567383,11567468-11569497,11569567-11574175,
USP6NL	NM_014688	chr10	11505849-11523767,11523922-11526968,11527070-11527166,11527234-11527814,11527911-11531099,11531222-11532829,11532880-11535116,11535228-11543098,11543208-11551592,11551675-11560532,11560574-11567383,11567468-11569497,11569567-11639628,11639717-11653440,
USP8	NM_005154	chr15	50716712-50731204,50731375-50733544,50733691-50741595,50741683-50751195,50751360-50754475,50754520-50757242,50757389-50763828,50763993-50769044,50769191-50769471,50769697-50773676,50774263-50776470,50776559-50781996,50782079-50782458,50782723-50784896,50785111-50786265,50786478-50788043,50788282-50789284,50789429-50790791,50790926-50791098,
USP8	NM_001128611	chr15	50716852-50724533,50724697-50731204,50731375-50733544,50733691-50741595,50741683-50751195,50751360-50754475,50754520-50757242,50757389-50763828,50763993-50769044,50769191-50769471,50769697-50773676,50774263-50776470,50776559-50781996,50782079-50782458,50782723-50784896,50785111-50786265,50786478-50788043,50788282-50789284,50789429-50790791,50790926-50791098,
USP8	NM_001128610	chr15	50716852-50731204,50731375-50733544,50733691-50741595,50741683-50751195,50751360-50754475,50754520-50757242,50757389-50763828,50763993-50769044,50769191-50769471,50769697-50773676,50774263-50776470,50776559-50781996,50782079-50782458,50782723-50784896,50785111-50786265,50786478-50788043,50788282-50789284,50789429-50790791,50790926-50791098,
USP9X	NM_001039591	chrX	40945363-40982722,40982978-40988251,40988399-40990708,40990790-40993976,40994091-40996055,40996276-40999907,41000025-41000217,41000471-41000544,41000685-41002542,41002697-41003773,41003880-41007620,41007829-41010172,41010311-41012199,41012335-41022041,41022131-41025123,41025468-41026733,41026831-41027258,41027472-41029246,41029489-41029721,41029873-41031089,41031212-41043249,41043382-41043648,41043929-41045768,41045896-41047243,41047371-41048560,41048729-41055502,41055613-41055843,41055992-41056615,41056764-41057779,41058004-41060311,41060534-41064554,41064747-41069760,41069936-41073819,41073963-41075150,41075906-41076471,41076597-41077623,41077851-41078353,41078485-41082468,41082656-41083993,41084216-41084300,41084391-41088504,41088663-41088818,41089033-41089752,41089850-41091638,
USP9X	NM_001039590	chrX	40945363-40982722,40982978-40988251,40988399-40990708,40990790-40993976,40994091-40996055,40996276-40999907,41000025-41000217,41000471-41000544,41000685-41002542,41002697-41003773,41003880-41007620,41007829-41010172,41010311-41012199,41012335-41022041,41022131-41025123,41025468-41026733,41026831-41027258,41027472-41029246,41029489-41029721,41029873-41031089,41031212-41043249,41043382-41043648,41043929-41045768,41045896-41047243,41047371-41048560,41048729-41055502,41055613-41055843,41055992-41056615,41056764-41057779,41058004-41060311,41060534-41064554,41064747-41069760,41069936-41073819,41073963-41075150,41075906-41076471,41076597-41077623,41077851-41078353,41078485-41082468,41082656-41083993,41084216-41084300,41084391-41088504,41088663-41088818,41089081-41089752,41089850-41091638,
VAMP1	NM_014231	chr12	6573653-6574054,6574108-6575006,6575167-6575389,6575518-6579694,
VAMP1	NM_016830	chr12	6572009-6574054,6574108-6575006,6575167-6575389,6575518-6579694,
VAMP1	NM_199245	chr12	6574108-6575006,6575167-6575389,6575518-6579694,
VAT1	NM_006373	chr17	41168162-41168322,41168566-41169856,41169948-41170051,41170224-41170607,41170817-41173951,
VCX3B	NM_001001888	chrX	8433032-8433344,8433594-8433784,
VDAC2	NM_003375	chr10	76970697-76970890,76970948-76971986,76972057-76973777,76973829-76978819,76978974-76979060,76979115-76980499,76980729-76982008,76982161-76989400,76989460-76990654,
VDAC2	NM_001184783	chr10	76970697-76970890,76970948-76971238,76971418-76971986,76972057-76973777,76973829-76978819,76978974-76979060,76979115-76980499,76980729-76982008,76982161-76989400,76989460-76990654,
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VDAC2	NM_001184823	chr10	76969971-76970890,76970948-76971986,76972057-76973777,76973829-76978819,76978974-76979060,76979115-76980499,76980729-76982008,76982161-76989400,76989460-76990654,
VEGFA	NM_001171628	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43752276,

