(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
20 November 2008 (20.11.2008)

PCT

(10) International Publication Number
WO 2008/140484 A2

(51) International Patent Classification: Not classified

(21) International Application Number:
PCT/US2007/023675

(22) International Filing Date:
9 November 2007 (09.11.2007)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/858,147 9 November 2006 (09.11.2006) US

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, MT, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

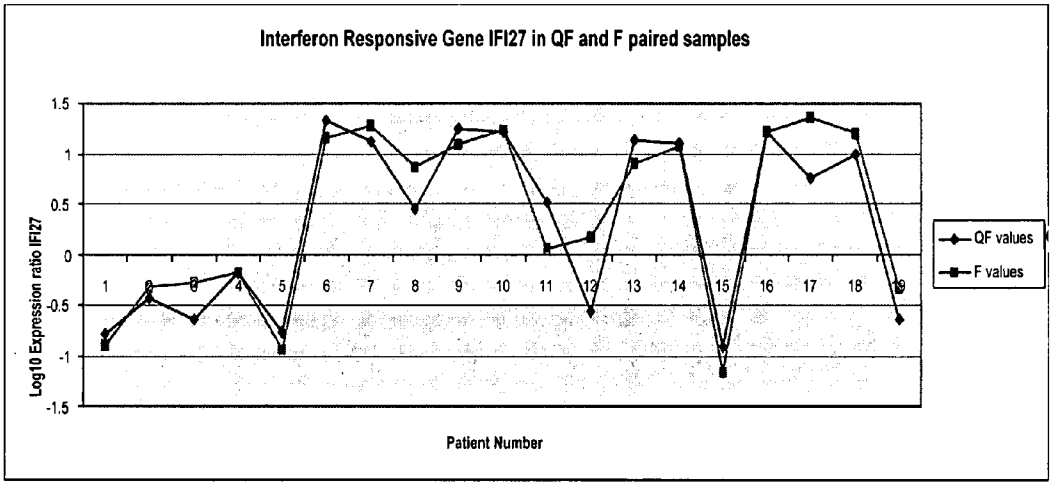
Published:

— *without international search report and to be republished upon receipt of that report*

[Continued on next page]

(54) **Title:** METHODS FOR DIAGNOSING AND MONITORING THE STATUS OF SYSTEMIC LUPUS ERYTHEMATOSUS

FIGURE 1



(57) **Abstract:** The invention presents a method of diagnosing or monitoring the status of systemic lupus erythematosus (SLE) in a subject or patient comprising detecting the expression of all genes of a diagnostic set in the subject or patient wherein the diagnostic set comprises two or more genes having expression correlated with the classification or status of SLE; and diagnosing or monitoring the status of SLE in the subject or patient by applying at least one statistical method to the expression of the genes of the diagnostic set.

WO 2008/140484 A2

— *with sequence listing part of description published separately in electronic form and available upon request from the International Bureau*

METHODS FOR DIAGNOSING AND MONITORING THE STATUS OF SYSTEMIC LUPUS ERYTHEMATOSUS

PRIORITY

[0001] This application claims the benefit of U.S. Prov. App. No. 60/858,147, filed November 9, 2006, which is incorporated by reference herein in its entirety.

TECHNICAL FIELD

[0002] The invention provides for the use of gene expression and statistical analysis to diagnose and monitor the status of systemic lupus erythematosus.

BACKGROUND OF THE INVENTION

[0003] Systemic lupus erythematosus (SLE) is an autoimmune rheumatic disease characterized by dysregulation of the immune system and differential expression of genes in immunological pathways. In the United States, SLE affects about 2 million patients and 90% of these patients are female. Targeted tissues and organs include the blood, central nervous system (CNS), joints, kidneys, lungs, skin, and vasculature. Symptoms include abnormal blood panels, arthralgias, atherosclerosis, CNS disorders, infections, joint pain, malaise, rashes, ulcers, and the production of autoantibodies. Since disease severity, symptomology, and response to therapy vary widely, SLE is difficult to diagnose, manage and treat.

[0004] As described in USSN 20040033498, SLE clearly involves differential gene expression in SLE patients as compared to normal controls. Two laboratories have reported on the role of the interferon (INF)-α inducible genes in SLE and on high levels of anti-RNA binding protein, anti-Ro antibodies, and renal disease (Baechler et al (2003) PNAS 100:2610-2615; Kirou et al (2004) Arthritis and Rheumatism 50:3958-3967). However, low positive correlation between disease activity and IFN-inducible genes, the apparent heterogeneity of SLE patients, and lack of longitudinal studies continue to present challenges for clinicians (Kirou et al. (2005) Arthritis and Rheumatism 52:1491-1503).

[0005] These challenges point to a need in the art for better diagnosis, characterization, and

follow-up of patients with SLE. To this end, longitudinal data from SLE patients was used with methods for detecting and analyzing gene expression to monitor status, quiescence versus flare, and to classify a patient as having type 1 SLE or type 2 SLE.

SUMMARY

[0006] The invention presents methods and compositions for diagnosing and monitoring systemic lupus erythematosus (SLE). The methods use gene expression based on nucleic acid or protein technologies, and statistical methods to classify patients as having type 1 SLE or type 2 SLE and to monitor disease activity, predict flare, and assess the efficacy of treatment administered to the patient.

[0007] The invention provides a method of diagnosing or monitoring the status of systemic lupus erythematosus (SLE) in a subject or patient includes detecting the expression of all genes of a diagnostic set in the subject or patient wherein the diagnostic set comprises two or more genes having expression correlated with the classification or status of SLE; and diagnosing or monitoring the status of SLE in the subject or patient by applying at least one statistical method to the expression of the genes of the diagnostic set. In one aspect, the statistical method is a prediction algorithm that produces a number or single value indicative of the status of SLE in the subject or patient. In another aspect, the statistical method further comprises classification of the subject or patient into one of at least two classes of SLE, and is optimized to maximize the separation among longitudinally stable classes of SLE. The method also provides a diagnostic set further comprising at least one gene selected from each of at least two gene clusters selected from cluster 1, cluster 2, cluster 3, cluster 4, cluster 5, cluster 6, cluster 7, cluster 8, cluster 9, cluster 10, cluster 11; cluster 12, cluster 13, cluster 14, and cluster 15 of Table 1. The invention further provides classification of the subject or patient into one of at least two classes of SLE further comprising detecting the expression of two or more gene whose expression correlates with the expression of the IFI27 from about 0.5 to about 1.0 and from about -0.5 to about -1.0 calculated using a Pearson correlation; and classifying a subject or patient as having type 1 or type 2 SLE based on the expression of the two or more genes. In one aspect, one of the two or more genes is selected from Table 2 and

the classifying step uses a linear algorithm to produce an interferon response (INFr) score wherein a high IFNr score is correlated with type I SLE and a low IFNr score is correlated with type II SLE. The invention additionally provides at least one linear algorithm producing an IFNr score comprising IFI27 + IFI144*(1.1296) + OAS3*(1.8136). The invention still further provides a Pearson correlation that is selected from a range of 0.5, 0.4, 0.3, and 0.2 of the expressed genes.

[0008] The invention provides a method of diagnosing or monitoring the status of systemic lupus erythematosus (SLE) in a subject or patient comprising detecting the expression of all genes of a diagnostic set in a subject or patient wherein the diagnostic set includes at least one gene from each of at least two gene clusters selected from cluster 1, cluster 2, cluster 3, cluster 4, cluster 5, cluster 6, cluster 7, cluster 8, cluster 9, cluster 10, cluster 11; cluster 12, cluster 13, cluster 14, and cluster 15 of Table 1; and diagnosing or monitoring the status of SLE in the subject or patient based on expression of the genes in the diagnostic set. In one aspect, the expression of all genes in the diagnostic set is detected using a nucleic acid technology further including hybridization in solution or on a substrate or amplification in a quantitative real-time polymerase chain reaction. In another aspect, expression of all genes is proportional to the amount of RNA isolated from a subject or patient sample further including a body fluid selected from whole blood or a blood fraction, ascites, cerebrospinal fluid, lymph, sputum, and urine or a tissue selected from central nervous system, joints, kidneys, liver, lungs, oral cavity, sinuses, skin, and vasculature obtained by any sampling means selected from aspiration of a body fluid, a biopsy of a tissue or an organ, drawing of peripheral blood, endoscopy, and lavage followed by aspiration.

[0009] The invention provides for the use of at least one primer or probe set to detect the expression of each of the genes in the diagnostic set. In one aspect, the primers or probe sets are oligonucleotides selected from natural or synthetic cDNA, genomic DNA, locked nucleic acids, peptide nucleic acids, and RNA and can be used in a diagnostic kit. The invention also provides a method of diagnosing a patient as having a longitudinally stable classification of SLE by detecting the expression of two or more genes whose expression correlates with the

expression of the IFI27 from about 0.5 to about 1.0 and from about -0.5 to about -1.0 calculated using Pearson correlation; and diagnosing the patient as having type I or type II SLE based on analyzing the expression of the two or more genes using a statistical method. The invention further provides for assigning a subject or patient to a clinical trial based on their classification as type 1 SLE or type 2 SLE.

[0010] The invention provides for monitoring the status of SLE in a subject or patient by predicting incipient flare or disease activity, and assessing response to a therapeutic agent administered to the patient or to an immunosuppressant administered to a patient. The invention also provides for screening a subject exhibiting symptoms of a rheumatic disease selected from ankylosing spondylitis, dermatomyositis, autoimmune hepatitis, hepatitis-C (hep-C), polymyalgia rheumatica, polymyositis, rheumatoid arthritis (RA), scleroderma, systemic sclerosis, Sjogren's disease, systemic vasculitis, and Whipple's disease.

[0011] The invention provides method of producing a probe set for diagnosing or monitoring SLE in a subject or patient by selecting at least one gene from each of at least two of the gene clusters of Table 1 and at least two genes from Table 2; and producing a probe set consisting of at least one oligonucleotide that detects the expression of each of the selected genes. In one aspect, the probe set is used in a diagnostic kit.

[0012] The invention provides a method for predicting flare in a patient diagnosed with SLE by analyzing gene expression in a sample from the patient to produce a gene expression profile wherein a first portion of the analysis includes using expression of at least one gene selected from each of at least two of the clusters 1 through 15 of Table 1 and at least one statistical method to produce a patient expression profile, and a second portion of the analysis includes using expression of at least two genes selected from Table 2 and a linear algorithm to classify the patient as having type 1 SLE or type 2 SLE; and predicting flare by comparing the patient gene expression profile at least one reference profile. In one aspect, the reference profile is selected from at least one normal subject, at least one patient classified as having type 1 SLE with quiescent status, at least one patient classified as having type 1 SLE in flare, at least one patient classified as having type 2 SLE with quiescent status, at least one patient

classified as having type 2 SLE in flare.

BRIEF DESCRIPTION OF THE FIGURES

[0013] Figure 1 shows the Log_{10} expression ration for Interferon Responsive Gene IFI27 in QF and F paired samples.

[0014] Figure 2 shows the Interferon Response (INFr) score for normal controls and SLE patient.

[0015] Figure 3 shows the bimodal distribution for IFI27, IFI44, and OAS3 of SLE patients.

DESCRIPTION OF THE TABLES

[0016] Table 1 shows 15 clusters of correlated genes that are differentially expressed as SLE patients change status from quiescence to flare and can be used with at least one statistical method to predict flare. Cell types corresponding to each cluster are indicated as well as Array ID, Genbank ID, Gene ID, and the source of each gene. 60-mer sequences, which are unique identifiers for the genes, are also displayed in Table 1. The Sequence Listing provides the 60-mer sequences listed in Table 1.

[0017] Table 2 lists INFr genes with expression that positively correlates with IFI27 expression and can be used with at least one statistical method to classify a patient as having either type 1 SLE or type 2 SLE. 60-mer sequences, which are unique identifiers for the genes, are also displayed in Table 2.

[0018] Table 3 presents longitudinal data for SLE patients showing stability in an individual's INFr score and its lack of correlation with SLEDAI.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

[0019] Unless defined otherwise, all scientific and technical terms are understood to have the same meaning as commonly used in the art to which they pertain. In this application, the singular form—"a", "an", and "the"--includes plural references unless the context clearly dictates otherwise. For example, the term "an agent" includes a plurality of agents and

mixtures thereof. For the purpose of this invention, the following terms are defined below.

[0020] "Amplification" refers to any device, method or technique that can make copies of a nucleic acid. It can be achieved using polymerase chain reaction (PCR) techniques such as linear amplification (cf. USPN 6,132,997), rolling circle amplification, and the like. Further, amplification and detection can be combined as in TAQMAN Real-Time PCR (RT-PCR) using the TAQMAN protocols and the Prism 7900HT Sequence detection system and software (Applied Biosystems (ABI), Foster City CA).

[0021] "Array" refers to an ordered arrangement of at least two reagents--antibodies, nucleic acids or proteins--in solution or on a substrate where at least one of the reagents represents a normal control and the other, a sample of diagnostic or prognostic interest. The ordered arrangement insures that the size and signal intensity of each labeled complex, formed between at least one reagent and at least one nucleic acid or protein to which the reagent specifically binds, is individually distinguishable.

[0022] The term "diagnostic set" generally refers to a set of two or more genes that, when evaluated for differential expression of their products, collectively yields predictive data. Such predictive data typically relates to diagnosis, prognosis, monitoring of therapeutic outcomes, and the like. In general, the components of a diagnostic set are distinguished from nucleotide sequences that are evaluated by analysis of the DNA to directly determine the genotype of an individual as it correlates with a specified trait or phenotype, such as a disease, in that it is the pattern of expression of the components of the diagnostic set, rather than mutation or polymorphism of the DNA sequence that provides predictive value. It will be understood that a particular component (or member) of a diagnostic set can, in some cases, also present one or more mutations, or polymorphisms that are amenable to direct genotyping by any of a variety of well known analysis methods, e.g., Southern blotting, RFLP, AFLP, SSCP, SNP, and the like.

[0023] "cDNA" refers to an isolated polynucleotide, nucleic acid molecule, or any fragment or complement thereof that originated recombinantly or synthetically, is double- or single-stranded, represents coding and noncoding 3' or 5' sequence, and generally lacks introns.

[0024] "Classification" refers to the categorization of a subject or patient based on gene expression as having type 1 SLE or type 2 SLE. SLE is considered to be type 1 if it primarily involves Type 1 T helper cells and type 1-linked cytokines, such as interferon-gamma. SLE is considered to be type 2 if there is more involvement of Type 2 helper cells which activate an antibody-driven immune response.

[0025] "Expression" refers differential gene expression--an increased (i.e., upregulated) or a decreased (i.e., downregulated) expression as detected by absence, presence, or change in the amount of messenger RNA or protein for a gene in a sample.

[0026] "Flare" refers to onset of disease activity in a patient diagnosed with an immune disorder; in SLE, mild flare has been defined by an increase in systemic lupus erythematosus disease activity index (SLEDAI) by $\geq$ four units over a previous score for that patient and severe flare, as an increase in SLEDAI by $\geq$ 12 units. SLEDAI represents a composite assessment of disease activity based on 16 clinical manifestations and eight laboratory measures including two immunological tests with a possible range of overall score from 0 to 105.

[0027] A "gene expression profile" refers to the identification, characterization, quantification, and representation of a plurality of genes expressed in a sample as measured using nucleic acid or protein technologies. A nucleic acid expression profile is produced using mature mRNA transcript and/or regulatory sequences such as promoters, enhancers, introns, mRNA-processing intermediates, and 3' untranslated regions in nucleic acid technologies. A protein expression profile, although time delayed, mirrors the nucleic acid expression profile and is produced using protein technologies and proteins and/or antibodies to detect protein expression in a sample. Results from subject or patient samples are compared with reference profiles based on normal, diseased, or treated samples.

[0028] "Immunosuppressant" refers to any therapeutic agent that suppresses immune response in a patient such as anticoagulents, antimalarials, heart drugs, non-steroidal anti-inflammatory drugs (NSAIDs), and steroids including but not limited to aspirin, azathioprine, chloroquine, corticosteroids, cyclophosphamide, cyclosporin A, dehydroepiandrosterone,

deoxyspergualin, dexamethasone, everolimus, fenoprofen, hydralazine, hydroxychloroquine, immunoglobulin, ibuprofen, indomethacin, leflunomide, ketoprofen, meclophenamate, mepacrine, 6-mercaptopurine, methotrexate, mizoribine, mycophenolate mofetil, naproxen, prednisone, methyprenisone, rapamycin (sirolimus), solumedrol, tacrolimus (FK506), thymoglobulin, tolmetin, tresperimus, triamcinoline, and the like.

[0029] "Longitudinally stable" refers to the behavior of one or more interferon response (INFr) genes expressed in samples collected at different time points from an individual or data derived from those samples.

[0030] "Diagnosis or monitoring" refers to the detection of gene expression at the nucleic acid or protein level to provide useful information about an individual's medical status. Monitoring status can include determination of prognosis or complication, following progression of a disease, prediction of disease activity or flare, providing information relating to a patient's health over a period of time, selection of a therapeutic agent and/or determining response or resistance to that agent, selecting an individual patient or small subsets of patients most likely to benefit from an experimental therapy or clinical trial, and determining classification of a patient as having a particular disease status.

[0031] "Normal" refers to the medical status of an individual, or a sample from an individual, who does not have SLE or any diagnosis or manifestation of an infection or immune disorder and can be used as a negative control.

[0032] "Nucleic acid technology" refers to any device, means or system used to detect gene expression or produce a gene expression profile and includes but is not limited to methods using arrays for amplification in PCR, TAQMAN RT-PCR, quantitative RT-PCR, and the like, or hybridization in solution or on a substrate containing cDNAs, genomic DNAs, locked nucleic acids, oligonucleotide primers or probes, peptide nucleic acids, polynucleotides, and RNAs of any length either natural or synthetic, and the like.

[0033] "Patient" refers to a human subject who is genetically predisposed to a rheumatic disease or has been diagnosed with a SLE.

[0034] "Prediction" refers to the use of gene expression assessed using nucleic acid or protein technologies, algorithms and statistical analyses to provide information about an individual's status; for example, being predisposed to, diagnosed with, or effectively treated for disease activity or flare.

[0035] "Protein technology" includes but is not limited to activity assays, affinity antibody or protein arrays, chromatographic separation, colorimetric assays, two-dimensional gel electrophoresis, enzyme-linked immunosorbent assays (ELISA), fluorescent-activated cell sorting (FACS), mass spectrophotometric detection, western analysis, and the like.

[0036] A "reference profile" refers to gene expression or gene expression profiles from well-characterized normal, diseased or treated samples taken from at least one subject and giving repeatable results whenever used in or with a particular nucleic acid or protein technology.

[0037] A "rheumatic disease" is a condition or disorder selected from ankylosing spondylitis, dermatomyositis, autoimmune hepatitis, hepatitis-C (hep-C), polymyalgia rheumatica, polymyositis, rheumatoid arthritis (RA), scleroderma, systemic sclerosis, Sjogren's disease, systemic vasculitis, Whipple's disease and the like.

[0038] "Sample" is used in its broadest sense and refers to any biological material used to obtain histological information or to measure gene expression obtained by any means from a subject. A sample can be a body fluid such as ascites, bile, blood, cerebrospinal fluid, synovial fluid, lymph, pus, semen, sputum, urine; the soluble fraction of a cell preparation, an aliquot of media in which cells were grown; a chromosome, an organelle, or membrane isolated or extracted from a cell; cDNA, genomic DNA, or RNA in solution or bound to a substrate; a cell; a tissue biopsy, and the like. Preferred samples for diagnosis, prognosis, or monitoring of SLE patients are leukocytes or serum derived from whole blood, biopsies of the central nervous system (CNS), joints, kidneys, liver, lungs, oral cavity, sinuses, skin, vasculature, and any other tissues or organs affected by SLE.

[0039] "Sampling means" refers to aspiration, biopsy, endoscopy, lavage, needle aspiration or biopsy, puncturing with a lancet; bleeding, ejaculating, expectorating, seeping, or urinating

into or onto a collection device, container, substrate, and the like.

[0040] "Status" refers to the deterioration, improvement, progression, remission, or stability of a patient with SLE, as determined from analyzing one or more samples from that patient. Status, or a change therein, can be used to evaluate the need for administration of a therapeutic agent, to adjust dosage of such an agent, to change or use another agent or treatment regime, and the like.

[0041] "Statistical methods" include but are not limited to analysis of variance, classification algorithms, classification and regression trees, Fisher's Exact Test, linear algorithm, linear discriminatory analysis, linear regression, logistic algorithm, multiple regression, nearest shrunken centroids classifier, Pearson correlation, prediction algorithm, significance analysis of microarrays, one-tailed T-tests, two-tailed T-tests, voting algorithm, Wilcoxon's signed ranks test, and the like.

[0042] "Substrate" refers to any rigid or semi-rigid support to which antibodies, nucleic acids or proteins are bound and includes magnetic or nonmagnetic beads, capillaries or other tubing, chips, fibers, filters, gels, membranes, microparticles, plates, polymers, slides, and wafers with a variety of surface forms including channels, columns, pins, pores, trenches, wells and the like.

[0043] "Therapeutic agent" refers to any pharmaceutical molecule or compound that will bind specifically to a polynucleotide or to an epitope of a protein and stabilize or modulate the activity of the polynucleotide or protein. It can be composed of inorganic and/or organic substances including minerals, cofactors, nucleic acids, proteins, carbohydrates, fats, and lipids and includes but is not limited to Ace inhibitors, aspirin, azathioprine, B7RP-1-fc, ß-blockers, brequinar sodium, campath-1H, celecoxib, chloroquine, corticosteroids, coumadin, cyclophosphamide, cyclosporin A, dehydroepiandrosterone, deoxyspergualin, dexamethasone, diclofenac, dolobid, etodolac, everolimus, FK778, feldene, fenoprofen, flurbiprofen, heparin, hydralazine, hydroxychloroquine, CTLA-4 or LFA3 immunoglobulin, ibuprofen, indomethacin, ISAtx-247, ketoprofen, ketorolac, leflunomide, meclophenamate, mefenamic acid, mepacrine, 6-mercaptopurine, meloxicam, methotrexate, mizoribine, mycophenolate

mofetil, naproxen, oxaprozin, Plaquenil, NOX-100, prednisone, methyprenisone, rapamycin (sirolimus), sulindac, tacrolimus (FK506), thymoglobulin, tolmetin, tresperimus, UO126, and antibodies including but not limited to alpha lymphocyte antibodies, adalimumab, anti-CD3, anti-CD25, anti-CD52 anti-IL2R, and anti-TAC antibodies, basiliximab, daclizumab, etanercept, hu5C8, infliximab, OKT4, natalizumab and the like.

DETAILED DESCRIPTION OF THE INVENTION

Description

[0044] Microarray experiments have been used to find genes that are differentially expressed in patients diagnosed with systemic lupus erythrematosus (SLE). These genes were described in USPN 6,905,827 and USSN 10/990,298, each incorporated by reference herein in its entirety.

[0045] The invention provides methods of diagnosing or monitoring the status of SLE in a subject or patient by detecting the expression of all genes of a diagnostic set in the subject or patient wherein the diagnostic set has two or more genes having expression correlated with the classification or status of SLE; and diagnosing or monitoring the status of SLE in the subject or patient by applying at least one statistical method to the expression of the genes of the diagnostic set.

[0046] The methods of the invention also include classifying the subject or patient as having type 1 SLE or type 2 SLE, predicting flare, and monitoring disease activity and treatment efficacy.

Diagnostic Genes of the Invention

[0047] The invention provides diagnostic sets containing genes that can be used to diagnosis and monitor SLE disease status. The diagnostic sets can also be used to predict occurrence and future complication of the disease.

[0048] Diagnostic genes were identified and validated for use in diagnosing and monitoring of SLE status by identifying genes for which a correlation exists between the SLE status of an individual as determined based on various disease criteria and the individual's expression of

RNA or protein products corresponding to the gene. Disease criteria may include clinical data such as symptom rash, joint pain, malaise, rashes, blood counts (white and red), tests of renal function (e.g. creatinine, blood urea nitrogen, creative clearance), data obtained from laboratory tests, including complete blood counts with differentials, CRP, ESR, ANA, Serum IL6, Soluble CD40 ligand, LDL, HDL, Anti-DNA antibodies, rheumatoid factor, C3, C4, serum creatinine and any medication levels, the need for pain medications, cumulative doses or immunosuppressive therapy, symptoms or any manifestation of carotid atherosclerosis (e.g. ultrasound diagnosis or any other manifestations of the disease), data from surgical procedures such as gross operative findings and pathological evaluation of resected tissues and biopsies (e.g., renal, CNS), information on pharmacological therapy and treatment changes, clinical diagnoses of disease "flare", hospitalizations, death, response to medications, quantitative joint exams, results from health assessment questionnaires (HAQs), and other clinical measures of patient symptoms and disability. Disease criteria also include the clinical score known as SLEDAI (Bombadier C, Gladman D D, Urowitz M B, Caron D, Chang C H and the Committee on Prognosis Studies in SLE: Derivation of the SLEDAI for Lupus Patients. Arthritis Rheum 35:630-640, 1992.).

