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(54) Title: GENE EXPRESSION MARKERS FOR PREDICTING RESPONSE TO INTERLEUKIN-6 RECEPTOR-INHIBITING MONOCLONAL ANTIBODY DRUG TREATMENT

(57) Abstract: This invention provides methods, compositions, and kits relating to gene product biomarkers where gene expression levels are correlated with therapeutic response of rheumatoid arthritis patients to treatment with an IL-6 receptor antagonist, such as an IL6 antibody. The methods, compositions, and kits of the invention can be used to identify rheumatoid arthritis patients who are likely, or not likely, to respond to IL-6 receptor antagonist treatments.

Gene Expression Markers For Predicting Response To Interleukin-6 Receptor-Inhibiting Monoclonal Antibody Drug Treatment

BACKGROUND OF THE INVENTION

Tocilizumab is the first humanized interleukin-6 receptor (IL-6R)-inhibiting monoclonal antibody that has been developed to treat rheumatoid arthritis. As with other treatments, the antibody exhibits a range of therapeutic efficacy in patients. Thus, there is a need to determine those patients that are more likely to respond positively to treatment with tocilizumab and/or patients that are likely to not respond to treatment. The present invention addresses this need.

BRIEF SUMMARY OF THE INVENTION

The invention is based, in part, on the discovery of changes in gene expression that are associated with a positive therapeutic response to treatment with an agent that modulate IL-6-mediated signal transduction, such as an anti-IL-6 antibody that inhibits transduction or an IL-6R-inhibiting monoclonal antibody such as tocilizumab.

Thus, in one aspect, the invention provides a method of identifying a rheumatoid arthritis patient that is likely to respond to treatment with tocilizumab; or of identifying a patient that is likely not to respond to treatment with tocilizumab; wherein the method comprises identifying the levels of expression of a gene set forth in Table 1, Table 2, or Table 3. Such genes can be identified using a variety of techniques, including array probe sets and amplification techniques. The level of expression of the marker gene is then compared to the expression level shown in the data set used to establish a correlation.

In a further aspect, the invention provides, a kit for predicting the therapeutic response of a rheumatoid arthritis patient to a treatment regimen that comprises administration of an IL-6R antibody such as tocilizumab. In some embodiments, the kit also includes an electronic device or computer software to compare the marker gene expression level of a biomarker

gene set forth in Table 1, Table 2, or Table 3 from the patient to a dataset. The endpoint for evaluating therapeutic response can be any symptom of rheumatoid arthritis, *e.g.,* the endpoints evaluated in Example 1.

In some embodiments, the marker gene is any one of the genes set forth in Table 1. In some embodiments, the marker genes are at least two genes set forth in Table 1. Thus, in some embodiments any one of from 2 to 20, 30, 40, 50, 60, 70, 80, or all of the genes set forth in Table 1.

In some embodiments, the marker gene is any one of the genes set forth in Table 2. In some embodiments, the marker genes are at least two genes set forth in Table 2. Thus, in some embodiments any one of from 2 to 20, 30, 40, 50, 60, 70, 80, or all of the genes set forth in Table 2.

In some embodiments, the marker gene is any one of the genes set forth in Table 3. In some embodiments, the marker genes are at least two genes set forth in Table 3. Thus, in some embodiments any one of from 2 to 20, 30, 40, 50, 60, 70, 80, or all of the genes set forth in Table 3.

In some embodiments, the step of determining the level of expression of the biomarker gene comprises measure the level of RNA expressed by the marker gene. The amount of RNA expressed may be determined, *e.g.,* using an amplification area reaction such as qPCR, or by using a probe array. For example, a nucleic acid array forming a probe set may be used to detect RNA expressed of the biomarker gene. RNA expression levels are typically determined by measuring the level of cDNA transcribed from the RNA isolated from the patient. RNA expression levels can be determined using known probesets to quantify expression level. As known in the art, such probes sets may comprises multiple probes that hybridize to the target sequence of interest. Alternatively, expression of a marker gene can be determined by measuring the level of expression of a protein encoded by the gene.

The levels of expression are compared to standard control data, *e.g.,* the expression data set generated in Example 1 and 2. An increased level of expression of the marker gene or decreased level of expression of the biomarker gene may be determined by using statistical

models for determining whether expression of the biomarker gene is indicative of therapeutic response of a patient to treatment with an IL-6R antibody such as tocilizumab. In some the invention provides an electronic device or computer software that employs the use of a statistical model to determine likelihood of therapeutic responses.

In some embodiments, the levels of expression of genes set forth in Table 5 are evaluated to identify rheumatoid arthritis patients that are likely to be responsive, or unresponsive, to treatment with an IL-6R antagonist such as tocilizumab. In typical embodiments, anywhere from 2 to 10, 20, 30, 40, 50, 60, 70, 80, or 90, or all of the genes in column C, column D, column E, column F, column G, column H, column I, or column J are analyzed to determined likelihood of a therapeutic response.

DETAILED DESCRIPTION OF THE INVENTION

As used herein, a "positive therapeutic response" or "therapeutic benefit" refers to an improvement in, and/or delay in the onset of, any symptom of rheumatoid arthritis.

As used herein "negative therapeutic response" refers to a lack of improvement of one or more symptoms of rheumatoid arthritis.

An "interleukin-6 receptor (IL-6R) inhibiting antibody" refers to an antibody to IL-6 receptor where the antibody binds to IL-6 receptor and antagonizes (i.e., inhibits) IL-6 receptor activity. An example of such an antibody is tocilizumab, a humanized IL-6R monoclonal antibody (*see, e.g.,* Sato et al., *Cancer Res* 1993; 53: 851-6; and U.S. Patent No. 7479543) that is used for the treatment of rheumatoid arthritis.

In the current invention, a "gene set forth in Table 1" refers to the gene that corresponds to the probesets annotated in Table 1. Similarly, a "gene set forth in" Tables 2, 3, or 5 refers to the gene that corresponds to the probesets annotated in the respective Table. For Tables 1-3, the "Representative Public ID" is listed as the accession number Table 1. The "Representative Public ID" is the accession number of a representative sequence. For consensus-based probe sets, the representative sequence is only one of several sequences (sequence sub-clusters) used to build the consensus sequence in the probe set used in the Examples and it is not directly used to derive the probe sequences. The representative

sequence is chosen during array design as a sequence that is best associated with the transcribed region being interrogated by the probe set. As understood in the art, there are naturally occurring polymorphisms for many gene sequences. Genes that are naturally occurring allelic variations for the purposes of this invention are those genes encoded by the same genetic locus. The proteins encoded by allelic variations of a gene set forth in Table 1, Table 2, or Table 3 typically have at least 95% amino acid sequence identity to one another, *i.e.*, an allelic variant of a gene indicated in Table 1, Table 2, or Table 3 typically encodes a protein product that has at least 95% identity, often at least 96%, at least 97%, at least 98%, or at least 99%, or greater, identity to the amino acid sequence encoded by the nucleotide sequence denoted by the accession number shown in the Table for that gene. For example, an allelic variant of a gene encoding Eph receptor B2 (gene: EPHB2, representative accession number AF025304) typically has at least 95% identity, often at least 96%, at least 97%, at least 98%, or at least 99%, or greater, to the Eph receptor b2 protein encoded by the sequence available under accession number AF025304.

The terms "identical" or "100% identity," in the context of two or more nucleic acids or proteins refer to two or more sequences or subsequences that are the same sequences. Two sequences are "substantially identical" or a certain percent identity if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (i.e., 70% identity, optionally 75%, 80%, 85%, 90%, or 95% identity, over a specified region, or, when not specified, over the entire sequence), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using known sequence comparison algorithms, e.g., BLAST using the default parameters, or by manual alignment and visual inspection.

A "gene product" or "gene expression product" in the context of this invention refers to an RNA or protein encoded by the gene.

The term "evaluating a biomarker" in a patient that has rheumatoid arthritis refers to determining the level of expression of a gene product encoded by a gene, or allelic variant of the gene, listed in Table 1, Table 2, Table 3, or Table 5. Typically, the RNA expression level is determined.

Introduction

The invention is based, in part, on the identification of specific genes/transcripts whose gene expression level, prior to drug dosing or 8 weeks subsequent to dosing, are correlated with response to tocilizumab.

The invention therefore relates to measurement of expression level of a biomarker prior to the patient receiving the drug. In some embodiments, probes to detect such transcripts may be applied in the form of a diagnostic device to predict which rheumatoid arthritis patients will respond or not respond to an IL-6 receptor antagonist such as an IL-6 receptor antagonizing antibody, *e.g.,* tocilizumab. Transcripts may also be measured to predict which RA patients will respond tocilizumab at a later time point. Further, the identification of proteins/metabolites and/or related transcripts and associated product that are linked by pathway or cell type or tissue expression to the transcripts identified herein in the Examples section can be used as alternative biomarkers for measurement of response to tocilizumab.

The expression levels of any gene expression product of one of the genes set forth in Table 1, Table 2, or Table 3 may be measured, however, typically expression of multiple genes is assessed. Gene expression levels may be measured using any number of methods known in the art. In typical embodiments, the method involves measuring the level of RNA. RNA expression can be quantified using any method, *e.g.,* employing a quantitative amplification method such as qPCR. In other embodiments, the methods employ array-based assays. In still other embodiments, protein products may be detected. The gene expression patterns are determined using a whole blood or peripheral blood lymphocyte samples from the patient.

In some embodiments, gene products, typically RNA, encoded by a gene that is in the same pathway as a biomarker shown in Table 1, Table 2, or Table 3 may be quantified. In some embodiments, at least one of the biomarkers that is evaluated to identify a rheumatoid arthritis patient that is a candidate for treatment with tocilizumab is selected from the group consisting of JAM3, CD41, CD61, ephrin receptor B2. In some embodiments, at least one of the biomarkers selected for evaluation is JAM3, CD41, CD61, and a second biomarker evaluated is ephrin receptor B2. In some embodiments, a biomarker that is evaluated in a patient is a component of the inflammasome, caspase 1, caspase 5, IL-1 receptor, or

CARD16. In some embodiments, at least one of the biomarkers that is evaluated is serine palmitoyltransferase long chain base subunit 2 or sphingosine-1-phosphate (S1P), ceramide or related sphingolipids.

In some embodiments, the methods of the invention comprise analyzing gene expression products of two or more biomarkers of Table 5 that have a value over "0" shown in one of columns C-J. Such biomarkers may be used in combination to predict likelihood of a rheumatoid arthritis patient's response to treatment in an IL-6R antagonist such as tocilizumab. Thus, for example, analysis of gene expression levels of at least two biomarkers, preferably three, four, five, or any number up to 100 of the biomarkers having a value above "0" in column C can be used in combination to predict response to treatment is tocilizumab. Similarly, at least two biomarkers, preferably three, four, five, or more, or all of the biomarkers from column D that have values above "0" can be analyzed for expression levels to identify rheumatoid arthritis patients likely to be responsive, or not responsive, to treatment with an IL-6R antagonist such as tocilizumab. In typical embodiments, those expression levels of those genes that have lower numbers, are evaluated. Thus, for example, a gene in column C that has a value of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, for example, is typically included in the analysis of gene expression. In some embodiments, the methods of the invention comprise analyzing expression level of two or more genes in column C; and analyzing expression levels of two or more genes in column D, or two or more genes in column E, etc.

In Table 5, the column "ID" refers to a probeset for the corresponding gene (Table 5B). One of skill understands that the probeset annotation in Table 5B and column L of Table 5A can be obtained through the database of the maker of the chip used for this analysis (Affymetrix).

Methods for Quantifying RNA

The quantity of RNA encoded by a gene set forth in Table 1 can be readily determined according to any method known in the art for quantifying RNA. Various methods involving amplification reactions and/or reactions in which probes are linked to a solid support and used to quantify RNA may be used. Alternatively, the RNA may be linked to a solid support and quantified using a probe to the sequence of interest.

An "RNA nucleic acid sample" analyzed in the invention is obtained from peripheral blood lymphocytes. An "RNA nucleic acid sample" comprises RNA, but need not be purely RNA, *e.g.,* DNA may also be present in the sample. Techniques for obtaining an RNA sample from peripheral blood lymphocytes are well known in the art.

In some embodiments, the target RNA is first reverse transcribed and the resulting cDNA is quantified. In some embodiments, RT-PCR or other quantitative amplification techniques are used to quantify the target RNA. Amplification of cDNA using PCR is well known (see U.S. Patents 4,683,195 and 4,683,202; PCR PROTOCOLS: A GUIDE TO METHODS AND APPLICATIONS (Innis et al., eds, 1990)). Methods of quantitative amplification are disclosed in, e.g., U.S. Patent Nos. 6,180,349; 6,033,854; and 5,972,602, as well as in, e.g., Gibson et al., Genome Research 6:995-1001 (1996); DeGraves, et al., Biotechniques 34(1):106-10, 112-5 (2003); Deiman B, et al., Mol Biotechnol. 20(2):163-79 (2002). Alternative method for determining the level of a mRNA of interest in a sample may involve other nucleic acid amplification methods such as ligase chain reaction (Barany (1991) Proc. Natl. Acad. Sci. USA 88:189-193), self-sustained sequence replication (Guatelli et al. (1990) Proc. Natl. Acad. Sci. USA 87:1874-1878), transcriptional amplification system (Kwoh et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), Q-Beta Replicase (Lizardi et al. (1988) Bio/Technology 6:1197), rolling circle replication (U.S. Patent No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art.

In general, quantitative amplification is based on the monitoring of the signal (e.g., fluorescence of a probe) representing copies of the template in cycles of an amplification (e.g., PCR) reaction. One method for detection of amplification products is the 5'-3' exonuclease "hydrolysis" PCR assay (also referred to as the TaqMan™ assay) (U.S. Pat. Nos. 5,210,015 and 5,487,972; Holland et al., PNAS USA 88: 7276-7280 (1991); Lee *et al., Nucleic Acids Res.* 21: 3761-3766 (1993)). This assay detects the accumulation of a specific PCR product by hybridization and cleavage of a doubly labeled fluorogenic probe (the "TaqMan™" probe) during the amplification reaction. The fluorogenic probe consists of an oligonucleotide labeled with both a fluorescent reporter dye and a quencher dye. During PCR, this probe is cleaved by the 5'-exonuclease activity of DNA polymerase if,

and only if, it hybridizes to the segment being amplified. Cleavage of the probe generates an increase in the fluorescence intensity of the reporter dye.

Another method of detecting amplification products that relies on the use of energy transfer is the "beacon probe" method described by Tyagi and Kramer, *Nature Biotech.* 14:303-309 (1996), which is also the subject of U.S. Patent Nos. 5,119,801 and 5,312,728. This method employs oligonucleotide hybridization probes that can form hairpin structures. On one end of the hybridization probe (either the 5' or 3' end), there is a donor fluorophore, and on the other end, an acceptor moiety. In the case of the Tyagi and Kramer method, this acceptor moiety is a quencher, that is, the acceptor absorbs energy released by the donor, but then does not itself fluoresce. Thus, when the beacon is in the open conformation, the fluorescence of the donor fluorophore is detectable, whereas when the beacon is in hairpin (closed) conformation, the fluorescence of the donor fluorophore is quenched. When employed in PCR, the molecular beacon probe, which hybridizes to one of the strands of the PCR product, is in "open conformation," and fluorescence is detected, while those that remain unhybridized will not fluoresce (Tyagi and Kramer, Nature Biotechnol. 14: 303-306 (1996)). As a result, the amount of fluorescence will increase as the amount of PCR product increases, and thus may be used as a measure of the progress of the PCR. Those of skill in the art will recognize that other methods of quantitative amplification are also available.

Various other techniques for performing quantitative amplification of nucleic acids are also known. For example, some methodologies employ one or more probe oligonucleotides that are structured such that a change in fluorescence is generated when the oligonucleotide(s) is hybridized to a target nucleic acid. For example, one such method involves is a dual fluorophore approach that exploits fluorescence resonance energy transfer (FRET), e.g., LightCycler™ hybridization probes, where two oligo probes anneal to the amplicon. The oligonucleotides are designed to hybridize in a head-to-tail orientation with the fluorophores separated at a distance that is compatible with efficient energy transfer. Other examples of labeled oligonucleotides that are structured to emit a signal when bound to a nucleic acid or incorporated into an extension product include: Scorpions™ probes (e.g., Whitcombe et al., Nature Biotechnology 17:804-807, 1999, and U.S. Pat. No. 6,326,145),

Sunrise™ (or Amplifluor™) probes (e.g., Nazarenko et al., Nuc. Acids Res. 25:2516-2521, 1997, and U.S. Pat. No. 6,117,635), and probes that form a secondary structure that results in reduced signal without a quencher and that emits increased signal when hybridized to a target (e.g., Lux probes™).

In other embodiments, intercalating agents that produce a signal when intercalated in double stranded DNA may be used. Exemplary agents include SYBR GREEN™ and SYBR GOLD™. Since these agents are not template-specific, it is assumed that the signal is generated based on template-specific amplification. This can be confirmed by monitoring signal as a function of temperature because melting point of template sequences will generally be much higher than, for example, primer-dimers, etc.

In other embodiments, the mRNA is immobilized on a solid surface and contacted with a probe, *e.g.,* in a dot blot or Northern format. In an alternative embodiment, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the probe(s), for example, in a gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in detecting the level of mRNA encoding the biomarkers or other proteins of interest.

In some embodiments, microarrays, *e.g.,* are employed. DNA microarrays provide one method for the simultaneous measurement of the expression levels of large numbers of genes. Each array consists of a reproducible pattern of capture probes attached to a solid support. Labeled RNA or DNA is hybridized to complementary probes on the array and then detected by laser scanning. Hybridization intensities for each probe on the array are determined and converted to a quantitative value representing relative gene expression levels. See, U.S. Patent Nos. 6,040,138, 5,800,992 and 6,020,135, 6,033,860, and 6,344,316. High-density oligonucleotide arrays are particularly useful for determining the gene expression profile for a large number of RNA's in a sample.

Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, e.g., U.S. Patent No. 5,384,261. Although a planar array surface is often employed the array may be fabricated on a surface of virtually any shape or even a multiplicity of surfaces. Arrays may be peptides or nucleic acids on beads, gels, polymeric surfaces, fibers such as fiber optics, glass or any other appropriate substrate, see U.S. Patent

Nos. 5,770,358, 5,789,162, 5,708,153, 6,040,193 and 5,800,992. Arrays may be packaged in such a manner as to allow for diagnostics or other manipulation of an all-inclusive device.

Primer and probes for use in amplifying and detecting the target sequence of interest can be selected using well-known techniques.

In the context of this invention, "determining the levels of expression" of an RNA interest encompasses any method known in the art for quantifying an RNA of interest.

Detection of protein levels

In some embodiments, *e.g.,* where the expression level of a protein encoded by a biomarker gene set forth in Table 1 is measured. Often, such measurements may be performed using immunoassays. Although the protein expression level may be determined using a cellular sample, such as a peripheral blood lymphocyte sample, the protein expression is typically determined using a serum sample.

A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988) and Harlow & Lane, *Using Antibodies* (1999). Methods of producing polyclonal and monoclonal antibodies that react specifically with an allelic variant are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *supra*; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature* 256:495-497 (1975)). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (*see, e.g.*, Huse *et al.*, *Science* 246:1275-1281 (1989); Ward *et al.*, *Nature* 341:544-546 (1989)).

Polymorphic alleles can be detected by a variety of immunoassay methods. For a review of immunological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*. For a review of the general immunoassays, see also

Methods in Cell Biology: Antibodies in Cell Biology, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991).

Commonly used assays include noncompetitive assays, *e.g.*, sandwich assays, and competitive assays. Typically, an assay such as an ELISA assay can be used. The amount of the polypeptide variant can be determined by performing quantitative analyses.

Other detection techniques, *e.g.*, MALDI, may be used to directly detect the presence of proteins correlated with treatment outcomes.

Devices and Kits

In a further aspect, the invention provides diagnostic devices and kits for identifying gene expression products associated with improved responsiveness of a rheumatoid arthritis patient to a therapeutic agents that antagonizes IL-6 receptor signaling, such as an IL-6R antibody, *e.g.*, tocilizumab.

In some embodiments, a diagnostic device comprises probes to detect at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 50, 60, 70, or 80, or all of, the gene expression products set forth in Table 1. In some embodiments, the present invention provides oligonucleotide probes attached to a solid support, such as an array slide or chip, *e.g.*, as described in DNA Microarrays: A Molecular Cloning Manual, 2003, Eds. Bowtell and Sambrook, Cold Spring Harbor Laboratory Press. Construction of such devices are well known in the art, for example as described in US Patents and Patent Publications U.S. Patent No. 5,837,832; PCT application W095/11995; U.S. Patent No. 5,807,522; US Patent Nos. 7,157,229, 7,083,975, 6,444,175, 6,375,903, 6,315,958, 6,295,153, and 5,143,854, 2007/0037274, 2007/0140906, 2004/0126757, 2004/0110212, 2004/0110211, 2003/0143550, 2003/0003032, and 2002/0041420. Nucleic acid arrays are also reviewed in the following references: *Biotechnol Annu Rev* 8:85-101 (2002); Sosnowski *et al*, *Psychiatr Genet* 12(4):181-92 (Dec. 2002); Heller, *Annu Rev Biomed Eng* 4: 129-53 (2002); Kolchinsky et al, *Hum. Mutat* 19(4):343-60 (Apr. 2002); and McGail et al, Adv Biochem Eng Biotechnol 77:21-42 (2002).