VEGFA	NM_001171626	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43749691,43749825-43752276,
VEGFA	NM_001171629	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43749691,43749825-43752342,
VEGFA	NM_001033756	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43749691,43749825-43752342,
VEGFA	NM_001171630	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43752276,
VEGFA	NM_001171627	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43749691,43749790-43752276,
VEGFA	NM_001171622	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43752276,
VEGFA	NM_001025368	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43749691,43749825-43752276,
VEGFA	NM_001025370	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43752276,
VEGFA	NM_001025369	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43749691,43749790-43752276,
VEGFA	NM_001025367	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43748467,43748523-43749691,43749825-43752276,
VEGFA	NM_001171624	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43748467,43748541-43749691,43749825-43752276,
VEGFA	NM_001171625	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43748467,43748523-43749691,43749825-43752276,
VEGFA	NM_001171623	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43748467,43748592-43749691,43749825-43752276,
VEGFA	NM_003376	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43748467,43748541-43749691,43749825-43752276,
VEGFA	NM_001025366	chr6	43739050-43742076,43742130-43745204,43745403-43746195,43746274-43746624,43746656-43748467,43748592-43749691,43749825-43752276,
VILL	NM_015873	chr3	38035224-38035387,38035464-38035750,38035958-38037228,38037339-38038566,38038679-38038972,38039177-38039579,38039660-38039755,38039856-38040401,38040542-38040828,38040931-38042945,38043085-38043191,38043352-38043885,38044067-38044657,38044805-38045744,38045891-38047281,38047466-38047670,38047744-38047938,38048192-38048431,
VNN3	NR_028290	chr6	133044194-133044871,133045047-133045743,133046119-133047859,133048152-133049878,133050119-133055390,133055523-133055617,
VNN3	NR_028291	chr6	133044194-133044871,133045047-133045743,133046119-133047859,133048152-133049878,133050073-133055390,133055523-133055617,
VPS13B	NM_152564	chr8	100025576-100025986,100026164-100050649,100050795-100108538,100108661-100115179,100115349-100123324,100123508-100127926,100128103-100133403,100133674-100146858,100146956-100147241,100147366-100147822,100147962-100148891,100148981-100155200,100155394-100160067,100160239-100168775,100168972-100182265,100182392-100205102,100205286-100286424,100286561-100287307,100287483-100396434,100396546-100403783,100403933-100443763,100443893-100454627,100454864-100479640,100479863-100493825,100494031-100513913,100514087-100515062,100515179-100519363,100519432-100523330,100523741-100533125,100533239-100568676,100568882-100587884,100588013-100589716,100589862-100654037,100654727-100673580,100673720-100711751,100712161-100729397,100729602-100732571,100732781-100733089,100733276-100779000,100779199-100789001,100789185-100790908,100791260-100796541,100796705-100821601,100821759-100829766,100830032-100830677,100830763-100830939,100831117-100831638,100831811-100832147,100832351-100833520,100833711-100836058,100836207-100844595,100844881-100847423,100847553-100847765,100847967-100861002,100861123-100865677,100866485-100871530,100871709-100874002,100874175-100880515,100880694-100883011,100883116-100883674,100883926-100887644,
VPS13B	NM_181661	chr8	100025576-100025986,100026164-100050649,100050795-100108538,100108661-100115179,100115349-100123324,100123508-100127926,100128103-100133403,
VPS13B	NM_017890	chr8	100025576-100025986,100026164-100050649,100050795-100108538,100108661-100115179,100115349-100123324,100123508-100127926,100128103-100133403,100133674-100146858,100146956-100147241,100147366-100147822,100147962-100148891,100148981-100155200,100155394-100160067,100160239-100168775,100168972-100182265,100182392-100205102,100205286-100286424,100286561-100287307,100287483-100396434,100396546-100403783,100403933-100443763,100443893-100454627,100454864-100479640,100479863-100493825,100494031-100513913,100514087-100515062,100515179-100519996,100520140-100523330,100523741-100533125,100533239-100568676,100568882-100587884,100588013-100589716,100589862-100654037,100654727-100673580,100673720-100711751,100712161-100729397,100729602-100732571,100732781-100733089,100733276-100779000,100779199-100789001,100789185-100790908,100791260-100796541,100796705-100821601,100821759-100829766,100830032-100830677,100830763-100830939,100831117-100831638,100831811-100832147,100832351-100833520,100833711-100836058,100836207-100844595,100844881-100847423,100847553-100847765,100847967-100861002,100861123-100865677,100866485-100871530,100871709-100874002,100874175-100880515,100880694-100883011,100883116-100883674,100883926-100887644,