[0049] The diagnostic genes of this invention include sequences corresponding those provided by the accession numbers and Unigene numbers provided in Table 1 and 2. The 60-mer sequences provided in the Tables are unique identifiers for the diagnostic genes of this invention. Therefore, the diagnostic genes of this invention also include sequences containing the 60-mer sequence provided in the Tables. In other words, the diagnostic genes may be partially or totally contained in (or derived from) the full-length gene sequences referenced in Tables 1 and 2.

[0050] In certain embodiments, the diagnostic genes of this invention include any sequences whose expression correlates with the expression of all genes which correlate with IFI27, such as the sequences provided by the accession numbers and Unigene numbers provided in Table 2.

[0051] Homologs and variants of the nucleic acid molecules in Table 1 and Table 2 may also be part of the diagnostic gene set. Homologs and variants of these nucleic acid molecules

will possess a relatively high degree of sequence identity when aligned using standard methods. The sequences encompassed by the invention have at least 40-50, 50-60, 70-80, 80-85, 85-90, 90-95, or 95-100% sequence identity to the sequences disclosed herein.

[0052] The diagnostic gene set may also include other genes that are coexpressed with the correlated sequence or full-length gene. Genes may share expression patterns because they are regulated in the same molecular pathway or in the same cell type. Because of the similarity of expression behavior, these genes are identified as surrogates in that they can substitute for a diagnostic gene in a diagnostic gene set.

[0053] In some embodiments, diagnostic genes of the invention are used as a diagnostic gene set in combination with genes that are known to be associated with a disease state ("known markers"). The use of the diagnostic genes in combination with the known markers can provide information that is not obtainable through the known markers alone.

Gene Clusters

[0054] In some embodiments, the diagnostic genes of this invention are segregrated into "clusters". In preferred embodiments the diagnostic genes of this invention are sorted into clusters as indicated in Table 1 and diagnostic gene sets of this invention include at least one gene from each of at least two of gene clusters 1 through 15.

[0055] As used herein the term "gene cluster" or "cluster" refers to a group of genes related by expression pattern. In other words, a cluster of genes is a group of genes with similar regulation across different conditions, such as a patient having SLE or a patient without SLE. The expression profile for each gene in a cluster should be correlated with the expression profile of at least one other gene in that cluster. Correlation may be evaluated using a variety of statistical methods.

[0056] As used herein the term "surrogate" refers to a gene with an expression profile such that is so highly correlated with gene expression of another gene that it can substitute for a diagnostic gene in a diagnostic assay. Such genes are typically members of the same gene cluster as the diagnostic gene. For each member of a diagnostic gene set, a set of potential surrogates can be identified through identification of genes with similar expression patterns as

described below.

[0057] Many statistical analyses produce a correlation coefficient to describe the relatedness between two gene expression patterns. Patterns may be considered correlated if the correlation coefficient is greater than or equal to 0.8. In preferred embodiments, the correlation coefficient should be greater than 0.85, 0.9 or 0.95. Other statistical methods produce a measure of mutual information to describe the relatedness between two gene expression patterns. Patterns may be considered correlated if the normalized mutual information value is greater than or equal to 0.7. In preferred embodiments, the normalized mutual information value should be greater than 0.8, 0.9 or 0.95. Patterns may also be considered similar if they cluster closely upon hierarchical clustering of gene expression data (Eisen et al. 1998). Similar patterns may be those genes that are among the 1, 2, 5, 10, 20, 50 or 100 nearest neighbors in a hierarchical clustering or have a similarity score (Eisen et al. 1998) of >0.5, 0.7, 0.8, 0.9, 0.95 or 0.99. Similar patterns may also be identified as those genes found to be surrogates in a classification tree by CART (Breiman et al. 1994).

[0058] Often, but not always, members of a gene cluster have similar biological functions in addition to similar gene expression patterns. For example, all genes in a particular cluster may be associated with a particular biological pathway or cell type. Representative cell types associated with diagnostic genes of this invention include granulocytes, NK cells, red blood cells, and platelets. Is is expected that the expression pattern of other genes in the same pathway or cell type will also be part of the same cluster and may be useful as surrogates.

[0059] Correlated genes, clusters and surrogates are all useful as diagnostic genes of the invention. These surrogates may be used as diagnostic genes in an assay instead of, or in addition to, the diagnostic genes for which they are surrogates.

[0060] Clusters also provide a means to ensure that the diagnostic gene sets do not contain redundant information. Diagnostic gene sets of the invention therefore preferably include genes from different clusters. For example, diagnostic gene sets of the invention preferably include at least one gene from at least two gene clusters.

Primer and Probe Sets

[0061] The invention further provides methods for producing diagnostic primer sets or probe sets. It is understood that a probe includes any reagent capable of specifically identifying genes in diagnostic setss, and include but are not limited to DNA, RNA, cDNA, splice variants, primers, probe sets, peptide nucleic acids, locked nucleic acids; amplicons, synthetic oligonucleotide, and partial or full-length nucleic acid sequences. In addition, the probe may identify the protein product of a diagnostic gene, and include, for example, antibodies and other affinity reagents. In some applications, a probe set may include one or more oligonucleotide that detects the expression of one or more of the selected genes for the diagnostic set.

[0062] It is also understood that each probe can correspond to one gene, or multiple probes can correspond to one gene, or both, or one probe can correspond to more than one gene.

[0063] In some embodiments, a diagnostic probe set is immobilized on an array. The array may be a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, a polynucleotide array or a cDNA array, a microtiter plate, a pin array, a bead array, a membrane or a chip.

Obtaining DNA, RNA and Protein Samples for Detection of Expression

[0064] Gene expression can be evaluated at the level of DNA, or RNA or protein products. A variety of techniques are available for the isolation of DNA, RNA and protein from bodily fluids.

[0065] A variety of techniques are available for the isolation of RNA from samples. Any technique that allows isolation of mRNA from cells (in the presence or absence of rRNA and tRNA) can be utilized. For example, by means of aspiration of body fluid, biopsy of a tissue or organ, drawing of peripheral blood, endoscopy, and lavage followed by aspiration, RNA can be isolated from ascites, bile, blood, cerebronspinal fluid, lymph, sputum, and/or urine. By the same methods, RNA can also be isolated from the central nervous system, joints, kidneys, liver, lungs, oral cavity, sinuses, skin, and vasculature.

Methods for Obtaining Expression Data

[0066] Numerous methods for obtaining expression data are known, and any one or more of these techniques, singly or in combination, are suitable for detecting expression in the context of the present invention.

[0067] For example, expression patterns can be evaluated by northern analysis, PCR, RT-PCR, Taq Man analysis, FRET detection, monitoring one or more molecular beacons, hybridization to an oligonucleotide array, hybridization to a cDNA array, hybridization to a polynucleotide array, hybridization to a liquid microarray, hybridization to a microelectric array, cDNA sequencing, clone hybridization, cDNA fragment fingerprinting, serial analysis of gene expression (SAGE), subtractive hybridization, differential display and/or differential screening (see, e.g., Lockhart and Winzeler (2000) Nature 405:827-836, and references cited therein). Oligonucleotide hybridization may occur in solution or on substrates including, but not limited to magnetic or nonmagnetic beads, chips, fibers, filters, gels, membranes, microparticles, plates, polymers, slides, capillary tubing, and wafers with surface features selected from channels, columns, pins, pores, trenches, and wells.

[0068] It is understood that for detection of gene expression, variations in the disclosed sequences will still permit detection of gene expression. The degree of sequence identity required to detect gene expression varies depending on the length of the oligomer. For a 60 mer, 6-8 random mutations or 6-8 random deletions in a 60 mer do not affect gene expression detection. Hughes, T R, et al. "Expression profiling using microarrays fabricated by an ink-jet oligonucleotide synthesizer. Nature Biotechnology, 19:343-347(2001). As the length of the DNA sequence is increased, the number of mutations or deletions permitted while still allowing the detection of gene expression is increased.

[0069] Alternatively, expression at the level of protein products of gene expression can be performed. For example, protein expression in a disease patient can be evaluated by one or more methods including, but not limited to Western analysis, two-dimensional gel analysis, chromatographic separation, mass spectrometric detection, protein-fusion reporter constructs, colorimetric assays, binding to a protein array and characterization of polysomal mRNA. One particularly favored approach involves binding of labeled protein expression products to an array of antibodies specific for members of the candidate library. Methods for producing and

evaluating antibodies are widespread in the art, see, e.g., Coligan, supra; and Harlow and Lane (1989) Antibodies: A Laboratory Manual, Cold Spring Harbor Press, NY ("Harlow and Lane"). Additional details regarding a variety of immunological and immunoassay procedures adaptable to the present invention by selection of antibody reagents specific for the products of candidate nucleotide sequences can be found in, e.g., Stites and Terr (eds.)(1991) Basic and Clinical Immunology, 7.sup.th ed., and Paul, supra. Another approach uses systems for performing desorption spectrometry. Commercially available systems, e.g., from Ciphergen Biosystems, Inc. (Fremont, Calif.) are particularly well suited to quantitative analysis of protein expression. Indeed, Protein Chip.RTM. arrays (see, e.g., the website, ciphergen.com) used in desorption spectrometry approaches provide arrays for detection of protein expression. Alternatively, affinity reagents (e.g., antibodies, small molecules, etc.) are developed that recognize epitopes of the protein product. Affinity assays are used in protein array assays, e.g. to detect the presence or absence of particular proteins. Alternatively, affinity reagents are used to detect expression using the methods described above. In the case of a protein that is expressed on the cell surface of leukocytes, labeled affinity reagents are bound to populations of leukocytes, and leukocytes expressing the protein are identified and counted using fluorescent activated cell sorting (FACS).

Expression Profiles

[0070] Expression patterns, or profiles, of a plurality of genes corresponding to members of the diagnostic set are evaluated in one or more SLE patients. These expression patterns constitute a set of relative or absolute expression values for some number of RNA or protein products corresponding to the plurality of genes evaluated, which is referred to herein as the subject's "expression profile" for those genes. While expression patterns for as few as one independent member of the diagnostic set can be obtained, it is generally preferable to obtain expression patterns corresponding to a larger number of genes, e.g., about 2, about 5, about 10, about 20, about 50, about 100, about 200, about 500, or about 1000, or more. The expression pattern for each differentially expressed component member of the set provides a finite specificity and sensitivity with respect to predictive value, e.g., for diagnosis, prognosis, monitoring, and the like.

Evaluation of Expression Data and Profiles

[0071] Expression profiles can be evaluated by qualitative and/or quantitative measures. Certain techniques for evaluating gene expression (as RNA or protein products) yield data that are predominantly qualitative in nature. That is, the methods detect differences in expression that classify expression into distinct modes without providing significant information regarding quantitative aspects of expression. For example, a technique can be described as a qualitative technique if it detects the presence or absence of expression of a diagnostic nucleotide sequence, i.e., an on/off pattern of expression. Alternatively, a qualitative technique measures the presence (and/or absence) of different alleles, or variants, of a gene product.

[0072] In contrast, some methods provide data that characterizes expression in a quantitative manner. That is, the methods relate expression on a numerical scale. It will be understood that the numerical, and symbolic examples provided are arbitrary, and that any graduated scale (or any symbolic representation of a graduated scale) can be employed in the context of the present invention to describe quantitative differences in nucleotide sequence expression. Typically, such methods yield information corresponding to a relative increase or decrease in expression.

[0073] Any method that yields either quantitative or qualitative expression data is suitable for evaluating expression of diagnostic nucleotide sequence in a SLE subject or patient. In some cases, e.g., when multiple methods are employed to determine expression patterns for a plurality of diagnostic nucleotide sequences, the recovered data, e.g., the expression profile for the nucleotide sequences is a combination of quantitative and qualitative data.

[0074] In some applications, expression of the plurality of diagnostic nucleotide sequences is evaluated sequentially. This is typically the case for methods that can be characterized as low- to moderate-throughput. In contrast, as the throughput of the elected assay increases, expression for the plurality of diagnostic nucleotide sequences in a sample or multiple samples of SLE subjects or patients is assayed simultaneously. Again, the methods (and throughput) are largely determined by the individual practitioner, although, typically, it is preferable to employ methods that permit rapid, e.g. automated or partially automated,

preparation and detection, on a scale that is time-efficient and cost-effective.

[0075] In one some embodiments, once expression levels for a diagnostic set of genes are determined, a diagnostic classifier (a mathematical function that assigns samples to diagnostic categories based on expression data) is applied to unknown sample expression levels in order to diagnose or monitor the status of the SLE in a subject or patient.

[0076] The diagnostic classifier is typically derived from a prediction algorithm derived from statistical methods including, but not limited to, analysis of variance, classification algorithms, classification and regression trees, Fisher's Exact Test, linear algorithm. linear discriminatory analysis, linear regression, logistic algorithm, multiple regression, nearest shrunken centroids classifier, Pearson correlation, prediction algorithm, significance analysis of microarrays, one-tailed T-test, two tailed T-tests, voting algorithm, Wilcoxon's signed ranks test and the like.

Expression Reference Standards

[0077] In other embodiments, comparison of patient gene expression with reference profiles is used to evaluate expression data and to monitor the status of SLE, to predict flare, and to assess treatment efficacy.

[0078] For example, expression profiles derived from a patient (i.e., subjects diagnosed with, or exhibiting symptoms of, or exhibiting a disease criterion, or under a doctor's care for a disease) sample are compared to a control or standard expression RNA to facilitate comparison of expression profiles (e.g. of a set of candidate nucleotide sequences) from a group of patients relative to each other (i.e., from one patient in the group to other patients in the group, or to patients in another group).

[0079] The reference RNA used should have desirable features of low cost and simplicity of production on a large scale. Additionally, the reference RNA should contain measurable amounts of as many of the genes of the candidate library as possible.

[0080] For example, in one approach to identifying diagnostic gene sets and evaluating expression data, expression profiles derived from patient samples are compared to an expression reference "standard." Standard expression reference can be derived from samples

from at least one normal subject and from at least one patient diagnosed with SLE and include but are not limited to a gene expression from one or more patients with quiescent type 1 SLE, from one or more patients with quiescent type 2 SLE, from one or more patients with type 1 SLE showing increased disease activity or flare, from one or more patients with type 2 SLE showing increased disease activity or flare, from one or more patients with type 1 SLE that had been treated with an immunosuppressant, from one or more patients with type 2 SLE that had been treated with an immunosuppressant, from one or more patients with type 1 SLE that had been treated with a therapeutic agent, and from one or more patients with type 2 SLE that had been treated with a therapeutic agent..

[0081] Use of an expression reference standard is particularly useful when the expression of large numbers of nucleotide sequences is assayed, e.g. in an array, and in certain other applications, e.g. qualitative PCR, RT-PCR, etc., where it is desirable to compare a sample profile to a standard profile, and/or when large numbers of expression profiles, e.g. a patient population, are to be compared. Generally, an expression reference standard should be available in large quantities, should be a good substrate for amplification and labeling reactions, and should be capable of detecting a large percentage of candidate nucleic acids using suitable expression profiling technology.

[0082] Alternatively, the expression reference standard can be derived from any subject or class of subjects including healthy subjects or subjects diagnosed with the same or a different disease or disease criterion. Expression profiles from subjects in two distinct classes are compared to determine which subset of genes in the diagnostic set best distinguish between the two subject classes. It will be appreciated that in the present context, the term "distinct classes" is relevant to at least one distinguishable criterion relevant to a disease of interest, a "disease criterion." The classes can, of course, demonstrate significant overlap (or identity) with respect to other disease criteria, or with respect to disease diagnoses, prognoses, or the like. The mode of discovery involves, e.g., comparing the molecular signature of different subject classes to each other (such as patient to control, patients with a first diagnosis to patients with a second diagnosis, etc.) or by comparing the molecular signatures of a single individual taken at different time points. The invention can be applied to a broad range of

diseases, disease criteria, conditions and other clinical and/or epidemiological questions, as further discussed above/below.

[0083] In some applications, when a single patient sample is obtained, it may still be desirable to compare the expression profile of that sample to some reference expression profile. In this case, one can determine the change of expression between the patient's sample and a reference expression profile that is appropriate for that patient and the medical condition in question. For example, a reference expression profile can be determined for all patients without the disease criterion in question who have similar characteristics, such as age, sex, race, diagnoses, etc.

Classification of SLE Patients into Longitudinally Stable Classes of SLE

[0084] In some embodiments, the invention provides methods for diagnosis of a patient as having a longitudinally stable classification of SLE by detecting the expression of genes whose expression correlates with the expression of IFI27. In some embodiments, the method is practiced as part of a method to diagnose or monitor the status of SLE in a patient.

[0085] In preferred embodiments, a subject is classified into one of at least two classes of SLE by detecting the expression of at least two genes whose expression corrrelates with the expression of IFI27 from about 0.5 to about 1.0 and from about -0.5 to about -1.0 caclulated using Pearson correlation and classifying the subject as having type I or type II SLE based on the expression of these two genes. In preferred embodiments, the genes are provided in Table 2.

Pharmacogenomics

[0086] Pharmocogenomics is the study of the individual propensity to respond to a particular drug therapy (combination of therapies). In this context, response can mean whether a particular drug will work on a particular patient, e.g. some patients respond to one drug but not to another drug. Response can also refer to the likelihood of successful treatment or the assessment of progress in treatment. Titration of drug therapy to a particular patient is also included in this description, e.g. different patients can respond to different doses of a given

medication. This aspect may be important when drugs with side-effects or interactions with other drug therapies are contemplated.

[0087] Diagnostic gene sets are developed and validated for use in assessing whether a patient will respond to a particular therapy and/or monitoring response of a patient to drug therapy (therapies). Disease criteria correspond to presence or absence of clinical symptoms or clinical endpoints, presence of side-effects or interaction with other drug(s). The diagnostic nucleotide set may further include nucleotide sequences that are targets of drug treatment or markers of active disease.

[0088] Example 1 describes the SLE patients, criteria for their diagnosis, and collection and characterization of blood and tissue samples from normal subjects and patients in periods of quiescence and flare. Although analyses determined that expression profiles contained a subset of genes, designated interferon response genes (INFr), whose expression generally correlated with disease severity, but not with change in patient status from quiescence to flare. Based on this fact, subject and patient samples can be queried for expression of the subset of INFr genes.

[0089] Example 2 describes the analysis of gene expression in samples from SLE patients. Pearson correlation was used to identify 15 different, pathway or cell-type specific, gene clusters that were differentially expressed in patient samples during periods of disease quiescence versus periods when that patient was converting from quiescence to flare. These clusters are also shown and described in Table 1. Column 1 shows the number of the cluster; column 2, the array ID; column 3, the GenBank ID; column 4, the gene ID; and column 5, a short description of the gene.

[0090] To diagnose and monitor the status of a subject or patient, a sample from the subject or patient is analyzed for differential expression of at least one gene selected from each of at least two different gene clusters shown in Table 1. Comparison of patient gene expression with reference profiles can also serve to monitor the status of SLE, to predict flare, and to assess treatment efficacy.

[0091] Prediction algorithms were developed using gene expression representing quiescent

(QQ) versus flare (QF) samples. Multiple regression analysis was used to associate gene expression with flare, and linear regression was used to examine individual genes. In general, prediction algorithms were trained using 90% of the samples; and cross-validated, using 10% of samples in 100 iterations as explained in Example 3. Prediction algorithms can be also used to assess patient prognosis--presence or likelihood of developing premature carotid atherosclerosis or progressing to end-stage organ damage--and to monitor treatment of SLE patients. Of particular interest are samples and expression profiles from patients who responded to a given steroid or immunosuppressant treatment regime versus samples or profiles from those same patients where the medication stopped working or from different patients who did not respond or were resistant to a specific medication or treatment regime.

[0092] Gene expression was analyzed using at least one statistical method selected from analysis of variance, classification algorithms, classification and regression trees, Fisher's Exact Test, linear algorithm, linear discriminatory analysis, linear regression, logistic algorithm, multiple regression, nearest shrunken centroids classifier, Pearson correlation, prediction algorithm, significance analysis of microarrays, one-tailed T-tests, two-tailed T-tests, voting algorithm, Wilcoxon's signed ranks test and the like. One or more of these methods were used to process and evaluate the normal and patient samples and to choose those samples used as reference profiles.

[0093] Example 4 describes the classification of SLE patients into type 1 SLE and type 2 SLE is based on IFNr score. A linear algorithm was used in the analysis of the expression of at least two INFr genes selected from Table 2. Expression of IFI27 was chosen as the basis to which all of other genes expressed in SLE were compared, and Table 2 shows the 190 features (probes on a microarray) that represent those INFr genes positively correlated with IFI27 (cutoff of ≥ 0.5 or <-0.5 using Pearson correlation). Column 1 of Table 2 shows the feature ID on the Human Genome CGH 44A microarrays (Agilent Technologies, Palo Alto CA) array; column 2, the name of probe; column 3, symbol or identifier for the gene; column 5, description of the gene; and column 6, correlation with IFI27. For purposes of demonstration, IFI27 and the two other INFr genes highlighted in Table 2 were used to develop an exemplary

algorithm, IFI27 + IFI144*(1.1296) + OAS3* (1.8136), that can be used to produce an INFr score.

[0094] The analysis and validation of data from paired, longitudinal samples as described in Example 4 are summarized in Table 3. Exemplary data is shown for the first 25 of 81 patients. The data shows lack of correlation with SLEDAI and the stability of IFNr score in individual patients during periods of quiescence and flare. Regardless of disease activity or flare, a high INFr score classified a patient as having type 1 SLE, a condition characterized by more severe SLE symptoms such as increased organ involvement and dysfunction, low complement levels, and high titer of anti-double-stranded DNA (dsDNA) antibodies; and a low INFr score classified a patient as having type 2 SLE which is generally characterized by less severe symptoms. It is contemplated that many combinations of at least two INFr genes and algorithms developed using them can be used to classify SLE patients.

[0095] Examples 5-8 describe how normal and patient samples were purified and handled. Examples 9-11 describe the nucleic acid technologies (microarray and polymerase chain reaction) used to detect gene expression and produce gene expression patient and reference profiles.

[0096] Methods are presented for screening subjects for SLE, for classifying a patient already diagnosed with SLE as having type 1 SLE or type 2 SLE, for predicting disease activity or flare, for selecting an effective immunosuppressant and/or therapeutic agent for treatment of SLE, and for identifying subjects with SLE from subjects with other rheumatic diseases.

[0097] Useful reference profiles were derived from samples from at least one normal subject and from at least one patient diagnosed with SLE and include but are not limited to a gene expression from one or more patients with quiescent type 1 SLE, from one or more patients with quiescent type 2 SLE, from one or more patients with type 1 SLE showing increased disease activity or flare, from one or more patients with type 2 SLE showing increased disease activity or flare, from one or more patients with type 1 SLE that had been treated with an immunosuppressant, from one or more patients with type 2 SLE that had been

treated with an immunosuppressant, from one or more patients with type 1 SLE that had been treated with a therapeutic agent, and from one or more patients with type 2 SLE that had been treated with a therapeutic agent.

[0098] Reagents used to establish a gene expression profile include but are not limited to: 1) genes and their splice variants, primers, probe sets, peptide nucleic acids, locked nucleic acids and amplicons that can be used in nucleic acid technologies including but not limited to hybridization on arrays and amplification using quantitative RT-PCR; and 2) proteins and their fragments, antibodies, and affinity reagents that can be used in protein technologies including but not limited to protein or antibody arrays and enzyme-linked immunosorbent assays (ELISAs). These reagents can be used in assays or diagnostic kits to screen subjects for SLE.