An array can be composed of a large number of unique, single-stranded polynucleotides, usually either synthetic antisense polynucleotides or fragments of cDNAs, fixed to a solid

support. Typical polynucleotides are preferably about 6-60 nucleotides in length, more preferably about 15-30 nucleotides in length, and most preferably about 18-25 nucleotides in length. For certain types of arrays or other detection kits/systems, it may be preferable to use oligonucleotides that are only about 7-20 nucleotides in length. In other types of arrays, such as arrays used in conjunction with chemiluminescent detection technology, preferred probe lengths can be, for example, about 15-80 nucleotides in length, preferably about 50-70 nucleotides in length, more preferably about 55-65 nucleotides in length, and most preferably about 60 nucleotides in length.

A person skilled in the art will recognize that, based on the known sequence information, detection reagents can be developed and used to assay any gene expression product set forth in Table 1, Table 2, or Table 3 and that such detection reagents can be incorporated into a kit. The term "kit" as used herein in the context of biomarker detection reagents, are intended to refer to such things as combinations of multiple biomarker detection reagents, or one or more biomarker detection reagents in combination with one or more other types of elements or components (e.g., other types of biochemical reagents, containers, packages such as packaging intended for commercial sale, substrates to which biomarker detection reagents are attached, electronic hardware components, etc.). Accordingly, the present invention further provides biomarker detection kits and systems, including but not limited to, packaged probe and primer sets (e.g., TaqMan probe/primer sets), arrays/microarrays of nucleic acid molecules where the arrays/microarrays comprise probes to detect the level of biomarker transcript, and beads that contain one or more probes, primers, or other detection reagents for detecting one or more biomarkers of the present invention. The kits can optionally include various electronic hardware components; for example, arrays ("DNA chips") and microfluidic systems ("lab-on-a-chip" systems) provided by various manufacturers typically comprise hardware components. Other kits (e.g., probe/primer sets) may not include electronic hardware components, but may be comprised of, for example, one or more biomarker detection reagents (along with, optionally, other biochemical reagents) packaged in one or more containers.

In some embodiments, a biomarker detection kit typically contains one or more detection reagents and other components (e.g. a buffer, enzymes such as DNA polymerases) necessary to carry out an assay or reaction, such as amplification for detecting the level of

biomarker transcript. A kit may further contain means for determining the amount of a target nucleic acid, and means for comparing the amount with a standard, and can comprise instructions for using the kit to detect the biomarker nucleic acid molecule of interest. In one embodiment of the present invention, kits are provided which contain the necessary reagents to carry out one or more assays to detect one or more biomarkers disclosed herein. In one embodiment of the present invention, biomarker detection kits/systems are in the form of nucleic acid arrays, or compartmentalized kits, including microfluidic/lab-on-a-chip systems.

Biomarker detection kits/systems may contain, for example, one or more probes, or pairs or sets of probes, that hybridize to a nucleic acid molecule encoded by a gene set forth in Table 1, Table 2, or Table 3. In some embodiments, the presence of more than one biomarker can be simultaneously evaluated in an assay. For example, in some embodiments probes or probe sets to different biomarkers are immobilized as arrays or on beads. For example, the same substrate can comprise biomarkers probes for detecting at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or 20 or more of the biomarkers set forth in Table 1, Table 2, or Table 3.

Using such arrays or other kits/systems, the present invention provides methods of identifying the biomarkers described herein in a test sample. Such methods typically involve incubating a test sample of nucleic acids obtained from peripheral blood lymphocytes from a patient with an array comprising one or more probes that selectively hybridizes to a nucleic acid encoded by a gene set forth in Table 1, Table 2, or Table 3. Conditions for incubating a biomarker detection reagent (or a kit/system that employs one or more such biomarker detection reagents) with a test sample vary. Incubation conditions depend on such factors as the format employed in the assay, the detection methods employed, and the type and nature of the detection reagents used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification and array assay formats can readily be adapted to detect a biomarker set forth in Table 1, Table 2, or Table 3.

A biomarker detection kit of the present invention may include components that are used to prepare nucleic acids from a test sample for the subsequent amplification and/or detection of a biomarker nucleic acid molecule.

Correlating Gene Expression Levels with Therapeutic response

The present invention provides methods of determining the levels of a gene expression product to evaluate the likelihood that a rheumatoid arthritis patient will respond to treatment with an IL-6R antibody, such as tocilizumab. Either female or male rheumatoid arthritis patients can be analyzed for gene expression levels.

The presence of certain markers, *e.g.,* base line expression markers in Table 1 that are associated with an improvement in therapeutic outcomes, are indicative of patients who are expected to exhibit a positive therapeutic response to treatment with an IL-6R antibody, such as tocilizumab. Typically, the likelihood of the positive therapeutic response is increased with increasing amounts of the gene expression marker.

Similarly, a patient may have a gene expression marker, *e.g.,* baseline expression of a biomarker set forth in Table 1, that is associated with a negative therapeutic outcome. Accordingly, such a patient is not likely to response to IL-6R antibody, *e.g.,* tocilizumab. Typically, the likelihood of the negative therapeutic response is increased with increased amount of the biomarker.

In Tables 1, 2, and 3, the "co-efficient" column represents the effect of the gene expression value on the response measured by change in DAS28 score, adjusted for baseline DAS (data in Table 3 are also adjusted for baseline platelet number). The sign of the coefficient represent the direction of the effect. For example, a coefficient of -1.6 means that higher expression is associated with better response. Every 2-fold increase in gene expression value corresponds to a further reduction on DAS score by 1.6 unit. Likewise, a positive coefficient indicates that higher expression value is associated with poorer response (higher DAS28 score). Table 1 show biomarkers in which the baseline expression (i.e., level prior to undergoing treatment with an IL-6R antibody such as tocilizumab) of a biomarker is predictive for a therapeutic response. Thus, for example, the level of a gene expression product encoded by a gene set forth in Table 1 can be determined in a peripheral blood

sample obtained from a rheumatoid arthritis patient. A biomarker positive/negative groups is defined using a threshold in gene expression level. The exact thresholds for each marker can be determined using algorithms well known in the art and will depend on the particular platform and assay used and the desired performance parameters, *e.g.,* sensitivity, specificity, of the assay.

For example, a patient is determined to be likely to exhibit a therapeutic response, or not to exhibit a therapeutic response to the IL-6 antagonizing agent, *e.g.,* tocilizumab, if the level of expression of a biomarker in Table 1 is either above (predicted to exhibit a positive therapeutic response) or below (predicted to the not exhibit a positive therapeutic response) a threshold.

Measurement of the level of expression of a gene set forth in Table 2 also provides the ability to measure the likelihood of a patient to respond to treatment with an IL6-R antagonist, *e.g.,* an IL-6R antibody such as tocilizumab, at later time points. For example, measurement of the expression of a gene set forth in Table 2 is made at base line and, *e.g.,* at 8 weeks following treatment. The change in gene expression between the two measurements is used to calculate likelihood of response at a later time point, such as 16 or 24 weeks. Here again, a threshold of change in response may be applied.

Alternatively, a measurement can be made after initiation of treatment, *e.g.,* at week 8, and an observed ' normalization' of a level of gene expression against a predetermined value may be used to make the response predication.

Gene expression can also be evaluated for genes listed in Table 5. Each of columns A-J of Table 5 represent genes that were analyzed for the clinical response noted in the column head. The top 100 genes for ACR are listed in the table with the rank > 0. If the value is 0, the gene is not selected for ACR. For each column at least two, typically most, or all of the genes indicated with a value > 0 can be analyzed. The gene expression values are used as a linear combination of expression signals from multiple genes in order to predict the classification of clinical response as outlined in the Examples section of 'class index's' in the description relating to Table 5. The cutoffs for these linear combinations of gene expression levels are determined by classification algorithms known in the art, such as support vector machines (SVM) (*see, e.g.,* Vapnik, The Nature of Statistical Learning,

Springer, NY, 1995; Cristianini & Shawe-Taylor, An Introduction to Support Vector Machines, Cambridge University Press, Cambridge, UK, 2000.)

The methods of the invention typically involve recording the level of a gene expression product associated with a beneficial therapeutic outcome, or a negative therapeutic outcome, in a rheumatoid arthritis patient treated with an IL-6R antibody such as tocilizumab. This information may be stored in a computer readable form. Such a computer system typically comprises major subsystems such as a central processor, a system memory (typically RAM), an input/output (I/O) controller, an external device such as a display screen via a display adapter, serial ports, a keyboard, a fixed disk drive via a storage interface and a floppy disk drive operative to receive a floppy disc, and a CD-ROM (or DVD-ROM) device operative to receive a CD-ROM. Many other devices can be connected, such as a network interface connected via a serial port.

The computer system also be linked to a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The computer system can comprise code for interpreting the results of an expression analysis evaluating the baseline level of one or more gene expression products encoded by a gene noted in Table 1. Thus in an exemplary embodiment, the expression analysis results are provided to a computer where a central processor executes a computer program for determining the propensity for a therapeutic response to treatment with an IL-6 receptor antibody.

The invention also provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding the expression results obtained by the methods of the invention, which may be stored in the computer; (3) and, optionally, (4) a program for determining the likelihood for a positive therapeutic response.

The invention further provides methods of generating a report based on the detection of gene expression products in a patient that has rheumatoid arthritis. Such a report is based on the detection of gene expression products encoded by the genes set forth in Table 1 that are associated with either a positive or negative therapeutic outcome.

A patient that has an increased likelihood of having a positive therapeutic response to treatment with IL-6R antibody has at least one gene expression product in Table 1 that is associated with a positive therapeutic response. Typically such a patient has an expression pattern where at least two products encoded by a gene set forth in Table 1 are determined. In some embodiments, the patient may be evaluated for expression levels of products encoded by 3, 4, 5, 6, 7, 8, 9, or 10 or more of the genes set forth in Table 1.

EXAMPLES

Example 1. Analysis of gene expression profiles of rheumatoid arthritis patients treated with tocilizumab.

Analysis of gene expression data for association with response to change in DAS28 score.

RNA samples collected from patients with active RA dosed with 8 mg/Kg tocilizumab as a monotherapy in the AMBITION study (Jones, *et al., Ann Rheum Dis* 2 69:88-96, 2010) were collected at baseline and at week 8 post dose. Two hundred and nine samples (113 baseline samples and 96 "week 8" samples) underwent gene expression profiling through use of an Affymetrix GeneChip® Human Genome U133 Plus 2.0 Array.

After a number of quality control steps on the gene expression data, 2 samples were highlighted as having lower quality, and 207 samples were subjected to further analysis.

The Affymetrix RMA algorithm was used in generating the normalized gene expression data for further analysis. Only probesets with high expression levels (max > 4) and those with larger dynamic range (max-min >2) were included. The max and min were taken over all samples. Linear regression was performed for the following analyses. In all analyses, change in Disease Activity Score 28 (DAS28) at week 16 (cDAS28) was used as response endpoint. Week 16 was chosen because it was the earliest time point for escape therapy in

the most tocilizumab clinical trials). Baseline DAS was used as a covariate in all analysis since it has significant effect on cDAS.

1. Baseline gene expression versus cDAS28. 111 subjects were included in the analysis.

2. Linear Regression with LASSO Variable Selection using baseline expression data. This is a multivariate analysis method that include all probesets in the model, with L1 penalty on the coefficients of the probesets added to the objective function. (Tibshirani, R. (1996). *J. Royal. Statist.* Soc B., Vol. 58(1): 267-288)). A subset of the probesets was selected by the model. The number of probesets selected by the model depends on the level of penalty. The optimal level of penalty, which subsequently determined optimal number of probesets selected to achieve the best prediction, was determined using 10-fold cross validation.

3. Change in gene expression at week 8 versus cDAS28. Ninety four subjects were included in the analysis.

4. Linear Regression with LASSO Variable Selection using change in gene expression

5. Baseline gene expression versus cDAS28, adjusting for baseline platelets

Analysis (1) identified a number of probesets that represented activated platelet expressed genes e.g. ITGA2B (CD41), ITGB3 (CD61), JAM3 were present at the top of the list of data ordered by p-value (see, Table 1). There is a correlation of expression of these genes with cDAS28.

This observation prompted a regression analysis of baseline platelet count against change in DAS28. The analysis demonstrated a modest but statistically significant link to baseline platelet count. A far stronger effect size is noted through the correlation of ITGA2B, ITGB3, JAM3 to cDAS28, suggesting that markers of platelet activation are a better predictors of response than platelet count alone.

From analysis (1), it was determined that baseline expression levels of EPHB2 (Ephrin receptor B2) has a correlation to cDAS28. EPHB2 transduces signals that regulate cell

attachment and migration and is expressed at higher levels in synovial fibroblasts and exudate lymphocytes in RA, than in those from OA. It's ligand, EphrinB1, is expressed at levels higher in RA peripheral blood lymphocytes (PBL) than healthy controls.

Recombinant EphrinB1 stimulates normal PBL's to exhibit enhanced migration and TNF production, and RA synovial cells to produce IL-6. These results indicate that it is also a useful biomarker for predicting response to tocilizumab.

We reasoned that the high correlation of platelet expressed genes with cDAS observed in analysis (1) could be 'masking' the identification of other important response signals. Baseline correction of platelet number in the regression model was therefore performed. From this analysis, ordered by p-value 3 out of 4 components of the NALP1 inflammasome were identified. Inflammasomes are multi-protein cytoplasmic complexes that mediate activation of pro-inflammatory caspases. The NALP1 inflammasome activates caspase 1 and caspase 5. Caspase 1 cleaves pro-IL-1β to IL-1β,and also activates IL-18 and potentially IL-33. We also identified the association of baseline expression of CARD16, a negative regulator of Caspase 1, and the baseline expression of IL-1 receptor, with cDAS. Serum levels of IL1B/IL-18/IL-33 and gene expression signature of transcripts identified above also may be used as biomarkers to predict response to tocilizumab.

From analysis (3), a number of transcripts have been identified that may be used to predict response through change in gene expression 8 weeks from tocilizumab administration. (Table 2). These include caspase 1, a link to the IL-1β/ IL-18/IL-33 pathway (and see (4) above), serine palmitoyltransferase, long chain base subunit 2, a link to de novo sphingolipid synthesis of molecules such ceramide and sphingosine-1-phosphate (S1P), and platelet expressed genes such as CD41, CD61, and JAM3.

Lasso variable selection multivariate methodology (analyses 2 and 4) allows identification of transcripts that each contribute a different 'component' to the prediction of response. An optimal number of probesets (n=12 and n=13 respectively) were determined by 10 fold cross validation. This analysis identified a number of genes that may be used as predictive biomarkers.

The list of probesets/genes identified by these analyses are shown in Table 1. Table 1 cDASvs.bExp contains probesets/genes whose baseline expression is predictive of tocilizumab treatment response. This list consists of 95 probesets, 12 of which were unmapped, the remaining probesets mapped to 72 unique gene symbols. Among the probesets, 88 were identified by univariate linear regression (analysis 1) and 12 were identified using the multivariate LASSO analysis (analysis 2), with 5 probesets identified by both analyses.

Table 2 cDASvs.cEXP contains probeset/gene expression change from baseline to week 8 that is predictive of tocilizumab treatment response. This list consists of 104 probesets, 6 of which were unmapped, the remaining mapped to 92 unique genes symbols. Among the probesets, 97 were identified by univariate linear regression analysis (analysis 3) and 13 were identified using the multivariate LASSO analysis (analysis 4), with 6 probesets identified by both analyses.

Table 3 (cDASvs.bEXP.AdjustforPlatelet) contains probeset/genes whose baseline expression, combined with baseline platelet count, is predictive of tocilizumab treatment response. This list consists of 81 probesets, 10 of which were unmapped, the remaining mapped to 61 unique genes symbols. All of the probesets were identified by univariate linear regression analysis (analysis 5).

All of the biomarkers may be used univariately or in combination in a multivariate model.

Example 2. Identification of groups of probesets with predicative value for extreme response to tocilizumab

An analysis to identify groups of probesets with predictive value of extreme response to tocilizumab, namely ACR response and EULAR response, was also undertaken.

Two hundred nine CEL files (Affymetrix expression data files) were generated for patients treated with tocilizumab. Two CEL files were excluded from the dataset for technical reasons. One hundred eleven of the remaining 207 CEL files are for the samples at the baseline. This example is focused on the dataset N111.

We considered the four classes of American College of Rheumatology (ACR) response are shown in Table 4.

Table 4

ClassIndex	ACR20	ACR50	ACR70
1	0	0	0
2	1	0	0
3	1	1	0
4	1	1	1

We also considered 3 classes of European League Against Rheumatism (EULAR) response at week 16 (1 for no response, 2 for moderate and 3 for good response). Change in DAS28 at beginning and DAS28 at week 16 ("dDAS28" or "cDAS28"), as well as DAS28 at week 16 was also evaluated. There is one missing data point in DAS28, we therefore have a dataset N110 for DAS28 at week 16 and cDAS28.

For DAS28 at week 16, we define C1 as the class with DAS28 value x >= 4 (non response), C2 as the class with x in the range of 2.6 to 4, and C3 as the class with x < 2.6 (good response). For ΔDAS28, we define C1 as the class with ΔDAS28 value y <= 2.5 (poor response), C2 as the class with y in the range of 2.5 to 3.6, and C3 as the class with y > 3.6 (good response).

In all the above class assignments, C1 represents the group with poor response and C4 (ACR) or C3 (other indicators) for good response. C2 (or C2 and C3 for ACR) is the class of moderate response.

Approaches for Probeset selection

For each indicator (ACR, EULAR, ΔDAS28, and DAS28 at week 16), we used Dn3 expression signals (see Liu, *et al., J. Theortical Biol* 243:273-278, 2006; and pending U.S. application no. 12/578,417) and two different ways of grouping. One grouping is the poor response class versus others (good and moderate response classes). The other grouping is to use only the extreme classes (poor response class versus the good response classes). The sample sizes for the first grouping method are given before, N111 or N110. The sample sizes for the grouping of extreme classes are N62 (ACR), N45 (EULAR), N70 (DAS28 at week 16) and N80 (ΔDAS28).

Dn3 signals (with improvements on MAS5 using differences of perfect match and mismatch intensities) are typically robust for classification results. For completeness, we also included the probe sets selected with Pn3 signals (using only perfect match intensities and similar to RMA in certain sense).

For each grouping method, we calculated the absolute values of t-statistics and selected the top 100 probe sets with highest absolute values of t-statistics. Their union for 4 different indicators, 2 different signals and 2 different grouping methods (total 8 groups) contains 628 probesets and are listed in Table 5. (For "union of the four different indicators, the 4 different indicators (or 4 different types of responses) are ACR, EULAR, DAS and cDAS. The union is the combination of all probe sets without counting the replicated ones. For example, if set 1 is {1, 3, 5, 7, 9}, set 2 is {1, 2, 3, 4}, Set 3 is {3, 5}, set 4 is {9, 10, 11}, then the union of these 4 sets is {1, 2, 3, 4, 5, 7, 9, 10, 11}).

Table 5 Description

In Table 5, the first column "N1:54630" lists the 1-based indices in the list of 54630 probe sets targeting human genes on the HG-U133 Plus 2.0 microarray. The second column "ID" lists the Affymetrix probe set IDs.

The next 8 columns provide the ranks of 8 groups of probesets and the information whether a probe set is selected in a particular group. The column names are indicator name, sample size, and signals (Dn3). The value 0 means the probe set is not selected in a particular group. The values 1 through 100 give the ranks of the selected probe sets, where 1 is the top (most significant) one.

The column "AverageScore" provides a score for the summary of the previous 8 columns. The value 0 has no contribution to the score (i.e., the score is 0). For all other values (1 through 100), we calculated (101 – value) (so the difference is in the range 1 through 100, but in the reverse order, the largest difference, 100, corresponds to the most significant rank 1). We calculated the average score for the 8 columns and list all average scores in the column. In general, the higher the score, the more significant a probeset for all groups.

The columns "Gene Symbol" and "Gene Title" provide annotations from Affymetrix web site for the selected probe sets.

For Table 5, each group of genes identified in columns C-J of table 5 may be used to form one or more linear combinations of expression signals from multiple genes in order to predict the clinical response as outlined in the description of 'class index's' in lines 0080-0084. The cutoffs for these linear combinations of gene expression levels will be determined by classification algorithms such as support vector machines (SVM, The Nature of Statistical Learning, Springer, NY, 1995; Cristianini and Shawe-Taylor, An Introduction to Support Vector Machines, Cambridge University Press, Cambridge, UK, 2000). For Table 5, each indications shows a number; expression of at least two genes that have a number greater than 0 can be used (within the same column).

Examples 3 and 4 below provide example of how two and three gene transcripts are used to predict patient response to treatment with an IL-6R antagonist, such as an IL-6R antibody, *e.g.,* tocilizumab. As understood in the art, a multivariate model can be employed that involves additional genes identified herein, *e.g.*, probe sets corresponding to those set forth in Table 1, Table 2, or Table 3.

Example 3. Combination on three probesets for predicting the response level

Gene transcripts in patient baseline blood samples are measured using Affymetrix human genome U133 plus v2 array. The raw data file are normalized against the data from a set of reference samples from which the algorithm was derived. Expression at the gene transcript level (RMA type of data) will be extracted, in this example, for at the three probesets 12345_at, 12346_at and 12347_at (denoted as e1, e2 and e3) and used in a linear model to give predictions of the week 24 change from baseline DAS28 score (cDAS) if the patient undergoes tocilizumab (TCZ) treatment at 8mg/kg in combination with methotrexate (MTX).