VPS13B	NM_015243	chr8	100025576-100025986,100026164-100050649,100050795-100108538,100108661-100115179,100115349-100123324,100123508-100127926,100128103-100133403,100133674-100146858,100146956-100147241,100147366-100147822,100147962-100148891,100148981-100155200,100155394-100160067,100160239-100168775,100168972-100182265,100182392-100205102,100205286-100221818,
VPS13D	NM_018156	chr1	12290178-12294246,12294421-12302568,12302648-12304301,12304494-12304592,12304675-12309278,12309397-12313777,12313884-12316388,12316561-12317042,12317145-12317990,12318161-12320748,12320852-12321003,12321207-12321956,12322138-12326936,12327069-12327900,12327978-12328761,12328934-12331049,12331182-12333058,12333193-12335880,12338096-12339554,12339708-12342760,12343794-12348278,12348371-12351053,12351182-12353579,12353762-12359257,12359442-12364561,12364786-12368486,12368699-12371509,12371683-12371868,12371983-12374170,12374385-12378127,12378395-12379552,12379688-12381864,12382022-12382591,12382804-12383761,12383838-12387703,12387912-12389884,12389976-12393281,12393424-12395760,12395885-12401835,12401943-12402954,12403109-12405429,12405567-12406660,12406710-12408878,12409031-12409219,12409432-12414029,12414279-12415954,12416148-12416453,12416582-12418513,12418658-12422774,12422907-12423126,12423304-12428521,12428647-12429520,12429758-12433803,12433914-12438480,12438646-12439540,12439651-12443033,12443215-12445317,12445433-12446242,12446394-12460236,12460388-12461659,12461758-12463876,12464027-12475138,12475275-12476711,12476881-12516052,12516187-12520254,12520452-12557552,12557686-12566905,12567148-12568945,
VPS13D	NM_015378	chr1	12290178-12294246,12294421-12302568,12302648-12304301,12304494-12304592,12304675-12309278,12309397-12313777,12313884-12316388,12316561-12317042,12317145-12317990,12318161-12320748,12320852-12321003,12321207-12321956,12322138-12326936,12327069-12327900,12327978-12328761,12328934-12331049,12331182-12333058,12333193-12335880,12338096-12339554,12339708-12342760,12343794-12348278,12348371-12351053,12351182-12353579,12353762-12359257,12359442-12364561,12364786-12368486,12368699-12371509,12371683-12371868,12371983-12374170,12374385-12378127,12378395-12379552,12379688-12381864,12382022-12382591,12382804-12383761,12383838-12387703,12387912-12389884,12389976-12393281,12393424-12395760,12395885-12398286,12398363-12401835,12401943-12402954,12403109-12405429,12405567-12406660,12406710-12408878,12409031-12409219,12409432-12414029,12414279-12415954,12416148-12416453,12416582-12418513,12418658-12422774,12422907-12423126,12423304-12428521,12428647-12429520,12429758-12433803,12433914-12438480,12438646-12439540,12439651-12443033,12443215-12445317,12445433-12446242,12446394-12460236,12460388-12461659,12461758-12463876,12464027-12475138,12475275-12476711,12476881-12516052,12516187-12520254,12520452-12557552,12557686-12566905,12567148-12568945,
VPS24	NM_016079	chr2	86733073-86734600,86734717-86737479,86737603-86756339,86756521-86769373,86769436-86790425,
VPS24	NM_001193517	chr2	86733073-86734600,86734717-86737479,86737553-86756409,86756521-86769373,86769436-86790425,
VPS24	NM_001005753	chr2	86733073-86734600,86734717-86737479,86737603-86756339,86756521-86790425,
VPS24	NR_036454	chr2	86733073-86734600,86734717-86737479,86737603-86790425,
VPS37B	NM_024667	chr12	123352155-123353025,123353110-123355435,123355609-123380497,
VPS41	NM_080631	chr7	38765927-38766507,38766589-38768140,38768187-38768290,38768392-38781583,38781722-38783000,38783143-38785157,38785214-38791774,38791914-38794300,38794353-38794493,38794537-38796436,38796583-38797952,38798082-38803053,38803148-38805178,38805262-38807135,38807199-38810796,38810855-38812120,38812238-38813713,38813845-38816277,38816377-38829399,38829468-38835063,38835212-38836343,38836465-38857415,38857483-38860801,38860866-38902143,38902223-38908744,38908854-38937689,38937730-38948752,
VPS41	NM_014396	chr7	38765927-38766507,38766589-38768140,38768187-38768290,38768392-38781583,38781722-38783000,38783143-38785157,38785214-38791774,38791914-38794300,38794353-38794493,38794537-38796436,38796583-38797952,38798082-38803053,38803148-38805178,38805262-38807135,38807199-38810796,38810855-38812120,38812238-38813713,38813845-38816277,38816377-38829399,38829468-38835063,38835212-38836343,38836465-38857415,38857483-38860801,38860866-38869852,38869929-38902143,38902223-38908744,38908854-38937689,38937730-38948752,
VSTM2B	NM_001146339	chr19	30017573-30018116,30018303-30019338,30019370-30020724,30021198-30054751,
VWA5A	NM_014622	chr11	123986190-123988202,123988262-123988378,123988583-123988894,123989119-123989238,123989416-123989680,123989797-123993665,123993837-123994071,123994162-123994365,123994512-123994942,123995024-124005625,124005742-124006834,124007001-124007279,124007382-124007720,124007976-124012303,124012449-124013147,124013280-124015942,124016071-124016571,
VWA5A	NM_001130142	chr11	123986190-123987271,123987388-123988202,123988262-123988378,123988583-123988894,123989119-123989238,123989416-123989680,123989797-123993665,123993837-123994071,123994162-123994365,123994512-123994942,123995024-124005625,124005742-124006834,124007001-124007279,124007382-124007720,124007976-124012303,124012449-124013147,124013280-124015942,124016071-