[0099] Assays or diagnostic kits based on the primers and probe sets as described in Example 9 can be used with a sample from a subject with symptoms of a rheumatic disease to diagnose, classify or rule out SLE; and with a sample from a patient diagnosed with type 1 SLE or type 2 SLE to select a clinical trial, to predict flare, to detect immunosuppressant responsiveness, to determine efficacy of a therapeutic agent, to design treatment regimes, to monitor the status of the patient or treatment regime. In one alternative, the diagnostic kit includes an array of nucleic acid molecules or antibodies; in another, the diagnostic kit includes probe sets for use in quantitative RT-PCR.

[0100] Pharmacogenomics is the study of an individual's response to a particular therapeutic agent, immunosuppressant or combinations of agents. In this context, response refers to whether a particular agent or drug will work better for a particular type 1 SLE or type 2 SLE patient. The methods disclosed provide for assigning a patient to a clinical trial based on classification as type 1 SLE or type 2 SLE and disease status (quiescent or flare).

[0101] Pharmacogenomics is also important in determining the dosage of a therapeutic agent based on classification and disease status of the patient. It is contemplated that a patient diagnosed with type 1 SLE will respond differently to a particular immunosuppressant or therapeutic agent than a patient diagnosed with type 2 SLE. Individual response must also be

taken into account relative to the side-effects or interactions of various immunosuppressant or therapeutic agents. Some potentially useful therapeutic agents and immunosuppressants are listed in the definitions and claims.

[0102] The present invention contains many preferred embodiments and includes material from patents, patent applications and other publications incorporated by reference in their entirety for all purposes, but especially for details in practicing the invention and known to those in the art.

EXAMPLES

Example 1 Characterization of Patients and Samples

[0103] Patients who met the American College of Rheumatology (ACR) criteria for the diagnosis of SLE (malar rash, discoid rash, photosensitivity, oral ulcers, arthritis, serositis, renal disorder, neurologic disorder, hematologic disorder, immunologic disorder, and antinuclear antibody) were identified (cf. Tan et al (1982) Arthritis Rheum 25:1271-7). After institutional review and approval, patients gave informed consent and were included in the Lupus Disease Activity Monitoring and Risk Stratification Archive Discovery Microarray Study. The samples and clinical data were available via the Autoimmune Biomarkers Collaborative Network (ABCoN).

[0104] Blood and/or tissue samples and clinical data have been collected from patients managed at Johns Hopkins Medical Center (JHMC) within the Hopkins Lupus Cohort. In this cohort, all SLE patients have been followed according to protocol with visits at a minimum of every 3 months. The table below has self-explanatory columns that show demographic information for the patients in the SLE cohort.

Age at Entry into cohort (yrs)		**Number (% of total cohort)**
	< 30	304 (32%)
	30 to 49	511 (53%)
	50 +	148 (15%)
Female		888 (92%)
Race		
	White	529 (55%)
	Black	403 (42%)
	Other	31 (3%)

Education	
< 12 yrs	124 (14%)
High School	281 (31%)
Some College	497 (55%)
Years in cohort	
0	191 (19%)
1 to 3	409 (41%)
4 +	391 (40%)
Number of cohort visits	
1	78 (8%)
2 to 8	320 (32%)
9 to 44	492 (50%)
45 +	101 (10%)
Years with SLE prior to cohort entry	
0	304 (31%)
1 to 4	325 (33%)
5+	362 (36%)

[0105] As seen above, the cohort was more or less racially balanced, and its individuals represented a broad socioeconomic spectrum. The patient samples and clinical data used in this investigation were from SLE patients who had been in the cohort for more than one year. In total, these patients visited the clinic 1782 times (an average of 5.9 quarterly visits for each patient). In the alternative, samples for training and validating prediction algorithms were obtained from the Autoimmune Disease Registry of the Hospital for Special Surgery (HSS; New York City NY).

[0106] Clinical data were examined for each patient in order to select samples for use in training or validation studies. Whereas additional samples can be added to the training set, a completely unique set must be used for validation. Both clinical and existing expression data were analyzed for 81 of the first 100 patients in the cohort and a subset of these patients was used for the training study. For the training study, the following classes of samples (Q=quiescent, F=flare) were defined as follows:

QF1: primary QF

quiescent sample that proceeds to flare within 150 days

No prior flare within 60 day

1 primary pair per patient only

SLEDAI $\geq$ 4

QF4: second QF1

A second, unique QF1 |F from the same patient

QF4 precedes a distinct F from the QF1

Can be combined with QF1 for analysis

QF5: earliest baseline

additional, earlier QF for a given QF1 |F

F: high current disease activity

SLEDAI increases ≥ 4 from previous visit

PGA (Physician's Global Assessment) = rating of disease activity as high or increasing

QQ: primary quiescent and stable

SLEDAI ≤ 4 and no flares in next 150 days or more

Sample Characteristics

[0107] The table below shows the comparison between the various classes. Column one lists the QF, F and QQ classes as defined above; column two, the groups within the class; column three, the number of patients in the class or group; column four, the average (avg) days (da) to flare; column five, the median days to flare; column six, the average (avg) increase in SLEDAI; column seven, the median (med) increase in SLEDAI; column eight, the average increase in SLEDAI at flare; and column nine, the number of visits prior to flare.

Class	Group	No.	Avg da to F	Med da to F	SLEDAI avg	SLEDAI med	F SLEDAI	Visits to F
QF	1	30	87	87	5.7	4	7.6	1.1
	4	3	78	84	6.7	4	8	1
	5	12	227	186				
F		37			7.7			
QQ		34	357	340				

Sample Matching

[0108] One of the most important class comparisons was QQ vs. QF. Molecular characterization of the samples that do not progress in disease activity or proceed to flare were particularly important for assessing risk and efficacy of treatment regime, determining prognosis, and the like. A typical subset of patients was characterized in the table below. In that the patients have similar clinical data, their samples showed that observed difference in class was due to activation at the molecular level (measured by gene expression) and not due

to observable differences. Column one shows class or T-test; column two, number of patients (No), column three, physician's global assessment (PGA); column four, SLEDAI score, column five, prednisone treatment (Pred); column six, percent of patients on immunosuppressant treatment (Immuno); column seven, percent of patients on intravenous treatment (IVS); and column seven, percent of the patients who are female.

	No	PGA	SLEDAI	Pred	Immuno	IVS	% Female
QF1	30	0.79	1.87	6.96	47%	17%	97
QQ	34	0.58	1.65	5.33	44%	12%	88
T-test		0.14	0.60	0.41	0.84	0.58	0.22
	No.	PGA	SLEDAI	Pred	Immuno	IVS	% Female
QF1+4	33	0.78	1.82	7.75	45%	45%	97%
QQ	34	0.58	1.65	5.33	44%	12%	88%
T-test		0.17	0.68	0.26	0.91	0.69	0.18

[0109] Although none of the clinical variables was statistically significant between classes, there was a slight trend towards more severe disease in the QF group. It must be noted that this trend was not clinically relevant; and as samples are added to the study, it is expected that even this slight trend will disappear.

[0110] The normal control sample was a pooled blood sample taken from equal numbers of male and female Expression Genetics employees. These donors were healthy at the time the sample was collected, and none had obvious disease symptoms or diagnosis of SLE or any other rheumatic disease.

Example 2 Analyses of Gene Expression Profiles of SLE Patients Proceeding to Flare.

[0111] The basis for diagnosing and monitoring the status of SLE in patients involved detecting differential gene expression between quiescence (QQ) and flare (QF) samples. K-means clustering of gene using GeneSpring GX 7.3 were done with the following criteria Number of clusters 15, Number of iterations 200, Similarity Measure Pearson Correlation and genes in which half of the samples did not have data were not used. Genes shown in Table 1were defined as those with a p-value ≤ 0.05 and a fold change ≥ 1.2. The genes were

clustered to group genes which represented a particular pathway or cell type. The table below shows the number of the cluster as presented in Table 1, the average Radius between the clusters and an all clusters average. Average Radius is calculated by the root mean square of the Euclidean distances between each gene and the centroid.

Cluster No	Cell Type	Average Radius
1	Granulocytes & B cells	5.15
2	NK cells	6.02
3	Granulocytes	7.23
4	Granulocytes	6.82
5	Platelet	6.31
6	All Cell Types	6.32
7	B cells	4.39
8	All Cell Types	6.85
9	B cells	5.88
10	All Cell Types	8.81
11	All Cell Types	8.34
12	All Cell Types	3.67
13	Red Blood Cells	6.87
14	Red Blood Cells	4.98
15	All Cell Types	2.19
All Clusters Ave		**5.99**

[0112] The genes shown in Table 1 were used with the statistical methods described below to diagnose and monitor the status of SLE patients, to predict flare and to assess treatment efficacy.

[0113] The various analyses were carried out using classification and prediction algorithms, software and programs including, but not limited to, analysis of variance, classification and regression trees (Brieman et al. (1984) Classification and Regression Trees, Wadsworth, Belmont CA), linear discriminatory analysis (Statsoft, Tulsa OK), multiple additive regression trees (Friedman (2002) Stanford University, Stanford CA), nearest shrunken centroids classifier (Tibshirani et al. (2002) PNAS 99:6567-6572), significance analysis of microarrays (Tusher et al. (2001) PNAS 98:5116-5121), one and two tailed T-tests, Wilcoxon's signed ranks test, and the like. The statistical analyses applied to both array and PCR expression data were also described in the Detailed Description of the Invention and in Example 5 of USPN 6,905,827 incorporated by reference herein in its entirety.

[0114] In addition to expression data, any piece of clinical data collected from patients can

be used in a correlation or classification analysis. Continuous variables including but not limited to albumin, autoantibodies, hemoglobin or other measures of organ function that contribute to SLEDAI score can be used for correlation analysis. In some cases, the logarithm of the values was used for the analysis. When these variables were included in the analysis, they were treated as another "gene". For example, samples from kidney biopsies can be used to divide SLE patients into groups with or without renal disease. From the analyses of clinical manifestations carried out in this study and differences in clinical manifestations reported by others, it is contemplated that categorical variables such gender, ethnicity and socioeconomic status can also contribute to classification, prediction of flare, and selection or modulation of effective therapeutics.

Example 3 Prediction Algorithms

[0115] After all the expression and clinical data were placed in a relational database, these data were used to build prediction algorithms. The prediction algorithms were applied to gene expression profiles from SLE patients converting from quiescence to flare to identify sets of differentially expressed genes for monitoring the status of SLE, specifically for predicting flare or disease activity and effective treatment regimes.

[0116] Once a set of genes and expression criteria for those genes have been established for classification, cross-validation was done. Validation of the algorithm by these means yielded an estimate of the predictive value of the algorithm on the target population. For example, a 10-fold cross-validation analysis excluded 10% of the training samples from the analysis, and the classification algorithm was built with the remaining 90%. The 10% of the samples that were initially excluded were then used as a test set for the algorithm. The process was repeated 10 times with 10% of the samples being used as a test set each time. Through this analysis, it was possible to derive a cross-validation error which helped estimate the robustness of the algorithm for use on previously untested samples (i.e., samples that were not included in the training analysis). Untested samples came from the JHMC or HSS archives. In the alternative, the samples can come from a new clinical study.

Example 4 Classification of Patients as Type 1 SLE and Type 2 SLE

[0117] Another step toward better monitoring the status of SLE patients was to classify them as having either type 1 SLE or type 2 SLE. A number of comparisons of data in the relational database were made and validated as described below.

Gene Expression Patterns

[0118] One of the comparisons of gene expression patterns was to analyze genes that were differentially expressed between paired QF1 and F samples from the same patient taken from about two to about six months apart. The first sample was from a time period when the patient's disease activity was low (SLEDAI 0-4), but the second sample from the same patient showed increased disease activity and a SLEDAI ≥ 4. In this process, examination of some of the genes known to be expressed in inflammation or immune disorders showed nearly parallel expression patterns in paired quiescent/flare (QF) and flare (F) patient. The expression of one of those genes, IFI27, is shown in Figure 1.

[0119] The x-axis of Figure 1 represents patient number and the y-axis, the Log_{10} expression ratio for IFI27. Figure 1 demonstrates that IFI27 was not differentially expressed according to disease activity or flare. Further examination of longitudinal data showed that expression of INFr genes placed SLE patients into at least two different groups.

INFr score

[0120] The relational database of SLE data was searched for genes whose expression correlated with IFI27 ≥ 0.5 or ≤ -0.5 using Pearson correlation; these designated INFr genes are listed in Table 2. Longitudinal data from an initial group of 81 patients covering a period of up to two years (including extra time points available in the QF4 and QF5 classes) was used to examine IFNr gene expression.

[0121] Although many different algorithms were contemplated, one exemplary algorithm was developed to demonstrate how to use three INFr genes to calculate an IFNr score. The genes that encode IFI27, IFI44 and OAS3, highlighted in Table 2, were used to develop the algorithm. The INFr score based on these three genes reflects the Log_{10} ratio of patient sample expression over reference sample expression on the microarray after normalization

using Feature Extraction v 7.5 software (Agilent Technologies). The standard deviation for each gene was normalized so that each of the genes would have the same influence on IFNr score. The exemplary algorithm is: IFI27 + IFI144*(1.1296) + OAS3*(1.8136).

[0122] The genes used to derive INFr score are described as follows: 1) IFI27 (also known as ISG12 and p27) maps to chromosome 14q32, the location of the serine protease inhibitor gene cluster. IFI27 is induced by alpha interferon and localizes to the nuclear membrane. Since IFI27 is expressed in breast, head and neck carcinomas, it has been used to predict patient sensitivity to cisplatin and paclitaxel; 2) IFI44 (also known as MTAP44) is induced by α and β interferons, but not by γ interferon and aggregates to form microtubular-like structures in hepatitus-C infected cells; and 3) OAS3 maps to chromosome 12q24.2 and is an interferon-induced protein that catalyzes the synthesis of 2'-5' oligomers of adenosine.

[0123] Table 3 presents longitudinal data for patients with SLE. Column one shows patient number; column two, ABCoN ID followed by sample number; column three, sample designated as quiescent (QF) or flare (F); column four, date sample taken; column five, SLEDAI score; column six, IFNr score (high or low); column seven, days from first sample; and INFr score. The cutoff for distinguishing between high IFNr and low IFNr scores was the average of all INFr scores. Table 3 demonstrated: 1) longitudinal stability of INFr score in an individual over time, 2) the existence of at least two types of SLE as defined by high and low expression of IFNr genes, and 3) lack of correlation between SLEDAI and IFNr scores as shown for patients 2, 4, 6, 9, and 15.

[0124] The change from high to low INFr score or from high to low to high INFr score as seen in the data for patients 10 and 13, respectively, were further analyzed. A Fisher's Exact Test was used to calculate a p-value for hypothesized random discordant results. The conversion of one high to low and one low to high produced the p-value = 0.000034 that the events happened at random.

[0125] Another way to look at IFNr score was to compare normal control and first visit patient samples. In Figure 2, all samples were sorted low to high and plotted according to INFr score. The normal subjects are presented on the left side of the graph, and the 81 SLE

(lupus) patients are presented on the right.

[0126] The x-axis shows the number assigned each normal subject or SLE patient, and the y-axis shows INFr score where the scale is fold. As shown on this graph, INFr scores varied by as much as 500-fold. Although they appeared healthy at the time of sampling, three of the normal subjects had slightly elevated IFNr scores that were attributed to infection, allergies, or other sub-acute, non-SLE conditions.

[0127] Since the INFr scores of the SLE patients appeared as a continuous slope in the graph above, the data was parsed. The graph for IFI27, IFI44, and OAS3 (Figure 3) clearly showed the bimodal distribution of SLE patients (type 2 SLE to the left of zero and type 1 SLE to the right, on the x-axis) when number of samples was graphed against $\log_{10}$ of the expression ratio.

[0128] Similar graphs or histograms can be plotted for any of the other INFr genes shown in Table 2, and any of these INFr genes can be used to develop an algorithm to classify SLE patients as type 1 SLE or type 2 SLE.

[0129] In further support of the stability of type 1 and type 2 SLE classification, a Fisher's Exact Test was applied to the hypothesis, "Do the highs stay high and the lows stay low?" The data presented in the table below produces a p-value = 8.01e-13 that further demonstrates the validity of the bimodal distribution and the presence of at least two groups, type 1 SLE and type 2 SLE.

		First	**First**
		high	low
Second	high	48	4
Second	low	4	25

[0130] Although SLEDAI scores are on average higher in type 1 SLE patients (who generally show more severe symptoms), SLEDAI did not correlate with high or low INFr score. The clinical manifestations that did associate with type 1 SLE included low serum complement levels, high anti-double stranded DNA antibodies, and more renal disease.

Example 5 Harvesting and Preparation of Blood Samples

[0131] One or more of the methods and/or procedures below were used to prepare samples from SLE patients and normal control subjects. In the first method, two tubes of blood were drawn from each patient or normal control subject using either a peripheral venous blood draw or directly from a large-bore intra-arterial or intravenous catheter inserted in the femoral artery or vein, subclavian vein or internal jugular vein. Care was taken to avoid sample contamination with heparin since it interferes with RNA preparation.

[0132] In the second method, 8 ml of blood was drawn into a VACUTAINER CPT tube (BD Biosciences (BD), San Jose CA) containing the anticoagulant sodium citrate, Ficoll Hypaque density fluid, and a thixotropic polyester gel barrier permeable upon centrifugation to red blood cells (RBCs) and granulocytes but not to mononuclear cells. The blood was mixed with the anticoagulant in the tube by inverting the tube 5-10 times. Then, mononuclear cells and plasma were separated using the following procedures.

[0133] In one procedure, the mononuclear cells and plasma moved to the top of the tube while the RBCs and the granulocytes were trapped beneath the gel barrier when the tube was centrifuged in a swinging bucket rotor at 1750 x g for 20 min at room temperature. After, the mononuclear cells and plasma were decanted into a 15 ml tube, 5 ml of phosphate-buffered saline (PBS) were added. The tubes was inverted 5 times and centrifuged for 5 min at 1750 x g to pellet the cells; the supernatant was discarded.

[0134] In a second procedure, the clear plasma layer that formed above the mononuclear cell layer during centrifugation was aspirated and discarded. Then the mononuclear cell layer was aspirated, and all of the mononuclear cells were washed from the surface of the gel barrier with PBS. Approximately 2 mls of mononuclear cell suspension were transferred to a microcentrifuge tube and centrifuged in a microcentrifuge for 3 min at 16,000 rpm to pellet the cells; the supernatant was discarded.

[0135] Following each of the methods and/or procedures above, 1.8 ml of RLT lysis buffer (Qiagen, Chatsworth CA) was added to the pellet, the cells and lysis buffer were pipetted up and down to ensure complete lysis. Cell lysate was frozen and stored at -80°C until total

RNA was isolated.

Example 6 RNA preparation

[0136] RNA was prepared from the RNA samples from SLE patients or normal controls using one of the following protocols. In the first protocol: 1) samples were thawed, 2) 4 ml of chloroform were added to each tube, 3) tubes were vortexed prior to centrifugation at 2000 x g for 5 min, and 5) the aqueous layer was moved to new tube and processed using the RNeasy Maxi kit (Qiagen) according to the manufacturer's instructions. RNA quality was assessed using spectrophotometry, A260/A280 spectrophotometric ratios were considered to be acceptable when they ranged between 1.6 and 2.0, and/or gel electrophoresis, when 2 µl of each sample were run on an agarose gel in the presence of ethidium bromide and no degradation of RNA and no DNA contamination were visible.

[0137] In the second protocol: 1) samples were thawed and held at room temperature for 5 min, 2) after adding 5 ml of chloroform, the samples were vortexed and incubated at room temperature for 3 min, 3) the aqueous layer was transferred to a new 50 ml tube and purified using the RNeasy Maxi kit (Qiagen), and 4) the columns were eluted twice with 1 ml RNAse free water and incubated for one min before each spin. RNAs isolated using the first and second protocols were combined when the normal control cell preparations demonstrated reproducibility. The RNAs were mixed in a 50 ml tube, aliquoted into two 15 ml storage or 1.5 ml microcentrifuge tubes (100 µl per), and stored at -80°C.

[0138] In the third protocol: total RNA was purified using the RNeasy Miniprep kit (Qiagen) according to the protocol provided. Cells were homogenized and DNAse treated on a QIASHREDDER columns (Qiagen) and purified RNA was eluted in 50 µl of water.

[0139] After the last two protocols, RNA using the Agilent 2100 bioanalyzer and RNA 6000 microfluidics chips (Agilent Technologies).

Example 7 cDNA Synthesis

[0140] cDNA was synthesized from RNA using reverse transcription with OLIGO-dT primers/random hexamers (Invitrogen, Carlsbad CA) at a final concentration of 0.5 ng/µl and

3 ng/μl, respectively.

[0141] For the first strand reaction, 0.5 μg of mononuclear RNA or 2 μg of whole blood RNA and 1 μl of the OLIGO-dT/random hexamers (Invitrogen) were added to water in a reaction tube to a final volume of 11.5 μl. The tube was incubated at 70°C for 10 min, chilled on ice, centrifuged, and 88.5 μl of first strand buffer mix (Invitrogen) was added to the tube.

[0142] The first strand buffer mix contained 1 x first strand buffer, 10 mM DTT (Invitrogen), 0.5 mM dATP (New England Biolabs (NEB), Beverly MA), 0.5 mM dGTP (NEB), 0.5 mM dTTP (NEB), 0.5 mM dCTP (NEB), 200 U of SUPERSCRIPT RNAse H reverse transcriptase (Invitrogen), and 18 U of RNAGUARD inhibitor (GE Healthcare (GEH), Piscataway NJ). After the reaction was incubated at 42°C for 90 min, the enzyme was heat-inactivated at 70°C for 15 min. After adding 2 U of RNAse H (NEB) to the reaction tube, it was incubated at 37°C for 20 min.

[0143] For second strand synthesis, 40 U of *E. coli* DNA polymerase (Invitrogen) and 2 U RNaseH (Invitrogen) were added to the previous reaction to bring the final volume to 150 μl. Salts and nucleotides were added to a final concentration of 20 mM Tris-HCl (pH 7.0; Fisher Scientific, Pittsburgh PA), 90 mM KCl (Teknova, Half Moon Bay CA) , 4.6 mM $MgCl_2$ (Teknova), 10 mM$(NH_4)_2SO_4$ (Fisher Scientific), 1 x second strand buffer (Invitrogen), 0.266 mM dGTP, 0.266 mM dATP, 0.266 mM dTTP, and 0.266 mM dCTP.

[0144] After second strand synthesis for 150 min at 16°C, the cDNA was purified away from the enzymes, dNTPs, and buffers using phenol-chloroform extraction followed by ethanol precipitation in the presence of glycogen. Alternatively, the cDNA was purified on a QIAQUICK silica-gel column (Qiagen) followed by ethanol precipitation in the presence of glycogen. The cDNA was centrifuged at >10,000 x g for 30 min; and after the supernatant was aspirated, the pellet was washed with 150 μl of 70% ethanol. Following recentrifugation, the supernatant was removed, and residual ethanol was evaporated at room temperature. Alternatively, the volume of column purified cDNA was reduced in a vacuum evaporator to 7.4 μl.

Example 8 Arrays

[0145] Arrays were used to produce a gene expression profile for diagnosing and monitoring the status of SLE in a patient. In one format, the array contains reagents specific for at least two genes or proteins, one that binds to a gene or protein of the invention, and one that binds to a control gene or protein.

Nucleic Acid Arrays

[0146] Human Genome CGH 44A microarrays (Agilent Technologies) were used to determine differential gene expression. These Cy3/Cy5 chips contained 41,675 probes (60-mers) that represented most the genes found in REFSEQ database (NCBI); additional genes on the chip represented various controls. The chips were run as recommended by the manufacturer and scanned using an Agilent DNA microarray scanner. The data was extracted using Feature Extraction v 7.5 software (Agilent Technologies).

[0147] In the alternative, Affymetrix U133A Human GeneChips (Affymetrix, Santa Clara CA) with probe sets representing about 14,500 full length genes and 22,000 features were used according to the manuals and product inserts supplied by the manufacturer. Affymetrix Microarray Suite (MAS) v 5.0 software was used to generate expression values for each gene. To correct for slight differences in overall chip hybridization intensity and allow for comparison between samples, each chip was scaled to an overall intensity of 1500.

[0148] In one alternative, the PAXgene Blood RNA system (PreAnalytix GmbH, Hombrechtikon Switzerland) was used for whole blood collection, stabilization, and RNA isolation from patient and/or normal samples. Five μg of total RNA was used to prepare biotinylated cRNA for hybridization using a standard protocol (Expression Analysis Technical Manual, Affymetrix). For samples with low RNA yields, two or more rounds of amplification were performed. Fifteen micrograms of each labeled cRNA was hybridized to Affymetrix U133A Human GeneChips.