For TCZ treatment: cDAS = a0 * DAS_baseline + a1 * e1 + a2 * e2 + a3 * e3

The predicted mean change in DAS for the patients will be from 1 to -7, depending on the baseline DAS and gene expression values of e1, e2 and e3. If the patient were to undergo treatment with MTX alone, the predicted mean change in DAS given by:

For MTX treatment: cDAS = b0 * DAS_baseline

The predicted mean change is DAS will be from 0 to -3, depending on the patient baseline DAS alone

The treatment choice for each patient is then made based on the difference of these predictions. For example, if patient A has a predicted change in DAS of -4.5 on tocilizumab, and -2 on MTX, the doctor may recommend TCZ treatment. Patient B has the predicted change in DAS of -3 on TCZ and -2.5 on MTX, the doctor may recommend treatment with MTX, as the small additional therapeutic benefit may be not worth the additional cost and any potential risk.

Example 4. Combination of two transcripts to predict patient response to treatment

Expression levels of two genes in patient baseline blood samples are measured using quantitative PCR (qPCR). The relative expression levels are represented by ΔCT. Biomarker groups are defined as following:

Positive: $a1*\Delta CT1 + a2*\Delta CT2 >= 2.1$

Negative: $a1*\Delta CT1 + a2*\Delta CT2 < 2.1$

Biomarker positive patients are likely to have better response rate compared with biomarker negative patients under tocilizumab treatment, (ACR50 response rate of 55% vs. 38%), while both group have similar response rate when treated with methotrexate, with ACR50 response rate of 35%.

It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims.

Table 1

probeset	Accession	gene. Symbol	gene.title	co-efficient	raw. p.value	exp. median	exp. min	exp. max	Diff	LASSO
240934_at	AI801975	PIP5K1B	Phosphatidylinositol-4-phosphate 5-kinase type-1 beta	-1.63	1.4E-04	3.51	2.16	4.93	2.77	
231721_at	AF356518	JAM3	junctional adhesion molecule 3	-0.67	2.5E-04	4.10	2.43	6.17	3.75	Y
1558938_at	BC043574	---	---	1.04	2.6E-04	4.45	3.09	5.77	2.68	
206494_s_at	NM_000419	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	-1.00	2.8E-04	3.97	2.64	5.76	3.12	
216956_s_at	AF098114	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	-0.68	4.1E-04	4.45	2.94	6.40	3.46	
212811_x_at	AI889380	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	1.07	5.6E-04	3.91	2.59	4.86	2.27	
209589_s_at	AF025304	EPHB2	EPH receptor B2	-0.90	7.1E-04	3.37	2.11	5.25	3.15	
234618_at	AL049434	PHTF1	Putative homeodomain transcription factor 1	0.93	9.2E-04	2.54	1.79	4.40	2.61	
239274_at	AV729557	PICALM	Phosphatidylinositol-binding clathrin assembly protein	1.13	9.7E-04	6.10	5.00	7.13	2.13	
217876_at	NM_012087	GTF3C5	general transcription factor IIIC, polypeptide 5, 63kDa	-1.22	1.2E-03	4.24	3.18	5.23	2.05	
240980_at	R61819	---	---	1.25	1.3E-03	2.22	1.58	4.29	2.71	
214364_at	W84525	MTERFD2	MTERF domain containing 2	-1.21	1.3E-03	3.30	2.00	4.62	2.61	
209006_s_at	AF247168	C1orf63	chromosome 1 open reading frame 63	1.08	1.5E-03	5.89	4.66	7.63	2.97	
234948_at	AK026640	SLC27A5	solute carrier family 27 (fatty acid transporter), member 5	-1.19	1.6E-03	3.73	2.92	4.97	2.05	
204626_s_at	J02703	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	-0.51	1.7E-03	7.30	4.89	9.40	4.51	Y
219476_at	NM_024115	C1orf116	chromosome 1 open reading frame 116	-1.04	1.9E-03	2.39	1.70	4.31	2.61	
206493_at	NM_000419	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	-0.56	2.0E-03	7.45	5.05	9.56	4.51	
239714_at	AA780063	---	---	-1.11	2.1E-03	3.41	2.55	4.80	2.25	
217179_x_at	X79782	---	---	0.90	2.2E-03	4.56	3.83	6.66	2.83	
225685_at	AI801777	---	---	0.99	2.6E-03	6.32	5.29	7.46	2.17	
1552309_a_at	NM_144573	NEXN	nexilin (F actin binding protein)	0.69	2.6E-03	3.63	1.94	5.33	3.39	
232472_at	AK022461	FNDC3B	Fibronectin type III domain-containing protein 3B	0.69	2.7E-03	3.86	2.60	5.60	3.00	
229643_at	AI857933	ITGA6	Integrin alpha 6B [human, mRNA Partial, 528 nt]	-0.98	2.7E-03	3.75	2.86	5.20	2.34	
238080_at	BF195052	B4GALNT4	beta-1,4-N-acetyl-galactosaminyl transferase 4	-1.06	2.7E-03	3.13	2.28	4.47	2.19	
243187_at	AA888821	PVRL2	Poliovirus receptor-related protein 2 Precursor	0.88	2.9E-03	2.25	1.48	4.09	2.61	
208792_s_at	M25915	CLU	clusterin	-0.55	3.0E-03	6.46	4.57	8.51	3.94	
208593_x_at	NM_004382	CRHR1	corticotropin releasing hormone receptor 1	-1.18	3.5E-03	3.24	2.25	4.28	2.04	
217472_at	J02963	---	---	-0.84	3.7E-03	3.98	2.98	5.66	2.68	

Table 1

243106_at	AA916861	CLEC12A	C-type lectin protein CLL-1	0.28	3.9E-03	3.93	1.90	7.11	5.22	Y
225680_at	BE896303	LRWD1	leucine-rich repeats and WD repeat domain containing 1	-1.10	3.9E-03	5.25	4.35	7.01	2.66	
212613_at	AI991252	BTN3A2	butyrophilin, subfamily 3, member A2	0.55	4.0E-03	6.00	2.43	6.98	4.56	
230888_at	AW300278	WDR91	CDNA FLJ23886 fis, clone LNG13909	0.76	4.0E-03	2.73	1.49	4.31	2.82	
212592_at	AV733266	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	0.32	4.0E-03	3.38	1.38	8.41	7.03	Y
216145_at	AL137713	---	---	-1.19	4.3E-03	2.81	2.20	4.25	2.05	
235971_at	AI147211	---	---	0.71	4.4E-03	3.59	2.63	5.66	3.04	
1562743_at	BC042873	ZNF33B	Zinc finger protein 33B (ZNF33B), mRNA	-1.03	4.4E-03	3.62	2.32	4.74	2.42	
208791_at	M25915	CLU	clusterin	-0.53	4.6E-03	5.47	3.72	7.37	3.65	
222411_s_at	AW087870	SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	0.87	4.8E-03	5.55	4.42	6.82	2.40	
212813_at	AA149644	JAM3	junctional adhesion molecule 3	-0.75	4.9E-03	5.14	4.07	6.61	2.54	
225831_at	AW016830	LUZP1	leucine zipper protein 1	-1.74	5.0E-03	4.16	3.58	6.99	3.41	
232079_s_at	BE867789	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	0.45	5.0E-03	3.15	2.33	6.76	4.42	
202112_at	NM_000552	VWF	von Willebrand factor	-0.72	5.1E-03	3.34	2.31	5.50	3.20	
231057_at	AU144266	MTMR2	Myotubularin-related protein 2	1.11	5.3E-03	2.91	2.07	4.22	2.15	
220476_s_at	NM_019099	C1orf183	chromosome 1 open reading frame 183	-0.90	5.5E-03	5.53	4.21	6.32	2.11	
232726_at	AK024956	MAML3	Mastermind-like protein 3	0.75	5.5E-03	3.71	2.61	4.94	2.33	
1552398_a_at	NM_138337	CLEC12A	C-type lectin domain family 12, member A	0.31	5.7E-03	5.84	4.09	8.70	4.61	
238183_at	AI632259	PRKAR1B	cAMP-dependent protein kinase type I-beta regulatory subunit	-0.60	6.0E-03	5.73	3.24	7.26	4.02	
231174_s_at	H92979	---	---	0.83	6.2E-03	2.00	1.11	4.39	3.28	
203545_at	NM_024079	ALG8	asparagine-linked glycosylation 8, alpha-1,3-glucosyltransferase homolog (S. cerevisiae)	0.72	6.6E-03	3.73	2.08	5.29	3.21	
227551_at	BE856596	FAM108B1	family with sequence similarity 108, member B1	0.77	6.8E-03	3.98	2.17	5.30	3.13	
229530_at	BF002625	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	-0.62	6.9E-03	3.07	1.99	4.73	2.74	
233852_at	AK025631	POLH	polymerase (DNA directed), eta	0.85	6.9E-03	4.78	3.86	6.77	2.91	
231720_s_at	AF356518	JAM3	junctional adhesion molecule 3	-0.78	7.0E-03	4.48	3.49	5.99	2.50	
218435_at	NM_013238	DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15	0.64	7.0E-03	5.15	3.55	6.54	2.99	
202874_s_at	NM_001695	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	0.73	7.2E-03	5.48	4.00	6.98	2.98	
244308_at	BF514096	SYT15	Chr10 synaptotagmin (CHR10SYT gene)	0.73	7.3E-03	2.48	1.57	5.12	3.55	
238589_s_at	AW601184	ATXN2	Ataxin-2	0.67	7.3E-03	4.82	3.32	6.35	3.03	
203064_s_at	NM_004514	FOXK2	forkhead box K2	0.79	7.5E-03	4.33	3.01	7.04	4.03	
231886_at	AL137655	DKFZP434B2016	similar to hypothetical protein LOC284701	0.50	7.6E-03	4.49	2.87	6.21	3.33	

Table 1

221942_s_at	AI719730	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	-0.52	7.6E-03	2.75	1.40	4.54	3.14	
1564155_x_at	BC041466	---	---	0.61	7.7E-03	4.06	2.58	5.71	3.13	
228040_at	AW294192	MGC21881	hypothetical locus MGC21881	0.77	7.7E-03	3.31	2.13	5.03	2.90	
207500_at	NM_004347	CASP5	caspase 5, apoptosis-related cysteine peptidase	0.60	7.8E-03	3.89	2.30	6.14	3.85	
211637_x_at	L23516	IGH	immunoglobulin heavy locus	0.59	8.1E-03	5.36	4.09	7.61	3.52	
232030_at	AK023817	KIAA1632	KIAA1632	0.61	8.1E-03	2.31	1.30	4.36	3.06	
210219_at	U36501	SP100	SP100 nuclear antigen	0.65	8.2E-03	1.67	1.10	6.37	5.28	
209610_s_at	BF340083	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	0.64	8.2E-03	2.76	1.53	4.32	2.78	
1558120_at	BE379787	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	0.89	8.4E-03	4.10	2.82	5.14	2.32	
210127_at	BC002510	RAB6B	RAB6B, member RAS oncogene family	-0.46	8.5E-03	3.49	2.15	5.71	3.56	
210456_at	AF148464	PCYT1B	phosphate cytidylyltransferase 1, choline, beta	-0.88	8.5E-03	3.93	3.07	5.19	2.12	
1559810_at	BF724577	LOC642313	hypothetical LOC642313	0.79	8.6E-03	2.91	1.56	4.71	3.15	
209651_at	BC001830	TGFB1I1	transforming growth factor beta 1 induced transcript 1	-0.48	8.7E-03	1.55	0.91	5.59	4.68	
239442_at	BF589179	CEP68	centrosomal protein 68kDa	0.86	8.7E-03	5.28	4.08	6.17	2.09	
1558742_at	BE899474	DEXI	Dexamethasone-induced protein	0.74	8.7E-03	2.98	1.67	4.76	3.09	
238894_at	AW665144	RABGAP1L	RAB GTPase-activating protein 1-like	0.80	8.8E-03	3.76	2.59	5.04	2.45	
209846_s_at	BC002832	BTN3A2	butyrophilin, subfamily 3, member A2	0.40	8.8E-03	6.65	1.82	7.73	5.91	Y
215093_at	U82671	NSDHL	NAD(P) dependent steroid dehydrogenase-like	0.53	8.9E-03	3.50	1.82	6.28	4.46	
213814_s_at	AA741303	SNTB2	CDNA clone IMAGE:5263917	-0.69	9.2E-03	4.24	2.90	5.32	2.42	
219348_at	NM_018467	USE1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	-1.11	9.5E-03	6.10	5.30	8.00	2.70	
240482_at	AI955094	HDAC3	Histone deacetylase 3 (HD3)	0.74	9.6E-03	5.31	3.99	6.47	2.49	
201058_s_at	NM_006097	MYL9	myosin, light chain 9, regulatory	-0.44	9.6E-03	5.68	3.84	8.28	4.44	
225900_at	AW294630	EXOC6B	exocyst complex component 6B	0.73	9.7E-03	3.23	1.91	5.03	3.12	
230788_at	BF059748	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	0.46	9.8E-03	3.91	2.57	6.90	4.34	
211368_s_at	U13700	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	0.73	9.8E-03	6.41	4.86	7.73	2.86	
235066_at	AI078534	MAP4	microtubule-associated protein 4	-1.25	9.8E-03	2.81	2.21	4.25	2.03	
206176_at	NM_001718	BMP6	bone morphogenetic protein 6	-0.72	9.9E-03	3.27	2.13	4.85	2.73	
232078_at	BE867789	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	0.38	9.9E-03	2.53	1.29	6.24	4.95	
211026_s_at	BC006230	MGLL	monoglyceride lipase	-0.75	1.0E-02	3.28	2.30	5.05	2.74	
1557012_a_at	BC040670	---	---							Y
203911_at	NM_002885	RAP1GAP	RAP1 GTPase activating protein							Y

Table 1

209728_at	BC005312	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	Y	
217207_s_at	AK025267	BTNL3	butyrophilin-like 3	Y	
220281_at	AI632015	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1		Y
230720_at	AI884906	RNF182	ring finger protein 182		Y
235446_at	AW856618	---	---		Y

Table 2

probeset	Accession	gene. symbol	gene.title	co-efficient	raw. p.value	exp. median	exp. min	exp. Max	diff	LASSO
1562743_at	BC042873	ZNF33B	Zinc finger protein 33B (ZNF33B), mRNA	1.18	3.1E-04	3.62	2.32	4.74	2.42	
242109_at	AI038577	SYTL3	CDNA FLJ61334 complete cds, moderately similar to Synaptotagmin-like protein 3	-1.01	4.3E-04	2.83	1.90	4.43	2.53	
232354_at	AK022083	VPS37B	Vacuolar protein sorting-associated protein 37B	-0.88	6.1E-04	4.36	3.04	5.60	2.55	
226865_at	AW130600	---	---	-1.00	8.1E-04	5.64	3.75	6.66	2.90	
224091_at	AF116642	---	---	-0.82	8.7E-04	5.38	4.30	6.69	2.39	
211367_s_at	U13699	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	-1.07	1.2E-03	7.44	6.20	9.01	2.81	
218728_s_at	NM_014184	CNIH4	cornichon homolog 4 (Drosophila)	-0.88	1.2E-03	5.95	4.56	7.10	2.55	
216203_at	U15555	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	-0.93	1.3E-03	3.00	2.23	5.29	3.07	
219476_at	NM_024115	C1orf116	chromosome 1 open reading frame 116	0.88	1.5E-03	2.39	1.70	4.31	2.61	
233660_at	BG540685	EHD4	EH-domain containing 4	0.95	1.5E-03	3.97	2.48	5.06	2.59	
215431_at	AI033054	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	1.07	1.6E-03	3.34	2.45	4.70	2.26	
219731_at	NM_024343	FLJ34077	weakly similar to zinc finger protein 195	-0.99	1.8E-03	5.81	4.52	7.18	2.66	
241339_at	BF437886	TTC39B	Tetratricopeptide repeat protein 39B	0.96	1.8E-03	4.59	3.45	5.74	2.29	
211368_s_at	U13700	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	-0.82	1.9E-03	6.41	4.86	7.73	2.86	
209006_s_at	AF247168	C1orf63	chromosome 1 open reading frame 63	-0.88	2.0E-03	5.89	4.66	7.63	2.97	
1559469_s_at	BC006013	SIPA1L2	signal-induced proliferation-associated 1 like 2	-0.54	2.1E-03	6.17	4.01	8.18	4.18	Y
239613_at	AA833846	TMED3	Transmembrane emp24 domain-containing protein 3 Precursor	0.83	2.2E-03	3.20	2.39	4.56	2.17	
206494_s_at	NM_000419	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	0.87	2.4E-03	3.97	2.64	5.76	3.12	
231721_at	AF356518	JAM3	junctional adhesion molecule 3	0.57	2.6E-03	4.10	2.43	6.17	3.75	Y
227461_at	AA632295	STON2	stonin 2	0.55	2.8E-03	2.49	1.44	4.47	3.03	Y
213810_s_at	AW007137	AKIRIN2	CDNA FLJ10342 fis, clone NT2RM2000837	-0.97	2.8E-03	5.88	4.85	7.36	2.51	
211366_x_at	U13698	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	-0.96	2.8E-03	7.42	6.32	8.70	2.37	
209499_x_at	BF448647	TNFSF12	tumor necrosis factor (ligand) superfamily, member 12	-0.69	2.9E-03	4.43	2.78	5.75	2.97	
228040_at	AW294192	MGC21881	hypothetical locus MGC21881	-0.73	3.0E-03	3.31	2.13	5.03	2.90	
202254_at	AB007900	SIPA1L1	KIAA0440	-0.81	3.4E-03	3.72	2.19	4.88	2.69	
239936_at	AA126428	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	-0.85	3.5E-03	3.44	1.74	4.26	2.52	

Table 2

1570165_at	BC027983	CHST11	Carbohydrate sulfotransferase 11	0.90	3.5E-03	3.09	1.94	4.44	2.50		
232030_at	AK023817	KIAA1632	KIAA1632	-0.64	3.7E-03	2.31	1.30	4.36	3.06		
209970_x_at	M87507	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	-0.80	3.7E-03	6.58	5.06	7.70	2.64		
201615_x_at	AI685060	CALD1	caldesmon 1	0.76	3.7E-03	5.11	3.82	6.65	2.83		
238979_at	BE501771	C10orf33	chromosome 10 open reading frame 33	0.86	3.7E-03	4.15	3.33	5.68	2.35		
239824_s_at	BF971873	TMEM107	transmembrane protein 107	0.81	3.7E-03	3.01	2.19	4.57	2.38		
218988_at	NM_018656	SLC35E3	solute carrier family 35, member E3	-0.70	3.9E-03	4.22	3.19	5.69	2.49		
221942_s_at	AI719730	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	0.58	3.9E-03	2.75	1.40	4.54	3.14	Y	
215739_s_at	AJ003062	TUBGCP3	tubulin, gamma complex associated protein 3	0.79	3.9E-03	3.71	1.83	4.79	2.96		
223501_at	AW151360	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	-0.60	4.0E-03	4.50	2.96	6.73	3.77		
204629_at	NM_013327	PARVB	parvin, beta	0.76	4.1E-03	3.92	2.54	5.41	2.86		
211908_x_at	M87268	IGHG1	Immunoglobulin lambda heavy chain	-0.89	4.1E-03	5.59	4.59	7.12	2.53		
1554744_at	BC033638	CARD16	caspase recruitment domain family, member 16	-0.52	4.2E-03	4.71	3.17	7.41	4.24		
202270_at	NM_002053	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	-0.37	4.3E-03	3.81	1.90	6.97	5.06	Y	
208593_x_at	NM_004382	CRHR1	corticotropin releasing hormone receptor 1	0.95	4.6E-03	3.24	2.25	4.28	2.04		
1561171_a_at	AK093450	FLJ36131	hypothetical protein FLJ36131	-0.90	4.8E-03	4.00	2.95	5.20	2.25		
244752_at	AI563915	ZNF438	zinc finger protein 438	-0.64	4.8E-03	5.10	2.46	6.79	4.32		
209651_at	BC001830	TGFB1I1	transforming growth factor beta 1 induced transcript 1	0.50	4.9E-03	1.55	0.91	5.59	4.68		
235900_at	AW016030	SPNS3	spinster homolog 3 (Drosophila)	0.84	5.0E-03	3.32	2.23	5.01	2.78		
235040_at	BG168618	RUNDC1	RUN domain containing 1	0.55	5.0E-03	3.36	2.10	4.98	2.88		
214009_at	R10150	MSL3	male-specific lethal 3 homolog (Drosophila)	-1.17	5.2E-03	4.43	3.29	5.36	2.08		
226388_at	AI675780	TCEA3	transcription elongation factor A (SII), 3	0.57	5.2E-03	4.47	2.97	6.33	3.35		
232840_at	AK025004	FNDC3B	Fibronectin type III domain-containing protein 3B	-0.82	5.8E-03	5.31	4.07	6.46	2.39		
227640_s_at	AI492167	RP9	retinitis pigmentosa 9 (autosomal dominant)	0.84	5.9E-03	4.94	3.98	6.03	2.05		
244308_at	BF514096	SYT15	Chr10 synaptotagmin (CHR10SYT gene)	-0.62	6.0E-03	2.48	1.57	5.12	3.55		
232472_at	AK022461	FNDC3B	Fibronectin type III domain-containing protein 3B	-0.63	6.0E-03	3.86	2.60	5.60	3.00		
1562458_at	AL833723	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	-0.76	6.1E-03	3.77	2.35	5.05	2.70		
224009_x_at	AF240697	DHRS9	dehydrogenase/reductase (SDR family) member 9	-0.48	6.1E-03	5.12	2.97	7.43	4.46		
228428_at	AA521285	FAM102A	CDNA FLJ37031 fis, clone BRACE2011199	1.01	6.1E-03	7.54	6.36	8.44	2.08		
202688_at	NM_003810	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	-0.54	6.2E-03	6.23	4.73	8.52	3.79		
238669_at	BE613133	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	0.68	6.3E-03	7.18	5.33	8.58	3.25		
234948_at	AK026640	SLC27A5	solute carrier family 27 (fatty acid transporter), member 5	0.91	6.4E-03	3.73	2.92	4.97	2.05		
223519_at	AW069181	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	-0.63	6.4E-03	2.33	1.24	4.28	3.04		
206361_at	NM_004778	GPR44	G protein-coupled receptor 44	0.76	6.5E-03	5.20	3.55	7.85	4.30		