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VWA5A	NM_198315	chr11	123986190-123988202,123988262-123988378,123988583-123988894,123989119-123989238,123989416-123989680,123989797-123993665,123993837-123994071,123994162-123994365,123994512-123994942,
WARS2	NM_201263	chr1	119576012-119576716,119576837-119584885,119584973-119588203,119588286-119618971,119619231-119683176,
WARS2	NM_015836	chr1	119575983-119576716,119576837-119584885,119584973-119588203,119588286-119618971,119619231-119683176,
WASF3	NM_006646	chr13	27131957-27187096,27187196-27216396,27216541-27239163,27239300-27241652,27241808-27246007,27246127-27250684,27250862-27255189,27255458-27256742,27257112-27259823,
WDR16	NM_145054	chr17	9480083-9489088,9489290-9490013,9490152-9497508,9497639-9501549,9501651-9503382,9503501-9511434,9511537-9515624,9515797-9531987,9532138-9536203,9536351-9538720,9538874-9541924,9542029-9545039,9545153-9546338,
WDR16	NM_001080556	chr17	9480083-9490017,9490152-9497508,9497639-9501549,9501651-9503382,9503501-9511434,9511537-9515624,9515797-9531987,9532138-9536203,9536351-9538720,9538874-9541924,9542029-9545039,9545153-9546338,
WDR19	NM_025132	chr4	39184184-39187344,39187438-39188157,39188225-39191274,39191402-39196162,39196280-39201096,39201214-39205260,39205343-39206772,39206887-39207181,39207357-39216219,39216292-39217459,39217634-39217714,39217831-39218752,39218861-39219601,39219726-39226502,39226654-39229828,39229978-39230104,39230311-39233415,39233577-39233780,39233893-39236384,39236496-39241895,39241955-39245866,39246009-39246088,39246173-39246987,39247073-39254764,39254913-39255524,39255651-39257466,39257581-39259104,39259175-39267681,39267761-39269613,39269712-39271594,39271721-39274598,39274682-39276426,39276579-39278638,39278764-39279749,39279828-39280157,39280284-39287105,
WDR62	NM_173636	chr19	36546051-36549680,36549774-36550868,36550933-36556858,36556918-36557157,36557330-36558206,36558346-36558728,36558913-36562456,36562619-36564242,36564434-36572333,36572473-36573963,36574144-36575553,36575647-36577587,36577715-36579938,36580008-36580085,36580209-36581345,36581423-36582100,36582214-36582302,36582368-36583589,36583714-36584931,36585067-36587927,36587982-36590299,36590520-36591648,36591778-36592114,36592220-36592564,36592677-36592914,36593054-36593652,36593754-36593848,36593977-36594056,36594110-36594243,36594884-36595418,36595578-36595668,
WDR62	NM_001083961	chr19	36546051-36549680,36549774-36550868,36550933-36556858,36556918-36557157,36557330-36558206,36558346-36558728,36558913-36562456,36562619-36564242,36564434-36572333,36572473-36573963,36574144-36575553,36575647-36577587,36577715-36579938,36580008-36580085,36580209-36581345,36581423-36582100,36582214-36582302,36582368-36583589,36583714-36584931,36585067-36587927,36587982-36590299,36590520-36591648,36591778-36592114,36592220-36592564,36592677-36592914,36593054-36593637,36593754-36593848,36593977-36594056,36594110-36594243,36594884-36595418,36595578-36595668,
WDR65	NM_001195831	chr1	43638125-43638404,43638582-43647203,43647522-43649260,43649549-43650818,43651028-43652376,43652531-43663222,43663364-43664150,43664318-43665059,43665175-43672389,43672604-43675412,43675588-43680924,43681088-43685051,43685209-43687041,43687137-43687774,43687967-43688493,43688669-43689715,43689876-43692652,43692798-43698177,43698296-43699948,43700085-43700164,43700310-43708896,43709031-43719646,
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WDR67	NM_145647	chr8	124085087-124089349,124089498-124094940,124095058-124096400,124096581-124105829,124105983-124109520,124109682-124113045,124113248-124117526,124117705-124121555,124121637-124121712,124121861-124132293,124132429-124138294,124138430-124138746,124138928-124140519,124140754-124141304,124141459-124142436,124142574-124146352,124146447-124152999,124153142-