[0149] In another alternative, a low density array containing amplicons produced using probe sets for genes selected from Table 1 and Table 2 are harvested from PCR reactions,

purified using Sephacryl-400 beads (GEH) and arrayed on a membrane. The membrane is UV irradiated, washed in 0.2% SDS at room temperature and rinsed three times in distilled water. Non-specific binding sites on the array are blocked by incubation in 0.2% casein in PBS for 30 min at 60°C, and the arrays are washed in 0.2% SDS and rinsed in distilled water.

[0150] In another alternative, purified amplicons are robotically arranged and immobilized on polymer-coated glass slides using the procedure described in USPN 5,807,522 (which is hereby incorporated in its entirety). Polymer-coated slides are prepared by cleaning glass microscope slides (Corning Life Sciences, Corning NY) ultrasonically in 0.1% SDS and acetone, etching in 4% hydrofluoric acid (VWR Scientific Products, West Chester PA), coating with 0.05% aminopropyl silane (Sigma-Aldrich) in 95% ethanol, and curing in a 110°C oven. The slides are washed extensively with distilled water between and after treatments.

Antibody arrays

[0151] Monoclonal antibodies specific to at least two IFNr proteins and at least two proteins selected from the clusters of Table 1 are immobilized on a membrane, slide or dipstick or added to the wells of an ELISA plate using methods well known in the art. The array is incubated in the presence of serum or cell lysate until protein:antibody complexes are formed. The proteins encoded by genes or their splice variants are identified by the known position and labeling of the antibody that binds an epitope of that protein on the array. Quantification is normalized using the antibody:protein complex of various controls.

Example 9 Designing and Selecting Primers and Probe Sets

[0152] Primers and probe sets were designed and selected for each gene having utility in the diagnosis and monitoring of SLE using the PRIMER3 program (Whitehead Research Institute (WRI), Cambridge MA). Default values were used for all parameters but melting temperature (Tm). Tm was set between 71.7 and 73.7°C; amplicon size, between 50 and 150 bases in length (optimum, about 100 bases); and primers or probes were allowed to be 36 nucleotides in length. Salt concentration, a critical parameter affecting the Tm of the probes and primers,

was used at the default concentration, 50 mM.

[0153] The C source code for the PRIMER3 program was downloaded from the WRI website and complied on a Sun Enterprise 250 server (Sun Microsystems, Palo Alto CA) using the GCC compiler (Free Software Foundation, Boston MA). A subsequent version was compiled for machines running the Windows operating system (Microsoft, Redmond WA). The program was run from the command line which also dictated the use of an input file that contained the sequences and the parameters for primer design as described in the help files that accompanied the software. A script was written to input a number of sequences and automatically generate a number of potential primers. The following batch approach was used to design primers for the genes.

[0154] The first step in designing primers was to mask out repetitive sequences in the mRNA using the REPEATMASKER program (Institute for Systems Biology, University of Washington, Seattle WA). The second step was to mask out all known SNPs for the genes as annotated in the SNP database at NCBI (Bethesda MD) that have an allelic heterozygosity higher than 1%. The masked sequence was submitted to PRIMER3 using parameters as outlined above, and the top eight sequences were selected. Alternatively, the Primer3 program was used on the MIT website (Massachusetts Institute of Technology, Cambridge MA) to examine a specific region on the mRNA of a particular gene. The final step was to test several of the top pairs of primers for correct size and efficiency.

[0155] Primers were ordered from Integrated DNA Technologies (Coralville IA) or an alternative commercial source.

Example 10 Testing of Primers and Probe Sets for RT-PCR

[0156] Control genes: With both microarrays and RT-PCR, variation was monitored by adding one or more genes from bacteria, plants, or animals in one or more wells. Although human β-actin and β-GUS were used to validate the control RNAs, several other genes were also tested for variability between samples, for expression in mononuclear and whole blood RNA from control subjects and SLE patients, on samples prepared using various protocols,

and in the RT-PCR assays.

[0157] Based on criteria of low variability between control and patient samples and high expression across samples, β-actin, β-GUS, 18s ribosomal subunit, GAPDH, and β2-microglobulin were selected as the control genes and used in the various assays.

[0158] Primer Testing: Primers were tested once using RT-PCR protocol (without Rox and Sybr green dyes) to see whether they produced an amplicon of the correct size without amplifying non-specific sequences. Each primer pair/probe set was tested on cDNA made from mononuclear cell control RNA described in Example 2. The PCR reaction contained 1 x RealTime-PCR buffer (Ambion, Austin TX), 2 mM MgCl2 (ABI), 0.2 mM dATP (NEB), 0.2 mM dTTP (NEB), 0.2 mM dCTP (NEB), 0.2 mM dGTP (NEB), 0.625 U AMPLITAQ Gold enzyme (ABI), 0.3 μM of each primer to be used (Sigma Genosys, The Woodlands TX), 5 μl of the reverse transcription reaction, and water added to a final volume of 19 μl.

[0159] Following 40 cycles of PCR, 10 μl of each product were combined with Sybr Green dye at a final dilution of 1:72,000. Melt curves for each PCR product were determined on a PRISM 7900HT Sequence detection system (ABI), and primer pairs yielding a product with one clean peak were chosen for further analysis. One μl of product from each probe set assay was examined by agarose gel electrophoresis or using a DNA 1000 chip kit and an Agilent 2100 bioanalyzer (Agilent Technologies). From primer design and the genomic sequence, the expected size of the amplicon was known. Only primer pairs showing amplification of the single desired product, and minimal amplification of contaminants, were used in assays.

[0160] Primers were tested a second time to determine their efficiency in an RT-PCR reactions. cDNA was synthesized as described above. A set of 5 serial dilutions of cDNA in water: 1:10, 1:20, 1:40, 1:80, and 1:160 was tested using RT-PCR.

Example 11 RT-PCR Assays and Analysis

[0161] TAQMAN: PCR reactions were performed using the TAQMAN Universal PCR Master mix (ABI). The master mix was aliquoted into light tight tubes, one for each gene. The primer pair for each gene was added to the tube of PCR master mix labeled for that gene.

A FAM/TAMRA dual labeled TAQMAN probe (Biosearch Technologies, Novato CA) was added to each tube. Alternatively, different combinations of commercially available fluorescent reporter dyes and quenchers were used such that the absorption wavelength for the quencher matches the emission wavelength for the reporter.

In one alternative, a Sybr green RT-PCR reaction can be performed using the TAQMAN PCR reagent kit (ABI). In the alternative, Universal ProbeLibrary (LNAs; Roche Diagnostics, Pleasanton CA), were substituted for Taqman probes.

[0162] RT-PCR Assays and Analysis: 18 µl of master mix were dispensed into each well of a 384 well plate (ABI), and 2 µl of the template sample were dispensed into triplicate wells for each primer pair. The final concentration of each reagent was: 1 x TAQMAN Universal PCR Master Mix, 300 nM each primer, 0.25 nM TAQMAN probe, and 21 µl of 1:10 diluted template. PCR reactions were run on the PRISM 7900HT Sequence Detection system (ABI) with the following conditions: 10 min at 95°C; 40 cycles of 95°C for 15 sec, 60°C for 1 min.

[0163] Sequence detection system v2.0 software (ABI) was used to analyze the fluorescent signal from each reaction. Standard deviation (Stdev) and coefficient of variation (CV) were calculated for triplicate wells. If the CV was greater than 2, an outlier among the three wells was identified and deleted; and the average was recalculated. In each plate, the difference in CT (ΔCT) was calculated for each gene and control combination by subtracting the average CT of the gene from the average CT of the control. The expression relative to the control was calculated by taking two to the power of the ΔCT of the gene.

[0164] In each case, all plates were run in duplicate and analyzed in the same manner. The percent variation was determined for each sample and gene combination (relative expression, RE) by taking the absolute value of the RE for the second plate from the RE for the first plate, and dividing that by the average. If more than a quarter of the variation calculations on a plate were greater than 50%, then a third plate was run. The cycle number at which each amplification curve crossed CT was recorded, and the file was transferred to MS Excel for further analysis. CT values for triplicate wells were averaged, and data were plotted as a function of the $\log_{10}$ of the calculated starting concentration of RNA. The starting RNA

concentration for each cDNA dilution was determined based on the original amount of RNA used in the reverse transcription reaction, the dilution of the reverse transcription reaction, and the amount used in the RT-PCR reaction (usually 5 µl). For each gene, a linear regression line was plotted through all points of the dilution series. The slope of the line was used to calculate efficiency of the reaction for each primer set using the equation, $E = 10^{(-1/\text{slope})} - 1$. This efficiency equation was used to compare the expression of primers or probe sets for each gene, and a primer pair was considered successful if the efficiency was reproducibly determined to be 0.85-1.2.

[0165] Since variation of RT-PCR assays can arise from unequal amounts of RNA starting material, probe sets for control genes can be run in the same reaction as the probe set for the diagnostic gene to reduce variation. Different fluorescent dyes were used to amplify the control, differentiating their expression from that of the diagnostic gene.

[0166] Quantitative RT-PCR: RT-PCR was used to compare the expression of each gene using the primers described above. cDNA was synthesized from normal control, patient, and reference samples. Ten µl RT-PCR reactions were performed using a PRISM 7900 Sequence Detection system (ABI) using FAM-TAMRA labeled probes and the standard TAQMAN protocols described above. RT-PCR amplification product was measured as CT (threshold cycle = the point at which an amplification curve crosses a threshold fluorescence value) during the PCR reaction to observe amplification before any reagent became rate limiting. Threshold was set to a point where all of the reactions were in their linear phase of amplification. A lower CT indicated a higher amount of starting material (greater expression in the sample) since an earlier cycle number meant the threshold was crossed more quickly. A CT of less than 30 based on appropriate cDNA dilutions provided linear results for the blood samples from SLE patients.

[0167] In the alternative, other labeling moieties or technologies can be used to measure amplification product in RT-PCR. Molecular beacons (Invitrogen) use FRET technology, and fluorescence is measured when a hairpin structure is relaxed by the specific probe binding to the amplicon.

[0168] Other labeling moieties can be used for detection of an antibody, nucleic acid or protein in any of the assays or diagnostic kits described herein. These labeling moieties include fluorescent, chemiluminescent, or chromogenic agents, cofactors, enzymes, inhibitors, magnetic particles, radionuclides, reporters/quenchers, substrates and the like that can be attached to or incorporated into the antibody, nucleic acid or protein. Visible labels and dyes include but are not limited to anthocyanins, avidin-biotin, ß glucuronidase, biotin, BIODIPY, Coomassie blue, Cy3 and Cy5, 4,6-diamidino-2-phenylindole (DAPI), digoxigenin, ethidium bromide, FAM/TAMRA, FITC, fluorescein, gold, green fluorescent protein, horseradish peroxidase, lissamine, luciferase, phycoerythrin, reporter/quencher pairs (HEX/TAMRA, JOE/TAMRA, ROX/BHQ2, TAMRA/BHQ2, TET/BHQ1, VIC/BHQ1, and the like), rhodamine, spyro red, silver, streptavidin, and the like. Radioactive markers include radioactive forms of hydrogen, iodine, phosphorous, sulfur, and the like.

Example 12 Protein Expression

[0169] Adapter sequences for subcloning are added at either end of a coding region specific to a gene or a portion thereof and amplified using PCR. An epitope or affinity tag (6 x his) or sequences for secretion from a cell can be added to the adapter sequence to facilitate purification and/or detection of the protein. The amplified cDNA is inserted into a shuttle or expression vector that can replicate in bacteria, insect, yeast, plant, or mammalian cells. Such vectors typically contain a promoter that operably links to the coding region, replication start sites, and antibiotic resistance or metabolite selection sequences.

[0170] The expression vector can be used in an in vitro translation system or to transfect cells. For example, Spodoptera frugiperda (Sf9) insect cells are infected with recombinant Autographica californica nuclear polyhedrosis virus (baculovirus). The polyhedrin gene is replaced with the cDNA by homologous recombination, and the polyhedrin promoter drives transcription. The protein is synthesized as a fusion protein with an affinity tag that enables purification.

[0171] Clones of transformed cells are analyzed to ensure that the inserted sequence is expressed. Once expression is verified, the cells are grown under selective conditions; and the

protein is isolated from cells, or if secreted, from the growth media using chromatography, size exclusion chromatography, immunoaffinity chromatography, or other methods including cell fractionation, ion exchange, or selective precipitation.

[0172] The isolated and purified protein is then used as a reagent on an array or as an antigen to produce specific antibodies.

Example 13: Antibody Production and Testing

[0173] If antibodies are to be used as reagents, the sequence of the gene or splice variant is analyzed to determine regions of high immunogenicity (LASERGENE software; DNASTAR, Madison WI), and an appropriate oligopeptide is synthesized and conjugated to keyhole lympet hemocyanin (KLH; Sigma-Aldrich, St Louis MO).

Immunization

[0174] Rabbits are injected with the oligopeptide-KLH complexes in complete Freund's adjuvant, and the resulting antisera is tested for specific recognition of the protein or fragments thereof. Antisera that react positively with the protein are affinity purified on a column containing beaded agarose resin to which the synthetic oligopeptide has been conjugated (SULFOLINK kit; Pierce Chemical, Rockford IL). The column is equilibrated using 12 ml IMMUNOPURE Gentle Binding buffer (Pierce Chemical). Three ml of rabbit antisera is combined with one ml of binding buffer and poured into the column. The column is capped (on the top and bottom), and antisera is allowed to bind with the oligopeptide by gentle shaking at room temperature for 30 min. The column is allowed to settle for 30 min, drained by gravity flow, and washed with 16 ml binding buffer (4 x 4 ml additions of buffer). The antibody is eluted in one ml fractions with IMMUNOPURE Gentle Elution buffer (Pierce Chemical), and absorbance at 280 nm is determined. Peak fractions are pooled and dialyzed against 50 mM Tris, pH 7.4, 100 mM NaCl, and 10% glycerol. After dialysis, the concentration of the purified antibody is determined using the BCA assay (Pierce Chemical), aliquoted, and frozen.

Electrophoresis and Blotting

[0175] Samples containing protein are mixed in 2 x loading buffer, heated to 95°C for 3-5 min, and loaded on 4-12% NUPAGE Bis-Tris precast gel (Invitrogen). Unless indicated, equal amounts of total protein are loaded into each well. The gel is electrophoresed in 1 x MES or MOPS running buffer (Invitrogen) at 200 V for approximately 45 min on an XCELL II apparatus (Invitrogen) until the RAINBOW marker (GEH) resolves and the dye front approaches the bottom of the gel. The gel is soaked in 1 x transfer buffer (Invitrogen) with 10% methanol for a few minutes; and a PVDF membrane (Millipore, Billerica MA) is soaked in 100% methanol for a few seconds to activate it. The membrane, the gel, and supports are placed on the TRANSBLOT SD transfer apparatus (Biorad, Hercules CA) and a constant current of 350 mA is applied for 90 min.

Conjugation with Antibody and Visualization

[0176] After the proteins are transferred to the membrane, it is blocked in 5% (w/v) non-fat dry milk in 1 x phosphate buffered saline (PBS) with 0.1% Tween 20 detergent (blocking buffer) on a rotary shaker for at least 1 hr at room temperature or at 4°C overnight. After blocking, the buffer is removed, and 10 ml of primary antibody in blocking buffer is added and incubated on the rotary shaker for 1 hr at room temperature or overnight at 4°C. The membrane is washed 3 times for 10 min each with PBS-Tween (PBST), and secondary antibody, conjugated to horseradish peroxidase, is added at a 1:3000 dilution in 10 ml blocking buffer. The membrane and solution are shaken for 30 min at room temperature and washed three times for 10 min with PBST.

[0177] The wash solution is carefully removed, and the membrane is moistened with ECL+ chemiluminescent detection system (GEH) and incubated for approximately 5 min. The membrane, protein side down, is placed on x-ray film (Eastman Kodak, Rochester NY) and developed for approximately 30 seconds. Antibody:protein complexes are visualized and/or scanned and quantified.