Table 2

227699_at	BF511003	C14orf149	chromosome 14 open reading frame 149	-0.71	6.6E-03	3.23	2.02	4.26	2.24	
218167_at	NM_016627	AMZ2	archaelysin family metallopeptidase 2	-0.83	6.7E-03	5.02	3.11	5.93	2.82	
1562955_at	BC028181	WDFY1	WD repeat and FYVE domain-containing protein 1	-0.69	6.7E-03	3.37	2.23	4.91	2.68	
236132_at	AI870477	TLN1	talin 1	-0.72	6.7E-03	4.19	3.23	6.24	3.01	
1560867_a_at	AF085926	NEDD9	Enhancer of filamentation 1	-0.73	6.8E-03	2.33	1.69	4.88	3.19	
1557455_s_at	AF086333	MOSPD1	motile sperm domain containing 1	-0.82	6.9E-03	3.42	2.58	5.24	2.65	
201481_s_at	NM_002862	PYGB	phosphorylase, glycogen; brain	0.73	7.0E-03	4.57	3.40	6.21	2.81	
210904_s_at	U81380	IL13RA1	interleukin 13 receptor, alpha 1	-0.67	7.0E-03	7.05	5.34	8.57	3.22	
239467_at	AI806747	---	---	-0.41	7.0E-03	2.36	0.70	5.45	4.76	Y
238428_at	BG542347	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	-0.73	7.1E-03	5.53	3.82	6.92	3.10	
226459_at	AW575754	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	-0.52	7.2E-03	6.28	4.62	7.91	3.29	
1568658_at	BU069195	C2orf74	chromosome 2 open reading frame 74	0.60	7.3E-03	3.00	1.58	4.78	3.20	
201921_at	NM_004125	GNG10	guanine nucleotide binding protein (G protein), gamma 10	-0.65	7.3E-03	7.74	6.19	9.25	3.06	
211254_x_at	AF031549	RHAG	Rh-associated glycoprotein	-0.88	7.5E-03	2.50	1.70	4.32	2.62	
1555338_s_at	AF159174	AQP10	aquaporin 10	0.73	7.8E-03	3.09	1.86	5.46	3.61	
237306_at	AA447558	ZNF829	zinc finger protein 829	0.73	7.8E-03	2.07	1.33	4.11	2.78	
240934_at	AI801975	PIP5K1B	Phosphatidylinositol-4-phosphate 5-kinase type-1 beta	0.91	8.1E-03	3.51	2.16	4.93	2.77	
241603_at	BE745453	ATP11A	ATPase, class VI, type 11A	-0.79	8.2E-03	5.18	3.93	6.23	2.30	
1553697_at	NM_145257	C1orf96	chromosome 1 open reading frame 96	-0.58	8.2E-03	3.63	1.96	5.89	3.93	
1552701_a_at	NM_052889	CARD16	caspase recruitment domain family, member 16	-0.61	8.3E-03	6.99	5.50	8.51	3.01	
209686_at	BC001766	S100B	S100 calcium binding protein B	0.94	8.5E-03	2.20	1.61	4.23	2.62	
1555968_a_at	AA362254	---	---	-0.57	8.5E-03	4.11	2.54	5.51	2.97	
241834_at	AW299520	IPW	imprinted in Prader-Willi syndrome (non-protein coding)	0.58	8.8E-03	3.09	1.80	5.04	3.25	
230585_at	AI632692	---	---	-0.47	8.9E-03	3.84	1.87	5.75	3.88	
214523_at	NM_001805	CEBPE	CCAAT/enhancer binding protein (C/EBP), epsilon	0.77	8.9E-03	4.94	4.18	8.28	4.10	
218204_s_at	NM_024513	FYCO1	FYVE and coiled-coil domain containing 1	0.72	8.9E-03	3.45	2.28	4.54	2.27	
213860_x_at	AW268585	CSNK1A1	casein kinase 1, alpha 1	-0.57	9.0E-03	5.28	3.51	6.66	3.14	
213803_at	BG545463	KPNB1	Importin subunit beta-1	-0.68	9.1E-03	5.96	4.71	7.02	2.30	
217986_s_at	NM_013448	BAZ1A	bromodomain adjacent to zinc finger domain, 1A	-0.49	9.1E-03	5.42	2.67	6.94	4.27	
210093_s_at	AF067173	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)	0.71	9.4E-03	4.69	3.34	6.30	2.96	
212892_at	AW130128	ZNF282	zinc finger protein 282	0.82	9.4E-03	2.98	1.89	4.13	2.25	
240793_at	BF224054	TTN	Titin	-0.68	9.5E-03	3.86	2.91	5.08	2.16	
241812_at	AV648669	LOC26010	viral DNA polymerase-transactivated protein 6	-0.63	9.5E-03	1.48	0.88	5.30	4.42	
233587_s_at	AK022852	SIPA1L2	signal-induced proliferation-associated 1 like 2	-0.58	9.5E-03	5.36	3.64	7.70	4.06	
213988_s_at	BE971383	SAT1	spermidine/spermine N1-acetyltransferase 1	-0.79	9.6E-03	7.68	6.40	9.33	2.93	

Table 2

241599_at	AW014922	LSM11	LSM11, U7 small nuclear RNA associated	0.88	9.8E-03	2.89	1.81	4.14	2.33	
241368_at	AI190693	LSDP5	lipid storage droplet protein 5	-0.69	9.9E-03	4.32	2.86	5.77	2.91	
200032_s_at	NM_000661	RPL9	ribosomal protein L9							Y
202948_at	NM_000877	IL1R1	interleukin 1 receptor, type I							Y
212512_s_at	AA551784	CARM1	coactivator-associated arginine methyltransferase 1							Y
225453_x_at	BE733510	CCDC124	Full length insert cDNA clone ZD51E04							Y
230393_at	BF448201	CUL5	cullin 5							Y
238364_x_at	BG231548	GLI4	GLI-Kruppel family member GLI4 (GLI4), mRNA							Y
239866_at	AA705933	---	---							Y

Table 3

probeset	Accession	gene.symb	gene.title	co-efficient	raw. p.value	exp. median	exp. min	exp. max	exp. diff
239714_at	AA780063	PIP5K1B	Phosphatidylinositol-4-phosphate 5-kinase type-1 beta	-1.57	6.9E-05	3.41	2.55	4.80	2.25
1558938_a	BC043574	---	---	1.06	3.6E-04	4.45	3.09	5.77	2.68
214364_at	W84525	MTERFD2	MTERF domain containing 2	-1.35	4.6E-04	3.30	2.00	4.62	2.61
240934_at	AI801975	PIP5K1B	Phosphatidylinositol-4-phosphate 5-kinase type-1 beta	-1.51	5.7E-04	3.51	2.16	4.93	2.77
240980_at	R61819	---	---	1.32	7.1E-04	2.22	1.58	4.29	2.71
243187_at	AA888821	PVRL2	Poliovirus receptor-related protein 2 Precursor	1.02	1.1E-03	2.25	1.48	4.09	2.61
225831_at	AW016830	LUZP1	leucine zipper protein 1	-2.06	1.1E-03	4.16	3.58	6.99	3.41
234618_at	AL049434	PHTF1	Putative homeodomain transcription factor 1	1.02	1.2E-03	2.54	1.79	4.40	2.61
232079_s_	BE867789	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	0.52	1.5E-03	3.15	2.33	6.76	4.42
231886_at	AL137655	DKFZP434	similar to hypothetical protein LOC284701	0.62	2.0E-03	4.49	2.87	6.21	3.33
1562743_a	BC042873	ZNF33B	Zinc finger protein 33B (ZNF33B), mRNA	-1.14	2.0E-03	3.62	2.32	4.74	2.42
242109_at	AI038577	SYTL3	CDNA FLJ61334 complete cds, moderately similar to Synaptotagmin-like protein 3	1.10	2.2E-03	2.83	1.90	4.43	2.53
239274_at	AV729557	PICALM	Phosphatidylinositol-binding clathrin assembly protein	1.08	2.4E-03	6.10	5.00	7.13	2.13
212811_x_	AI889380	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	0.99	2.4E-03	3.91	2.59	4.86	2.27
229643_at	AI857933	ITGA6	Integrin alpha 6B [human, mRNA Partial, 528 nt]	-1.02	2.5E-03	3.75	2.86	5.20	2.34
235971_at	AI147211	---	---	0.88	2.5E-03	3.59	2.63	5.66	3.04
210113_s_	AF310105	NLRP1	NLR family, pyrin domain containing 1	-1.18	2.8E-03	5.50	4.01	6.55	2.54
216145_at	AL137713	---	---	-1.28	2.9E-03	2.81	2.20	4.25	2.05
206494_s_	NM_000419	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	-0.89	3.0E-03	3.97	2.64	5.76	3.12
240671_at	H38635	GYPC	Glycophorin-C	-0.92	3.0E-03	3.54	2.49	5.20	2.71
231721_at	AF356518	JAM3	junctional adhesion molecule 3	-0.58	3.2E-03	4.10	2.43	6.17	3.75
217876_at	NM_012087	GTF3C5	general transcription factor IIIC, polypeptide 5, 63kDa	-1.13	3.3E-03	4.24	3.18	5.23	2.05
217179_x_	X79782	---	---	0.87	3.3E-03	4.56	3.83	6.66	2.83
225685_at	AI801777	---	---	0.97	3.7E-03	6.32	5.29	7.46	2.17
219348_at	NM_018467	USE1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	-1.30	3.7E-03	6.10	5.30	8.00	2.70
243106_at	AA916861	CLEC12A	C-type lectin protein CLL-1	0.30	3.7E-03	3.93	1.90	7.11	5.22
209589_s_	AF025304	EPHB2	EPH receptor B2	-0.79	3.8E-03	3.37	2.11	5.25	3.15
209006_s_	AF247168	C1orf63	chromosome 1 open reading frame 63	1.03	4.0E-03	5.89	4.66	7.63	2.97
238080_at	BF195052	B4GALNT4	beta-1,4-N-acetyl-galactosaminyl transferase 4	-1.04	4.3E-03	3.13	2.28	4.47	2.19
1564443_a	AF529010	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	0.75	4.3E-03	4.55	3.00	6.47	3.47

Table 3

1568706_s	AF318328	AVIL	Advillin, mRNA (cDNA clone MGC:133244 IMAGE:40035028)	0.88	4.5E-03	5.08	3.85	6.02	2.16
238987_at	AL574435	B4GALT1	Clone p4betaGT/3 beta-1,4-galactosyltransferase	0.93	4.5E-03	3.24	1.82	4.52	2.70
216956_s_	AF098114	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	-0.60	4.5E-03	4.45	2.94	6.40	3.46
231057_at	AU144266	MTMR2	Myotubularin-related protein 2	1.14	4.7E-03	2.91	2.07	4.22	2.15
234948_at	AK026640	SLC27A5	solute carrier family 27 (fatty acid transporter), member 5	-1.12	4.7E-03	3.73	2.92	4.97	2.05
228040_at	AW294192	MGC2188	hypothetical locus MGC21881	0.89	4.8E-03	3.31	2.13	5.03	2.90
202874_s_	NM_001695	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	0.81	5.0E-03	5.48	4.00	6.98	2.98
234047_at	AK024127	---	---	1.06	5.6E-03	3.83	2.96	4.98	2.02
231174_s_	H92979	---	---	1.06	5.8E-03	2.00	1.11	4.39	3.28
212592_at	AV733266	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	0.31	6.0E-03	3.38	1.38	8.41	7.03
218618_s_	NM_022763	FNDC3B	fibronectin type III domain containing 3B	0.75	6.2E-03	5.19	3.78	6.54	2.76
1552703_s	NM_052889	CARD16	caspase recruitment domain family, member 16	0.97	6.2E-03	8.38	7.16	9.60	2.44
236458_at	BE875072	---	---	-1.06	6.2E-03	2.07	1.33	4.02	2.69
202948_at	NM_000877	IL1R1	interleukin 1 receptor, type I	0.43	6.3E-03	3.44	1.49	5.81	4.33
1562137_a	AF147388	ADAM10	Disintegrin and metalloproteinase domain-containing protein 10 Precursor	0.96	6.4E-03	3.57	2.05	4.72	2.67
1552398_a	NM_138337	CLEC12A	C-type lectin domain family 12, member A	0.31	6.4E-03	5.84	4.09	8.70	4.61
222692_s_	BF444916	FNDC3B	fibronectin type III domain containing 3B	0.90	6.6E-03	5.33	4.36	6.62	2.26
203129_s_	BF059313	KIF5C	kinesin family member 5C	-0.92	7.2E-03	4.77	3.49	5.99	2.50
1555281_x	BC007934	ARMC8	armadillo repeat containing 8	-0.88	7.4E-03	5.82	4.00	6.87	2.88
229180_at	AI685931	WWC1	KIBRA protein (KIBRA)	-1.34	7.5E-03	3.00	2.24	4.54	2.31
207500_at	NM_004347	CASP5	caspase 5, apoptosis-related cysteine peptidase	0.70	7.5E-03	3.89	2.30	6.14	3.85
232963_at	BF725688	RFWD2	ring finger and WD repeat domain 2	0.82	7.5E-03	4.55	3.54	5.93	2.39
233504_at	AA629020	C9orf84	chromosome 9 open reading frame 84	0.70	7.6E-03	5.06	3.39	6.48	3.09
222693_at	BF444916	FNDC3B	fibronectin type III domain containing 3B	0.60	7.6E-03	3.94	2.88	5.73	2.85
222411_s_	AW087870	SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	0.86	8.0E-03	5.55	4.42	6.82	2.40
211368_s_	U13700	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	0.79	8.0E-03	6.41	4.86	7.73	2.86
232472_at	AK022461	FNDC3B	Fibronectin type III domain-containing protein 3B	0.63	8.1E-03	3.86	2.60	5.60	3.00
218435_at	NM_013238	DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15	0.64	8.3E-03	5.15	3.55	6.54	2.99
215093_at	U82671	NSDHL	NAD(P) dependent steroid dehydrogenase-like	0.54	8.3E-03	3.50	1.82	6.28	4.46
209091_s_	AF263293	SH3GLB1	SH3-domain GRB2-like endophilin B1	1.02	8.3E-03	7.39	6.50	8.58	2.08

Table 3

238589_s_	AW601184	ATXN2	Ataxin-2	0.71	8.3E-03	4.82	3.32	6.35	3.03
1558011_a	BM823647	---	---	0.64	8.4E-03	6.95	5.39	8.67	3.28
205877_s_	NM_017590	ZC3H7B	zinc finger CCCH-type containing 7B	-1.06	8.4E-03	4.80	3.36	5.74	2.38
239603_x_	AI082479	FBXO11	F-box only protein 11	0.91	8.6E-03	5.78	4.81	8.59	3.78
214594_x_	BG252666	ATP8B1	ATPase, class I, type 8B, member 1	0.81	8.6E-03	6.40	4.97	7.27	2.30
206267_s_	NM_002378	MATK	megakaryocyte-associated tyrosine kinase	-0.87	8.8E-03	3.65	2.62	4.63	2.01
209970_x_	M87507	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	0.80	8.9E-03	6.58	5.06	7.70	2.64
232078_at	BE867789	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	0.40	9.0E-03	2.53	1.29	6.24	4.95
228718_at	AI379070	ZNF44	zinc finger protein 44	-0.94	9.0E-03	3.32	2.63	5.23	2.60
232417_x_	AU150300	ZDHHC11	zinc finger, DHHC-type containing 11	-1.17	9.1E-03	4.70	3.97	5.99	2.02
224917_at	BF674052	MIR21	microRNA 21	0.74	9.1E-03	6.66	5.36	8.32	2.96
239124_at	AA002064	PITPNA	Phosphatidylinositol transfer protein alpha isoform	0.83	9.1E-03	3.23	1.98	4.50	2.52
219476_at	NM_024115	C1orf116	chromosome 1 open reading frame 116	-0.91	9.2E-03	2.39	1.70	4.31	2.61
218415_at	NM_018668	VPS33B	vacuolar protein sorting 33 homolog B (yeast)	-0.67	9.4E-03	4.31	2.31	5.85	3.55
219700_at	NM_020405	PLXDC1	plexin domain containing 1	-0.65	9.4E-03	4.36	2.52	5.65	3.13
243980_at	AW978739	ZNF594	MRNA; cDNA DKFZp667J055 (from clone DKFZp667J055)	-0.96	9.4E-03	3.31	1.93	4.40	2.47
1554482_a	BC002847	SAR1B	SAR1 homolog B (S. cerevisiae)	0.66	9.5E-03	4.05	2.56	5.37	2.81
215191_at	AW836210	FBXL11	Lysine-specific demethylase 2A	0.56	9.7E-03	3.39	1.96	5.14	3.18
211366_x_	U13698	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	0.93	9.9E-03	7.42	6.32	8.70	2.37
244308_at	BF514096	SYT15	Chr10 synaptotagmin (CHR10SYT gene)	0.73	9.9E-03	2.48	1.57	5.12	3.55
210219_at	U36501	SP100	SP100 nuclear antigen	0.64	1.0E-02	1.67	1.10	6.37	5.28

Table 5a

N1:54630	ID	ACR111 Dn3	ACR62 Dn3	EULAR111 Dn3	EULAR 45Dn3	DAS28wk 16_110Dn3	DAS28wk1 6_70Dn3	cDAS28_11 0Dn3	cDAS28_80 Dn3	Average Score	Gene Symbol	Accession Number
91	200053_at	0	0	45	0	0	0	0	0	7	SPAG7	NM_004890
145	200600_at	0	0	94	84	0	0	0	0	3	MSN	NM_002444
210	200665_s_at	0	0	41	0	0	0	0	0	7,5	SPARC	NM_003118
495	200950_at	0	81	0	0	0	0	0	0	2,5	ARPC1A	NM_006409
523	200978_at	0	56	0	0	0	0	0	0	5,625	MDH1	NM_005917
617	201072_s_at	0	83	0	0	0	0	0	0	2,25	SMARCC1	AW152160
670	201125_s_at	0	0	19	33	0	0	0	0	18,75	ITGB5	NM_002213
708	201163_s_at	0	0	0	0	0	0	0	79	2,75	IGFBP7	NM_001553
771	201226_at	0	33	0	0	0	0	0	0	8,5	NDUFB8 /// SEC31B	NM_005004
846	201301_s_at	0	0	0	0	85	0	0	0	2	ANXA4	BC000182
915	201370_s_at	0	0	0	0	0	0	0	30	8,875	CUL3	AU145232
931	201386_s_at	0	0	0	0	0	0	15	0	10,75	DHX15	AF279891
962	201417_at	0	0	0	0	0	0	47	0	6,75	SOX4	AL136179
1005	201460_at	26	0	0	0	0	0	0	0	9,375	MAPKAPK2	AI141802
1007	201462_at	56	0	0	0	0	0	0	0	5,625	SCRN1	NM_014766
1013	201468_s_at	0	0	0	86	0	0	0	0	1,875	NQO1	NM_000903
1056	201511_at	0	0	0	0	0	0	21	0	10	AAMP	NM_001087
1081	201536_at	0	0	0	0	0	43	0	0	7,25	DUSP3	AL048503
1226	201681_s_at	0	0	93	97	0	0	0	0	1,5	DLG5	AB011155
1429	201884_at	0	0	0	73	0	0	0	0	3,5	CEACAM5	NM_004363
1450	201905_s_at	0	0	0	0	0	0	0	98	0,375	CTDSPL	BF590317
1456	201911_s_at	0	0	0	0	0	78	0	0	2,875	FARP1	NM_005766
1519	201974_s_at	0	71	0	0	0	0	0	0	3,75	C7orf28A	NM_015622
1528	201983_s_at	0	0	0	0	0	0	23	78	12,625	EGFR	AW157070
1581	202036_s_at	0	53	0	0	0	0	0	0	6	SFRP1	AF017987
1686	202141_s_at	0	0	0	0	0	0	50	0	6,375	COPS8	BC003090
1869	202324_s_at	0	0	0	0	0	0	65	0	4,5	ACBD3	NM_022735
1910	202365_at	48	0	0	0	0	0	0	0	6,625	UNC119B	BC004815
2062	202517_at	97	0	0	0	0	0	0	0	0,5	CRMP1	NM_001313
2124	202579_x_at	0	0	28	0	0	0	0	0	9,125	HMGN4	NM_006353
2235	202690_s_at	0	0	0	0	0	37	0	0	8	SNRPD1	BC001721
2327	202782_s_at	0	0	91	0	0	0	0	0	1,25	INPP5K	NM_016532
2411	202866_at	0	0	27	26	0	0	0	0	18,625	DNAJB12	BG283782
2614	203068_at	9	0	0	0	0	0	0	0	11,5	KLHL21	NM_014851
2717	203172_at	0	0	0	0	0	47	0	0	6,75	FXR2	NM_004860
2767	203222_s_at	0	0	0	0	0	0	86	0	1,875	TLE1	NM_005077