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WDR70	NM_018034	chr5	37379495-37379589,37379657-37381702,37381788-37392100,37392223-37396475,37396673-37438022,37438084-37443339,37443475-37479934,37480090-37516614,37516693-37605164,37605341-37697755,37697857-37701158,37701245-37703049,37703190-37721215,37721318-37722955,37723037-37725034,37725153-37726983,37727148-37752586,
WDR75	NM_032168	chr2	190306305-190313103,190313235-190315627,190315695-190316529,190316622-190320044,190320171-190322035,190322108-190323477,190323599-190324060,190324151-190327208,190327369-190328418,190328480-190328570,190328688-190329803,190329981-190331149,190331309-190332192,190332375-190333199,190333296-190334068,190334166-190334800,190334972-190335543,190335605-190338910,190339059-190339441,190339535-190339937,
WDR78	NM_024763	chr1	67279864-67288042,67288201-67292501,67292730-67293493,67293594-67299266,67299390-67299672,67299832-67301307,67301461-67303391,67303480-67306150,67306355-67313165,67313362-67327828,67327986-67337051,67337193-67340462,67340621-67356835,67356950-67358910,67359097-67370882,67371059-67390343,
WDR78	NM_207014	chr1	67303480-67306150,67306355-67313165,67313362-67327828,67327986-67337051,67337193-67340462,67340621-67356835,67356950-67358910,67359097-67370882,67371059-67390343,
WDR91	NM_014149	chr7	134871068-134871722,134871922-134873183,134873298-134874094,134874205-134877981,134878152-134878328,134878425-134879684,134879837-134880894,134881090-134882743,134882904-134889018,134889186-134890678,134890811-134891870,134891955-134893541,134893751-134894326,134894508-134896130,
WDTC1	NM_015023	chr1	27561443-27587445,27587594-27589641,27589727-27608728,27608777-27609827,27609941-27614163,27614353-27618704,27618889-27620511,27620608-27621003,27621121-27622815,27622893-27623540,27623648-27624427,27624603-27627715,27627953-27630110,27630287-27631490,27631685-27632675,
WFDC12	NM_080869	chr20	43752585-43752746,43752907-43753008,
WFS1	NM_001145853	chr4	6271742-6279180,6279415-6288818,6288903-6290712,6290859-6292922,6293095-6293642,6293725-6296766,6296917-6302382,
WFS1	NM_006005	chr4	6271742-6279176,6279415-6288818,6288903-6290712,6290859-6292922,6293095-6293642,6293725-6296766,6296917-6302382,
WWP2	NM_199424	chr16	69959388-69963349,69963433-69964031,69964162-69965053,69965131-69965410,69965484-69965703,69965794-69967871,69968033-69969754,69969890-69970213,69970356-69971019,69971142-69971449,69971556-69972928,69973027-69973242,69973317-69973742,
WWP2	NM_007014	chr16	69796295-69810090,69810145-69820897,69820984-69832583,69832733-69833075,69833199-69874027,69874167-69875925,69876024-69905705,69905835-69921940,69922153-69942662,69942754-69951610,69951787-69959331,69959388-69963349,69963433-69964031,69964162-69965053,69965131-69965410,69965484-69965703,69965794-69967871,69968033-69969754,69969890-69970213,69970356-69971019,69971142-69971449,69971556-69972928,69973027-69973242,69973317-69973742,
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XPA	NM_000380	chr9	100437870-100447203,100447323-100449376,100449544-100451814,100451922-100455929,100456042-100459401,
XPO1	NM_003400	chr2	61706102-61708318,61708417-61709513,61709675-61710090,61710227-61711070,61711241-61712901,61713098-61715298,61715407-61715721,61715907-61717775,61717912-61719168,61719334-61719458,61719617-61719700,61719884-61720048,61720189-61721027,61721227-61722588,61722749-61724012,61724143-61725806,61725928-61725998,61726049-61726846,61727030-61729129,61729176-61729382,61729446-

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XPOT	NM_007235	chr12	64798585-64803740,64803876-64808685,64808770-64810476,64810535-64811824,64811896-64812654,64812875-64813848,64814035-64814131,64814302-64815013,64815252-64816783,64816824-64816960,64817025-64818377,64818504-64818816,64818963-64819116,64819238-64819593,64819690-64821829,64821901-64823827,64824068-64825316,64825604-64827192,64827384-64828285,64828404-64828572,64828690-64829405,64829455-64833022,64833096-64838853,64838912-64841883,
YEATS2	NM_018023	chr3	183415782-183432930,183433051-183435437,183435537-183436286,183436381-183439677,183439925-183442205,183442320-183446476,183446640-183454504,183454618-183465458,183465505-183469859,183470042-183471912,183472154-183474314,183474478-183476648,183476754-183479293,183479403-183479883,183480068-183490091,183490352-183491419,183491583-183493701,183493912-183495328,183495489-183503911,183504090-183508583,183508769-183515709,183515840-183516677,183516778-183518252,183518357-183519241,183519317-183521042,183521124-183521773,183521977-183524652,183524881-183525816,183525893-183526883,183526959-183528261,
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YWHAE	NR_024058	chr17	1248794-1257503,1257642-1264384,1264593-1265194,1265303-1268151,1268353-1273001,1273036-1303339,
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YWHAZ	NM_001135701	chr8	101932981-101936181,101936279-101936361,101936527-101937142,101937268-101960822,101961129-101963412,
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YWHAZ	NM_145690	chr8	101932981-101936181,101936279-101936361,101936527-101937142,101937268-101960822,101961129-101964155,
YWHAZ	NM_003406	chr8	101932981-101936181,101936279-101936361,101936527-101937142,101937268-101960822,101961129-101965495,
ZBED4	NM_014838	chr22	50247638-50276980,
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ZBTB34	NM_001099270	chr9	129623019-129641667,
ZC3H18	NM_144604	chr16	88636975-88643516,88644135-88653006,88653093-88664584,88664735-88665026,88665121-88666197,88666357-88675340,88675460-88677674,88677945-88688603,88688797-88689625,88689753-88690364,88690471-88691008,88691154-88691608,88691676-88694028,88694191-88694326,88694528-88695164,88695263-88696891,88696990-88697507,
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ZFP112	NM_013380	chr19	44834090-44840774,44840872-44844566,44844695-44860776,
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ZFP28	NM_020828	chr19	57050596-57050992,57051086-57058875,57059004-57059174,57059272-57060325,57060491-57061434,57061551-57061877,57061975-57065051,
ZFP3	NM_153018	chr17	4981871-4994790,
ZFP42	NM_174900	chr4	188916995-188920260,188920428-188920761,188920840-188923865,
ZFR	NM_016107	chr5	32356046-32364052,32364152-32364268,32364382-32379219,32379317-32380179,32380279-32385612,32385756-32387653,32387806-32388573,32388781-32390379,32390544-32395263,32395411-32397323,32397445-32400110,32400309-32403209,32403503-32404009,32404203-32406877,32407127-32415072,32415293-32417751,32417898-32419924,32420209-32444333,32444435-32444726,
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ZNF263	NM_005741	chr16	3334206-3335057,3335240-3335679,3335755-3336021,3336150-3338452,3338571-3339391,
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ZNF384	NM_001039919	chr12	6777282-6778195,6778356-6779924,6780005-6782380,6782607-6787291,6787627-6788110,6788350-6788619,6788692-6797331,6797393-6798532,