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
1		Granulocytes and B cells					
1			A_23_P113258	NM_005739	RASGRP1	Homo sapiens RAS guanyl releasing protein 1 (calcium and DAG-regulated) (RASGRP1), mRNA	AGAAGAAAATAGAATCCCTCCAGCTTGAAAAA AGCAATCATGTCTTAGCTCAAATGGAGC (SEQ ID NO: 1)
1			A_23_P117599	NM_012111	AHSA1	Homo sapiens AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast) (AHSA1), mRNA	ATTAGTGTGAGCCTTGCCAAAGATGAGCCTGA CACAAATCTCGTGGCCTTAATGAAGGAA (SEQ ID NO: 2)
1			A_23_P128230	NM_002135	NR4A1	Homo sapiens nuclear receptor subfamily 4, group A, member 1 (NR4A1), transcript variant 1, mRNA	AATGACAGATTCTGACATTTATATTTGTGTATTT TCCTGGATTTATAGTATGTGACTTTT (SEQ ID NO: 3)
1			A_23_P134078	NM_004824	CDYL	Homo sapiens chromodomain protein, Y-like (CDYL), transcript variant 1, mRNA	AGGTACAGATACCTCAGATTCGGGAAACTCAA AATCAAAAGACTTAGCTTCTAGGATAAA (SEQ ID NO: 4)
1			A_23_P251686	NM_005160	ADRBK2	Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA	GTCAAAATGGGTTAACTGTGTATATTGACTTTC ATGTCGTCATGCATCTGTCATGAATGA (SEQ ID NO: 5)
1			A_23_P43580	NM_007018	CEP1	Homo sapiens centrosomal protein 1 (CEP1), mRNA	AACCTAGAAGGAGAATTGGAAAGCTTGAAAGA GAACCTTCCATTTACCATGAATGAGGGA (SEQ ID NO: 6)
1			A_23_P46781	NM_003638	ITGA8	Homo sapiens integrin, alpha 8 (ITGA8), mRNA	CCCATTATGGGTAATAATACTAGCAATACTTCT TGGATTGTTGGTTCTCGCCATTTTAAC (SEQ ID NO: 7)
1			A_23_P54170	NM_005466	MED6	Homo sapiens mediator of RNA polymerase II transcription, subunit 6 homolog (yeast) (MED6), mRNA	AGGCACCAGACTTGGGATCAGTTATAAACTCT AGAGTGCTTACTGCAGTGCATGGTATTC (SEQ ID NO: 8)
1			A_23_P64689	NM_014871	USP52	Homo sapiens ubiquitin specific peptidase 52 (USP52), mRNA	CCAGATGGAAAGTAATTGGTATTCTTAATATCC TGGGTGACTAATATCCAGGCAGAGAAG (SEQ ID NO: 9)
1	3	Granulocyte	A_24_P115932	NM_004778	GPR44	Homo sapiens G protein-coupled receptor 44 (GPR44), mRNA	TGGATGAAATGTCAGTGGAAGAAGCAGATGAG AAACTCTTGAGATCTTGGTCCTGTGTTT (SEQ ID NO: 10)
1			A_24_P227585	NM_018559	KIAA1704	Homo sapiens KIAA1704 (KIAA1704), mRNA	TGATGACACATCTGGAGATCGATCAATCTGGA CAGATACTCCAGCTGATAGGGAAAGGAA (SEQ ID NO: 11)
1			A_24_P229658				GAAGGGCGTAGTCACAGAACTCGAAGTAGGA GCCGAGATAAATCCCATAGGCATAAAAAA (SEQ ID NO: 12)
1			A_24_P312692	NM_006595	API5	Homo sapiens apoptosis inhibitor 5 (API5), mRNA	TTGCTATTCAAATCAACTGCCTGAATGACATTT CTAGTAGTCTGATGTATTTTTCTGAGG (SEQ ID NO: 13)
1			A_24_P341489	AC003043		Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.	ATCTGAAGTCTGTCCAGGAACTCATTTTGAAAC ATGGACAAGCCAAGATAAGGAATAAGA (SEQ ID NO: 14)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
1	3	Bcells	A_24_P359165	AC026250		Homo sapiens chromosome 11, clone RP11-540A21, complete sequence.	TGGATAATTGAAGCCAGTGGTTTTTTAACCAATGTTATGTATCAGAATCACCTCACAAAG (SEQ ID NO: 15)
1			A_24_P4426	NM_014937	INPP5F	Homo sapiens inositol polyphosphate-5-phosphatase F (INPP5F), transcript variant 1, mRNA	TCTCATTTGATCCTAATTTTCCCCGTATTCTACTTGAACACATTAAAAATACTCTGCTGC (SEQ ID NO: 16)
1			A_24_P8140	AK124166		Homo sapiens cDNA FLJ42172 fis, clone THYMU2029676.	AGCTACTTAGGGTGAGCCTGCCTTCTTCCATTCTATCCGAAGTCTCTTCTAAAGTTGCGG (SEQ ID NO: 17)
1			A_24_P861009	NM_001007246	BRWD1	Homo sapiens bromodomain and WD repeat domain containing 1 (BRWD1), transcript variant 3, mRNA	AGTCACAGATCCTACGTATGTGCTCTTCAGTAGAGGATTTTCTGTGATCCTACAATGAAG (SEQ ID NO: 18)
1			A_24_P865672	AC018347		Homo sapiens chromosome 15 clone RP11-410F2, complete sequence.	AAAGCACCGGTGAAGAAATCTATAAAGATGCTCCAGCCGAAAATGCACAGAAGTCAAATC (SEQ ID NO: 19)
1			A_32_P90551	NM_014230	SRP68	Homo sapiens signal recognition particle 68kDa (SRP68), mRNA	GACTTACATCAAGCTGTCAATGGCAATCAAGCGTAATGAGAGCATGGCCAAAGGTCTGCA (SEQ ID NO: 20)
1			A_32_P98683	AC006449		Homo sapiens chromosome 17, clone hCIT.58_E_17, complete sequence.	TGAGGGGTGCCTTCATTCCCCTTTGTTCACTTTCTCCAGCTCAACTTGGGACTTGGGTGG (SEQ ID NO: 21)
2		NK cells					
2			A_23_P10025	NM_006159	NELL2	Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA	ACATCACCATGTAGAAGAATGGGCGTACAGTATATACCGTGACATCCTGAACCCTGGATA (SEQ ID NO: 22)
2			A_23_P103765	NM_002001	FCER1A	Homo sapiens Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A), mRNA	AGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTT (SEQ ID NO: 23)
2			A_23_P103775	NM_032270	LRRC8C	Homo sapiens leucine rich repeat containing 8 family, member C (LRRC8C), mRNA	AAACTCTGAAGATTGGAAAAAACAGCCTATCTGTACTTTCACCGAAAATTGGAAATTTGC (SEQ ID NO: 24)
2			A_23_P107283	NM_002145	HOXB2	Homo sapiens homeo box B2 (HOXB2), mRNA	ATTAAACTCTAGGGGGACTTTCTTAAAAATAACTAGAGGGACCTATTTTCCTCTTTTTTA (SEQ ID NO: 25)
2			A_23_P117662	NM_002112	HDC	Homo sapiens histidine decarboxylase (HDC), mRNA	CCGAGGGTAGACAGGCAGCTTCTGTGGTTCAGCTTGTGACATGATATATAACACAGAAAT (SEQ ID NO: 26)
2			A_23_P119418	NM_003796	C19orf2	Homo sapiens chromosome 19 open reading frame 2 (C19orf2), transcript variant 1, mRNA	TCGCAAATCCATCCTGAAGTCTCGAAGTAGAGAGAATAGTGTGTGTAGCGACACTAGTGA (SEQ ID NO: 27)
2			A_23_P12572	NM_001227	CASP7	Homo sapiens caspase 7, apoptosis-related cysteine peptidase (CASP7), transcript variant alpha, mRNA	AGTTCTATAAGTGAGGAAGAGTTTATGGCAAAGATTTTTGGCACTTTGTTTTCAAGATGG (SEQ ID NO: 28)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
2			A_23_P126057	NM_001007099	SCP2	Homo sapiens sterol carrier protein 2 (SCP2), transcript variant 3, mRNA	ACATTGGCAAATAGCGTGGGATAGATTTGTTT CTTAATGGGTGTGACCAATCCTGTTTTT (SEQ ID NO: 29)
2			A_23_P127676	NM_014633	CTR9	Homo sapiens SH2 domain binding protein 1 (tetratricopeptide repeat containing) (SH2BP1), mRNA	TAAACCCAGATGCTAAATCATTCCTACAAAGGT TTGACTGAAACTGTGGCAGATGTCTCA (SEQ ID NO: 30)
2			A_23_P129128	NM_152334	TARSL2	Homo sapiens threonyl-tRNA synthetase-like 2 (TARSL2), mRNA	TGACCCTTAAAAATGTATTTTTCTTAACATGTTA GTACTTCTACGACTTTGGAGCCACTG (SEQ ID NO: 31)
2			A_23_P133543	NM_017415	KLHL3	Homo sapiens kelch-like 3 (Drosophila) (KLHL3), mRNA	TGGCTGTTAGGGACTGTATATCTTGTAAAAGA ACACTTGTCACATGCTTGATCAGTTACA (SEQ ID NO: 32)
2			A_23_P135857	NM_004836	EIF2AK3	Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA	CCTCCAATAAAGGGAAAATGAAGCTTTTTATGT AAATTGGTTGAAAGGTCTAGTTTTGGG (SEQ ID NO: 33)
2			A_23_P14543	NM_006020	ALKBH	Homo sapiens alkB, alkylation repair homolog (E. coli) (ALKBH), mRNA	TTGGCTGTAATGTATGTTGAGAAGTCAGTCCA AGGAGGTATGTTCTTCCACAACAGCCTT (SEQ ID NO: 34)
2			A_23_P14804	NM_005724	TSPAN3	Homo sapiens tetraspanin 3 (TSPAN3), transcript variant 1, mRNA	GGCTTTATAGGAGGAGTATAATGTATGCACTA CTGTTTTAAAAGAATTAGTGTGAGTGTG (SEQ ID NO: 35)
2			A_23_P152353	NM_133451	KIAA1970	Homo sapiens KIAA1970 protein (KIAA1970), mRNA	TGGCCAATCTTGTCTGAGTTCTTTGATGGCGA CACATGAACTACAGCCGTTTTGTTGTTG (SEQ ID NO: 36)
2			A_23_P200015	NM_012093	AK5	Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA	AATGCAGAGGGAACACCAGAGGACGTTTTTCT TCAACTCTGCACAGCTATTGACTCTATT (SEQ ID NO: 37)
2			A_23_P208477	NM_001419	ELAVL1	Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (ELAVL1), mRNA	GGAGGCGTAAAATGGCTCTGTATTTTAATAAC ACAGAAACATTTGAGCATTGTATTTCTC (SEQ ID NO: 38)
2			A_23_P213045	NM_016269	LEF1	Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA	AGCAGGAGCCAAAAAGACCTCACATTAAGAAG CCTCTGAATGCTTTTATGTTATACATGA (SEQ ID NO: 39)
2			A_23_P214882	NM_019041	MTRF1L	Homo sapiens mitochondrial translational release factor 1-like (MTRF1L), mRNA	CATAAAGTCAAAAAATCCTAAAACATAAGTTGG TGACCATCTGTAATCATGATGTGGTGG (SEQ ID NO: 40)
2			A_23_P215566	NM_001621	AHR	Homo sapiens aryl hydrocarbon receptor (AHR), mRNA	AATGGCTTCGGACAAAATATCTCTGAGTTCTGT GTATTTTCAGTCAAAACTTTAAACCTG (SEQ ID NO: 41)
2			A_23_P215956	NM_002467	MYC	Homo sapiens v-myc myelocytomatosis viral oncogene homolog (avian) (MYC), mRNA	TTCAAATGCATGATCAAATGCAACCTCACAACC TTGGCTGAGTCTTGAGACTGAAAGATT (SEQ ID NO: 42)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
2			A_23_P217187	HS333E23		Human DNA sequence from clone RP3-333E23 on chromosome Xq21.1 Contains the P2RY10 gene for purinergic receptor P2Y G-protein coupled 10, complete sequence.	TTTTTCTAACAGGCAAGACAGTGTGAAGAATT GAAGCAATATGTGCATAAATTTCAGGAC (SEQ ID NO: 43)
2			A_23_P25566	NM_004951	EBI2	Homo sapiens Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) (EBI2), mRNA	CTGAAACGGCAAGTCAGTGTATCGATTTCTAG TGCTGTGAAGTCAGCCCCTGAAGAAAAT (SEQ ID NO: 44)
2	3	NK	A_23_P302018	NM_003328	TXK	Homo sapiens TXK tyrosine kinase (TXK), mRNA	GCTGAGAGTGCTTCCTTCTTGAAGACGAGTGT CATTCATCACTTCAGTGATCCATGCATA (SEQ ID NO: 45)
2			A_23_P31376	NM_018334	LRRN3	Homo sapiens leucine rich repeat neuronal 3 (LRRN3), mRNA	GCCTCTCTCCAGAAATGAACTGTGATGGTGGA CACAGCTATGTGAGGAATTACTTACAGA (SEQ ID NO: 46)
2			A_23_P33643	XM_937367	IL7R	PREDICTED: Homo sapiens interleukin 7 receptor (IL7R), mRNA	GCAATGAGTGAACTGACTGTGGCTACATTCTT GAAGATATACGGGAGAGACGTATTATTA (SEQ ID NO: 47)
2			A_23_P338919	NM_005876	APEG1	Homo sapiens aortic preferentially expressed gene 1 (APEG1), mRNA	GCAGGGGGCCACTGTAGTGAGCGTGGAGAAA TTTGGAAACACCTATTTCTTAACTCAAAT (SEQ ID NO: 48)
2			A_23_P343398	NM_001838	CCR7	Homo sapiens chemokine (C-C motif) receptor 7 (CCR7), mRNA	AAGAGAGCAACATTTTACCCACACACAGATAA AGTTTTCCCTTGAGGAAACAACAGCTTT (SEQ ID NO: 49)
2			A_23_P345460	NM_015432	PLEKHG4	Homo sapiens pleckstrin homology domain containing, family G (with RhoGef domain) member 4 (PLEKHG4), mRNA	GACTTGATGCCTTTTGAATAACTTTCAATAGAA TTGTCTAAAATTATCTTACTGGTTGTT (SEQ ID NO: 50)
2			A_23_P354151	NM_005546	ITK	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA	TTGAACACTTCATGAGGAGGGACATTCCCTGA TATAAGAGAGGATGGTGTTGCAATTGGC (SEQ ID NO: 51)
2			A_23_P384085	NM_014635	GCC2	Homo sapiens GRIP and coiled-coil domain containing 2 (GCC2), transcript variant 2, mRNA	TCTCTTAAGCCTTCAGTTTATACTCTTAATTTAA TTTTCTTTCTGAGCTGGAGAACTGGC (SEQ ID NO: 52)
2			A_23_P404481	NM_001400	EDG1	Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA	GCTGAGGCCAAAGTTTCCATGTAAGCGGGATC CGTTTTTTGGAATTTGGTTGAAGTCACT (SEQ ID NO: 53)
2			A_23_P436117	NM_018200	HMG20A	Homo sapiens high-mobility group 20A (HMG20A), mRNA	CACTTGACAGTGACTTGAAACATTTGCATATTC AGGAATGCATGAGATTTCAAGAGAGCC (SEQ ID NO: 54)
2			A_23_P45726	NM_005826	HNRPR	Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA	GGGATAGATTACATAGGAGTATGGAGTATGCT GTAAATAAAAATACAAGCTAGTGCTTTG (SEQ ID NO: 55)
2			A_23_P55682	NM_023926	ZNF447	Homo sapiens zinc finger protein 447 (ZNF447), mRNA	GCAAGTGGTCACCAGCATTACACAGCAATGAA GCAGAATAAAGTAGGCCAGAATGCATCA (SEQ ID NO: 56)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
2			A_23_P68198	NM_015677	SH3YL1	Homo sapiens SH3 domain containing, Ysc84-like 1 (S. cerevisiae) (SH3YL1), mRNA	TGGAGACAGAATCACAGTTATATCAAAAACAG ATTCACATTTTGATTGGTGGGAAGGAAA (SEQ ID NO: 57)
2			A_23_P78268	NM_016080	C17orf25	Homo sapiens chromosome 17 open reading frame 25 (C17orf25), mRNA	TAATCCCGACAGAACATCATGTGAGATTTCTTT AAAATGGATTAAACGATTTCTTCAGCC (SEQ ID NO: 58)
2			A_23_P83931	NM_005863	NET1	Homo sapiens neuroepithelial cell transforming gene 1 (NET1), mRNA	TCTTTGAAAGGGGGGAGGAGGAGTAAAAGCC CGATTATAATGGTGATCAATTCAAGTCAG (SEQ ID NO: 59)
2			A_23_P91991	NM_138381	MGC15763	Homo sapiens hypothetical protein BC008322 (MGC15763), mRNA	ATGTACCCAAAGAACACATTTGCTTTGAGAAGT GGTGGTAGGAGGCAGACAAAGGCAGAA (SEQ ID NO: 60)
2			A_23_P94889	AC103817		Homo sapiens chromosome 8, clone CTD-3083F21, complete sequence.	TAAGTTTTGTAAAAAGGAGCATCTTGAATCCAC TTAGATAAAGACAGACTGTGTGTGTAG (SEQ ID NO: 61)
2			A_24_P108291	NM_018439	IMPACT	Homo sapiens Impact homolog (mouse) (IMPACT), mRNA	AGAGCCTTTCTGAAGAGAATTATATCAAACTAA TTACAACCAAGAAATAATAGTATGAAG (SEQ ID NO: 62)
2			A_24_P117528	NM_002765	PRPS2	mRNA	CAAGGCCTAAAGCCAACTGACTTAAAGGTAAT CATTTCAGCTAAGATTAAATTTAAAGCC (SEQ ID NO: 63)
2			A_24_P12521	NM_138811	C7orf31	Homo sapiens chromosome 7 open reading frame 31 (C7orf31), mRNA	GGTGCACAAAAGCGTTTCCATAAATCAATTCTA GAAGACCATAAAGACCTCAGGGATAAT (SEQ ID NO: 64)
2			A_24_P136438	NM_014915	ANKRD26	Homo sapiens ankyrin repeat domain 26 (ANKRD26), mRNA	ATGTTGATGAAGTGCACAAAAATAATAGAAGTG ATATGATGTCCGCATTAGGATTAGGAC (SEQ ID NO: 65)
2			A_24_P157424	NM_007362	NCBP2	Homo sapiens nuclear cap binding protein subunit 2, 20kDa (NCBP2), mRNA	CCCGTTAAACTGAGTGTAGAAATCTGAATTTTT AAAAGAGCTGTAACTAGTTGTAAGTGC (SEQ ID NO: 66)
2			A_24_P16361				ACCAAAAAATTCATGAGAGATCCAATTAATTCT GGTGAAAAAGGATTGACCCTTGAAGGA (SEQ ID NO: 67)
2			A_24_P170103				AACGACAACAGAAAAACAATCTTATTCCAAGTC ATTCCAGTAACTTTTTTGGGTACGTAC (SEQ ID NO: 68)
2			A_24_P170186	AL589796		Human DNA sequence from clone RP13-469O16 on chromosome 6 Contains a nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1)(B23, NPM) pseudogene and a CpG island, complete sequence.	ATGCACAAAAGTCAAATCAGAATGGAGACTCA AAACCATCAAAGCTAAGATCAAAAGGTC (SEQ ID NO: 69)
2			A_24_P202555	NM_015073	SIPA1L3	Homo sapiens signal-induced proliferation-associated 1 like 3 (SIPA1L3), mRNA	TGCAAAAACAGATCTATTTAATTTGAGGTTGAT GTTCTATCCAATGGCCGAAGATAGCAG (SEQ ID NO: 70)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
2			A_24_P208345	NM_033102	SLC45A3	Homo sapiens solute carrier family 45, member 3 (SLC45A3), mRNA	GTGCCGTTTGCAATAATGTCGTCTTATTTATTT AGCGGGGTGAATATTTTATACTGTAAG (SEQ ID NO: 71)
2			A_24_P212596	AC019288		Homo sapiens chromosome 15, clone RP11-139F4, complete sequence.	TTTTCAACAGTACAGAAAAATTGAAAAAAGGGG CTTTGCCTTTGTAACCTTTGATGACCA (SEQ ID NO: 72)
2			A_24_P218970	NM_001417	EIF4B	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA	TTTTTAAGCTTCCCTTGAGAGAATAAATGGTAA TGGAGAGAACTATTTAACAAGGTCCTG (SEQ ID NO: 73)
2			A_24_P234921	NM_004367	CCR6	Homo sapiens chemokine (C-C motif) receptor 6 (CCR6), transcript variant 1, mRNA	AAGCTTTAACTATATCTCTCTTTAAAATGCAAAA TAATGTCTTAAGATTCAAAGTCTGTA (SEQ ID NO: 74)
2			A_24_P251381	NM_024782	XLF	Homo sapiens XRCC4-like factor (XLF), mRNA	ACCTTGAAAGAAGCTTACATGGCAGCAATATTT CTAAAATAGTGATACAGTCAGAGGCCT (SEQ ID NO: 75)
2			A_24_P26073	NM_133259	LRPPRC	Homo sapiens leucine-rich PPR-motif containing (LRPPRC), mRNA	AGAGAAAGATGTCACATCTGCTAAAGCACTGT ATGAACATTTGACTGCAAAGAATACAAA (SEQ ID NO: 76)
2			A_24_P299911	NM_015148	PASK	Homo sapiens PAS domain containing serine/threonine kinase (PASK), mRNA	ATCTTGCTGACTATACATGGGAAGAGGTGTTT CGAGTAAACAAGCCAGAAAGTGGAGTTC (SEQ ID NO: 77)
2			A_24_P302506	AL355145		Human DNA sequence from clone RP5-831G13 on chromosome 1	AATTGGAGAATTGAATAATCAGCATATGTAAGC GCACTAGAACCCTGTGTTGAAAACTGC (SEQ ID NO: 78)
2			A_24_P307384	XM_927265	LOC643288	PREDICTED: Homo sapiens similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60) (LOC643288), mRNA	CTAGTGAATATGAAAAGGAAAAACTGAATGAA CTGGCAAAACTTTCAGATGGAGTAGCTG (SEQ ID NO: 79)
2			A_24_P354451	AC104825		Homo sapiens BAC clone RP11-774O3 from 4, complete sequence.	CATAACCTTATTAATTTGCACATAGATCATCTG AATGTCGTGGTTTAAGACTTAAGGAGG (SEQ ID NO: 80)
2			A_24_P366465				GGATAAGATTGTCATTCAGAAATACCATCCTAA TGGCTACAACTTTGAAGTAAGAAAAGC (SEQ ID NO: 81)
2			A_24_P382113	NM_006107	CROP	Homo sapiens cisplatin resistance-associated overexpressed protein (CROP), transcript variant 2, mRNA	GCAGAGTGAAGACACAAACACTGAATCGAAGG AAAGTGATACTAAGAATGAGGTCAATGG (SEQ ID NO: 82)
2			A_24_P385341	NM_014388	C1orf107	Homo sapiens chromosome 1 open reading frame 107 (C1orf107), mRNA	TTTCTATGAACTGCCGACATATCCACACTTTTA CAGTGAAATCTGTAATATGCTGAGAGC (SEQ ID NO: 83)
2			A_24_P388528	NM_003032	ST6GAL1	Homo sapiens ST6 beta-galactosamide alpha-2,6-sialyltranferase 1 (ST6GAL1), transcript variant 2, mRNA	ATGCAAATTATGATATGGACGTTATCATTGGTC TGGTGAGATGTTTCATATTTGTGACAG (SEQ ID NO: 84)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
2			A_24_P393838	NM_014765	TOMM20	Homo sapiens translocase of outer mitochondrial membrane 20 homolog (yeast) (TOMM20), mRNA	CTAGCTGTGTCGAGTTAAAGAAAAAATCAGCA GTTTTTTCTCCCAGAAATGTAATTGCCA (SEQ ID NO: 85)
2			A_24_P402690	NM_001012514	ITM2C	Homo sapiens integral membrane protein 2C (ITM2C), transcript variant 3, mRNA	ACTCTTAAATGCTTTGTATATTTTCTCAATTAGA TCTCTTTTCAGAAGTGTCTATAGAAC (SEQ ID NO: 86)
2			A_24_P419300	AC010442		Homo sapiens chromosome 5 clone CTD-2228K2, complete sequence.	TTACAGAGTTCAATATACTGTGTACCATTGATC TTCTATTGTGAAAGCAAAGAATTTCAT (SEQ ID NO: 87)
2			A_24_P472455	HSM801157		Homo sapiens mRNA; cDNA DKFZp564M0264 (from clone DKFZp564M0264).	ACCCTCATGTTAAATCTTAAATGTAGTATTTCT AACTTGTGAAGACAGATTGGTAGGCAG (SEQ ID NO: 88)
2			A_24_P4877	NM_033114	ZCRB1	Homo sapiens zinc finger CCHC-type and RNA binding motif 1 (ZCRB1), mRNA	GAAAAATTAATACTATCATGTTAATACTATTATT GTCATCCCAAGAAAAAAGATATTTTA (SEQ ID NO: 89)
2			A_24_P542375	NM_002823	PTMA	Homo sapiens prothymosin, alpha (gene sequence 28) (PTMA), mRNA	ACTATAAGTAGTTGGTTTGTATGAGATGGTTAA AAAGGCCAAAGATAAAAGGTTTCTTTT (SEQ ID NO: 90)
2			A_24_P579826	AC090419		Homo sapiens chromosome 17, clone CTD-2107B16, complete sequence.	GAAGAAAAGTATAAGAGTTGCTAGGTGTGACA ATCTCAAGACTTTTCAACCACTACAAAT (SEQ ID NO: 91)
2			A_24_P59239				CATCATCAACACCAAAAAAGGACAAGAATCCTT CAAAACAGGAAAAAACTCCTAAAACAC (SEQ ID NO: 92)
2			A_24_P595460	AK097398		Homo sapiens cDNA FLJ40079 fis, clone TESTI2001498, highly similar to DNA-BINDING PROTEIN NEFA PRECURSOR.	AAATTGTATGTGATATTCCAACAGCAAGTTGGA TGCAATGTGTCATAAAAATGACCTCAG (SEQ ID NO: 93)
2			A_24_P6725	NM_001010914	LOC400986	Homo sapiens protein immuno-reactive with anti-PTH polyclonal antibodies (LOC400986), mRNA	AATCTGGGACAGTGTCTCCTCAGAAACAATCA GCCTGGAAGGTTATATTTAAAAAGAAAG (SEQ ID NO: 94)