Table 5a

2815	203271_s_at	95	0	0	0	0	0	0	0	0,75	UNC119	NM_005148
2823	203279_at	0	27	0	0	0	0	0	0	9,25	EDEM1	NM_014674
2837	203293_s_at	0	0	16	99	0	0	0	0	10,875	LMAN1	NM_005570
2997	203453_at	0	0	0	0	100	0	0	0	0,125	SCNN1A	NM_001038
3131	203587_at	0	0	0	58	0	0	0	0	5,375	ARL4D	U25771
3435	203891_s_at	0	0	49	94	0	0	0	0	7,375	DAPK3	NM_001348
3446	203902_at	0	0	0	0	30	0	0	0	8,875	HEPH	AU148222
3455	203911_at	0	0	0	0	0	0	35	8,25	RAP1GAP	NM_002885	
3511	203967_at	0	0	0	0	49	0	0	6,5	CDC6	U77949	
3585	204041_at	0	0	87	31	0	0	0	10,5	MAOB	NM_000898	
3661	204117_at	0	67	0	0	0	0	0	4,25	PREP	NM_002726	
3937	204393_s_at	0	68	0	0	0	0	0	4,125	ACPP	NM_001099	
3942	204398_s_at	0	0	26	0	0	0	0	9,375	EML2	NM_012155	
3966	204422_s_at	0	0	0	0	0	0	0	3,125	FGF2	NM_002006	
3982	204438_at	0	63	0	0	0	0	0	4,75	MRC1 /// MRC1L1	NM_002438	
4000	204456_s_at	0	0	0	0	0	0	34	8,375	GAS1	AW611727	
4171	204627_s_at	0	0	39	65	0	0	0	12,25	ITGB3	M35999	
4316	204772_s_at	0	0	0	0	6	81	0	14,375	TTF1	NM_007344	
4346	204802_at	0	0	0	0	0	41	0	7,5	RRAD	NM_004165	
4493	204949_at	0	0	17	0	0	0	0	10,5	ICAM3	NM_002162	
4497	204953_at	77	61	0	0	0	0	0	8	SNAP91	NM_014841	
4506	204962_s_at	0	0	24	77	0	0	0	12,625	CENPA	NM_001809	
4528	204984_at	0	15	0	0	0	0	0	10,75	GPC4	NM_001448	
4805	205261_at	0	32	0	0	0	34	0	17	PGC	NM_002630	
4825	205281_s_at	0	0	0	0	79	0	39	8	22,125	PIGA	NM_002641
4838	205294_at	0	0	0	0	0	77	0	0	3	BAIAP2	NM_017450
4976	205432_at	0	0	0	0	0	90	0	0	1,375	OVGP1	NM_002557
5175	205631_at	0	0	0	8	0	0	85	27	22,875	KIAA0586	NM_014749
5405	205861_at	0	0	0	0	0	91	0	0	1,25	SPIB	NM_003121
5414	205870_at	0	0	0	60	0	0	0	0	5,125	BDKRB2	NM_000623
5536	205992_s_at	0	0	0	0	0	0	0	43	7,25	IL15	NM_000585
5622	206079_at	64	0	0	0	0	0	0	0	4,625	CHML	NM_001821
5689	206146_s_at	0	0	0	82	0	0	0	0	2,375	RHAG	AF178841
5868	206325_at	0	0	0	0	62	0	0	0	4,875	SERPINA6	NM_001756
5970	206427_s_at	0	0	0	0	0	0	0	99	0,25	MLANA	U06654
6036	206493_at	0	0	14	38	0	0	0	0	18,75	ITGA2B	NM_000419
6046	206503_x_at	99	0	0	0	0	0	0	0	0,25	PML	NM_002675
6104	206561_s_at	0	0	0	0	0	0	77	0	3	AKR1B10	NM_020299
6116	206573_at	98	0	0	0	0	0	0	0	0,375	KCNQ3	NM_004519

Table 5a

6152	206609_at	0	0	0	0	5	0	0	0	12	MAGEC1	NM_005462
6177	206634_at	0	48	0	0	95	0	0	0	7,375	SIX3	NM_005413
6178	206635_at	0	0	0	0	0	0	0	100	0,125	CHRNB2	NM_000748
6254	206711_at	0	0	0	0	57	0	0	0	5,5	CXorf1	NM_004709
6273	206730_at	32	55	0	0	18	0	0	0	24,75	GRIA3	NM_007325
6341	206798_x_at	0	0	0	0	0	11	0	0	11,25	DLEC1	NM_005106
6495	206952_at	0	0	0	4	0	0	0	0	12,125	G6PC	NM_000151
6637	207094_at	80	0	0	0	0	0	0	0	2,625	IL8RA	NM_000634
6639	207096_at	0	0	0	0	83	26	0	0	11,625	SAA4	NM_006512
6777	207235_s_at	0	0	0	0	4	0	0	0	12,125	GRM5	NM_000842
6869	207328_at	0	72	0	0	0	0	0	0	3,625	ALOX15	NM_001140
6905	207365_x_at	83	0	0	0	0	0	0	0	2,25	USP34	NM_014709
6968	207429_at	0	46	0	0	0	57	0	0	12,375	SLC22A2	NM_003058
7108	207570_at	0	0	32	74	0	0	0	0	12	SHOX	NM_000451
7136	207598_x_at	60	0	0	0	0	0	0	0	5,125	XRCC2	NM_005431
7201	207663_x_at	0	0	0	0	0	97	0	0	0,5	GAGE3	NM_001473
7231	207693_at	0	0	0	78	0	0	0	0	2,875	CACNB4	NM_000726
7268	207730_x_at	53	0	0	0	0	0	0	0	6	---	NM_017932
7353	207817_at	0	0	0	0	0	0	76	49	9,625	IFNW1	NM_002177
7400	207864_at	46	0	0	0	0	0	0	0	6,875	SCN7A	NM_002976
7545	208019_at	0	0	0	0	82	0	0	0	2,375	ZNF157	NM_003446
7634	208108_s_at	0	0	0	0	0	0	4	42	19,5	AVPR2	AF030626
7709	208186_s_at	0	0	0	0	0	0	0	86	1,875	LIPE	NM_005357
7731	208209_s_at	0	0	0	23	0	0	0	0	9,75	C4BPB	NM_000716
7749	208227_x_at	86	0	0	0	0	0	0	0	1,875	ADAM22	NM_021721
7812	208291_s_at	0	0	0	0	0	68	0	0	4,125	TH	NM_000360
7901	208383_s_at	0	0	0	0	0	0	0	85	2	PCK1	NM_002591
7991	208476_s_at	0	0	0	0	0	0	0	70	3,875	FRMD4A	NM_018027
8286	208774_at	71	0	0	0	0	0	0	0	3,75	CSNK1D	AV700224
8401	208889_s_at	0	0	0	0	0	72	0	0	3,625	NCOR2	AI373205
8631	209120_at	0	0	79	0	0	0	0	0	2,75	NR2F2	AL037401
8799	209288_s_at	0	0	0	0	0	0	37	0	8	CDC42EP3	AL136842
8874	209364_at	0	0	0	0	88	0	0	0	1,625	BAD	U66879
9068	209559_at	0	0	0	0	0	0	72	69	7,625	HIP1R	AB013384
9157	209651_at	0	0	0	0	0	0	0	55	5,75	TGFB1I1	BC001830
9240	209735_at	0	0	0	80	0	0	0	0	2,625	ABCG2	AF098951
9296	209791_at	0	0	2	0	0	0	0	0	12,375	PADI2	AL049569
9337	209834_at	0	0	0	0	55	0	0	0	5,75	CHST3	AB017915
9362	209859_at	0	0	0	92	0	0	0	0	1,125	TRIM9	AF220036
9525	210023_s_at	66	0	0	0	0	0	0	0	4,375	PCGF1	BC004952

Table 5a

9541	210039_s_at	0	22	0	0	0	19	0	0	20,125	PRKCQ	L01087
9596	210095_s_at	0	0	0	0	0	85	0	0	2	IGFBP3	M31159
9633	210132_at	0	0	0	0	0	0	69	88	5,625	EFNA3	AW189015
9696	210195_s_at	0	28	0	0	0	0	0	0	9,125	PSG1	M34715
9728	210230_at	85	0	0	0	0	0	0	0	2	---	BC003629
9742	210245_at	0	75	0	0	0	0	0	0	3,25	ABCC8	L78207
9766	210269_s_at	0	0	0	0	0	0	53	0	6	SFRS17A	M99578
9826	210330_at	0	0	0	0	71	42	0	0	11,125	SGCD	U58331
9915	210420_at	40	8	0	0	52	10	0	0	36,75	SLC24A1	AB014602
10007	210520_at	0	0	0	59	0	0	0	0	5,25	FETUB	AB017551
10093	210611_s_at	16	39	0	0	0	0	0	0	18,375	DTNA	U26744
10143	210661_at	0	0	0	0	0	62	0	0	4,875	GLRA3	U93917
10447	210983_s_at	0	0	1	1	0	0	0	0	25	MCM7	AF279900
10489	211026_s_at	0	0	0	0	0	0	36	3	20,375	MGLL	BC006230
10757	211320_s_at	0	0	0	0	0	0	31	0	8,75	PTPRU	U71075
10773	211338_at	0	0	0	0	41	0	0	0	7,5	IFNA2	M54886
10797	211364_at	0	0	0	0	70	0	0	0	3,875	MTAP	AF109294
10884	211458_s_at	0	0	0	63	0	0	0	0	4,75	GABARAPL1 /// GABARAPL3	AF180519
10893	211467_s_at	0	5	0	0	0	0	0	0	12	NFIB	U70862
10895	211469_s_at	0	43	0	0	0	0	0	0	7,25	CXCR6	U73531
10992	211570_s_at	0	0	0	0	0	0	0	75	3,25	RAPSN	BC004196
11058	211637_x_at	0	0	97	0	0	0	0	0	0,5	IGH@ /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHG4 /// IGHM /// IGHV3-23 /// IGHV4-31 /// LOC100126583 /// LOC642131 /// LOC652128 /// VSIG6	0

Table 5a

11061	211640_x_at	0	0	51	39	0	0	0	0	14	IGHA1 /// IGHG1 /// LOC1001338 62	L23519
11240	211827_s_at	0	0	0	0	3	0	0	0	12,25	KCND3	AF187964
11328	211923_s_at	57	10	0	0	2	2	0	0	41,625	ZNF471	AF352026
11495	212092_at	0	0	0	82	0	0	0	0	2,375	PEG10	BE858180
11500	212097_at	0	34	0	0	0	32	0	37	25	CAV1	AU147399
11645	212242_at	0	0	37	0	0	0	0	0	8	TUBA4A	AL565074
11867	212465_at	0	0	0	46	0	0	0	0	6,875	SETD3	AA524500
11918	212516_at	0	0	38	0	0	0	0	0	7,875	ARAP1	AB018325
11930	212528_at	0	0	0	0	73	0	0	0	3,5	---	AI348009
12160	212758_s_at	20	0	0	44	31	0	0	0	26	ZEB1	AI373166
12199	212797_at	0	58	0	0	0	0	0	0	5,375	SORT1	BE742268
12294	212892_at	0	0	0	0	0	0	0	72	3,625	ZNF282	AW130128
12391	212991_at	0	90	0	0	0	0	0	0	1,375	FBXO9	AL137520
12680	213282_at	0	0	0	0	0	0	1	4	24,625	APOOL	BE501952
12698	213300_at	0	0	83	0	0	0	0	0	2,25	ATG2A	AW168132
12721	213323_s_at	0	0	0	0	17	0	0	0	10,5	ZC3H7B	BE855831
12750	213352_at	62	0	0	0	0	0	0	0	4,875	TMCC1	AB018322
12820	213422_s_at	0	0	6	21	0	0	0	0	21,875	MXRA8	AW888223
13420	214024_s_at	0	74	0	0	0	0	0	0	3,375	DGCR6L	AA631156
13433	214037_s_at	0	0	25	52	0	0	0	0	15,625	CCDC22	BF224247
13576	214180_at	0	0	0	13	0	0	0	0	11	MAN1C1	AW340588
13717	214321_at	47	0	0	0	36	0	0	0	14,875	NOV	BF440025
13806	214410_at	0	0	0	0	0	0	0	90	1,375	TRPM1	N32151
13834	214438_at	0	0	48	0	0	0	0	0	6,625	HLX	M60721
13970	214575_s_at	3	0	0	0	0	0	0	0	12,25	AZU1	NM_001700
14067	214674_at	0	0	0	0	97	17	0	0	11	USP19	AW451502
14135	214742_at	0	0	0	0	0	0	11	29	20,25	AZI1	AB029041
14159	214766_s_at	92	0	0	0	37	0	0	0	9,125	AHCTF1	AL080144
14162	214769_at	0	0	54	72	0	0	0	0	9,5	CLCN4	AF052117
14170	214777_at	0	0	61	0	0	0	0	0	5	IGKV4-1	BG482805
14213	214821_at	0	0	0	0	0	0	10	0	11,375	---	AF052119
14276	214884_at	0	0	0	0	0	0	44	0	7,125	MCF2	AL033403
14290	214898_x_at	0	0	0	0	27	0	0	0	9,25	MUC3B	AB038783
14350	214958_s_at	0	1	0	0	65	23	0	0	26,75	TMC6	AK021738
14398	215006_at	94	0	0	0	0	0	0	0	0,875	---	AK023816
14407	215016_x_at	0	14	0	0	0	0	0	0	10,875	DST	BC004912
14446	215055_at	0	0	0	0	0	0	82	5	14,375	B3GNTL1	U79265

Table 5a

14581	215190_at	0	0	0	0	0	48	0	0	6,625	EIF3M	AV717062
14642	215251_at	0	0	0	0	0	0	7	0	11,75	---	AA595276
14913	215523_at	73	0	0	0	0	0	0	0	3,5	ZNF391	AL031118
14980	215590_x_at	0	0	0	0	44	0	0	0	7,125	LOC100128640	AK025619
14994	215604_x_at	18	0	0	0	0	0	0	0	10,375	---	AK023783
15045	215655_at	0	0	0	0	0	60	0	0	5,125	GRIK2	AU156204
15099	215709_at	100	0	0	0	0	0	0	0	0,125	LOC100134355 /// PRIM2	AL121975
15122	215732_s_at	0	0	80	66	0	0	0	0	7	DTX2 /// LOC100134197	AK023924
15127	215737_x_at	0	0	46	0	0	0	0	0	6,875	USF2	X90824
15233	215843_s_at	49	0	0	0	21	0	0	0	16,5	TLL2	AK026106
15309	215919_s_at	0	0	0	0	0	0	56	18	16	MRPS11	BC000200
15525	216136_at	0	0	0	0	0	65	0	0	4,5	---	AF113683
15612	216223_at	0	26	0	0	0	0	0	0	9,375	CPN2	J05158
15618	216229_x_at	19	0	0	0	0	0	0	0	10,25	HCG2P7	X81001
15818	216430_x_at	0	0	52	0	0	0	0	0	6,125	IGL@	AF043586
15871	216483_s_at	0	0	90	19	0	0	0	0	11,625	C19orf10	AC005339
15953	216566_at	0	0	11	29	0	0	0	0	20,25	---	D84140
16315	216928_at	0	0	0	0	0	0	74	0	3,375	TAL1	X51990
16393	217006_x_at	0	0	0	55	0	0	0	0	5,75	FASN	U52428
16398	217011_at	0	89	0	0	11	20	0	0	22,875	GBX1	L11239
16421	217034_at	0	0	99	79	0	0	0	0	3	NTN3	AF103529
16510	217126_at	63	42	0	0	0	7	0	0	23,875	---	K00627
16521	217137_x_at	0	0	22	6	0	0	0	0	21,75	---	K00627
16547	217163_at	0	0	0	0	0	0	38	0	7,875	ESR1	X63118
16560	217176_s_at	28	0	0	0	0	0	0	0	9,125	ZFX	X59740
16584	217200_x_at	0	0	0	0	0	0	45	0	7	CYB561	U06715
16606	217222_at	0	0	65	0	0	0	0	0	4,5	LOC642131	S74639
16673	217291_at	0	0	0	0	0	0	13	0	11	CEACAM5	Z21818
16686	217304_at	0	0	0	0	0	0	0	13	11	SHMT1	Y14488
16863	217481_x_at	0	0	85	0	0	0	0	0	2	---	AL110201
16865	217483_at	0	0	0	0	7	0	0	0	11,75	FOLH1	AF254357
16922	217540_at	0	0	0	0	9	1	0	0	24	FAM55C	AA721025
16961	217579_x_at	0	0	0	96	0	0	0	0	0,625	---	AW301806
17051	217669_s_at	69	0	0	0	0	0	0	0	4	AKAP6	AW451230
17091	217709_at	0	0	0	0	0	0	42	0	7,375	---	AV647366

Table 5a

17248	217866_at	34	0	0	0	0	0	0	0	8,375	CPSF7	NM_024811
17294	217912_at	65	78	0	0	0	0	0	0	7,375	DUS1L	NM_022156
17514	218132_s_at	29	0	0	0	0	0	0	0	9	TSEN34	NM_024075
17526	218144_s_at	0	0	0	0	0	0	0	82	2,375	INF2	NM_022489
17680	218298_s_at	0	0	0	0	0	0	92	0	1,125	C14orf159	NM_024952
17736	218354_at	0	0	0	53	0	0	0	0	6	TRAPPC2L	NM_016209
17757	218375_at	0	0	0	0	0	25	0	0	9,5	NUDT9	NM_024047
17785	218403_at	0	0	0	0	0	0	99	0	0,25	TRIAP1	NM_016399
17803	218421_at	12	0	0	0	0	0	0	0	11,125	CERK	NM_022766
17821	218439_s_at	0	0	0	0	96	0	0	0	0,625	COMMD10	NM_016144
17943	218561_s_at	0	3	0	0	0	0	0	0	12,25	LYRM4	NM_020408
17955	218573_at	0	0	0	0	0	0	91	0	1,25	MAGEH1	NM_014061
17959	218577_at	0	0	0	0	0	0	9	12	22,625	LRRC40	NM_017768
18051	218670_at	0	0	21	49	0	0	0	0	16,5	PUS1	NM_025215
18066	218685_s_at	0	0	0	0	0	0	28	93	10,125	SMUG1	NM_014311
18074	218693_at	0	0	0	0	35	0	0	0	8,25	TSPAN15	NM_012339
18196	218815_s_at	0	0	0	0	61	0	0	0	5	TMEM51	NM_018022
18263	218882_s_at	0	0	0	0	0	0	75	0	3,25	WDR3	NM_006784
18295	218914_at	0	80	0	0	0	0	0	0	2,625	C1orf66	NM_015997
18325	218944_at	0	0	0	0	81	0	0	0	2,5	PYCRL	NM_023078
18344	218963_s_at	0	0	0	37	0	0	0	0	8	KRT23	NM_015515
18474	219093_at	0	0	0	0	0	0	3	9	23,75	PID1	NM_017933
18663	219282_s_at	0	0	0	61	0	0	0	0	5	TRPV2	NM_015930
18692	219311_at	0	0	0	0	62	0	0	0	4,875	CEP76	NM_024899
18790	219409_at	0	9	0	0	0	0	0	0	11,5	SNIP1	NM_024700
18870	219489_s_at	0	0	0	0	0	0	0	54	5,875	NXN	NM_017821
18930	219549_s_at	0	0	70	0	0	0	0	0	3,875	RTN3	NM_006054
18946	219565_at	0	0	0	0	0	0	73	0	3,5	CYP20A1	NM_020674
19008	219627_at	82	0	0	0	0	0	0	0	2,375	ZNF767	NM_024910
19024	219643_at	0	0	0	0	0	0	6	51	18,125	LRP1B	NM_018557
19452	220071_x_at	21	0	0	0	0	0	0	0	10	HAUS2	NM_018097
19474	220093_at	0	0	73	0	0	0	0	0	3,5	ANTXR1	NM_018153
19680	220299_at	0	0	0	0	0	0	14	0	10,875	SPATA6	NM_019073
19733	220352_x_at	23	0	0	0	0	0	0	0	9,75	FLJ42627	NM_024305
19837	220456_at	0	0	0	54	0	0	0	0	5,875	SPTLC3	NM_018327
19887	220506_at	0	0	0	0	0	0	49	0	6,5	GUCY1B2	NM_004129
19973	220592_at	0	98	0	0	0	0	0	0	0,375	CCDC40	NM_017950
20125	220744_s_at	0	0	0	0	0	0	0	50	6,375	IFT122	NM_018262
20192	220811_at	0	0	0	0	0	52	0	0	6,125	PRG3	NM_006093
20209	220828_s_at	0	0	0	98	0	0	0	0	0,375	FLJ11292	NM_018382