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ZNF71	NM_021216	chr19	57106797-57112873,57112960-57132634,
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ZNF721	NM_133474	chr4	438222-466362,466491-492843,
ZNF738	NR_027130	chr19	21541946-21544566,21544661-21558038,21558167-21558669,21558767-21560189,
ZNF763	NM_001012753	chr19	12076027-12087842,12087980-12088184,12088247-12088929,
ZNF768	NM_024671	chr16	30537373-30537645,
ZNF782	NM_001001662	chr9	99582061-99589360,99589464-99607170,99607299-99614227,99614288-99615133,99615352-99616368,
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ZSCAN30	NM_001166012	chr18	32834346-32843475,32843622-32843907,32844420-32847438,32847644-32870046,
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TABLE B

GENE	Accession No.	GENE	Accession No.	GENE	Accession No.
TRPS1	NM_014112	C3orf18	NM_001171743	LRRC49	NM_001199018
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MICA	NR_036523	C3orf15	NM_033364	CYBASC3	NM_001161454
MICA	NM_182924	DIS3L	NM_001143688	CLINT1	NM_014666
MICA	NR_036523	DIS3L	NM_152383	CLINT1	NM_001195556
MICA	NR_036523	DIS3L	NM_133375	CLINT1	NM_001195555
MICA	NR_036523	PSMD8	NM_002812	CLCA2	NM_006536
MICA	NM_000247	B4GALT5	NM_004776	RPRD1A	NM_018170
MICA	NM_000247	ARPC1B	NM_005720	TSPAN10	NM_031945
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MICA	NR_036523	SLC26A5	NM_206884	BCL2	NM_001040668
MICA	NM_000247	SLC26A5	NM_206883	BCL2	NM_004049
MICA	NR_036524	SLC26A5	NM_198999	BCL2	NM_001199864
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MICA	NM_033386	ZNF837	NM_138466	BCL2	NM_020396
MICA	NM_001122731	ZNF837	NM_001129730	BCL2	NM_138639
MICA	NM_153206	BEND5	NM_024603	BCL2	NM_138723
MICA	NM_022765	LOC100128675	NR_024561	BCL2	NM_001191
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MICA	NM_001098526	GRTP1	NM_024719	BCL2	NM_006538
MICA	NM_032867	AP1M1	NM_032493	BCL2	NM_001010922
MICA	NM_001159291	AP1M1	NM_001130524	BCL2	NM_030766
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MICA	NR_036524	MAGI1	NM_001033057	BCL2	NM_001114735
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PIP4K2B	NM_003559	NEDD4L	NM_001144967	CAMK2G	NM_172173
CWC25	NM_017748	NEDD4L	NM_001144971	CAMK2G	NM_172170
SLITRK2	NM_001144009	NEDD4L	NM_001144964	CAMK2G	NM_001222
SLITRK2	NM_001144005	NEDD4L	NM_015277	TSPAN14	NM_030927
SLITRK2	NM_001144008	NEDD4L	NM_001144968	TSPAN14	NM_001128309
SLITRK2	NM_001144010	NEDD4L	NM_001144970	RWDD3	NM_015485
SLITRK2	NM_001144006	TMEM56	NM_152487	RWDD3	NM_001128142
SLITRK2	NM_001144003	TMEM56	NM_001199691	RWDD3	NM_001199691

SLITRK2	NM_001144004	TMEM56	NM_001199679	RWDD3	NR_037643
SLITRK2	NM_032539	LRRC49	NM_017691	RWDD3	NM_001199682
C3orf18	NM_016210	LRRC49	NM_001199017	TRAK1	NM_001042646
TRAK1	NM_014965	EML2	NR_034098	MTR	NM_000254
LOC730668	NR_027240	EML2	NM_012155	MTR	NM_002454
ZNF621	NM_198484	EML2	NR_002794	MTR	NM_001190470
ZNF621	NM_001098414	LAPTM4B	NM_018407	MTR	NM_001190472
PELI3	NM_001098510	SLC38A2	NM_018976	MTR	NM_001190452
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NCOA3	NM_001174087	MID2	NM_052817	MTR	NM_019041
NCOA3	NM_181659	MID2	NM_012216	MTR	NM_001190487
NCOA3	NM_006534	SLC26A8	NM_052961	MTR	NM_001190706
PSMB3	NM_002795	SLC26A8	NM_138718	MTR	NM_001190708
ZNF763	NM_001012753	SLC26A8	NM_001193476	MTR	NM_001190702
CHDH	NM_018397	NKAPP1	NR_027131	WBSCR27	NM_152559
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KRT4	NM_182497	RPL14	NM_003973	TSNAXIP1	NM_018430
KRT4	NR_033415	RPL14	NM_001034996	BAIAP3	NM_003933
KRT4	NM_002272	C6orf155	NR_026807	BAIAP3	NM_001199099
STK3	NM_015690	ABCA3	NM_001089	BAIAP3	NM_001199097
STK3	NM_001112724	LOC723809	NR_027374	BAIAP3	NM_001199096
STK3	NM_018401	EPB49	NM_001114139	BAIAP3	NM_001199098
STK3	NM_006281	EPB49	NM_001114138	TSC1	NM_001162427
STK3	NM_173575	EPB49	NM_001114137	TSC1	NM_000368
STK3	NM_015000	EPB49	NM_001978	TSC1	NM_001162426
STK3	NM_007271	EPB49	NM_001114136	LDLRAD3	NM_174902
STK3	NM_031414	EPB49	NM_001114135	NPY1R	NM_000909
STK3	NM_013233	PLEKHA7	NM_175058	IKBIP	NM_153687
STK3	NM_080836	RNU6ATAC	NR_023344	IKBIP	NM_201613
STK3	NM_030906	LAMC2	NM_005562	IKBIP	NM_201612
STK3	NM_145001	LAMC2	NM_018891	WDR67	NM_145647
STK3	NM_001122833	MST1	NR_027504	WDR67	NM_001145088
STK3	NM_032944	MST1	NM_002447	HMGCR	NM_000859
CCDC24	NM_152499	MST1	NM_020998	HMGCR	NM_001130996
IQCH	NM_001031715	MST1	NR_002729	ZNF415	NM_001136038
IQCH	NM_022784	GSTM2	NM_001142368	ZNF415	NM_001164309
NCRNA00173	NR_027346	GSTM2	NR_002932	ZNF415	NR_028343
NCRNA00173	NR_027345	GSTM2	NM_000848	ZNF415	NM_018355
GTPBP10	NM_001042717	ZNF337	NM_015655	LMX1B	NM_001174147