2			A_24_P686992	NM_001010914	LOC400986	Homo sapiens protein immuno-reactive with anti-PTH polyclonal antibodies (LOC400986), mRNA	TCCAGGAAAAGTGTCTTCTCAGAAACAACCAG CTGAGAAGGCTACAAGTGACGACAAAGA (SEQ ID NO: 95)
2			A_24_P736638	NM_002156	HSPD1	K (LOC646447), mRNA	GTTGAGAAAATTATGCAAAGTTCCTCAGAAGTT GGTTATGATACTATGTTAGGAGATGTC (SEQ ID NO: 96)
2			A_24_P808100	AC011890		Homo sapiens PAC clone RP4-655L22 from Xq23, complete sequence.	TAAAAGTCAGGTTGCAGTTTCCATTGCATTCAA GAAAATCAGAAAAATAAATACAACTTT (SEQ ID NO: 97)
2			A_24_P82142	NM_003205	TCF12	Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 3, mRNA	TCAGGATGATTCCTAACAAGTCAGTCATTTGTG AACTTAGTGGACTTTTTGGTTACTTTA (SEQ ID NO: 98)
2			A_24_P832113	NM_001004419	CLEC2D	Homo sapiens C-type lectin domain family 2, member D (CLEC2D), transcript variant 2, mRNA	CTTTGAAATAACACCACCAGTAGTCTTACGGTT GAAGTGTGGTTCAGGGCCAGTGCATAT (SEQ ID NO: 99)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
2			A_24_P883109	AC073089		Homo sapiens BAC clone RP11-324F21 from 7, complete sequence.	GGGCAACTAGTCATCTACTAGTTAGCTTAGTA AGCTAAGCATTAAATCTAAGAAATAGCA (SEQ ID NO: 100)
2			A_24_P927189	NM_138381	OXNAD1	oxidoreductase NAD-binding domain containing 1	AGTGTGTTGTCGTTATTAATTTGCTATTCCTTG TCCTATTCAGAAAGGATTTCAAGAGGC (SEQ ID NO: 101)
2			A_24_P930963	AC009041		Homo sapiens chromosome 16 clone RP11-161M6, complete sequence.	GCCCCATTTCAAGTATAACCAGGAGGGAAAAT GGTGCTTGAAATAAGCATGCCACAAAGG (SEQ ID NO: 102)
2			A_24_P941188	XM_375697	OTUD3	PREDICTED: Homo sapiens OTU domain containing 3 (OTUD3), mRNA	CCACGGATTGTGTTCATCTGAACCATTTTATTT TTTATTTACCAAAGTACTGTACTTGGC (SEQ ID NO: 103)
2			A_24_P943263	NM_006989	RASA4	Homo sapiens RAS p21 protein activator 4 (RASA4), mRNA	TCCTGCATAGTCTATCTTTGTATATCTTTGAAC TTTTCAAGAATAAAAAAGCTTAAAAAG (SEQ ID NO: 104)
2			A_32_P119604	AC090948		Homo sapiens chromosome 3 clone RP11-415F23 map 3p, complete sequence.	CAGAACTCTACTTCAGCAGACACTCAACTCAA AAAGACTGGCAAATGGACATGTATTTAC (SEQ ID NO: 105)
2			A_32_P133213	AC006480		Homo sapiens BAC clone RP11-166O4 from 7, complete sequence.	TCAAGAGAGATCCTAAAGAAAGCAAAATCACT GTGGACTGAAATGAGCAGACAAGGTTTT (SEQ ID NO: 106)
2			A_32_P149492	XM_496391	NBPF9	PREDICTED: Homo sapiens neuroblastoma breakpoint family, member 9, transcript variant 1 (NBPF9), mRNA	TTCTGGATTGTTTTTTACATTCAGTGTTATAATA TTTGATTATGCTGATTGGTTTTGGTG (SEQ ID NO: 107)
2			A_32_P155506	NM_152653	UBE2E2	Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) (UBE2E2), mRNA	TGCAAACAATGTTGGAGCTGTAATAGTAAGAG CTTTCTTACAAAGCTTTGTATTACTGTG (SEQ ID NO: 108)
2			A_32_P159787	NM_005520	HNRPH1	Homo sapiens heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1), mRNA	AAATAAAAGCATGTCTTTCAACATGCATCCAAA ACAGTGTTCAATTTAACGTGGCAAAGG (SEQ ID NO: 109)
2			A_32_P162306	NM_001004419	CLEC2D	Homo sapiens C-type lectin domain family 2, member D (CLEC2D), transcript variant 2, mRNA	GCTGACAAAGATGATCACTTTAAGGTGGATAA TGATGAAAATGAGCACCAGTTATCTTTA (SEQ ID NO: 110)
2			A_32_P181548	AC087407		Homo sapiens 3 BAC CTC-269B10 (CalTech Clone Library C) complete sequence.	ATATTCTTCCAATATGTAGGGGAAAAGACATAT GAATAAGACAAATGAAAAATTGCATAT (SEQ ID NO: 111)
2			A_32_P187009	AC010260		Homo sapiens chromosome 5 clone CTC-458I2, complete sequence.	ATTCACATGAGTAAAATGATGGAAGAACTCTTT AAGGTAATCCTTTGGGATAAAGGATCC (SEQ ID NO: 112)
2			A_32_P193646	NM_002139	RBMX	Homo sapiens RNA binding motif protein, X-linked (RBMX), mRNA	GACTTGTACTGGTGTTGTAACTTTCCAAGTAAA AGTATCCCTAAAGGCCACTTCCTATCT (SEQ ID NO: 113)
2			A_32_P217510	NM_032168	WDR75	Homo sapiens WD repeat domain 75 (WDR75), mRNA	TTACCGAAAAAGTCCAGGATACAAGTAACACA GGTTTAGGAGAAGACATTATACATCAGT (SEQ ID NO: 114)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
2			A_32_P225604	NM_000969	RPL5	Homo sapiens ribosomal protein L5 (RPL5), mRNA	AAGCACTTCATGGGCCAGAATGTTGCAGATTA CATGCGCTACTTAATGGAAGAAGATGAC (SEQ ID NO: 115)
2			A_32_P34149	NM_005520	HNRPH1	Homo sapiens heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1), mRNA	TGAAGACTTAAGGCCCAGTATTTTTTAATAGAA TACTCATCTAGGATGTAACAGTGAAGC (SEQ ID NO: 116)
2			A_32_P49423	NM_002520	NPM1	Homo sapiens nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), transcript variant 1, mRNA	AAACAGGAAAAAACTCCTAAAACACCTAAAAG GACCTAGTTCTGTAGAAGACATTAAAGC (SEQ ID NO: 117)
2			A_32_P63013	HUMYY74A12		Homo sapiens full length insert cDNA clone YY74A12.	CCCGGGAGTGTTGCAAGTTAAACTGATGAAAA GACGTTTAGTATTTAATTGCTCCTCATG (SEQ ID NO: 118)
2			A_32_P80068	NM_001004419	CLEC2D	Homo sapiens C-type lectin domain family 2, member D (CLEC2D), transcript variant 2, mRNA	TGAACTGCACATTGTTGAAGCAGAGGCCATGA ATTACGAAGGCAGTCCAATTAAAGTAAC (SEQ ID NO: 119)
3		Granulocytes					
3			A_23_P11926	XR_001410	FLJ21272	PREDICTED: Homo sapiens hypothetical protein FLJ21272 (FLJ21272), misc RNA	ATCTTCCTAATCTCGTGGGATCACAATATGAAT AACAAGGATGAACATAAGACACATCTG (SEQ ID NO: 120)
3			A_23_P135769	NM_001101	ACTB	Homo sapiens actin, beta (ACTB), mRNA	TTTAAAAACTGGAACGGTGAAGGTGACAGCAG TCGGTTGGAGCGAGCATCCCCCAAAGTT (SEQ ID NO: 121)
3			A_23_P19590	NM_003379	VIL2	Homo sapiens villin 2 (ezrin) (VIL2), mRNA	GATTATTCTCGAATCACCTCCTGTGTTGTGCT GGGAGCAGGACTGATTGAATTACGGAAA (SEQ ID NO: 122)
3			A_23_P20894	NM_024757	EHMT1	Homo sapiens euchromatic histone-lysine N-methyltransferase 1 (EHMT1), mRNA	TGATTTCAGACTCAGAAGCCGACGTTCGAGAG GAAGATTCTTACCTCTTTGATCTCGACA (SEQ ID NO: 123)
3			A_23_P257503	NM_003922	HERC1	Homo sapiens hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1), mRNA	TTTGGTCACTTTTGATAAGTTTGCATGAAACCA TTTTGGTGCATTTTTAGTTGGGAATGG (SEQ ID NO: 124)
3			A_23_P259901	NM_012253	TKTL1	Homo sapiens transketolase-like 1 (TKTL1), mRNA	GATGTCCTGTGCTGCTTGTGATGAGAGCCTCC ACACTGTACTGTTCAAGTCAATGTTAAT (SEQ ID NO: 125)
3			A_23_P26759	NM_138793	CANT1	Homo sapiens calcium activated nucleotidase 1 (CANT1), mRNA	AATGTTGCCTTTTTCTAGGAACTGTCAGAAATC CTCATGCCTTTCAAGACTTCTGTGAAT (SEQ ID NO: 126)
3			A_23_P31686	NM_021174	KIAA1967	Homo sapiens KIAA1967 (KIAA1967), transcript variant 1, mRNA	AGAAAAAGGCTTTTCGAGTGTGGGACAAGGTC TGATGTCAGTGAACGGAATTGAAGAGCA (SEQ ID NO: 127)
3			A_23_P319895	XM_037523	KIAA1076	PREDICTED: Homo sapiens KIAA1076 protein (KIAA1076), mRNA	TGCAACTGAGGAAATAATTTATTTTTCACATGA GGAAATGCGTAGCTTGTAGAGACGGCT (SEQ ID NO: 128)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
3			A_23_P332190	NM_002163	IRF8	Homo sapiens interferon regulatory factor 8 (IRF8), mRNA	GGGATGCCTTACTTTGCACTTAATTTAATAAGG GCATTCTCGGAGGAGTAGACGTTTAAT (SEQ ID NO: 129)
3			A_23_P359430	NM_015383	NBPF14	Homo sapiens neuroblastoma breakpoint family, member 14 (NBPF14), mRNA	ACCCTGGTTTCAATGAACCTAACCTCATTCTTT GTGTCTTCAGTGTTGGCTTGTTTTAGC (SEQ ID NO: 130)
3			A_23_P388681	NM_001419	ELAVL1	Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (ELAVL1), mRNA	AGATAATTAAGAGTGAAGGAGTTGAAACTTTTC TTGTTAGTGTACAACTCATTTTGCGCC (SEQ ID NO: 131)
3			A_23_P406330	NM_022733	SMAP1L	Homo sapiens stromal membrane-associated protein 1-like (SMAP1L), mRNA	CAGCAGCCTAAAACTGTTGTGTTTTTCTTATGG TTTAAAAAACGCCATGTCATTGATAAC (SEQ ID NO: 132)
3			A_23_P416434	NM_015288	PHF15	Homo sapiens PHD finger protein 15 (PHF15), mRNA	ATATATTGAAAAGAGCAATTTTAAATTATTTTTG GCTTATGTTGCAATATTTATTTTCTT (SEQ ID NO: 133)
3			A_23_P417200	NM_005652	TERF2	Homo sapiens telomeric repeat binding factor 2 (TERF2), mRNA	TCCCTGGTAATCTGTAGAACCTTCTCCTAGGA AATGGTGAAGTCTATTAGGAGCCACTTG (SEQ ID NO: 134)
3			A_23_P44581	NM_001004060	NOMO2	Homo sapiens NODAL modulator 2 (NOMO2), transcript variant 1, mRNA	AATGTGATCACTTCCTCTGAATACCTTCCTACA TTATGGGTCAAGCTTTACAAAAGCGAA (SEQ ID NO: 135)
3			A_23_P44734	NM_032557	USP38	Homo sapiens ubiquitin specific peptidase 38 (USP38), mRNA	GGATGCTATAACAAAAGACAATAAACTATATTT ACAGGAACAAGAGTTGAATGCTCGAGC (SEQ ID NO: 136)
3			A_23_P60354	NM_003070	SMARCA2	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transcript variant 1, mRNA	TATCATCATCGTCTATAAACTAGCTTTAGGATA GTGCCAGACAAACATATGATATCATGG (SEQ ID NO: 137)
3			A_23_P73593	NM_002444	MSN	Homo sapiens moesin (MSN), mRNA	GAAGCTTTCAGTATTAGTGATGTCATCTGTCAC TATAGGTCATACAATCCATTCTTAAAG (SEQ ID NO: 138)
3			A_23_P97770	NM_020216	RNPEP	Homo sapiens arginyl aminopeptidase (aminopeptidase B) (RNPEP), mRNA	ACCAGGAAGATTTCTGGAAAGTGAAGGAGTTC CTGCATAACCAGGGGAAGCAGAAGTATA (SEQ ID NO: 139)
3			A_24_P174257	NM_019044	CCDC93	coiled-coil domain containing 93	AAAGAGAGGGAAGAACTACACTAATGTTAGAG ATAAGGTATGTTTTGGCTCAAAATGTGT (SEQ ID NO: 140)
3			A_24_P18190	NM_005347	HSPA5	Homo sapiens heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) (HSPA5), mRNA	TTCTACAGCTTCTGATAATCAACCAACTGTTAC AATCAAGGTCTATGAAGGTGAAAGACC (SEQ ID NO: 141)
3			A_24_P186030	NM_002760	PRKY	Homo sapiens protein kinase, Y-linked (PRKY), mRNA	CCAGTTTTCTCTGTACCTGTGTGTATAGAAATA GATCAGAGCACAGTTGAAATTCATGGA (SEQ ID NO: 142)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
3			A_24_P187626	AC055811		Homo sapiens chromosome 17, clone RP11-45M22, complete sequence.	GAAGTGTGATGTGGACATCTGCAAAGACTTATATGCCAACGTGCTGTCTGGCGGCACCAC (SEQ ID NO: 143)
3			A_24_P222599	NM_002613	PDPK1	Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDPK1), transcript variant 1, mRNA	GCTGGTAAAAGCCTCTATTACGACTGTAAGTAAGTTGGATGTTGGCAAAATTAAATTGTT (SEQ ID NO: 144)
3			A_24_P225325	NM_022733	SMAP1L	Homo sapiens stromal membrane-associated protein 1-like (SMAP1L), mRNA	CATGTTCTCATGATTTATGGGAATGAAGCAAGTACTGAAATCAAATTAAATACTCCCTGG (SEQ ID NO: 145)
3			A_24_P226037	NM_001003810	HNRPD	Homo sapiens heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa) (HNRPD), transcript variant 4, mRNA	AGAAATACCACAATGTTGGTCTTAGTAAATGTGAAATAAAAGTAGCCATGTCGAAGGAAC (SEQ ID NO: 146)
3			A_24_P226554	NM_001101	ACTB	Homo sapiens actin, beta (ACTB), mRNA	GCACCCAGCACAATGAAGATCAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCGTGTGG (SEQ ID NO: 147)
3			A_24_P238744	XM_292982	LOC653269	PREDICTED: Homo sapiens similar to protein expressed in prostate, ovary, testis, and placenta 15, transcript variant 1 (LOC653269), mRNA	TGTGGCATCCACGAAACTACCTTCAACTCCATCATGAAGTCGGATGTGGACATCTACAAA (SEQ ID NO: 148)
3			A_24_P255786	AL359844		Human DNA sequence from clone RP11-314J18 on chromosome 10	GTCCTCCTGGGAGAAGAGCTATGAGCTGTCAGATGGCCAGGTCATCACCAGCAGCAACAA (SEQ ID NO: 149)
3			A_24_P261169	NM_006378	SEMA4D	Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (SEMA4D), mRNA	AACTTCCTTTTGCTAAATGCATTCTTTCTGCTTTTAGAAATGTAGACATAAACACTCCCC (SEQ ID NO: 150)
3			A_24_P273666	NM_000516	GNAS	Homo sapiens GNAS complex locus (GNAS), transcript variant 1, mRNA	CCCCGAGTGATTTTGCGAAACCCCCTTTTCCCTTCAGCTTGCTTAGATGTTCCAAATTTA (SEQ ID NO: 151)
3			A_24_P287272	XM_498427	NBPF1	PREDICTED: Homo sapiens neuroblastoma breakpoint family, member 1, transcript variant 1 (NBPF1), mRNA	ACCTAACCTCATTCTTTGTATCTTCAGTGTTGAATTGTTTTAGCTGATCCATCTTTAACG (SEQ ID NO: 152)
3			A_24_P325333	NM_002600	PDE4B	Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA	ACTTCTACACAGATAAGCTTTCAAAGTTGACAAACTTTTTTGACTCTTTCTGGAAAAGGG (SEQ ID NO: 153)
3			A_24_P331998	NM_203447	DOCK8	Homo sapiens dedicator of cytokinesis 8 (DOCK8), mRNA	CCTACATACAGATCACTTTTGTGGAGCCCTACTTTGATGAGTATGAGATGAAAGACAGGG (SEQ ID NO: 154)
3			A_24_P354724	NM_054114	TAGAP	Homo sapiens T-cell activation GTPase activating protein (TAGAP), transcript variant 2, mRNA	GGCCATACGCCATGCCATAGCTTGTGCTATCTGTAAATATGAGACTTGTAAAGAACTGCC (SEQ ID NO: 155)
3			A_24_P369154	NM_002721	PPP6C	Homo sapiens protein phosphatase 6, catalytic subunit (PPP6C), mRNA	AATATTGCTTCGATCATGGTCTTCAAAGATGTAAATACAAGAGAACCAAAGTTATTCCGG (SEQ ID NO: 156)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
3			A_24_P375076	AL390237		Human DNA sequence from clone RP11-278J20 on chromosome 6 Contains a retinoblastoma binding protein 4 (RBBP4) pseudogene and a KIAA0797 pseudogene, complete sequence.	GACAATATTATGCAAGTGTGGCAAATGGCAGA GAACATTTACAACAATGAAGACCCTGAA (SEQ ID NO: 157)
3			A_24_P383901	HSBA12M9		Human DNA sequence from clone RP11-12M9 on chromosome 22, complete sequence.	CATGTACCCTGGCATCACCAACAGGATGCAGA AGAAGATCACCGCCCTAGCACCCAGCAT (SEQ ID NO: 158)
3			A_24_P391568	NM_001668	ARNT	Homo sapiens aryl hydrocarbon receptor nuclear translocator (ARNT), transcript variant 1, mRNA	GGCTTTGGCCAGTAGCTAAAGTGCAAGACTGA ATTAATGAGAAGATATATTAAATGTAGT (SEQ ID NO: 159)
3			A_24_P393151	AC009892		Homo sapiens chromosome 19 clone CTB-83J4, complete sequence.	AAGAAATCTTATCATTCGCCATCTACCCTGTAG AATAAAGAAATCTTATCATTCACCGTC (SEQ ID NO: 160)
3			A_24_P401090	AL354702		Human DNA sequence from clone RP11-334L9 on chromosome 1 Contains a heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) (HSPA5) pseudogene, complete sequence.	TTTTCTACAGCTTTTGATAATCAAGTTACAATC AAGGTCTATGAAGGTAAACAACCCCTG (SEQ ID NO: 161)
3			A_24_P408424	NM_002473	MYH9	Homo sapiens myosin, heavy polypeptide 9, non-muscle (MYH9), mRNA	CTGGTCTACACTGGTTGCCGAATTTACTTGTAT TCCTAACTGTTTTGTATATGCTGCATT (SEQ ID NO: 162)
3			A_24_P410017	NM_001017421	FKSG30	Homo sapiens actin-like protein (FKSG30), mRNA	ATGAAACTACCTTCAACTCCATCATGAAGTCTG ATGTGGACATCCGCAAAGACCTGTACA (SEQ ID NO: 163)
3			A_24_P42517	NM_006854	KDELR2	Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 (KDELR2), mRNA	CATCCTATACTGTGACTTCTTCTACTTGTACAT TACAAAAGTACTCAAGGGAAAGAAGCT (SEQ ID NO: 164)
3			A_24_P47182	NM_003373	VCL	Homo sapiens vinculin (VCL), transcript variant 2, mRNA	ATGGGGTTCAAGAGAGTAATGGGTTTCATATT TCTTATCACCACAGTAAGTTCCTACTAG (SEQ ID NO: 165)
3			A_24_P475115	AC097103		Homo sapiens 3 BAC RP11-319G6 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	ACTGACTACTTCATGAAGATCCTCATGGAGTG CAGCTACCGTTTCACCACCATGGCTGAG (SEQ ID NO: 166)
3			A_24_P63118	NM_013374	PDCD6IP	Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA	TAGTTTTTGCACGGAAGACAGAAAGAGATGAA CTCTTAAAGGACTTGCAACAAAGCATTG (SEQ ID NO: 167)
3	3	Granulocyte	A_24_P63136	NM_023914	P2RY13	Homo sapiens purinergic receptor P2Y, G-protein coupled, 13 (P2RY13), transcript variant 1, mRNA	ATGCCAGATTTTCTTGGTATCTCCCATAATACG ACCTACAGTCCATGGTCTACAGATGTT (SEQ ID NO: 168)
3			A_24_P63827	NM_005494	DNAJB6	Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 2, mRNA	CAACTTCAACTAAAATGGTTAATGGCAGAAAAA TCACTACAAAGAGAATTGTCGAGAACG (SEQ ID NO: 169)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
3			A_24_P643587	NM_024095	ASB8	Homo sapiens ankyrin repeat and SOCS box-containing 8 (ASB8), mRNA	GCTCTGTAATAACAGTAATAAATAGCTCTGAAA TAACAGTCCTAAGAACTCCTAAAGTCC (SEQ ID NO: 170)
3			A_24_P681011	HSM807522		Homo sapiens mRNA; cDNA DKFZp686K02111 (from clone DKFZp686K02111).	GTGTTAATCCATGTTAATCTGTGTGAAAATTAT TGCGTGCAACAGTATTTTCTCGTGTAC (SEQ ID NO: 171)
3			A_24_P68649	NM_020216	RNPEP	Homo sapiens arginyl aminopeptidase (aminopeptidase B) (RNPEP), mRNA	GCAACAGGAGAGAAGCTTTTTGGACCTTATGT TTGGGGAAGGTATGACTTGCTCTTCATG (SEQ ID NO: 172)
3			A_24_P693321				ATCACAACTATGCCAAATAATCAATCCTACAAT GTCCAAAATTTTACTTTAAAACTGGAA (SEQ ID NO: 173)
3			A_24_P714134	XR_019310	LOC646447	PREDICTED: Homo sapiens similar to heterogeneous nuclear ribonucleoprotein	AGAGTGCATAAAATTATCCTTGATCTTATATCT GAGTCTCCTACAGAGGATGTGCACAGA (SEQ ID NO: 174)
3			A_24_P787897	XM_001125986	LOC283824	PREDICTED: Homo sapiens hypothetical protein LOC283824	TGAACTATCTGAAATTGACCAGTAATCAAAGTT CCAATCATCTGAATGCTTTTCCTTGAG (SEQ ID NO: 175)
3			A_24_P79617	NM_014656	KIAA0040	Homo sapiens KIAA0040 (KIAA0040), mRNA	TGAAAATGAAAAGTCTTGATGTAGTCAGATGG TTACTCTCTTAACATTAGGTATTACCCC (SEQ ID NO: 176)
3			A_24_P7974	AF161369		Homo sapiens HSPC106 mRNA, partial cds.	GTTGCTTTATGTAGCAAATTCTCCGTTTGGAG CTTTTAAAATAGGATTATTTGCCAGAAC (SEQ ID NO: 177)
3			A_24_P808534	NM_001357	DHX9	Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 9 (DHX9), transcript variant 1, mRNA	GGAAAAGACAAAGATTCTCACCACTGAAGGGT GTAATGCACTTATCCACAAATCATCTGT (SEQ ID NO: 178)
3			A_24_P940059	NM_015553	PIP3-E	Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), mRNA	CCCAGGGTTTTGTAATACATAATTGAAAATAAA AGTCCCTGAAACTAAATGTTTGCAGCC (SEQ ID NO: 179)
3			A_32_P11359				AACTAAAAAGCATTAATTAAAAAGTACTTAACT CAGAAATTATAAAAATAGGAGACATCA (SEQ ID NO: 180)
3			A_32_P144920	NM_015509	NECAP1	Homo sapiens NECAP endocytosis associated 1 (NECAP1), mRNA	TTGAGTTTGAATTGTGTAACATCTTTGATCAGT GGGTGTATCTGTAATGAAGGAGGTTCA (SEQ ID NO: 181)
3			A_32_P155776	NM_001017421	FKSG30	Homo sapiens actin-like protein (FKSG30), mRNA	ATAGTGAAGTCTGATGTGGACATCCGCAAAGA CCTGTACACCAACACAGTGCTGTCTGGC (SEQ ID NO: 182)
3			A_32_P221958	NM_133446	CTGLF1	Homo sapiens centaurin, gamma-like family, member 1 (CTGLF1), mRNA	ATGGGAAAAATAAGGATAACTCAGAATTTCAAA AGGAAATCACAAATTCAGCTAGTAATA (SEQ ID NO: 183)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
3			A_32_P60551	HS661I20		Human DNA sequence from clone RP4-661I20 on chromosome 20q11.23-12 Contains the RPL12L2 gene for ribosomal protein L12-like 2 pseudogene, the 5' end of the CHD6 gene for chromodomain helicase DNA binding protein 6 and two CpG islands, complete sequence.	GCAGAAGTACAAGCTTTAGGGTGTATCTATTC ATCTATTCCTAGTACATAAAATTTAGCC (SEQ ID NO: 184)