Table 5a

20214	220833_at	93	0	0	0	0	0	0	0	1	---	NM_016241
20220	220839_at	0	0	0	0	75	0	0	0	3,25	METTL5	NM_014168
20258	220877_at	36	0	0	0	0	0	0	0	8,125	---	NM_018580
20390	221009_s_at	0	0	0	0	0	51	0	0	6,25	ANGPTL4	NM_016109
20401	221020_s_at	0	31	0	0	0	0	0	0	8,75	SLC25A32	NM_030780
20424	221043_at	0	0	81	0	0	0	0	0	2,5	---	NM_013395
20512	221132_at	0	0	0	0	0	0	40	0	7,625	CLDN18	NM_016369
20547	221167_s_at	0	0	0	0	53	0	0	0	6	CCDC70	NM_031290
20549	221169_s_at	0	44	0	0	0	0	0	0	7,125	HRH4	NM_021624
20690	221310_at	0	0	0	0	26	0	0	0	9,375	FGF14	NM_004115
20752	221372_s_at	0	0	29	18	0	0	0	0	19,375	P2RX2	NM_012226
20788	221408_x_at	0	0	0	0	0	86	0	0	1,875	PCDHB12	NM_018932
20816	221436_s_at	0	0	0	0	19	0	0	0	10,25	CDCA3	NM_031299
20956	221577_x_at	0	0	0	0	43	0	0	0	7,25	GDF15	AF003934
21196	221819_at	0	0	47	0	0	0	0	0	6,75	RAB35	BF791960
21238	221861_at	0	0	7	7	0	0	0	0	23,5	---	AL157484
21263	221886_at	0	0	0	0	0	0	0	26	9,375	DENND2A	AL037701
21281	221904_at	67	0	0	0	0	0	0	0	4,25	FAM131A	AI141670
21648	222272_x_at	90	0	0	0	0	0	0	0	1,375	SCIN	BG283584
21652	222276_at	0	0	0	0	42	0	0	0	7,375	---	AA837026
21833	34858_at	74	0	0	0	0	0	0	0	3,375	KCTD2	D79998
21843	35265_at	0	0	3	67	0	0	0	0	16,5	FXR2	AF044263
21925	38149_at	0	0	40	15	0	0	0	0	18,375	ARHGAP25	D29642
21974	40420_at	37	0	0	0	0	0	0	0	8	STK10	AB015718
22102	52837_at	0	0	0	0	0	64	0	0	4,625	KIAA1644	AL047020
22287	222439_s_at	0	0	0	51	0	0	0	0	6,25	THRAP3	BE967048
22352	222504_s_at	0	0	0	0	0	0	0	53	6	COX4NB	BC001472
22628	222780_s_at	33	0	0	0	0	0	0	0	8,5	BAALC	AI870583
22742	222894_x_at	43	50	0	0	0	0	0	0	13,625	C20orf7	AI640582
23095	223249_at	91	0	0	0	16	0	0	0	11,875	CLDN12	AL136770
23127	223281_s_at	0	0	0	0	89	0	0	0	1,5	COX15	AF026850
23130	223284_at	0	0	0	35	0	0	0	0	8,25	NAT14	AB038651
23337	223491_at	0	0	0	0	0	0	22	0	9,875	COMMD2	BC001228
23353	223507_at	0	0	0	0	0	0	71	0	3,75	CLPX	AL136922
23368	223523_at	0	0	44	0	0	0	0	0	7,125	TMEM108	BC000568
23788	223944_at	10	0	0	0	0	0	0	0	11,375	NLRP12	AF231021
23830	223987_at	0	0	0	0	0	0	0	83	2,25	CHRDL2	AF332891
23870	224027_at	0	0	0	0	0	98	0	0	0,375	CCL28	AF110384
23914	224071_at	0	0	0	0	0	31	0	0	8,75	IL20	AF224266
23943	224100_s_at	0	70	0	0	0	0	0	0	3,875	DPYSL5	BC002874

Table 5a

24025	224184_s_at	0	30	0	0	0	0	0	0	8,875	BOC	AY027658
24093	224254_x_at	0	0	66	0	0	0	0	0	4,375	---	AF116695
24121	224284_x_at	0	0	36	40	0	0	0	0	15,75	FKSG49	AF338193
24187	224351_at	0	0	0	0	46	0	0	0	6,875	LOC1001315 08	AF130064
24310	224480_s_at	0	0	89	0	0	0	0	0	1,5	AGPAT9	BC006236
24359	224529_s_at	0	12	0	0	0	0	0	0	11,125	NT5C1A	AY028778
24369	224539_s_at	0	0	0	64	0	0	0	0	4,625	PCDHAC2	AF152474
24463	224635_s_at	0	0	0	0	0	0	5	56	17,625	BIRC6	AI017106
24489	224661_at	0	0	0	17	0	0	0	0	10,5	PIGY	AW028485
24610	224783_at	22	0	0	0	0	56	0	0	15,5	FAM100B	AA831661
24619	224792_at	24	0	0	0	0	0	0	0	9,625	TNKS1BP1	AL566438
24752	224925_at	0	0	0	0	78	0	0	0	2,875	PREX1	AL445192
24753	224926_at	35	0	0	0	0	0	0	0	8,25	EXOC4	AB051486
24828	225001_at	0	0	9	69	0	0	0	0	15,5	RAB3D	AI744658
24903	225077_at	0	0	0	0	0	83	0	0	2,25	CHD2	AA890703
25062	225236_at	0	11	0	0	0	0	0	20	21,375	RBM18	AA167623
25121	225295_at	0	0	0	0	0	0	60	32	13,75	SLC39A10	AB033091
25156	225330_at	0	0	0	0	67	0	0	0	4,25	IGF1R	AL044092
25197	225371_at	0	0	0	14	0	0	0	0	10,875	GLE1	AI638714
25312	225486_at	6	0	0	0	0	0	0	0	11,875	ARID2	AB046777
25404	225578_at	0	0	0	0	0	0	89	0	1,5	C13orf37	AI885466
25461	225635_s_at	0	0	0	0	0	0	78	57	8,375	LOC401504	BG535378
25669	225843_at	0	0	78	0	0	0	0	0	2,875	ZFYVE19	AW015263
25815	225990_at	0	0	0	88	0	0	0	0	1,625	BOC	W72626
25816	225991_at	0	0	35	0	0	0	0	0	8,25	TMEM41A	BE644935
25854	226029_at	54	0	0	0	0	0	0	0	5,875	VANGL2	AB033041
25872	226047_at	51	0	0	0	0	0	0	0	6,25	MRVI1	N66571
25879	226054_at	0	0	4	16	0	0	0	0	22,75	BRD4	AA702437
25890	226065_at	0	0	0	0	0	87	0	0	1,75	PRICKLE1	N98595
26055	226230_at	76	0	0	0	0	0	0	0	3,125	SMEK2	AA541716
26321	226496_at	0	0	0	0	0	0	25	74	12,875	ZCCHC7	BG291039
26389	226564_at	0	0	0	0	0	28	0	0	9,125	ZFAT	BF941325
26474	226650_at	78	0	0	0	0	0	0	0	2,875	ZFAND2A	AI984061
26559	226735_at	0	93	0	0	0	0	0	0	1	TAPT1	AI239899
26729	226905_at	0	0	12	10	0	0	0	0	22,5	FAM101B	BG036514
26750	226926_at	0	0	58	100	0	0	0	0	5,5	DMKN	AA706316
26955	227131_at	61	0	0	0	0	0	0	0	5	MAP3K3	BG231756
27236	227412_at	0	0	0	0	48	0	0	0	6,625	PPP1R3E	AK024489
27331	227508_at	96	60	0	0	0	0	0	0	5,75	---	AI302271

Table 5a

27487	227664_at	0	0	0	0	14	0	0	0	10,875	hCG_200814 0	AW149809
27873	228050_at	0	0	0	0	0	0	43	0	7,25	UTP15	AA046406
27888	228065_at	31	0	0	0	0	0	0	0	8,75	BCL9L	AL353962
27915	228092_at	0	0	0	0	38	0	0	0	7,875	CREM	AL552470
27997	228174_at	0	0	0	0	20	0	0	0	10,125	C9orf126	AI832363
28042	228219_s_at	0	21	0	0	0	0	0	0	10	UPB1	AI770035
28091	228268_at	0	0	0	0	0	0	95	0	0,75	FMO2	AI758223
28163	228340_at	79	0	0	0	0	0	0	0	2,75	TLE3	BE967118
28281	228458_at	0	96	0	0	0	0	0	0	0,625	C6orf226	AI636501
28316	228493_at	0	0	0	0	0	0	67	62	9,125	NKAP	T87628
28462	228639_at	0	49	0	0	0	0	0	0	6,5	---	BG054835
28542	228719_at	0	88	0	0	0	0	0	0	1,625	ZSWIM7	BE645222
28601	228778_at	0	0	86	0	0	0	0	0	1,875	---	BE673677
28700	228877_at	0	0	0	0	0	0	34	0	8,375	RGL3	AI379517
28739	228916_at	0	0	0	0	0	0	0	65	4,5	CWF19L2	BE857467
28795	228972_at	0	0	0	0	0	39	0	0	7,75	---	AI028602
28954	229131_at	0	0	0	0	0	0	0	64	4,625	---	AI702450
29105	229282_at	0	0	0	0	0	0	16	0	10,625	GATA6	AI762621
29117	229294_at	0	0	0	0	0	0	0	71	3,75	JPH3	AL537395
29214	229391_s_at	0	0	0	0	0	24	0	0	9,625	FAM26F	AV734646
29502	229679_at	0	0	0	0	0	21	0	0	10	C12orf76	AI870880
29858	230035_at	38	0	0	0	0	0	0	0	7,875	BOC	BF447871
29949	230126_s_at	39	0	0	0	0	0	0	0	7,75	KDM4B	AI265747
29992	230169_at	8	0	0	0	0	0	0	0	11,625	THAP6	AI199523
30150	230327_at	0	0	0	0	0	69	0	0	4	LOC730098	AI203673
30320	230497_at	0	0	0	0	64	70	0	0	8,5	BRUNOL5	BE503640
30345	230522_s_at	0	0	0	0	0	94	0	0	0,875	C9orf100	BG028209
30397	230574_at	0	0	0	20	0	0	0	0	10,125	LOC1001309 38	AW139393
30428	230605_at	0	0	0	0	0	73	0	0	3,5	---	BF433830
30513	230690_at	0	0	42	42	0	0	0	0	14,75	TUBB1	N63244
30517	230694_at	0	0	0	0	0	0	46	0	6,875	---	AI340341
30543	230720_at	0	0	0	0	0	0	66	0	4,375	RNF182	AI884906
30559	230736_at	0	0	0	0	60	0	0	0	5,125	LOC387647	AW118878
30682	230859_at	0	84	0	0	0	0	0	0	2,125	---	BF111276
30758	230935_at	0	0	0	0	0	61	0	0	5	---	AI861874
30874	231051_at	0	87	0	0	0	0	0	0	1,75	---	W69743
30903	231080_at	0	0	0	0	0	0	0	38	7,875	CDAN1	AI951606
31011	231188_at	0	0	69	24	0	0	0	0	13,625	ZSCAN2	AW206602

Table 5a

31220	231397_at	0	59	0	0	1	0	0	0	17,75	PAP2D	AF131783
31296	231473_at	0	20	0	30	32	35	0	36	44	---	AI554926
31325	231502_at	0	0	0	0	0	0	12	48	17,75	---	BF591615
31501	231678_s_at	0	0	0	0	0	0	33	91	9,75	ADH4	AV651117
31544	231721_at	0	0	0	0	0	0	35	2	20,625	JAM3	AF356518
31826	232003_at	0	0	95	0	0	0	0	0	0,75	PNMAL2	AW299761
31897	232074_at	0	0	92	0	0	0	0	0	1,125	PRSS27	AW170323
31902	232079_s_at	0	0	0	32	0	0	0	0	8,625	PVRL2	BE867789
31946	232123_at	0	0	0	0	23	6	0	0	21,625	LOC283174	BF527412
32012	232189_at	0	0	0	0	0	0	0	11	11,25	---	AK026459
32031	232208_at	0	0	0	0	0	0	0	59	5,25	ISLR2	AW007241
32067	232244_at	75	0	0	0	0	0	0	0	3,25	KIAA1161	AB032987
32082	232259_s_at	0	0	0	0	0	46	0	0	6,875	LOC1000096 76	BC003066
32152	232329_at	0	0	0	95	0	0	0	0	0,75	RANBP10	AV717059
32361	232538_at	0	0	0	0	33	0	0	0	8,5	---	AK027226
32470	232647_at	0	0	0	0	0	0	93	0	1	PROCA1	AL137531
32506	232683_s_at	0	0	0	0	0	0	0	67	4,25	PARP6	AL122091
32536	232713_at	0	92	0	2	0	0	0	0	13,5	---	AL365407
32751	232929_at	0	0	0	0	0	13	0	0	11	---	AU154942
32959	233137_at	0	0	68	90	0	0	0	0	5,5	---	AF143887
32976	233154_at	0	0	0	50	0	0	0	0	6,375	---	AK022197
32998	233176_at	0	0	96	0	0	0	0	0	0,625	---	AK024243
33198	233378_at	0	0	0	0	10	0	0	0	11,375	---	AK025118
33318	233498_at	0	52	0	0	0	0	0	0	6,125	ERBB4	AK024204
33519	233699_at	0	0	20	27	0	0	0	0	19,375	---	AK025173
33553	233733_at	0	0	0	0	0	0	0	66	4,375	---	AL137552
33944	234125_at	59	0	0	0	0	0	0	0	5,25	---	AL137318
34212	234394_at	0	37	0	0	0	0	0	0	8	ZNF124	AB046850
34213	234395_at	0	0	0	0	0	0	81	45	9,5	---	AF065869
34280	234462_at	0	0	5	3	0	0	0	0	24,25	---	S51397
34315	234497_s_at	0	0	0	0	0	0	98	33	8,875	---	AK022113
34333	234515_at	4	0	0	0	34	0	0	0	20,5	PCGEM1	AF223389
34396	234578_at	0	0	0	34	0	0	0	0	8,375	---	AL157496
34491	234673_at	0	0	0	0	39	18	0	22	28	HHLA2	AK027132
34497	234679_at	0	0	0	0	0	0	0	87	1,75	KRTAP9-3	AJ406947
34503	234685_x_at	0	54	0	0	0	0	0	0	5,875	KRTAP4-9	AJ406941
34517	234699_at	0	6	0	0	0	0	0	0	11,875	RNASE7	AJ131212
34555	234737_at	0	4	0	0	0	0	0	0	12,125	NT5DC3	AK002128
34695	234877_x_at	0	0	43	9	0	0	0	0	18,75	---	L21961

Table 5a

34845	235027_at	0	0	0	0	0	0	51	0	6,25	---	R52023
34884	235066_at	0	0	0	0	0	93	0	0	1	MAP4	AI078534
34890	235072_s_at	0	0	33	0	0	0	0	0	8,5	---	BF594695
34896	235078_at	0	0	0	0	0	8	0	0	11,625	---	AI393725
35065	235247_at	0	0	0	0	0	0	0	58	5,375	---	AI224578
35189	235371_at	0	0	0	0	59	0	0	0	5,25	GLT8D4	AI452595
35268	235450_at	0	0	0	47	0	0	0	0	6,75	FBXL4	BF571480
35410	235592_at	0	0	72	0	0	0	0	0	3,625	---	AW960145
35564	235746_s_at	0	0	0	85	0	0	0	0	2	PLA2R1	BE048919
35645	235827_at	0	0	0	0	0	0	20	0	10,125	MAP3K7IP1	AW592369
36052	236234_at	0	0	0	0	28	0	0	0	9,125	PDE1A	AW614381
36312	236494_x_at	68	0	0	0	0	0	0	0	4,125	---	AW003845
36506	236688_at	0	0	53	12	80	0	0	0	19,75	FRMPD3	AL133943
36539	236721_at	0	0	0	0	0	44	0	0	7,125	ALKBH1	AI922200
36574	236756_at	0	0	0	0	0	0	94	0	0,875	LOC389857	BE466872
36694	236876_at	0	0	0	0	24	76	0	0	12,75	H1FNT	AW013835
36701	236883_at	5	16	0	0	77	0	0	0	25,625	---	AI769104
36721	236903_at	0	0	0	0	0	54	0	0	5,875	---	BF511686
36758	236940_at	0	0	63	0	0	0	0	0	4,75	---	W60647
36801	236983_at	0	0	0	0	50	0	0	0	6,375	TMC5	AI738488
37073	237255_at	0	0	0	0	0	0	84	0	2,125	---	BF222867
37229	237411_at	0	0	0	0	0	0	61	84	7,125	ADAMTS6	N71063
37239	237421_at	0	0	0	71	0	0	0	0	3,75	---	BF509605
37291	237473_at	45	0	0	0	0	0	0	0	7	LOC1001304 94 /// LOC728448	AW027469
37559	237741_at	0	0	0	0	0	0	0	77	3	SLC25A36	AW514168
37573	237755_s_at	0	0	0	0	0	0	0	81	2,5	WDR16	AW673231
37590	237772_at	0	0	62	0	0	0	0	0	4,875	LOC1001292 86	AI732275
37630	237812_at	0	0	0	0	40	0	0	0	7,625	---	AI684424
37647	237829_at	0	0	0	0	22	0	0	0	9,875	---	AI732280
37649	237831_x_at	0	0	0	0	0	0	48	94	7,5	MMAA	R15084
37735	237917_at	0	0	74	0	0	0	0	0	3,375	NBPF8	N62721
37752	237934_at	0	0	0	0	0	40	0	0	7,625	---	AI873296
37789	237971_at	0	0	0	0	90	0	0	0	1,375	---	AI341258
37872	238054_at	25	0	0	0	0	0	0	0	9,5	ADPRHL1	AI243209
37962	238144_s_at	0	0	0	58	0	0	0	0	5,375	---	BF514993
37966	238148_s_at	11	0	0	0	0	0	0	0	11,25	ZNF818P	AI651641
38158	238340_at	0	0	0	0	30	0	0	0	8,875	WDR42A	AL134577

Table 5a

38289	238471_at	0	0	0	0	100	0	0	0	0,125	---	AI684833
38445	238627_at	13	79	0	0	0	0	0	0	13,75	TRAPPC2L	AW827150
38536	238718_at	0	0	0	11	0	0	0	0	11,25	---	BF382322
38756	238938_at	0	0	0	0	0	0	0	73	3,5	---	AI674059
39035	239217_x_at	0	0	0	0	0	0	62	0	4,875	ABCC3	AI375341
39136	239318_at	0	76	0	0	0	0	0	0	3,125	FAM118B	AI632973
39161	239343_at	0	18	0	0	0	0	0	0	10,375	LOC728705	AW451176
39237	239419_at	0	0	0	0	0	99	26	1	22,125	PTPRA	AA652313
39241	239423_at	0	0	0	45	0	0	0	0	7	---	AW043836
39320	239502_at	0	0	0	0	13	0	0	0	11	---	AA478981
39340	239522_at	0	0	13	0	0	0	0	0	11	IL12RB1	AI637915
39361	239543_s_at	81	82	0	0	0	0	41	39	20,125	---	AW275049
39458	239640_at	0	0	0	87	0	0	0	0	1,75	LOC401320	AI221073
39477	239659_at	0	0	0	0	86	0	0	0	1,875	---	BF591259
39504	239686_at	0	0	34	5	0	0	0	0	20,375	---	AI694557
39625	239807_at	0	0	0	36	0	0	0	0	8,125	LOC728842	AI693407
39720	239902_at	0	0	76	83	0	0	0	0	5,375	---	AI766224
39744	239926_at	0	0	0	0	0	53	0	0	6	---	AI675753
39747	239929_at	0	0	0	0	0	12	0	0	11,125	PM20D1	AA918425
39832	240014_at	0	0	0	0	49	0	0	0	6,5	POLR2J4	AI821720
40016	240198_at	0	0	0	0	94	14	0	44	18,875	---	AA348683
40021	240203_at	0	0	0	28	0	0	0	0	9,125	---	AI921894
40081	240263_at	0	0	0	0	29	0	0	0	9	---	N74924
40134	240316_at	0	0	0	0	0	84	0	0	2,125	C9orf57	AW274388
40198	240380_at	0	69	0	0	0	0	0	0	4	---	N63808
40217	240399_at	44	57	0	0	0	0	0	0	12,625	---	AA668261
40245	240427_at	0	0	0	0	92	79	0	0	3,875	---	AW445087
40305	240487_at	30	0	0	0	0	0	0	0	8,875	---	AI184609
40422	240604_at	0	0	0	0	0	92	0	0	1,125	ERI2	AI688141
40613	240795_at	0	0	56	41	0	0	0	0	13,125	---	AA001970
40905	241087_at	0	0	0	0	0	0	0	28	9,125	---	AV654572
40958	241140_at	0	0	0	0	0	0	27	23	19	LMO7	AA702962
41050	241232_x_at	0	0	0	0	0	38	0	0	7,875	---	AW236797
41149	241331_at	0	0	0	0	0	0	0	80	2,625	SKAP2	BE671499
41215	241397_at	0	0	0	0	0	0	96	0	0,625	---	AW276866
41302	241484_x_at	0	0	0	0	0	0	97	0	0,5	---	AI668696
41374	241556_at	0	0	84	0	0	0	0	0	2,125	---	N27112
41443	241625_at	0	0	0	0	0	0	8	0	11,625	---	BE221330
41489	241671_x_at	0	0	0	0	0	58	0	0	5,375	FLJ22536	H14782
41500	241682_at	89	0	0	0	0	0	0	0	1,5	KLHL23	BE873351