GTPBP10	NM_033107	MTR	NM_024010	LMX1B	NM_001174146
EML2	NM_001193268	MTR	NM_001190476	LMX1B	NM_002316
EML2	NM_001193269	MTR	NM_001114184	RBBP8	NM_203292
EML2	NM_024807	MTR	NM_004294	RBBP8	NM_203291
RBBP8	NM_002894	PSD	NM_002779	PTPN18	NM_001142370
SORBS2	NM_001145673	PSD	NM_184231	PTPN18	NM_014369
SORBS2	NM_021069	PSD	NM_015310	ENTPD8	NM_198585
SORBS2	NM_003603	PSD	NM_032289	ENTPD8	NM_001033113
SORBS2	NM_001145674	PSD	NM_012217	MTFR1	NM_014637
SORBS2	NM_001145675	PSD	NM_012455	MTFR1	NM_001145839
SORBS2	NM_001145672	FAM201A	NR_027294	MTFR1	NM_001145838
SORBS2	NM_001145670	C9orf156	NM_016481	APC2	NM_013366
SORBS2	NM_001145671	LOC644759	NR_033737	APC2	NR_030717
LASP1	NM_001142273	PPP1R9A	NM_001166161	APC2	NM_005883
LASP1	NM_001142274	PPP1R9A	NM_001166163	PSD	NM_016453
LASP1	NM_006148	PPP1R9A	NM_001166162	PSD	NM_206909
LASP1	NM_015282	PPP1R9A	NM_017650	ARMCX6	NM_019007
PLCB3	NM_000932	PPP1R9A	NM_001166160	ARMCX6	NR_033669
PLCB3	NM_001184883	LRRN2	NM_006338	ARMCX6	NR_033670
CKAP4	NM_006825	LRRN2	NM_201630	ARMCX6	NM_001184768
RPPH1	NR_002312	OGFRL1	NM_024576	ARMCX6	NM_001009584
SCARNA16	NR_003013	OGDHL	NM_001143997		
MFSD2A	NM_032793	OGDHL	NM_001143996		
MFSD2A	NM_001136493	OGDHL	NM_018245		
ICA1	NM_138468	G6PD	NM_000402		
ICA1	NM_001136020	G6PD	NM_001042351		
ICA1	NM_153206	TMSB10	NM_021103		
ICA1	NM_001098526	VASP	NM_003370		
ICA1	NM_004968	SEC23A	NM_006364		
ICA1	NM_178231	TMEM86A	NM_153347		
ICA1	NM_022307	ZNF774	NM_001004309		
OPLAH	NM_017570	CLIC6	NM_053277		
C2orf55	NM_207362	ATL1	NM_080661		
ZNF48	NM_052852	ATL1	NM_181598		
ZNF48	NM_001007101	ATL1	NM_001127713		
ZNF48	NM_153034	ATL1	NM_015915		
ZNF48	NM_144684	ATL1	NM_152716		
ZNF48	NM_001007169	ATL1	NM_001012980		
ZNF48	NM_133464	ATL1	NM_032558		
ZNF48	NM_031486	C3orf23	NM_173826		
ZNF48	NR_026693	C3orf23	NM_001029840		
ZNF48	NM_145312	C3orf23	NM_001029839		
ZNF48	NM_152652	CHKB	NM_005198		
APC2	NM_003083	CHKB	NR_027928		

WHAT IS CLAIMED IS:

1. A method of predicting a likelihood of long-term survival without recurrence of breast cancer in a breast cancer patient, comprising:

determining a level of one or more breast cancer prognostic biomarkers in a breast cancer tumor sample obtained from the patient, wherein the one or more breast cancer prognostic biomarkers is selected from:

(a) one or more RNA transcripts, or expression products thereof, selected from Table 1 and/or Table 15,

(b) one or more RNA transcripts, or expression products thereof, selected from Table 2,

(c) one or more intronic RNAs selected from Table 3,

(d) one or more long intergenic non-coding regions (lincRNAs) selected from Table 4,