3			A_32_P79434	NM_002847	PTPRN2	Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA	TCTCTACATGGTATTGTAATGAATATCTGCTTT AATATAGCTATCATTTCTTTTCCAAAA (SEQ ID NO: 185)
3			A_32_P8666	NM_002140	HNRPK	Homo sapiens heterogeneous nuclear ribonucleoprotein K (HNRPK), transcript variant 1, mRNA	GGTCTGCAGATTAAACAAATCCGTCATGAGTC GGGAGCTTCGATCAAAATTGATGAGCCT (SEQ ID NO: 186)
4		Granulocytes					
4			A_23_P113762				AGACGCTGGACGAAGATGGGGATGGGGAGTG TGACTTCCAGGAGTTTATGGCCTTCGTCT (SEQ ID NO: 187)
4			A_23_P117992	NM_014861	KIAA0703	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA	TCCATCACCGGATCAGTTTTTCCTCTTAGGAAA GCTGCAGGAACCTCGTGGGCTCCAGGG (SEQ ID NO: 188)
4			A_23_P119222	NM_020415	RETN	Homo sapiens resistin (RETN), mRNA	CAATAAGCAGCATTGGCCTGGAGTGCCAGAG CGTCACCTCCAGGGGGGACCTGGCTACTT (SEQ ID NO: 189)
4	2	Granulocyte	A_23_P121622	NM_014465	SULT1B1	Homo sapiens sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), mRNA	GAAATAGAGATTGTCTGTAGTTGATTGAAACG AGGGCAGTTATGAATTGATTTGGGCAAT (SEQ ID NO: 190)
4	8	Granulocyte	A_23_P121716	NM_005139	ANXA3	Homo sapiens annexin A3 (ANXA3), mRNA	TGGACATTCGAACAGAGTTCAAGAAGCATTAT GGCTATTCCCTATATTCAGCAATTAAAT (SEQ ID NO: 191)
4			A_23_P122924	NM_002192	INHBA	Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA	AAACATCATCAAAAAGGACATTCAGAACATGAT CGTGGAGGAGTGTGGGTGCTCATAGAG (SEQ ID NO: 192)
4			A_23_P123645				AATGGTTTTGTGCAGTGAACAACACATGGCGA GGTACTAACTGAGAAACTTTTTCATGCT (SEQ ID NO: 193)
4			A_23_P126278	NM_003465	CHIT1	Homo sapiens chitinase 1 (chitotriosidase) (CHIT1), mRNA	GGGCCACCAAACAGAGAATCCAGGATCAGAA GGTGCCCTACATCTTCCGGGACAACCAGT (SEQ ID NO: 194)
4			A_23_P130961	NM_001972	ELA2	Homo sapiens elastase 2, neutrophil (ELA2), mRNA	AACGGCTACGACCCCGTAAACTTGCTCAACGA CATCGTGATTCTCCAGCTCAACGGGTCG (SEQ ID NO: 195)
4	4	Granulocyte	A_23_P131785	NM_001725	BPI	Homo sapiens bactericidal/permeability-increasing protein (BPI), mRNA	GACTCAGATTCAGAAATGATCTAAACACGAGG AAACATTATTCATTGGAAAAGTGCATGG (SEQ ID NO: 196)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
4			A_23_P140384	NM_001911	CTSG	Homo sapiens cathepsin G (CTSG), mRNA	TGTGACTGACTCTTCTTCTCGGGGACACAGGC CAGCTCCACAGTGTTGCCAGAGCCTTAA (SEQ ID NO: 197)
4			A_23_P141173	NM_000250	MPO	Homo sapiens myeloperoxidase (MPO), nuclear gene encoding mitochondrial protein, mRNA	CCTGTTCTGGGTGCAGCTGAGAAAATGAGTGA CTAGACGTTCATTTGTGTGCTCATGTAT (SEQ ID NO: 198)
4			A_23_P149301	NM_002105	H2AFX	Homo sapiens H2A histone family, member X (H2AFX), mRNA	GGCGCGCGACAACAAGAAGACGCGCATCATC CCGCGCCACCTGCAGCTGGCCATCCGCAA (SEQ ID NO: 199)
4			A_23_P151637	NM_002934	RNASE2	Homo sapiens ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA	GTGGTAACCCAAATATGACCTGTCCTAGTAAC AAAACTCGCAAAAATTGTCACCACAGTG (SEQ ID NO: 200)
4	3	Granulocyte	A_23_P156180	NM_003059	SLC22A4	Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA	AAACAAGAGACTCAATGGAGACAGAAGAAAAT CCCAAGGTTCTAATAACTGCATTCTGAA (SEQ ID NO: 201)
4			A_23_P161428	NM_144590	ANKRD22	Homo sapiens ankyrin repeat domain 22 (ANKRD22), mRNA	AATCCTTGTGACCACACCGATGGAGATACAGA AAAAGTTAACGACTGGATTCTATCTTCA (SEQ ID NO: 202)
4			A_23_P163025	NM_002934	RNASE2	Homo sapiens ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA	AGCCACAGCTCAGAGACTGGGAAACATGGTTC CAAAACTGTTCACTTCCCAAATTTGTCT (SEQ ID NO: 203)
4	4	Granulocyte	A_23_P166848	NM_002343	LTF	Homo sapiens lactotransferrin (LTF), mRNA	ATATTTGGGACCACAGTATGTCGCAGGCATTA CTAATCTGAAAAAGTGCTCAACCTCCCC (SEQ ID NO: 204)
4			A_23_P168014	NM_003509	HIST1H2AI	Homo sapiens histone 1, H2ai (HIST1H2AI), mRNA	TGAGGAGCTCAACAAGCTTCTGGGCAAAGTCA CCATCGCACAGGGTGGCGTCCTGCCCAA (SEQ ID NO: 205)
4			A_23_P169437	NM_005564	LCN2	Homo sapiens lipocalin 2 (oncogene 24p3) (LCN2), mRNA	GCTATGGTGTTCTTCAAGAAAGTTTCTCAAAAC AGGGAGTACTTCAAGATCACCCTCTAC (SEQ ID NO: 206)
4			A_23_P170233	NM_005213	CSTA	Homo sapiens cystatin A (stefin A) (CSTA), mRNA	AACTGGCTACTGAGTCATGATCCTTGCTGATA AATATAACCATCAATAAAGAAGCATTCT (SEQ ID NO: 207)
4			A_23_P19543	NM_003137	SRPK1	Homo sapiens SFRS protein kinase 1 (SRPK1), mRNA	CTGTCAAATTGCCACGATCTCACTAAAGGATTT CTATTTGCTGTCAGTTAAAAATAAAGC (SEQ ID NO: 208)
4			A_23_P200507	NM_014184	CNIH4	Homo sapiens cornichon homolog 4 (Drosophila) (CNIH4), mRNA	TGGTTGAAGTCAGCCTACACTACAGTGCACAG TTGAGGAGCCAGAGACTTCTTAAATCAT (SEQ ID NO: 209)
4			A_23_P206760	NM_005143	HP	Homo sapiens haptoglobin (HP), mRNA	GATAAGATGTGGTTTGAAGCTGATGGGTGCCA GCCCTGCATTGCTGAGTCAATCAATAAA (SEQ ID NO: 210)
4	3	Granulocyte	A_23_P218442	NM_002483	CEACAM6	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) (CEACAM6), mRNA	ACACTCATCTGACTCATTCTTTATTCTATTTTAG TTGGTTTGTATCTTGCCTAAGGTGCG (SEQ ID NO: 211)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
4			A_23_P23048	NM_002965	S100A9	Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA	GAGCTGGTGCGAAAAGATCTGCAAAATTTTCT CAAGAAGGAGAATAAGAATGAAAAGGTC (SEQ ID NO: 212)
4			A_23_P25235	NM_080387	CLEC4D	Homo sapiens C-type lectin domain family 4, member D (CLEC4D), mRNA	CATTTAACCCACGCAGAGTATTCTGGCATAAG AATGAACCCGACAACTCTCAGGGAGAAA (SEQ ID NO: 213)
4	18	Granulocyte	A_23_P253791	NM_004345	CAMP	Homo sapiens cathelicidin antimicrobial peptide (CAMP), mRNA	GAATTGTCCAGAGAATCAAGGATTTTTTGCGG AATCTTGTACCCAGGACAGAGTCCTAGT (SEQ ID NO: 214)
4			A_23_P258493	NM_005573	LMNB1	Homo sapiens lamin B1 (LMNB1), mRNA	AATATTAACCTAATCACCATGTAAGCACTCTGG ATGATGGATTCCACAAAACTTGGTTTT (SEQ ID NO: 215)
4	3	Granulocyte	A_23_P259506	NM_032412	ORF1-FL49	Homo sapiens putative nuclear protein ORF1-FL49 (ORF1-FL49), mRNA	TGGGATTCTAGATTAATGGGGGTTGCTACTGT TTAATTCAGTGACTTGATCTTTTTAATG (SEQ ID NO: 216)
4			A_23_P302470	NM_014465	SULT1B1	Homo sapiens sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), mRNA	TGTCTAAGTCACAAATCTGAAGAAATAAGAGAT TGTCTGTAGTTGATTGAAACGAGGGCA (SEQ ID NO: 217)
4			A_23_P306941	NM_153615	Rgr	Homo sapiens Ral-GDS related protein Rgr (Rgr), mRNA	CCATGGGACTTTTGTGAGTCAGGCGGGAGAC CATTTTATGTTTATTTTCTTTAGTGTATA (SEQ ID NO: 218)
4	2	Granulocyte	A_23_P309381	NM_003516	HIST2H2AA	Homo sapiens histone 2, H2aa (HIST2H2AA), mRNA	CGACTTTCCCGATCGCCAGGCAGGAGTTTCTC TCGGTGACTACTATCGCTGTCATGTCTG (SEQ ID NO: 219)
4			A_23_P312932	NM_175857	KRTAP8-1	Homo sapiens keratin associated protein 8-1 (KRTAP8-1), mRNA	GGCTATGGCTTCGGCTATGGCTACAACGGCT GTGGGGCTTTCGGCTACAGGAGATACTCG (SEQ ID NO: 220)
4	24	Granulocyte	A_23_P31816	NM_004084	DEFA1	Homo sapiens defensin, alpha 1 (DEFA1), mRNA	GAGAACGTCGCTATGGAACCTGCATCTACCAG GGAAGACTCTGGGCATTCTGCTGCTGAG (SEQ ID NO: 221)
4	13	Granulocyte	A_23_P326080	NM_001925	DEFA4	Homo sapiens defensin, alpha 4, corticostatin (DEFA4), mRNA	AGAGCTACAGGAAATGGTTGTTTCTCCTATACT TTGTCCTTAACATCTTTCTTGATCCTA (SEQ ID NO: 222)
4			A_23_P330561	NM_174918	MCEMP1	Homo sapiens mast cell-expressed membrane protein 1 (MCEMP1), mRNA	CTGTCTCCCTGTTTGTGTAAACATACTAGAGTA TACTGCGGCGTGTTTTCTGTCTACCCA (SEQ ID NO: 223)
4			A_23_P332042	NM_004259	RECQL5	Homo sapiens RecQ protein-like 5 (RECQL5), transcript variant 1, mRNA	CTTTCTGCTTGCAAAGCCTATAGACCCTTCTCA GAGCGGTCCTCATGGCTGGGTTTTCTG (SEQ ID NO: 224)
4			A_23_P344973	NM_021019	MYL6	Homo sapiens myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 1, mRNA	CCTATGAGGATTATGTCGAAGGACTTCGGGTG TTTGACAAGGAAGGAAATGGCACCGTCA (SEQ ID NO: 225)
4	2	Granulocyte	A_23_P370635	NM_138799	OACT2	Homo sapiens O-acyltransferase (membrane bound) domain containing 2 (OACT2), mRNA	TTGTTCCTAAATGGTATTTTCAAGTGTAATATT GTGAGAACGCTACTGCAGTAGTTGATG (SEQ ID NO: 226)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
4			A_23_P371495	XM_928461	LOC653626	PREDICTED: Homo sapiens similar to ARG99 protein (LOC653626), mRNA	ACCAGACTAAGTGCCAGTATATATATGACTGATATTTTCGTGACTCATAGAAGGTGTCCA (SEQ ID NO: 227)
4	5	Granulocyte	A_23_P380240	NM_001816	CEACAM8	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA	TAGTCCACCCAATGGCTGACAGTAACAGCATCTTTAACACAACTCTTTGTTCAAATGTAC (SEQ ID NO: 228)
4			A_23_P395438	NM_053044	HTRA3	Homo sapiens HtrA serine peptidase 3 (HTRA3), mRNA	AAGGGGCATTTGTGAGCTTTGCTGTAAATGGATTCCCAGTGTTGCTTGTACTGTATGTTT (SEQ ID NO: 229)
4			A_23_P4096	NM_000717	CA4	Homo sapiens carbonic anhydrase IV (CA4), mRNA	TAATATCCCCAAACCTGAGATGAGCACTACGATGGCAGAGAGCAGCCTGTTGGACCTGCT (SEQ ID NO: 230)
4			A_23_P41114	NM_005213	CSTA	Homo sapiens cystatin A (stefin A) (CSTA), mRNA	AAACAAATGAGACTTATGGAAAATTGGAAGCTGTGCAGTATAAAACTCAAGTTGTTGCTG (SEQ ID NO: 231)
4			A_23_P421493	NM_020995	HPR	Homo sapiens haptoglobin-related protein (HPR), mRNA	GGGGACAAAGTGACAACTTTAAACTTACTGACCATCTGAAGTATGTCATGCTGCCTGTGG (SEQ ID NO: 232)
4			A_23_P434809	NM_002964	S100A8	Homo sapiens S100 calcium binding protein A8 (calgranulin A) (S100A8), mRNA	AAAGCCATGAAGAAAGCCACAAAGAGTAGCTGAGTTACTGGGCCCAGAGGCTGGGCCCCT (SEQ ID NO: 233)
4			A_23_P60248	NM_003329	TXN	Homo sapiens thioredoxin (TXN), mRNA	GGACAAAAGGTGGGTGAATTTTCTGGAGCCAATAAGGAAAAGCTTGAAGCCACCATTAAT (SEQ ID NO: 234)
4			A_23_P63390	NM_000566	FCGR1A	Homo sapiens Fc fragment of IgG, high affinity Ia, receptor (CD64) (FCGR1A), mRNA	TTTAGTGAACACTGTTCTCTGGGTGACAATACGTAAAGAACTGAAAAGAAAGAAAAAGTG (SEQ ID NO: 235)
4	4	Granulocyte	A_23_P67847	NM_024572	GALNT14	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14) (GALNT14), mRNA	AAGCCTTCTTTTTCACTAGGCCAGGACTACATTGAGAGATGAAGAATGGAGGTTGTTTCC (SEQ ID NO: 236)
4			A_23_P74001	NM_005621	S100A12	Homo sapiens S100 calcium binding protein A12 (calgranulin C) (S100A12), mRNA	TGAAGGCTTTTTACCCAGCAATGTCCTCAATGAGGGTCTTTTCTTTCCCTCACCAAAACC (SEQ ID NO: 237)
4	3	Bcells	A_23_P85250	NM_013230	CD24	Homo sapiens CD24 antigen (small cell lung carcinoma cluster 4 antigen) (CD24), mRNA	CTGCCTCGACACACATAAACCTTTTTAAAAATAGACACTCCCCGAAGTCTTTTGTTTGTA (SEQ ID NO: 238)
4			A_23_P85903	NM_003268	TLR5	Homo sapiens toll-like receptor 5 (TLR5), mRNA	AACAGTAGAAAGATCGTTTGTCTTGTGAGCAGACACTTCCTTAGAGATGGCTGGTGCCTT (SEQ ID NO: 239)
4			A_23_P94230	NM_015364	LY96	Homo sapiens lymphocyte antigen 96 (LY96), mRNA	TGAAGCTATTTCTGGGAGCCCAGAAGAAATGCTCTTTTGCTTGGAGTTTGTCATCCTACA (SEQ ID NO: 240)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
4	3	Granulocyte	A_23_P99253	NM_004664	LIN7A	Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), mRNA	TTGAGGGAAAGCTACTTGATCAAACATCCGAT AGTCACAAATTTGAAACCGTGCTTCAGA (SEQ ID NO: 241)
4			A_24_P145066	NM_183416	KIF1B	Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, mRNA	TAGCTAGAACAGTTGAAGTCTTCAACTGAGGT TTTATAGCAGATTAGACATGGGTAAATG (SEQ ID NO: 242)
4	33	Granulocyte	A_24_P181254	NM_006418	OLFM4	Homo sapiens olfactomedin 4 (OLFM4), mRNA	TTTTTCCTTTGATGTTCAAGTCCTAGTCTATAG GATTGGCAGTTTAAATGCTTTACTCCC (SEQ ID NO: 243)
4			A_24_P252996	NM_000804	FOLR3	Homo sapiens folate receptor 3 (gamma) (FOLR3), mRNA	CCTGCAAAAGCAACTGGCACAAAGGCTGGAAT TGGACCTCAGGGATTAATGAGTGTCCGG (SEQ ID NO: 244)
4			A_24_P273143	NM_052871	MGC4677	Homo sapiens hypothetical protein MGC4677 (MGC4677), mRNA	ACAGGAAGCTCTATGACACACTTGATCGAATA TGACAGACACCGAAAATCACGACTCAGC (SEQ ID NO: 245)
4			A_24_P52004	NM_015200	SCC-112	Homo sapiens SCC-112 protein (SCC-112), mRNA	TGCATTGATAGGGACCTTTGTCTCTTCCTCCC TTTGATTAATTGCCCGGCATCACAGTTT (SEQ ID NO: 246)
4			A_24_P649624	BC063684		Homo sapiens cDNA clone IMAGE:4395035, partial cds.	CTGTTAGAGCCAAAATTGTGATGAGCAATACT GATAATTGTCCAGTTTATGTCATCTTTC (SEQ ID NO: 247)
4			A_24_P6921	NM_052871	MGC4677	Homo sapiens hypothetical protein MGC4677 (MGC4677), mRNA	CAGGAAGCTCTATGACACACTTGATCGAATAT GACAGACACTGAAAATCACGACTCATCC (SEQ ID NO: 248)
4			A_24_P759747	CNS01RGE		Human chromosome 14 DNA sequence BAC R-300J18 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence.	GGAGGAGCCCCACCTTCTGCTACTATTATGTT CTTCAGATGAGTAGAAGAGAGTGGGGAG (SEQ ID NO: 249)
4			A_24_P8151	AK098403		Homo sapiens cDNA FLJ25537 fis, clone CBR09136.	ATCTAGCAGGCGACTGAGTGCCGAGAAAATAC CTGGCAGAGGTGGGCACAAGGCGGGGTC (SEQ ID NO: 250)
4			A_24_P86389	NM_003514	HIST1H2AM	Homo sapiens histone 1, H2am (HIST1H2AM), mRNA	CTTGGTAAAGTTACCATCGCTCAGGGCGGTGT TCTGCCTAACATCCAGGCCGTACTGCTC (SEQ ID NO: 251)
4			A_32_P112452	NM_002965	S100A9	Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA	CGTGGGAGGTGTTGATGATGGTCTCTATGTTG CGTTCCAGCTGCGACATTTTGCAAGTCA (SEQ ID NO: 252)
4			A_32_P113646	NM_005544	IRS1	Homo sapiens insulin receptor substrate 1 (IRS1), mRNA	CAGTCTCTTCCTCTCTGGGAGCTGGCTGGAG CTGGGATGGACACCTGACAGAAGGAAATT (SEQ ID NO: 253)
4			A_32_P143589	AC018758	CD177	Homo sapiens chromosome 19, BAC CTB-61I7 (BC52850), complete sequence.	AGCTTGGATGGTAGCAGAGACTTCAGGGTGC TCCAGCCAAACGTATTTGGGCATCACCAT (SEQ ID NO: 254)
4			A_32_P146815	AC007528		Homo sapiens 12 BAC RP11-473N11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	TACCTTTTGCATATGCTTTTCTTGGCCTTAGGA TAGTACTGGACTTTGTTGTCCTCTGCT (SEQ ID NO: 255)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
4	2	Granulocyte	A_32_P198223	AC022784		Homo sapiens chromosome 8, clone RP11-10A14, complete sequence.	CAGGAATCACGGGAGTGAATCACATTCCAGAC ACTTGCTTGGACTTCATCACATCCTCAG (SEQ ID NO: 256)
4	26	Granulocyte	A_32_P228455	AC073172		Homo sapiens chromosome 11, clone RP11-531H8, complete sequence.	AGTTACTTGCCTCCAGATATCTTGGTGTGTGA GAACATTAAATCTGTATGTGTCTAAATC (SEQ ID NO: 257)
4			A_32_P41604	HS86F14		Human DNA sequence from clone RP1-86F14 on chromosome 1q23-24 Contains the F5 gene for coagulation factor V (proaccelerin labile factor) and the 3' end of the SELP gene for selectin P (granule membrane protein 140kDa antigen CD62), complete sequence.	GATCTGGAAAATACTTGTTTGGGGATCAATAAT ATGTTTGGGCTATTATCTAATGCTGTG (SEQ ID NO: 258)
4			A_32_P47754	HSM803756		Homo sapiens mRNA; cDNA DKFZp434F1129 (from clone DKFZp434F1129).	TTCACGTCAACTTCTGGCTCCTCAGTTTGGCA GTAAGGCAGGGAAGTTGTTTTCCTATTT (SEQ ID NO: 259)
4			A_32_P9753	AC004686		Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence.	ATTGGATAGGAAGAGGAATAAAATATAAAAATC AGAGAACTGCTGAAATTCTGTGACCCC (SEQ ID NO: 260)
5		Platelet					
5			A_23_P104624	XM_290546	KIAA0830	PREDICTED: Homo sapiens KIAA0830 protein, transcript variant 1 (KIAA0830), mRNA	GGAGAGAACACATGGTACAATCGTAACACATG AAGGACAAGTAAGTGCTGCAGTAAAGGT (SEQ ID NO: 261)
5			A_23_P118313	NM_007285	GABARAPL2	Homo sapiens GABA(A) receptor-associated protein-like 2 (GABARAPL2), mRNA	TGAGGTAGGTGCGGTATTAAAGTGAAAGGGAA GGTGATGCATTTATTCTGGGTTATGCTT (SEQ ID NO: 262)
5			A_23_P131646	NM_144563	RPIA	Homo sapiens ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase) (RPIA), mRNA	ACTTTTGCTAAGATCTGGGGGTTTCTTCATATT CCTGCTGTTGGAAGCAGTTGACCAGAA (SEQ ID NO: 263)
5			A_23_P134925	NM_004331	BNIP3L	Homo sapiens BCL2/adenovirus E1B 19kDa interacting protein 3-like (BNIP3L), mRNA	ATTTGGGGACAAAAAGGCAGGCTTCATTTTTC ATATGTTTGATGAAAACTGGCTCAAGAT (SEQ ID NO: 264)
5			A_23_P137434	NM_014372	RNF11	Homo sapiens ring finger protein 11 (RNF11), mRNA	TGTAGTATCCATATGTTGCTTAAATTTCCTTAT GAGCCCCATGATGGAAAGACTTAAAGA (SEQ ID NO: 265)
5			A_23_P140256	NM_000270	NP	Homo sapiens nucleoside phosphorylase (NP), mRNA	CTACTAGCTCTTTGAGATAATACATTCCGAGG GGCTCAGTTCTGCCTTATCTAAATCACC (SEQ ID NO: 266)
5			A_23_P141764	NM_003826	NAPG	Homo sapiens N-ethylmaleimide-sensitive factor attachment protein, gamma (NAPG), mRNA	CATGCCATTTCAAGGACTTGGGAATAGATTAG GGATATCCGTACTTCATTACAGTCATGA (SEQ ID NO: 267)
5			A_23_P144145	AC092953		Homo sapiens 3 BAC RP11-531F16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	TCTTTAGTGAATATCATCTGCATATCTCTGTAA GTTCAATTGTGTTTCTTACAGTCCCTG (SEQ ID NO: 268)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
5			A_23_P145114	NM_001498	GCLC	Homo sapiens glutamate-cysteine ligase, catalytic subunit (GCLC), mRNA	AGAATGCCTGGTTTTCGTTTGCAATTTGCTTGT GTAAATCAGGTTGTAAAAAGGCAGATA (SEQ ID NO: 269)
5	2	Platelet	A_23_P157795	NM_003798	CTNNAL1	Homo sapiens catenin (cadherin-associated protein), alpha-like 1 (CTNNAL1), mRNA	GGATAGTAAAACTTGAGAAGCTTTTGGGGTCA GATCTCTGGAACATCATGTGATGAAGCT (SEQ ID NO: 270)
5			A_23_P160359	NM_004437	EPB41	Homo sapiens erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked) (EPB41), transcript variant 3, mRNA	AGAGCAAGAGCAGTATGAAAGTACCATCGGAT TCAAACTTCCCAGTTACCGAGCAGCTAA (SEQ ID NO: 271)
5			A_23_P203558	NM_000518	HBB	Homo sapiens hemoglobin, beta (HBB), mRNA	GTCCAACTACTAAACTGGGGGATATTATGAAG GGCCTTGAGCATCTGGATTCTGCCTAAT (SEQ ID NO: 272)
5			A_23_P209426	NM_015049	TRAK2	Homo sapiens trafficking protein, kinesin binding 2 (TRAK2), mRNA	AGAAAATGTTGTGCTGTATGTTCTTGATTTGAC ATAAATGAATAGACTTTGGCAAGGGAG (SEQ ID NO: 273)
5			A_23_P21785	NM_022072	NSUN3	Homo sapiens NOL1/NOP2/Sun domain family, member 3 (NSUN3), mRNA	ACGGTAACATCATGCCTATGGACATTAAAGGA ATAGCAAGGACTTGCTCCCACGACTTCA (SEQ ID NO: 274)
5			A_23_P383377	NM_006563	KLF1	Homo sapiens Kruppel-like factor 1 (erythroid) (KLF1), mRNA	GGACCCGGGACGGTGGGCACTGGACTCGGG GGGACTGCAGAGGATCCAGGTGTGATAGCC (SEQ ID NO: 275)
5			A_23_P38757	NM_015865	SLC14A1	Homo sapiens solute carrier family 14 (urea transporter), member 1 (Kidd blood group) (SLC14A1), mRNA	GTATTAAAAATTAAACCCCCATAAACCCAACCT AAGCCTATGGAATCCACAGTCACAAAA (SEQ ID NO: 276)
5			A_23_P397999	NM_003468	FZD5	Homo sapiens frizzled homolog 5 (Drosophila) (FZD5), mRNA	GGGGCTTTACAATCCTAAGGTTGGCGTTGTAA TGAAGTTCCACTTGGTTCAGGTTTCTTT (SEQ ID NO: 277)
5	2	Platelet	A_23_P45304	NM_021083	XK	Homo sapiens X-linked Kx blood group (McLeod syndrome) (XK), mRNA	GCTTTCGTTGACTGCTTCTCTGCAGTCGTTGA TGCTAATAAATATTGTCCTGTTTCTTCA (SEQ ID NO: 278)