Table 5a

41719	241901_at	87	0	0	0	0	0	0	0	1,75	---	AA770235
41901	242083_at	0	0	0	0	0	95	0	0	0,75	ZNF81	AI028309
41911	242093_at	0	0	0	0	0	0	59	63	10	SYTL5	AW263497
42228	242410_s_at	14	0	0	0	0	0	0	0	10,875	CACNA1E	R15004
42244	242426_at	0	0	30	25	0	0	0	0	18,375	NRG4	BF793585
42287	242469_at	0	91	0	0	0	0	0	0	1,25	LOC120376	AI590055
42333	242515_x_at	0	36	0	0	0	16	0	0	18,75	C11orf17	AI933861
42415	242597_at	0	0	18	57	0	0	0	0	15,875	---	H11894
42424	242606_at	0	73	0	0	0	0	0	0	3,5	---	AL043482
42683	242865_at	0	0	0	0	0	0	54	0	5,875	---	AI332638
42726	242908_x_at	0	0	0	0	72	0	0	0	3,625	---	R46483
42965	243147_x_at	15	0	0	0	0	0	0	0	10,75	---	AW118707
43009	243191_at	0	0	0	0	0	0	17	14	21,375	---	BE044588
43041	243223_at	0	0	0	0	0	0	0	6	11,875	---	AA453526
43100	243282_at	0	0	0	75	0	0	0	0	3,25	CCDC93	AA504256
43210	243392_at	0	0	0	0	0	0	80	0	2,625	USP49	BF727345
43219	243401_at	0	0	0	0	0	0	18	0	10,375	---	AA806070
43415	243597_at	0	0	0	0	0	0	70	0	3,875	FANCB	BE550133
43420	243602_at	0	0	0	0	0	0	0	40	7,625	MGC40069	AI684979
43565	243747_at	0	0	0	89	0	0	0	0	1,5	ZNF599	AI222019
43618	243800_at	0	0	0	0	66	0	0	0	4,375	NR1H4	AI051958
43777	243959_at	0	0	0	0	0	0	0	46	6,875	---	N35099
43889	244071_at	0	0	0	0	0	0	29	0	9	FBLL1	AA868464
44334	244516_at	0	0	0	0	0	0	79	0	2,75	---	AW291120
44407	244589_at	1	64	0	0	0	0	0	0	17,125	---	AI026951
44411	244593_at	0	0	0	0	0	75	0	0	3,25	C17orf28	AL554277
44451	244633_at	0	85	0	0	0	0	0	0	2	---	AA404996
44582	244764_at	0	0	0	0	93	0	0	0	1	---	BG250907
44584	244766_at	0	0	64	0	0	0	0	0	4,625	LOC440354 /// LOC595101 /// LOC641298 /// LOC728423 /// LOC729513 /// SMG1	BG180003
44717	1552266_at	84	0	0	0	0	0	0	0	2,125	ADAM32	NM_145004
44778	1557411_s_at	0	0	0	0	0	63	0	0	4,75	SLC25A43	AK094254

Table 5a

44808	1552398_a_at	0	0	0	0	0	0	58	15	16,125	CLEC12A /// CLEC12B	NM_138337
45271	1553015_a_at	0	0	0	0	0	0	64	41	12,125	RECQL4	NM_004260
45312	1553063_at	0	0	0	0	0	0	0	24	9,625	GPR78	NM_080819
45349	1553114_a_at	41	41	0	0	0	0	0	0	15	PTK6	NM_005975
45403	1553186_x_at	0	0	98	0	0	0	0	0	0,375	RASEF	NM_152573
45407	1553192_at	0	0	67	0	0	0	0	0	4,25	ZNF441	NM_152355
45430	1553222_at	0	0	0	0	0	29	0	0	9	OXER1	AB083055
45440	1553237_x_at	0	0	0	0	0	50	0	0	6,375	PCDHAC1	NM_031882
45451	1553252_a_at	0	0	0	0	45	0	0	0	7	BRWD3	NM_153252
45814	1553713_a_at	0	0	0	0	0	82	0	0	2,375	RHEBL1	NM_144593
45877	1553801_a_at	0	0	57	91	0	0	0	0	6,75	C14orf126	NM_080664
45973	1553927_at	0	0	55	0	0	0	0	0	5,75	C7orf33	NM_145304
45996	1553960_at	88	0	0	0	0	0	0	0	1,625	SNX21	CA447177
46126	1554147_s_at	27	0	0	0	0	0	0	0	9,25	C3orf15	AB063297
46539	1554710_at	0	0	0	0	0	0	0	61	5	KCNMB1	BC025707
46892	1555181_a_at	0	0	0	0	69	0	0	0	4	ST3GAL3	AF425864
47027	1555356_a_at	0	38	0	0	0	0	0	0	7,875	SCML4	BC033286
47038	1555368_x_at	0	0	0	0	0	96	0	0	0,625	ZNF479	AF277624
47085	1555431_a_at	50	0	0	0	0	0	0	0	6,375	IL31RA	AF106913
47106	1555462_at	0	0	0	0	15	0	0	0	10,75	PPP1R1C	AF494535
47115	1555472_at	0	2	0	0	0	55	0	0	18,125	SORBS2	AF396457
47298	1555754_s_at	0	35	0	0	0	0	0	0	8,25	ATN1	Z22814
47323	1555786_s_at	0	0	0	0	8	0	0	0	11,625	C14orf34	BC008034
47374	1555853_at	0	77	0	0	0	0	0	0	3	---	BI524781
47470	1555990_at	0	0	0	93	0	0	0	0	1	C22orf42	CA775385
47482	1556006_s_at	0	0	0	0	0	0	63	89	6,25	CSNK1A1	BQ025347
47691	1556336_at	0	86	0	0	0	9	0	0	13,375	CCBL2 /// LOC1001317 35 /// RBMX	AA460960
47784	1556471_at	0	40	0	0	0	4	0	0	19,75	SCML4	CA448477
47858	1556597_a_at	0	0	0	0	0	0	100	0	0,125	LOC284513	AW169311
47868	1556616_a_at	0	0	0	0	0	0	32	21	18,625	LOC1001296 37	AA758799
47897	1556655_s_at	55	13	0	0	0	0	0	0	16,75	---	AI860021
47925	1556695_a_at	0	0	0	0	0	88	0	0	1,625	FLJ42709	AK095719
47926	1556696_s_at	0	0	0	0	54	33	0	0	14,375	FLJ42709	AK095719
47941	1556717_at	0	0	0	70	0	0	0	0	3,875	---	AK092802
48143	1557012_a_at	0	47	0	0	0	0	0	0	6,75	---	BC040670

Table 5a

48159	1557038_s_at	0	0	59	0	0	0	0	0	5,25	---	AK097488
48237	1557167_at	0	0	0	0	84	59	0	0	7,375	HCG11	AK024111
48265	1557217_a_at	0	0	0	0	91	0	0	0	1,25	FANCB	BC043596
48343	1557343_at	0	24	0	0	0	0	0	0	9,625	---	W95489
48404	1557437_a_at	0	0	60	0	0	0	0	0	5,125	---	AW273830
48540	1557633_at	0	0	0	0	51	0	0	0	6,25	POM121L8P	BC035394
48544	1557639_at	0	94	0	0	0	0	0	0	0,875	NFIA	AI220445
48783	1558017_s_at	0	0	0	0	0	0	24	10	21	---	BG109597
48789	1558034_s_at	0	0	0	0	0	15	0	0	10,75	CP	AL556703
48977	1558438_a_at	0	0	0	0	0	0	90	0	1,375	IGHG1	S55277
49079	1558624_at	0	0	0	0	12	66	0	0	15,5	---	BC033250
49168	1558770_a_at	0	17	0	0	0	0	0	0	10,5	PIK3R6	AK091819
49203	1558822_at	0	0	0	0	0	22	0	0	9,875	---	AF147412
49237	1558875_at	0	0	10	48	0	0	0	0	18	SREBF1	S66168
49250	1558897_at	0	25	0	0	0	0	0	0	9,5	PLK5P	AK054808
49357	1559086_at	0	0	0	0	0	27	0	0	9,25	---	AI678088
49377	1559124_at	0	0	0	0	0	45	0	0	7	LOC644135	BC038719
49385	1559133_at	0	0	77	76	0	0	0	0	6,125	---	BU176936
49404	1559163_at	0	0	0	0	0	0	0	68	4,125	LOC285954	AK096266
49429	1559218_s_at	0	0	0	0	87	0	0	0	1,75	NFYC	AL713771
49714	1559686_a_at	0	0	0	0	0	74	0	0	3,375	---	BC039376
49727	1559706_at	70	65	0	0	98	0	0	0	8,75	RGNEF	AB082529
49761	1559771_at	0	0	100	0	0	0	0	0	0,125	---	AI885742
49797	1559848_at	0	0	15	0	0	0	0	0	10,75	NSUN4	BC016907
49967	1560144_at	0	0	0	0	0	0	55	0	5,75	---	BC041865
50106	1560405_at	0	0	0	0	56	0	0	0	5,625	---	AL832499
50574	1561154_at	0	0	0	0	0	0	0	47	6,75	---	AF075113
50602	1561200_at	0	0	0	0	0	0	0	76	3,125	VWA3B	BM981856
50640	1561247_at	0	0	0	56	0	0	0	0	5,625	LOC283682	BC043440
50678	1561294_a_at	0	19	0	0	0	36	0	52	24,5	hCG_2015435	BC035235
50696	1561322_at	0	99	0	0	0	0	0	0	0,25	---	BC042427
50722	1569452_at	0	0	0	0	0	0	68	31	12,875	LOC692247	BG772667
50754	1561407_at	0	0	0	0	0	80	0	0	2,625	ARAP2	BC031283
50833	1561511_at	0	0	0	0	74	0	0	0	3,375	---	BC036630
50955	1561683_at	0	23	0	0	0	0	0	0	9,75	---	BC040600
50987	1561739_at	0	97	0	0	0	0	0	96	1,125	---	AL512742
51032	1561868_at	0	45	0	0	0	0	0	0	7	---	AL359058
51135	1562035_at	0	0	50	0	0	0	0	0	6,375	---	AK055464

Table 5a

51177	1562099_at	0	51	0	0	0	0	0	0	6,25	---	BC041050
51229	1562230_at	0	0	23	43	0	0	0	0	17	---	AF147390
51342	1562412_at	0	0	0	0	0	0	19	19	20,5	---	BC020562
51588	1562801_at	0	0	0	0	0	0	57	7	17,25	---	BC043373
51611	1562836_at	0	0	0	0	0	71	0	0	3,75	---	AK021715
51618	1562849_at	52	0	0	0	0	0	0	0	6,125	---	BQ002451
51639	1562880_at	0	0	0	0	68	0	0	0	4,125	---	BC043439
51802	1563106_at	0	0	0	0	0	0	83	0	2,25	---	BC032028
51928	1563348_at	0	0	0	0	0	0	0	95	0,75	---	AF087974
51940	1563376_at	58	0	0	0	0	0	0	0	5,375	---	BC038205
51960	1563450_at	0	66	0	0	0	0	0	0	4,375	DEFB107A /// DEFB107B	AF540979
51981	1563478_at	0	0	71	0	0	0	0	0	3,75	CTA-221G9.4	AL832019
52033	1563581_at	0	0	0	0	0	0	52	0	6,125	LOC285456	AK094992
52052	1563614_at	0	0	88	0	0	0	0	0	1,625	MTBP	AL832671
52063	1563655_at	7	0	0	0	0	0	0	0	11,75	TNNT2	AL832707
52114	1563800_at	42	0	0	0	0	0	0	0	7,375	LOC283140	AK095275
52135	1563853_at	0	0	8	81	0	0	0	0	14,125	LOC283045	AK095019
52354	1564402_at	0	0	31	68	0	0	0	0	12,875	LOC146795	AK057377
52414	1564600_a_at	0	0	0	0	0	89	0	0	1,5	CCDC36	AK058049
52547	1565065_at	0	0	0	0	25	0	0	0	9,5	OFCC1	AF520802
52828	1565935_at	0	0	0	0	0	0	0	16	10,625	LOC91431	AF075091
52968	1566294_at	72	0	0	0	0	0	0	0	3,625	---	AF085916
52985	1566425_at	0	0	0	0	0	0	2	17	22,875	---	AL833305
53014	1566469_at	0	0	0	0	63	0	0	0	4,75	---	AL831875
53063	1566550_at	0	0	0	0	99	0	0	0	0,25	---	AL137307
53125	1566698_at	0	95	0	0	0	0	0	0	0,75	---	AL117464
53155	1566775_at	0	0	0	0	0	0	0	97	0,5	DNAH1	AK093347
53225	1566902_at	0	7	0	0	0	3	0	0	24	---	AL831906
53309	1567079_at	0	29	0	0	0	0	0	0	9	CLN6	D17218
53332	1567240_x_at	0	0	0	0	0	0	0	92	1,125	OR2L2	X64978
53339	1567248_at	2	0	0	0	0	0	0	0	12,375	OR9A1P	X64982
53614	1568854_at	0	0	0	22	0	0	0	0	9,875	C6orf41	AI028608
53702	1569009_s_at	0	0	0	0	0	67	0	0	4,25	---	BC025967
53707	1569023_a_at	0	0	0	0	0	0	0	25	9,5	---	BC020935
53860	1569318_at	0	0	0	0	0	0	30	0	8,875	LOC284440	BC037856
54119	1569755_at	17	0	0	0	0	0	88	60	17,25	---	BC035112
54150	1569793_at	0	0	75	0	0	0	0	0	3,25	SLC25A18	BC016954

Table 5a

54206	1569882_at	0	0	0	0	47	0	0	0	6,75	NCRNA00119	BC036463
54295	1570033_at	0	0	0	0	0	0	87	0	1,75	WIPI2	BC016912
54482	1570318_at	0	62	0	0	0	0	0	0	4,875	---	BC030089
54485	1570327_at	0	0	0	0	0	5	0	0	12	C20orf62	BC030259
54541	1570433_at	0	100	0	0	0	0	0	0	0,125	TMPRSS2	BC015819

Table 5b

Gene Symbol	Gene Title
SPAG7	sperm associated antigen 7
MSN	moesin
SPARC	secreted protein, acidic, cysteine-rich (osteonectin)
ARPC1A	actin related protein 2/3 complex, subunit 1A, 41kDa
MDH1	malate dehydrogenase 1, NAD (soluble)
SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
ITGB5	integrin, beta 5
IGFBP7	insulin-like growth factor binding protein 7
NDUFB8 / SEC31B	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa /// SEC31 homolog B (S. cerevisiae)
ANXA4	annexin A4
CUL3	cullin 3
DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15
SOX4	SRY (sex determining region Y)-box 4
MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2
SCRN1	secernin 1
NQO1	NAD(P)H dehydrogenase, quinone 1
AAMP	angio-associated, migratory cell protein
DUSP3	dual specificity phosphatase 3
DLG5	discs, large homolog 5 (Drosophila)
CEACAM5	carcinoembryonic antigen-related cell adhesion molecule 5
CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like
FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)
C7orf28A	chromosome 7 open reading frame 28A
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
SFRP1	secreted frizzled-related protein 1
COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)
ACBD3	acyl-Coenzyme A binding domain containing 3
UNC119B	unc-119 homolog B (C. elegans)
CRMP1	collapsin response mediator protein 1
HMGN4	high mobility group nucleosomal binding domain 4
SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa
INPP5K	inositol polyphosphate-5-phosphatase K
DNAJB12	DnaJ (Hsp40) homolog, subfamily B, member 12
KLHL21	kelch-like 21 (Drosophila)
FXR2	fragile X mental retardation, autosomal homolog 2
TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
UNC119	unc-119 homolog (C. elegans)
EDEM1	ER degradation enhancer, mannosidase alpha-like 1
LMAN1	lectin, mannose-binding, 1
SCNN1A	sodium channel, nonvoltage-gated 1 alpha
ARL4D	ADP-ribosylation factor-like 4D
DAPK3	death-associated protein kinase 3
HEPH	hephaestin
RAP1GAP	RAP1 GTPase activating protein
CDC6	cell division cycle 6 homolog (S. cerevisiae)
MAOB	monoamine oxidase B
PREP	prolyl endopeptidase
ACPP	acid phosphatase, prostate
EML2	echinoderm microtubule associated protein like 2
FGF2	fibroblast growth factor 2 (basic)

Table 5b

MRC1 /// MRC1L1	mannose receptor, C type 1 /// mannose receptor, C type 1-like 1
GAS1	growth arrest-specific 1
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
TTF1	transcription termination factor, RNA polymerase I
RRAD	Ras-related associated with diabetes
ICAM3	intercellular adhesion molecule 3
SNAP91	synaptosomal-associated protein, 91kDa homolog (mouse)
CENPA	centromere protein A
GPC4	glypican 4
PGC	progastricsin (pepsinogen C)
PIGA	phosphatidylinositol glycan anchor biosynthesis, class A
BAIAP2	BAI1-associated protein 2
OVGP1	oviductal glycoprotein 1, 120kDa
KIAA0586	KIAA0586
SPIB	Spi-B transcription factor (Spi-1/PU.1 related)
BDKRB2	bradykinin receptor B2
IL15	interleukin 15
CHML	choroideremia-like (Rab escort protein 2)
RHAG	Rh-associated glycoprotein
SERPINA6	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6
MLANA	melan-A
ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)
PML	promyelocytic leukemia
AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)
KCNQ3	potassium voltage-gated channel, KQT-like subfamily, member 3
MAGEC1	melanoma antigen family C, 1
SIX3	SIX homeobox 3
CHRNB2	cholinergic receptor, nicotinic, beta 2 (neuronal)
CXorf1	chromosome X open reading frame 1
GRIA3	glutamate receptor, ionotrophic, AMPA 3
DLEC1	deleted in lung and esophageal cancer 1
G6PC	glucose-6-phosphatase, catalytic subunit
IL8RA	interleukin 8 receptor, alpha
SAA4	serum amyloid A4, constitutive
GRM5	glutamate receptor, metabotropic 5
ALOX15	arachidonate 15-lipoxygenase
USP34	ubiquitin specific peptidase 34
SLC22A2	solute carrier family 22 (organic cation transporter), member 2
SHOX	short stature homeobox
XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2
GAGE3	G antigen 3
CACNB4	calcium channel, voltage-dependent, beta 4 subunit
---	---
IFNW1	interferon, omega 1
SCN7A	sodium channel, voltage-gated, type VII, alpha
ZNF157	zinc finger protein 157
AVPR2	arginine vasopressin receptor 2
LIPE	lipase, hormone-sensitive
C4BPB	complement component 4 binding protein, beta
ADAM22	ADAM metallopeptidase domain 22
TH	tyrosine hydroxylase
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)
FRMD4A	FERM domain containing 4A
CSNK1D	casein kinase 1, delta
NCOR2	nuclear receptor co-repressor 2

Table 5b

NR2F2	nuclear receptor subfamily 2, group F, member 2
CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3
BAD	BCL2-associated agonist of cell death
HIP1R	huntingtin interacting protein 1 related
TGFB1I1	transforming growth factor beta 1 induced transcript 1
ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2
PADI2	peptidyl arginine deiminase, type II
CHST3	carbohydrate (chondroitin 6) sulfotransferase 3
TRIM9	tripartite motif-containing 9
PCGF1	polycomb group ring finger 1
PRKCQ	protein kinase C, theta
IGFBP3	insulin-like growth factor binding protein 3
EFNA3	ephrin-A3
PSG1	pregnancy specific beta-1-glycoprotein 1
---	---
ABCC8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
SFRS17A	splicing factor, arginine/serine-rich 17A
SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1
FETUB	fetuin B
DTNA	dystrobrevin, alpha
GLRA3	glycine receptor, alpha 3
MCM7	minichromosome maintenance complex component 7
MGLL	monoglyceride lipase
PTPRU	protein tyrosine phosphatase, receptor type, U
IFNA2	interferon, alpha 2
MTAP	methylthioadenosine phosphorylase
GABARAPL1 /// GABARAPL3	GABA(A) receptor-associated protein like 1 /// GABA(A) receptors associated protein like 3 (pseudogene)
NFIB	nuclear factor I/B
CXCR6	chemokine (C-X-C motif) receptor 6
RAPSN	receptor-associated protein of the synapse
IGH3 /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHG4 /// IGHM /// IGHV3-23 /// IGHV4-31 /// LOC100126583 /// LOC642131 /// LOC652128 /// VSIG6 /// IGHA1 /// IGHG1 /// LOC100133862	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant ga immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// similar to hCG1773549
KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3
ZNF471	zinc finger protein 471
PEG10	paternally expressed 10
CAV1	caveolin 1, caveolae protein, 22kDa
TUBA4A	tubulin, alpha 4a
SETD3	SET domain containing 3
ARAP1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1
---	---
ZEB1	zinc finger E-box binding homeobox 1
SORT1	sortilin 1
ZNF282	zinc finger protein 282