(e) one or more intergenic sequences selected from Table 5,

(f) one or more intergenic regions selected from intergenic regions 1-69 in Table 5,

(g) one or more RNA transcripts, or expression products thereof, selected from Tables 6-11, and

(h) one or more RNA transcripts, or expression products thereof, selected from Table 13,

normalizing the level of the one or more breast cancer prognostic biomarkers to obtain a normalized level of the one or more breast cancer prognostic biomarkers; and

predicting a likelihood of long-term survival without recurrence of breast cancer of said patient, wherein an increased normalized level of the one or more breast cancer prognostic biomarkers is negatively correlated with an increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the breast cancer prognostic biomarker is marked 1 in Tables 1, 2, 3, 4, 5, or 15, and wherein an increased normalized level of the one or more breast cancer prognostic biomarker is positively correlated with an increased likelihood of long-term survival without recurrence of breast cancer if the direction of association of the one or more breast cancer prognostic biomarker is marked -1 in Tables 1, 2, 3, 4, 5, or 15.

2. The method of claim 1, wherein the level of one or more breast cancer prognostic biomarkers is selected from (b) and/or (h) and the breast cancer patient is an estrogen receptor (ER)-positive breast cancer patient.

3. The method of claim 1, wherein the level of one or more intergenic regions of (f) is determined by determining the level of one or more intergenic sequences that comprises the one or more intergenic region.

4. The method of claim 1, further comprising assigning the one or more RNA transcripts, or an expression product thereof, of (g) to one or more gene networks selected from a cell cycle network, ESR1 network, Chr9q22 network, Chr17q23-24 network, Chr8q21-24 network, and olfactory receptor network;

determining a likelihood score for said one or more gene networks using the normalized level; and

predicting the likelihood of long-term survival without recurrence of breast cancer in a breast cancer patient based on the likelihood score,

wherein an increase in the likelihood score negatively correlates with an increased likelihood of long-term survival without breast cancer recurrence.

5. The method of claim 1, further comprising assigning the one or more RNA transcripts, or an expression product thereof, of (h) to an olfactory receptor network;

determining a likelihood score for said olfactory receptor network using the normalized level; and

predicting the likelihood of long-term survival without recurrence of breast cancer in a breast cancer patient based on the likelihood score,

wherein an increase in the likelihood score negatively correlates with an increased likelihood of long-term survival without breast cancer recurrence, and

wherein the breast cancer patient is an estrogen receptor (ER)-positive breast cancer patient.

6. A method of predicting a likelihood of long-term survival without recurrence of breast cancer in a breast cancer patient, comprising:

determining levels of at least three RNA transcripts, or expression products thereof, in a breast cancer tumor sample obtained from said patient, wherein the at least three RNA

transcripts, or expression products thereof, are selected from ENO1, IDH2, TMSB10, PGK1, and G6PD,

normalizing the levels of the at least three RNA transcripts, or expression products thereof, to obtain normalized expression levels of the at least three RNA transcripts or expression products thereof, and

predicting a likelihood of long-term survival without recurrence of breast cancer of said patient using the normalized expression levels, wherein increased normalized expression levels are negatively correlated with an increased likelihood of long-term survival without recurrence of breast cancer.

7. The method of claim 6, wherein the levels of at least IDH2, PGK1, and G6PD are determined.

8. The method of claim 6, wherein the levels of ENO1, IDH2, TMSB10, PGK1, and G6PD are determined.

9. A method of predicting a likelihood of long-term survival without recurrence of breast cancer in a breast cancer patient, comprising:

determining levels of at least five RNA transcripts, or expression product thereof, in a breast cancer tumor sample obtained from said patient, wherein the at least five RNA transcripts, or expression products thereof, are selected from PGD, TKT, TALDO1, G6PD, GP1, SLC1A5, SLC7A5, OGDH, SUCLG1, ENO1, PGK1, IDH2, ACO2, and FBP1,

normalizing the levels of the at least five RNA transcripts, or expression products thereof, to obtain normalized expression levels of the at least five RNA transcripts or expression products thereof, and

predicting a likelihood of long-term survival without recurrence of breast cancer of said patient using the normalized expression levels, wherein increased normalized expression levels of PGD, TKT, TALDO1, G6PD, GP1, SLC1A5, SLC7A5, OGDH, SUCLG1, ENO1, PGK1, IDH2, and ACO2 are negatively correlated with an increased likelihood of long-term survival without recurrence of breast cancer, and increased normalized expression level of FBP1 is positively correlated with an increased likelihood of long-term survival without recurrence of breast cancer.

10. The method of claim 9, wherein the levels of PGD, TKT, TALDO1, G6PD, GP1, SLC1A5, SLC7A5, OGDH, SUCLG1, ENO1, PGK1, IDH2, ACO2, and FBP1 are determined.

11. The method of any one of claims 1-10, wherein the level is determined by whole transcriptome sequencing.

12. The method of any one of claims 1-10, wherein the level is determined by reverse transcription polymerase chain reaction (RT-PCR).

13. The method of any one of claims 1-10, wherein the level is determined by array.

14. The method of any one of claims 1-13, wherein the breast cancer tumor sample is a fixed, wax-embedded tissue sample.

15. The method of any one of claims 1-14, wherein the breast cancer tumor sample is a fine needle biopsy sample.

16. The method of any one of claims 1-15, further comprising creating a report based on the level of the one or more RNA transcripts, or an expression product thereof.