Table 5b

FBXO9	F-box protein 9
APOOL	Apolipoprotein O-like
ATG2A	ATG2 autophagy related 2 homolog A (S. cerevisiae)
ZC3H7B	zinc finger CCCH-type containing 7B
TMCC1	transmembrane and coiled-coil domain family 1
MXRA8	matrix-remodelling associated 8
DGCR6L	DiGeorge syndrome critical region gene 6-like
CCDC22	coiled-coil domain containing 22
MAN1C1	mannosidase, alpha, class 1C, member 1
NOV	nephroblastoma overexpressed gene
TRPM1	Transient receptor potential cation channel, subfamily M, member 1
HLX	H2.0-like homeobox
AZU1	azurocidin 1
USP19	ubiquitin specific peptidase 19
AZI1	5-azacytidine induced 1
AHCTF1	AT hook containing transcription factor 1
CLCN4	chloride channel 4
IGKV4-1	immunoglobulin kappa variable 4-1
---	---
MCF2	MCF.2 cell line derived transforming sequence
MUC3B	mucin 3B, cell surface associated
TMC6	transmembrane channel-like 6
---	---
DST	dystonin
B3GNTL1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1
EIF3M	eukaryotic translation initiation factor 3, subunit M
---	---
ZNF391	zinc finger protein 391
LOC100128640	Hypothetical protein LOC100128640
---	---
GRIK2	Glutamate receptor, ionotropic, kainate 2
LOC100134355 ///	
PRIM2	similar to Primase, DNA, polypeptide 2 (58kDa) /// primase, DNA, polypeptide 2 (58kDa)
DTX2 ///	
LOC100134197	deltex homolog 2 (Drosophila) /// hypothetical protein LOC100134197
USF2	upstream transcription factor 2, c-fos interacting
TLL2	tolloid-like 2
MRPS11	mitochondrial ribosomal protein S11
---	---
CPN2	carboxypeptidase N, polypeptide 2
HCG2P7	HLA complex group 2 pseudogene 7
IGL@	immunoglobulin lambda locus
C19orf10	chromosome 19 open reading frame 10
---	---
TAL1	T-cell acute lymphocytic leukemia 1
FASN	fatty acid synthase
GBX1	gastrulation brain homeobox 1
NTN3	Netrin 3
---	---
---	---
ESR1	estrogen receptor 1
ZFX	zinc finger protein, X-linked
CYB561	cytochrome b-561
LOC642131	Similar to hCG1812074
CEACAM5	carcinoembryonic antigen-related cell adhesion molecule 5

Table 5b

SHMT1	serine hydroxymethyltransferase 1 (soluble)
---	---
FOLH1	folate hydrolase (prostate-specific membrane antigen) 1
FAM55C	family with sequence similarity 55, member C
---	---
AKAP6	A kinase (PRKA) anchor protein 6
---	---
CPSF7	cleavage and polyadenylation specific factor 7, 59kDa
DUS1L	dihydrouridine synthase 1-like (S. cerevisiae)
TSEN34	tRNA splicing endonuclease 34 homolog (S. cerevisiae)
INF2	inverted formin, FH2 and WH2 domain containing
C14orf159	chromosome 14 open reading frame 159
TRAPPC2L	trafficking protein particle complex 2-like
NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9
TRIAP1	TP53 regulated inhibitor of apoptosis 1
CERK	ceramide kinase
COMMD10	COMM domain containing 10
LYRM4	LYR motif containing 4
MAGEH1	melanoma antigen family H, 1
LRRC40	leucine rich repeat containing 40
PUS1	pseudouridylate synthase 1
SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1
TSPAN15	tetraspanin 15
TMEM51	transmembrane protein 51
WDR3	WD repeat domain 3
C1orf66	chromosome 1 open reading frame 66
PYCRL	pyrroline-5-carboxylate reductase-like
KRT23	keratin 23 (histone deacetylase inducible)
PID1	phosphotyrosine interaction domain containing 1
TRPV2	transient receptor potential cation channel, subfamily V, member 2
CEP76	centrosomal protein 76kDa
SNIP1	Smad nuclear interacting protein 1
NXN	nucleoredoxin
RTN3	reticulon 3
CYP20A1	cytochrome P450, family 20, subfamily A, polypeptide 1
ZNF767	zinc finger family member 767
LRP1B	low density lipoprotein-related protein 1B (deleted in tumors)
HAUS2	HAUS augmin-like complex, subunit 2
ANTXR1	anthrax toxin receptor 1
SPATA6	spermatogenesis associated 6
FLJ42627	hypothetical LOC645644
SPTLC3	serine palmitoyltransferase, long chain base subunit 3
GUCY1B2	guanylate cyclase 1, soluble, beta 2
CCDC40	coiled-coil domain containing 40
IFT122	intraflagellar transport 122 homolog (Chlamydomonas)
PRG3	proteoglycan 3
FLJ11292	hypothetical protein FLJ11292
---	---
METTL5	methyltransferase like 5
---	---
ANGPTL4	angiopoietin-like 4
SLC25A32	solute carrier family 25, member 32
---	---
CLDN18	claudin 18
CCDC70	coiled-coil domain containing 70

Table 5b

HRH4	histamine receptor H4
FGF14	fibroblast growth factor 14
P2RX2	purinergic receptor P2X, ligand-gated ion channel, 2
PCDHB12	protocadherin beta 12
CDCA3	cell division cycle associated 3
GDF15	growth differentiation factor 15
RAB35	RAB35, member RAS oncogene family
---	---
DENND2A	DENN/MADD domain containing 2A
FAM131A	family with sequence similarity 131, member A
SCIN	scinderin
---	---
KCTD2	potassium channel tetramerisation domain containing 2
FXR2	fragile X mental retardation, autosomal homolog 2
ARHGAP25	Rho GTPase activating protein 25
STK10	serine/threonine kinase 10
KIAA1644	KIAA1644
THRAP3	thyroid hormone receptor associated protein 3
COX4NB	COX4 neighbor
BAALC	brain and acute leukemia, cytoplasmic
C20orf7	chromosome 20 open reading frame 7
CLDN12	claudin 12
COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)
NAT14	N-acetyltransferase 14 (GCN5-related, putative)
COMMD2	COMM domain containing 2
CLPX	ClpX caseinolytic peptidase X homolog (E. coli)
TMEM108	transmembrane protein 108
NLRP12	NLR family, pyrin domain containing 12
CHRDL2	chordin-like 2
CCL28	chemokine (C-C motif) ligand 28
IL20	interleukin 20
DPYSL5	dihydropyrimidinase-like 5
BOC	Boc homolog (mouse)
---	---
FKSG49	FKSG49
LOC100131508	PRO2122
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9
NT5C1A	5'-nucleotidase, cytosolic IA
PCDHAC2	protocadherin alpha subfamily C, 2
BIRC6	baculoviral IAP repeat-containing 6
PIGY	phosphatidylinositol glycan anchor biosynthesis, class Y
FAM100B	family with sequence similarity 100, member B
TNKS1BP1	tankyrase 1 binding protein 1, 182kDa
PREX1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1
EXOC4	exocyst complex component 4
RAB3D	RAB3D, member RAS oncogene family
CHD2	chromodomain helicase DNA binding protein 2
RBM18	RNA binding motif protein 18
SLC39A10	solute carrier family 39 (zinc transporter), member 10
IGF1R	insulin-like growth factor 1 receptor
GLE1	GLE1 RNA export mediator homolog (yeast)
ARID2	AT rich interactive domain 2 (ARID, RFX-like)
C13orf37	chromosome 13 open reading frame 37
LOC401504	Hypothetical gene supported by AK091718
ZFYVE19	zinc finger, FYVE domain containing 19

Table 5b

BOC	Boc homolog (mouse)
TMEM41A	transmembrane protein 41A
VANGL2	vang-like 2 (van gogh, Drosophila)
MRVI1	murine retrovirus integration site 1 homolog
BRD4	bromodomain containing 4
PRICKLE1	prickle homolog 1 (Drosophila)
SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)
ZCCHC7	zinc finger, CCHC domain containing 7
ZFAT	zinc finger and AT hook domain containing
ZFAND2A	zinc finger, AN1-type domain 2A
TAPT1	transmembrane anterior posterior transformation 1
FAM101B	family with sequence similarity 101, member B
DMKN	dermokine
MAP3K3	mitogen-activated protein kinase kinase kinase 3
PPP1R3E	protein phosphatase 1, regulatory (inhibitor) subunit 3E
---	---
hCG_2008140	hypothetical LOC729614
UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)
BCL9L	B-cell CLL/lymphoma 9-like
CREM	cAMP responsive element modulator
C9orf126	chromosome 9 open reading frame 126
UPB1	ureidopropionase, beta
FMO2	flavin containing monooxygenase 2 (non-functional)
TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)
C6orf226	chromosome 6 open reading frame 226
NKAP	NFKB activating protein
---	---
ZSWIM7	zinc finger, SWIM-type containing 7
---	---
RGL3	ral guanine nucleotide dissociation stimulator-like 3
CWF19L2	CWF19-like 2, cell cycle control (S. pombe)
---	---
---	---
GATA6	GATA binding protein 6
JPH3	junctophilin 3
FAM26F	family with sequence similarity 26, member F
C12orf76	chromosome 12 open reading frame 76
BOC	Boc homolog (mouse)
KDM4B	Lysine (K)-specific demethylase 4B
THAP6	THAP domain containing 6
LOC730098	similar to chemokine (C-C motif) ligand 27
BRUNOL5	bruno-like 5, RNA binding protein (Drosophila)
C9orf100	chromosome 9 open reading frame 100
LOC100130938	hypothetical protein LOC100130938
---	---
TUBB1	tubulin, beta 1
---	---
RNF182	ring finger protein 182
LOC387647	patched domain containing 3 pseudogene
---	---
---	---
---	---
CDAN1	Congenital dyserythropoietic anemia, type I
ZSCAN2	zinc finger and SCAN domain containing 2
PAP2D	phosphatidic acid phosphatase type 2

Table 5b

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---	---
ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide
JAM3	junctional adhesion molecule 3
PNMAL2	PNMA-like 2
PRSS27	protease, serine 27
PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)
LOC283174	hypothetical LOC283174
---	---
ISLR2	immunoglobulin superfamily containing leucine-rich repeat 2
KIAA1161	KIAA1161
LOC100009676	hypothetical LOC100009676
RANBP10	RAN binding protein 10
---	---
PROCA1	protein interacting with cyclin A1
PARP6	poly (ADP-ribose) polymerase family, member 6
---	---
---	---
---	---
---	---
---	---
---	---
ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
---	---
---	---
---	---
ZNF124	zinc finger protein 124
---	---
---	---
---	---
PCGEM1	prostate-specific transcript 1 (non-protein coding)
---	---
HHLA2	HERV-H LTR-associating 2
KRTAP9-3	keratin associated protein 9-3
KRTAP4-9	keratin associated protein 4-9
RNASE7	ribonuclease, RNase A family, 7
NT5DC3	5'-nucleotidase domain containing 3
---	---
---	---
MAP4	microtubule-associated protein 4
---	---
---	---
---	---
GLT8D4	glycosyltransferase 8 domain containing 4
FBXL4	F-box and leucine-rich repeat protein 4
---	---
PLA2R1	phospholipase A2 receptor 1, 180kDa
MAP3K7IP1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1
PDE1A	phosphodiesterase 1A, calmodulin-dependent
---	---
FRMPD3	FERM and PDZ domain containing 3
ALKBH1	alkB, alkylation repair homolog 1 (E. coli)
LOC389857	hypothetical protein
H1FNT	H1 histone family, member N, testis-specific
---	---

Table 5b

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---	---
TMC5	transmembrane channel-like 5
---	---
ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif, 6
---	---
LOC100130494 ///	
LOC728448	hypothetical protein LOC100130494 /// peptidylprolyl isomerase E pseudogene
SLC25A36	Solute carrier family 25, member 36
WDR16	WD repeat domain 16
LOC100129286	Hypothetical protein LOC100129286
---	---
---	---
MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type
NBPF8	neuroblastoma breakpoint family, member 8
---	---
---	---
ADPRHL1	ADP-ribosylhydrolase like 1
---	---
ZNF818P	zinc finger protein 818 pseudogene
WDR42A	WD repeat domain 42A
---	---
TRAPPC2L	trafficking protein particle complex 2-like
---	---
---	---
ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
FAM118B	family with sequence similarity 118, member B
LOC728705	hypothetical protein LOC728705
PTPRA	Protein tyrosine phosphatase, receptor type, A
---	---
---	---
IL12RB1	interleukin 12 receptor, beta 1
---	---
LOC401320	Hypothetical LOC401320
---	---
---	---
LOC728842	hypothetical LOC728842
---	---
---	---
PM20D1	peptidase M20 domain containing 1
POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene
---	---
---	---
---	---
C9orf57	chromosome 9 open reading frame 57
---	---
---	---
---	---
---	---
ERI2	exoribonuclease 2
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LMO7	LIM domain 7
---	---
SKAP2	Src kinase associated phosphoprotein 2

Table 5b

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---	---
FLJ22536	hypothetical locus LOC401237
KLHL23	kelch-like 23 (Drosophila)
---	---
ZNF81	zinc finger protein 81
SYTL5	synaptotagmin-like 5
CACNA1E	calcium channel, voltage-dependent, R type, alpha 1E subunit
NRG4	neuregulin 4
LOC120376	Uncharacterized protein LOC120376
C11orf17	chromosome 11 open reading frame 17
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---	---
CCDC93	coiled-coil domain containing 93
USP49	ubiquitin specific peptidase 49
---	---
FANCB	Fanconi anemia, complementation group B
MGC40069	Hypothetical protein MGC40069
ZNF599	zinc finger protein 599
NR1H4	nuclear receptor subfamily 1, group H, member 4
---	---
FBLL1	fibrillarin-like 1
---	---
---	---
C17orf28	chromosome 17 open reading frame 28
---	---
---	---
LOC440354 ///	
LOC595101 ///	
LOC641298 ///	
LOC728423 ///	PI-3-kinase-related kinase SMG-1 pseudogene /// PI-3-kinase-related kinase SMG-1
LOC729513 ///	pseudogene /// SMG1 homolog, phosphatidylinositol 3-kinase-related kinase pseudogene ///
SMG1	hypothetical LOC728423 /// similar to PI-3-kinase-related kinase SMG-1 /// SMG1 homol
ADAM32	ADAM metallopeptidase domain 32
SLC25A43	solute carrier family 25, member 43
CLEC12A ///	
CLEC12B	C-type lectin domain family 12, member A /// C-type lectin domain family 12, member B
RECQL4	RecQ protein-like 4
GPR78	G protein-coupled receptor 78
PTK6	PTK6 protein tyrosine kinase 6
RASEF	RAS and EF-hand domain containing
ZNF441	zinc finger protein 441
OXER1	oxoeicosanoid (OXE) receptor 1
PCDHAC1	protocadherin alpha subfamily C, 1
BRWD3	bromodomain and WD repeat domain containing 3
RHEBL1	Ras homolog enriched in brain like 1
C14orf126	chromosome 14 open reading frame 126
C7orf33	chromosome 7 open reading frame 33

Table 5b

SNX21	sorting nexin family member 21
C3orf15	chromosome 3 open reading frame 15
KCNMB1	potassium large conductance calcium-activated channel, subfamily M, beta member 1
ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3
SCML4	sex comb on midleg-like 4 (Drosophila)
ZNF479	zinc finger protein 479
IL31RA	interleukin 31 receptor A
PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C
SORBS2	sorbin and SH3 domain containing 2
ATN1	atrophin 1
C14orf34	chromosome 14 open reading frame 34
---	---
C22orf42	chromosome 22 open reading frame 42
CSNK1A1	Casein kinase 1, alpha 1
CCBL2 ///	
LOC100131735 ///	cysteine conjugate-beta lyase 2 /// similar to RNA binding motif protein, X-linked /// RNA binding
RBMX	motif protein, X-linked
SCML4	sex comb on midleg-like 4 (Drosophila)
LOC284513	hypothetical protein LOC284513
LOC100129637	hypothetical LOC100129637
---	---
FLJ42709	hypothetical LOC441094
FLJ42709	hypothetical LOC441094
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---	---
HCG11	HLA complex group 11
FANCB	Fanconi anemia, complementation group B
---	---
---	---
POM121L8P	POM121 membrane glycoprotein-like 8 (rat) pseudogene
NFIA	Nuclear factor I/A
---	---
CP	ceruloplasmin (ferroxidase)
IGHG1	Immunoglobulin heavy constant gamma 1 (G1m marker)
---	---
PIK3R6	phosphoinositide-3-kinase, regulatory subunit 6
---	---
SREBF1	sterol regulatory element binding transcription factor 1
PLK5P	polo-like kinase 5 pseudogene
---	---
LOC644135	hypothetical LOC644135
---	---
LOC285954	hypothetical LOC285954
NFYC	nuclear transcription factor Y, gamma
---	---
RGNEF	Rho-guanine nucleotide exchange factor
---	---
NSUN4	NOL1/NOP2/Sun domain family, member 4
---	---
---	---
---	---
VWA3B	von Willebrand factor A domain containing 3B
LOC283682	Hypothetical protein LOC283682
hCG_2015435	hypothetical protein LOC100128554

Table 5b

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LOC692247	hypothetical locus LOC692247
ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
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---	---
DEFB107A ///	
DEFB107B	defensin, beta 107A /// defensin, beta 107B
CTA-221G9.4	KIAA1671 protein
LOC285456	hypothetical LOC285456
	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) binding protein,
MTBP	104kDa
TNNT2	troponin T type 2 (cardiac)
LOC283140	hypothetical protein LOC283140
LOC283045	hypothetical protein LOC283045
LOC146795	hypothetical protein LOC146795
CCDC36	coiled-coil domain containing 36
OFCC1	orofacial cleft 1 candidate 1
LOC91431	prematurely terminated mRNA decay factor-like
---	---
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---	---
---	---
DNAH1	dynein, axonemal, heavy chain 1
---	---
CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant
OR2L2	olfactory receptor, family 2, subfamily L, member 2
OR9A1P	olfactory receptor, family 9, subfamily A, member 1 pseudogene
C6orf41	chromosome 6 open reading frame 41
---	---
---	---
LOC284440	hypothetical LOC284440
---	---
SLC25A18	solute carrier family 25 (mitochondrial carrier), member 18
NCRNA00119	non-protein coding RNA 119
WIPI2	WD repeat domain, phosphoinositide interacting 2
---	---
C20orf62	chromosome 20 open reading frame 62
TMPRSS2	transmembrane protease, serine 2

WHAT IS CLAIMED IS:

1. A method of identifying a rheumatoid arthritis patient that is a candidate for treatment with an human interleukin-6 receptor antibody or a rheumatoid arthritis patient that should be excluded from treatment, the method comprising:

providing an RNA nucleic acid sample obtained from peripheral blood lymphocytes from the patient;

determining the level of expression of at least one gene product encoded by a gene set forth in Table 1, Table 2, or Table 3 that is associated with a therapeutic response to treatment with IL-6 receptor antibody; wherein when the level exceeds the threshold value, the level of the biomarker is indicative of a patient that is a candidate for treatment with the human interleukin-6 receptor antibody; or that a patient that should be excluded from treatment.

2. The method of claim 1, wherein the method comprises detecting the level of expression of gene products encoded by at least two, three, four, five, six, seven, eight, nine, ten, twenty, thirty, or forty or more, of the genes set forth in Table 1, Table 2, or Table 3.

3. The method of claim 1, wherein the step of determining the level of expression comprises an amplification reaction.

4. The method of claim 3, wherein the amplification reaction is a quantitative RT-PCR.

5. The method of claim 1, further comprising recording the correlation of the presence of the SNP with a positive response to treatment with IL-6 receptor antibody.

6. The method of claim 5, further comprising administering IL-6 receptor antibody to the patient.

7. A method of identifying a rheumatoid arthritis patient that is a candidate for treatment with an human interleukin-6 receptor antibody or patient that should be excluded from treatment, the method comprising:

providing a serum sample from the patient or a sample comprising protein from peripheral blood lymphocytes;

determining the level of expression of at least one gene product encoded by a gene set forth in Table 1, Table 2, or Table 3 that is associated with a therapeutic response to treatment with IL-6 receptor antibody.

8. A diagnostic device comprising two or more nucleic acid probes attached to a solid surface to detect RNA expression levels of two or more biomarkers set forth in Table 1, Table 2, or Table 3.

9. The diagnostic device of claim 8, wherein device comprises probes to detect RNA expression level of three, four, five, six, seven, eight, nine, ten, twenty, thirty, or forty or more, of the biomarkers set forth in Table 1, Table 2, or Table 3.

10. A method of identifying a rheumatoid arthritis patient that is a candidate for treatment with an human interleukin-6 receptor antibody or a rheumatoid arthritis patient that should be excluded from treatment, the method comprising:

providing an RNA nucleic acid sample obtained from peripheral blood lymphocytes from the patient;

determining the level of expression of at least two gene products having a value > 0 in column C of Table 5, or the level the level of expression of at least two gene products having a value > 0 in column D of Table 5, or the level of expression of at least two gene products having a value > 0 in column E of Table 5, or the level of expression of at least two gene products having a value > 0 in column F of Table 5, or the level of expression of at least two gene products having a value > 0 in column G of Table 5, or the level of expression of at least two gene products having a value > 0 in column H of Table 5, or the level of expression of at least two gene products

having a value > 0 in column I of Table 5, or the level of expression of at least two gene products having a value > 0 in column J of Table 5;

wherein the linear combination of the expression levels of the at least two gene products. that exceeds a threshold value is indicative of a patient that is a candidate for treatment with the human interleukin-6 receptor antibody; or that a patient that should be excluded from treatment.