5			A_23_P55578	NM_003831	RIOK3	Homo sapiens RIO kinase 3 (yeast) (RIOK3), transcript variant 1, mRNA	CTTTAGTGGGTAGAACAAATGGAAATTTGGTTT CAGAATGGCTGACAGAAATCGACATAA (SEQ ID NO: 279)
5			A_23_P60324	NM_016172	UBADC1	Homo sapiens ubiquitin associated domain containing 1 (UBADC1), mRNA	TTTAGCATCTGACAGGTGTTTACAAAAAAGTG GTTGTCGCACTGGGAAGTGGAGTGATGG (SEQ ID NO: 280)
5			A_23_P63547	XM_931256	CR1L	PREDICTED: Homo sapiens complement component (3b/4b) receptor 1-like, transcript variant 3 (CR1L), mRNA	AACACCTGTTTGTGACAGTGAGTTGAAATATG CATTCCTATTTCTTTTACCGATACATTC (SEQ ID NO: 281)
5			A_23_P67708	NM_003200	TCF3	Homo sapiens transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) (TCF3), mRNA	CGGAGAAATGGAAACATATCACTCAAGGGGGA TGCTGTGGAAACCTGGCTTATTCTTCTA (SEQ ID NO: 282)
5			A_23_P69695	NM_001008388	LOC493856	Homo sapiens similar to RIKEN cDNA 1500009M05 gene (LOC493856), mRNA	ATTTGTGTCTTACTAAAGCAGCTTATTGTAGGT GTTGGCGTTCTAAAACGTTTCCTGCCT (SEQ ID NO: 283)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
5			A_23_P70843	NM_001724	BPGM	Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 1, mRNA	TAGTAGAATTCCTCTTTGGCCACAAGAATAAG CAGCAAATAAACAACTATGGCTGTTGAG (SEQ ID NO: 284)
5			A_24_P132039	NM_004290	RNF14	Homo sapiens ring finger protein 14 (RNF14), transcript variant 1, mRNA	GGGTGTTAGAACCTAGATTCAAAATGGCTTGT CTTTGCTACTTTTGTTCCACATTCTCTC (SEQ ID NO: 285)
5			A_24_P173823	HSM800166		Homo sapiens mRNA; cDNA DKFZp586J2118 (from clone DKFZp586J2118).	ATGATACTAACACGGTGTAGGTTTTACAGTCTC CTAATTTGTACTGGTAATGCATATTCC (SEQ ID NO: 286)
5			A_24_P285880	NM_003262	TLOC1	Homo sapiens translocation protein 1 (TLOC1), mRNA	AAGGTATTTTTCCTTTTCCCTCTTACTGGATTT TTCAATTTTCAAACCATATGGCCTAGG (SEQ ID NO: 287)
5			A_24_P32790	NM_018566	YOD1	Homo sapiens YOD1 OTU deubiquinating enzyme 1 homolog (yeast) (YOD1), mRNA	CTAGGGATCTAATTAAGGACATTAAAGTACAAT TCTTGAGCTACTAACCATCAGCTCTTC (SEQ ID NO: 288)
5			A_24_P335620	NM_003486	SLC7A5	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (SLC7A5), mRNA	TTTCAGTCGTTGTGCTTTTTTGTTTTGTGCTAA CGTCTTACTAATTTAAAGATGCTGTCG (SEQ ID NO: 289)
5			A_24_P483083	NM_007111	TFDP1	Homo sapiens transcription factor Dp-1 (TFDP1), mRNA	AAACAGAAACAGTCTCAACTTCAAAACTTATTC TACAGCAAATTGCCTTCAAGAACCTGG (SEQ ID NO: 290)
5			A_24_P503866	XM_930101	LOC647087	PREDICTED: Homo sapiens hypothetical protein LOC647087 (LOC647087), mRNA	TATACCTTTTCACATTAAAAAAGGTATTTATATT ATTACTTTGTAGTGATTGTCTTAAGA (SEQ ID NO: 291)
5			A_24_P570806				TCTCAGAAGACAGAGGGTTTTCTTTTGAGGTA AATTTGATAGTACATTTTGATAGTACGG (SEQ ID NO: 292)
5			A_24_P599496	CNS01DVX		Human chromosome 14 DNA sequence BAC C-2555C10 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence.	GGCGGAAAACAAGTTTAGTCACAGAAGACTAC TCCATGTTTGAGCTTCTGTTTCAAGGGA (SEQ ID NO: 293)
5			A_24_P673786	AL513128		Human DNA sequence from clone RP11-301N24 on chromosome 10	GTCTATAACAAACAGTCTGTTCATTTATTTCTG TTGATAAACCATTTGGACAGAGTGAGG (SEQ ID NO: 294)
5			A_24_P67946	NM_019094	NUDT4	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), transcript variant 1, mRNA	GAACTCAGATTTGCAAACCAGGTTTCTGAAAC TTTGGGTAAGGTGTATGCTTTTAACTTT (SEQ ID NO: 295)
5			A_24_P886515	AC124287		Homo sapiens chromosome 17, clone RP13-991F5, complete sequence.	CGTTGCCTGTCTTGCTGGATAACTGCATATATT GTGTTCAGTTGTGTATTTGTTTTGCTT (SEQ ID NO: 296)
5			A_24_P926507	AC087685		Homo sapiens chromosome 18, clone RP11-618K16, complete sequence.	GAATAAACAGAAATAGGGAAGTAAACCTACAA ATATTTTAGGGAGAAGCTCACTTCTTCC (SEQ ID NO: 297)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
5			A_24_P935893	NM_017709	FAM46C	Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA	TTCACATGCAAGTTCTAATCTAAAGTTAAGCAG TCTCTTATTTGTTTCGGGACTCTGATT (SEQ ID NO: 298)
5	4	Platelet	A_32_P109653	AF163864		Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced.	TGTGGTTTGGTATTCCAAGTGGGGTCTTTTTC AGAATCTCTGCACTAGTGTGAGATGCAA (SEQ ID NO: 299)
5			A_32_P11181	AC034102		Homo sapiens 12 BAC RP11-603J24 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	GGCATGCTGTCCCAGGAAACTAGGGCTCCCA CTAACTTATGAGGTTTTTAAACACATTGA (SEQ ID NO: 300)
5			A_32_P122715	AC025300		Homo sapiens chromosome 11, clone RP11-573E11, complete sequence.	GAAAGTTCACATACAGGGGAAAGTGTACGATT TCATCTACTGTTTATCTTCTAACCTCAC (SEQ ID NO: 301)
5			A_32_P133840	NM_014858	TMCC2	Homo sapiens transmembrane and coiled-coil domain family 2 (TMCC2), mRNA	CTTCCATTCCATTTAGCCTTTGGATCATCCTGG CTGGGAGAAGTGGGACCGAGCCACCCA (SEQ ID NO: 302)
5			A_32_P159651	NM_003884	PCAF	Homo sapiens p300/CBP-associated factor (PCAF), mRNA	GAGTGGTGTCTAGATTTCTAATGAAGAATCAT GATACAGTTTGGATTAAGTATCTTGGAC (SEQ ID NO: 303)
5			A_32_P165297	HSJ842K24		Human DNA sequence from clone RP5-842K24 on chromosome Xq25-26.3 Contains the 3' end of the MBNL3 gene for muscleblind-like 3 (Drosophila) and a novel gene, complete sequence.	GAGGGGTATTTAGGGCCACTGTATTTTTGGTG CCACAATTTTCTACATTGTTGGCATTTT (SEQ ID NO: 304)
5			A_32_P1712	NM_002934	RNASE2	Homo sapiens ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA	TCCAGGTGCCTTTAATGTACTGTAACCTCACAA CTCCAAGTCCACAGAATATTTCAAACT (SEQ ID NO: 305)
5			A_32_P175183	AC019227	ZBTB44	Homo sapiens BAC clone RP11-567O18 from 11, complete sequence.	CAGTCAAGCTGTGGATGAAATGACCAGGAACG GAGAATGAAGTATGTAAATCCCAGCTTC (SEQ ID NO: 306)
5			A_32_P178945	NM_018566	YOD1	Homo sapiens YOD1 OTU deubiquinating enzyme 1 homolog (yeast) (YOD1), mRNA	TTGCCAGCATTTTTTGAAGTAATACACTGCTGC TACCTGGAAGATGTCTAACTTCATTTT (SEQ ID NO: 307)
5			A_32_P192480	HSJ842K24		Human DNA sequence from clone RP5-842K24 on chromosome Xq25-26.3 Contains the 3' end of the MBNL3 gene for muscleblind-like 3 (Drosophila) and a novel gene, complete sequence.	TAGTGCTGTAGTGCTTGTTTATGTTTAAAAGTG CACATTATGCAGCTCATTTTAGTATGC (SEQ ID NO: 308)
5			A_32_P204048	HSJ842K24		Human DNA sequence from clone RP5-842K24 on chromosome Xq25-26.3 Contains the 3' end of the MBNL3 gene for muscleblind-like 3 (Drosophila) and a novel gene, complete sequence.	GGGTGGGAAAGCATAAGATGGGGACTAAGAC TTTGCCTTTAACCTTCATGACATGAAGAA (SEQ ID NO: 309)
5			A_32_P23795	XM_929854	LOC646890	PREDICTED: Homo sapiens hypothetical protein LOC646890 (LOC646890), mRNA	GATGAAGAATTTGCCTTACTTTGTTGTTCGCTC AGTTCCTAAGACTGTGAGTTGTCAAAT (SEQ ID NO: 310)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
5			A_32_P36694	NM_175061	JAZF1	Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA	CAGGTAAGGATGGGAATATTTTGTTATACTGT GTATAGTGAATGTATTGTACTGTGTCTG (SEQ ID NO: 311)
5			A_32_P465742	NM_001031687	PIP5K1B	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), transcript variant 1, mRNA	TTCCTATGGACTTTTGCATTATTTCATTGTGCA TGCATCCAGTGATTATACATAAGCAAC (SEQ ID NO: 312)
6		all cell types					
6			A_23_P109133	NM_000490	AVP	Homo sapiens arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes insipidus, neurohypophyseal) (AVP), mRNA	CGAGAGCTGCGTGACCGAGCCCGAGTGCCGC GAGGGCTTTCACCGCCGCGCCCGCGCCAG (SEQ ID NO: 313)
6			A_23_P15174	NM_005949	MT1F	Homo sapiens metallothionein 1F (functional) (MT1F), mRNA	TGCCAGGACAACCTTTCTCCCAGATGTAAACA GAGAGACATGTACAAACCTGGATTTTTT (SEQ ID NO: 314)
6			A_23_P157943	NM_016219	MAN1B1	Homo sapiens mannosidase, alpha, class 1B, member 1 (MAN1B1), mRNA	AGCTATGACAACAGCAAGAGTTGGCGGCGGC GCTCGTGCTGGAGGAAATGGAAGCAACTG (SEQ ID NO: 315)
6			A_23_P159191	NM_000805	GAST	Homo sapiens gastrin (GAST), mRNA	AGCCTATGGATGGATGGACTTCGGCCGCCGC AGTGCTGAGGATGAGAACTAACAATCCTA (SEQ ID NO: 316)
6			A_23_P16483	NM_000455	STK11	Homo sapiens serine/threonine kinase 11 (STK11), mRNA	CCGTGGCCTCGTGCTCCGCAGGGCGCCCAGC GCCGTCCGGCGGCCCCGCCGCAGACCAGC (SEQ ID NO: 317)
6			A_23_P208900				GGGTCTCCGAGGTGCCGGTTAGGAGTTTGAA CCCCCCCCACTCTGCAGAGGGAAGCGGGG (SEQ ID NO: 318)
6			A_23_P211345	NM_080647	TBX1	Homo sapiens T-box 1 (TBX1), transcript variant C, mRNA	TGTAGATACTGTAGATACTGTAGATACCGCCC CGGCGCCGACTTGATAAACGGTTTCGCC (SEQ ID NO: 319)
6			A_23_P25790	NM_022478	CDH24	Homo sapiens cadherin-like 24 (CDH24), transcript variant 1, mRNA	CGAGACGTGTTGCCCCGGGCCCGGGTGTCGC GCCAGCCCAGACCCCCCGGCCCCGCCGAC (SEQ ID NO: 320)
6			A_23_P3413	NM_130901	OTUD7	Homo sapiens OTU domain containing 7 (OTUD7), mRNA	GCCGACGCGCCGACCGCGCGCTCGAACGGT GAGTGCGGCCGTGGCGGCCCGGGGCCGGTG (SEQ ID NO: 321)
6			A_23_P346309	NM_004324	BAX	Homo sapiens BCL2-associated X protein (BAX), transcript variant beta, mRNA	CCCGCGCGGACCCGGCGAGAGGCGGCGGCG GGAGCGGCGGTGATGGACGGGTCCGGGGAG (SEQ ID NO: 322)
6			A_23_P35534	NM_020999	NEUROG3	Homo sapiens neurogenin 3 (NEUROG3), mRNA	CATTCAAAGAATACTAGAATGGTAGCACTACC CGGCCGGAGCCGCCCACCGTCTTGGGTC (SEQ ID NO: 323)
6			A_23_P401626	NM_174919	LOC201175	Homo sapiens hypothetical protein LOC201175 (LOC201175), mRNA	GCAGCGACTCAGAGAACGTCTACGAGGTCAT CCAGGACTTGCACGTCCCGCCGCCGGAGG (SEQ ID NO: 324)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
6			A_23_P431346	NM_175887	LOC222171	Homo sapiens hypothetical protein LOC222171 (LOC222171), mRNA	CCCCAAACCAGACAAGTTATACGGGGACAAAT CCGGCAGCAGCCGCCGCAATTTGAAGAT (SEQ ID NO: 325)
6			A_23_P96072	NM_000832	GRIN1	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 1 (GRIN1), transcript variant NR1-1, mRNA	CAGGGTGCAGGCGCGCACCGCCCAACCCCCA CCTCCCGGTGTATGCAGTGGTGATGCCTA (SEQ ID NO: 326)
6			A_24_P108738	NM_153334	SCARF2	Homo sapiens scavenger receptor class F, member 2 (SCARF2), transcript variant 1, mRNA	CAGCGCCGCTGCAGCTGGCCGTGCGCCCTCA CCACCGCCGCCAGGCTCCGAGGCCGCGCC (SEQ ID NO: 327)
6			A_24_P112803	NM_005986	SOX1	Homo sapiens SRY (sex determining region Y)-box 1 (SOX1), mRNA	GCTGGGCTCTCTGGTGAAGTCGGAGCCCAGC GGCAGCCCGCCCGCCCCAGCGCACTCGCG (SEQ ID NO: 328)
6			A_24_P113725	NM_005634	SOX3	Homo sapiens SRY (sex determining region Y)-box 3 (SOX3), mRNA	GCCGCCCGCCATCGCATCGCACTCTCAGCGC GCGTGCCTCGGCGACCTGCGCGACATGAT (SEQ ID NO: 329)
6			A_24_P11737	XR_015426	LOC731268	PREDICTED: Homo sapiens similar to zinc finger protein 499 (LOC731268),	GTGAGAAGTTCTGCAGATGTATGTGGCGCACA GCCTCTACAGCCGCCGACTCCGACTCCT (SEQ ID NO: 330)
6			A_24_P117782	NM_033129	SCRT2	Homo sapiens scratch homolog 2, zinc finger protein (Drosophila) (SCRT2), mRNA	CTTCAAGCACTACCGCTGCCGCCAGTGCGAC AAGAGCTTCGCGCTCAAGTCCTACCTCCA (SEQ ID NO: 331)
6			A_24_P127719	NM_201589	MAFA	Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian) (MAFA), mRNA	GTTCGAGGTGAAGAAGGAGCCTCCCGAGGCC GAGCGCTTCTGCCACCGCCTGCCGCCAGG (SEQ ID NO: 332)
6			A_24_P144465	NM_022107	GPSM3	Homo sapiens G-protein signalling modulator 3 (AGS3-like, C. elegans) (GPSM3), mRNA	CAGACTGAACTCCTTCTGGACCTGGTGGCTGA AGCCCAGTCCCGCCGCCTGGAGGAGCAG (SEQ ID NO: 333)
6			A_24_P253293	NM_014360	NKX2-8	Homo sapiens NK2 transcription factor related, locus 8 (Drosophila) (NKX2-8), mRNA	GCGAGGTGGGAACCGCCGCGGCCCAGGAGA AGTGCGGCGCCCCTCCAGCCGCCGCCTGCC (SEQ ID NO: 334)
6			A_24_P273378	NM_006549	CAMKK2	Homo sapiens calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2), transcript variant 1, mRNA .	CCGGGCCGCCCCCCAGGATGAGCTGGGGGG TAGGGGCAGCAGCAGCAGCGAAAGCCAGAA (SEQ ID NO: 335)
6			A_24_P280660	NM_178174	TREML1	Homo sapiens triggering receptor expressed on myeloid cells-like 1 (TREML1), mRNA	GAGGGGTGCCAGCCCCTGGTGTCCTCAGCTG TGGATCGCAGAGCTCCAGCGGGCAGGCGT (SEQ ID NO: 336)
6			A_24_P315500	NM_014223	NFYC	Homo sapiens nuclear transcription factor Y, gamma (NFYC), mRNA	TCAGGAGTCCAGGAAGAGCAGGAGCCGCCCC CGCGCTCCTACGGAGTCGGGCAATGCAGA (SEQ ID NO: 337)
6			A_24_P328446	NM_016170	TLX2	Homo sapiens T-cell leukemia homeobox 2 (TLX2), mRNA	ACGGAGCCTCGGGCTACGGTCCCGCCGGCTC ACTTGCCCCGCTGCCCGGCAGCTCCGGAG (SEQ ID NO: 338)
6			A_24_P376451	NM_000514	GDNF	Homo sapiens glial cell derived neurotrophic factor (GDNF), transcript variant 1, mRNA	AACAGCAATGGTGCCGCCGCCGGACGGGACT TTAAGATGAAGTTATGGGATGTCGTGGCT (SEQ ID NO: 339)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
6			A_24_P37665	NM_022042	SLC26A1	Homo sapiens solute carrier family 26 (sulfate transporter), member 1 (SLC26A1), transcript variant 1, mRNA	TTATTTGAACAAGGGTCCCCCGCCATCATGCA GCCTCCAAGGTGCCAAGAGGACTCCCTA (SEQ ID NO: 340)
6			A_24_P40775	XM_290842	LRFN1	PREDICTED: Homo sapiens leucine rich repeat and fibronectin type III domain containing 1 (LRFN1), mRNA	AGGGGGCGCGGCCGGGGAGGATGGAGACCT GGGGCTGGGCTCCGCCAGGGCGTGCCTGGC (SEQ ID NO: 341)
6			A_24_P416595	NM_174945	ZNF575	Homo sapiens zinc finger protein 575 (ZNF575), mRNA	CAAGCTGGCCACGCACCGCTTAGCACACGGA GGCGCCCGACCCCACCCATGCCCAGACTG (SEQ ID NO: 342)
6			A_24_P471099				TGCAGGTTTTTGCCCCCGCCGTTGCGGCTGTT TTCCCCCCGTCAGCGAGGCTTTTTGTTG (SEQ ID NO: 343)
6			A_24_P535483	NM_207349	LOC284739	Homo sapiens hypothetical protein LOC284739 (LOC284739), mRNA	AGGAGGCCCGCCCTCCACGCGCCGAAGGCCT CAATAAACGGAGCTGGCGCTGCGGGTCCG (SEQ ID NO: 344)
6			A_24_P600087				GGGGGTTTCCCCCCCGGGAGGACCCCCCCTG GGGGCCCCCCTGTTTGTTACACGGCGGGT (SEQ ID NO: 345)
6			A_24_P75183	NM_199046	TEPP	Homo sapiens testis/prostate/placenta-expressed protein, isoform 2 (TEPP), transcript variant 1, mRNA	TCAGCGGCTACGCGGTGCGGTACTTGAAGCC CGACGTGACCCAGACCTGGCGGTACTGCC (SEQ ID NO: 346)
6			A_24_P780709				AGGCAGCCGCCGGGCCAGGTCGAGGCCGCC GCCGCCCGGCCAGAGCACGCCAGGGAGCAG (SEQ ID NO: 347)
6			A_24_P920135				CAAGTGGAAAAAAATATTAAAAAACTGATAATG GCCTCGGTTGGCCTCAGCGGCGGAACT (SEQ ID NO: 348)
6			A_32_P138359	NM_012331	MSRA	Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA	TGCGGCTCCGCTGCCGGTAGCGCCGTCCCCC GGGACCACCCTTCGGCTGGCGCCCTCCCA (SEQ ID NO: 349)
6			A_32_P336712	NM_173573	C11orf35	Homo sapiens chromosome 11 open reading frame 35 (C11orf35), mRNA	AGCCCCAAGGGCGAGGTCCTCAGTGAGCACC GGATCCCACGCCGCGAGACTCCGGCCCCG (SEQ ID NO: 350)
6			A_32_P509169	NM_207322	NLF1	Homo sapiens nuclear localized factor 1 (NLF1), mRNA	CCCCGCCTGGCCTTGGCTGCGCTCCGGAATT CTTGGGTCGAAGAAGCAGGGATGGACGAG (SEQ ID NO: 351)
7		B cells					
7	4	Bcells	A_23_P158817	NM_001040070	ELK2P1	ELK2, member of ETS oncogene family, pseudogene 1	ATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 352)
7	4	Bcells	A_23_P158868				ACACCTTCTACGGTATGGACGTCTGGGGCCAA GGGACCACGGTCACCGTCTCCTCAGCAT (SEQ ID NO: 353)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
7			A_23_P168229	NM_022085	TXNDC5	Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, mRNA	ATACGCAAGGGGATGTGGATACTTGGCCCAAA GTAACTGGTGGTAGGAATCTTAGAAACA (SEQ ID NO: 354)
7	7	Bcells	A_23_P21260				TAGGAGACAGAGTCACCATCACTTGCCGGGC AAGTCAGACCATTAGCAGCTATTTAAATT (SEQ ID NO: 355)
7	4	Bcells	A_23_P350782	XM_942302	LOC652694	PREDICTED: Homo sapiens similar to Ig kappa chain V-I region HK102 precursor (LOC652694), mRNA	GCAGCCTGCAGCCTGAAGATATTGCAACATAT TACTGTCAACAGTATGATAATCTCCCTC (SEQ ID NO: 356)
7	5	Bcells	A_23_P361654	AC073416		Homo sapiens BAC clone RP11-136K15 from 2, complete sequence.	TCAGGGTATTAGCAGCTGGTTAGCCTGGTATC AGCAGAAACCAGAGAAAGCCCCTAAGTC (SEQ ID NO: 357)
7	9	Bcells	A_23_P435390				AGACAGCACTGGTTCTTATTTGCTGTTCGGCG GAGGGACCAAGCTGACCGTCCTAGGTCA (SEQ ID NO: 358)
7	3	Bcells	A_23_P44053				AGCTCCTGATCTACGATGCATCCACTTTGGAA ACCGGGGTCCCATCAAGGTTCAGTGCAC (SEQ ID NO: 359)
7	7	Bcells	A_23_P61042	S55735		Homo sapiens immunoglobulin A1-A2 lambda hybrid GAU heavy chain mRNA, partial cds.	GAGTTGAAGACCCCACTAACCGCCAACATCAC AAAATCCGGAAACACATTCCGGCCCGAG (SEQ ID NO: 360)
7	8	Bcells	A_23_P61068				GCCTGAAGATCTTGCAGTATATTACTGTCAGC AGTATAGTAGTCCACCTCGGACTTTTGG (SEQ ID NO: 361)
7			A_23_P72330				AGATGGTGCAGCCACAGTTCGTTTGATCTCCA GCTCGAGCCGCTGCGTGTTTTCCTCTTG (SEQ ID NO: 362)
7	5	Bcells	A_23_P84596	NM_016459	PACAP	Homo sapiens proapoptotic caspase adaptor protein (PACAP), mRNA	GGACATGTTTGCACTACTTGGGGGAGTTTGGA GAAGACCAGATCTATGAAGCCCACCAAC (SEQ ID NO: 363)
7	4	Bcells	A_24_P100684				ATGGTATGATGGAAGTAATAAATACTATGCAGA CTCCGTGAAGGGCCGATTCACCATCTC (SEQ ID NO: 364)
7	5	Bcells	A_24_P144346				GTGGCACATACTATGCAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATGCCA (SEQ ID NO: 365)
7	6	Bcells	A_24_P15388				GCCAAGAACACGCTGTATCTGCAAATGAACAG TCTGAGAGCCGAGGACACGGCTGTGTAT (SEQ ID NO: 366)
7	2	Bcells	A_24_P15550				GCAGGGTGGAGGCTGAGGATGTTGGGGTTTA TTACTGCATGCAAGGTACACACTGGCCTC (SEQ ID NO: 367)
7			A_24_P169713	S80758		Ig VL=platelet glycoprotein IIIa leucine-33 form-specific antibody light chain variable region [human, plasma, mRNA Partial, 329 nt].	CATAGTTATAACCACCAACGTCACTGCTGGTT CCAGTGCAGGAGATGGTGATCGACTGTC (SEQ ID NO: 368)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
7	13	Bcells	A_24_P169873	HSM806780		Homo sapiens mRNA; cDNA DKFZp686O16217 (from clone DKFZp686O16217).	GTAAACCCACCCACATCAATGTGTCTGTTGTC ATGGCGGAGGCGGATGGCACCTGCTACT (SEQ ID NO: 369)
7			A_24_P204374				AGCCTGATGCCTGAACAGTGGAGATCCCGCA GCAGCTACAACTGCTGGGCCATGCATAAA (SEQ ID NO: 370)
7	4	Bcells	A_24_P204574	HUMIGLVE		Homo sapiens Ig germline lambda-chain gene variable region myeloma subgroup I (IGLV), complete exon.	GAGGATGAGGCTGATTATTACTGTGCAGCATG GGATGACAGCCTGAGTGGTCCCACAGTG (SEQ ID NO: 371)
7	5	Bcells	A_24_P212024				TGATCTATGCTGCATCCAGTTTGCAGTCGGGG GTCCCATCTCGGTTCAGTGGCAGTGGAT (SEQ ID NO: 372)
7	5	Bcells	A_24_P239076	NM_001013618	LOC91353	Homo sapiens similar to omega protein (LOC91353), mRNA	AACAAGGCCACACTGGTGTGTCTCATGAATGA CTTCTATCTGGGAATCTTGACGGTGACC (SEQ ID NO: 373)
7	4	Bcells	A_24_P24371				CACAAGCCCAGCAACACCAAGGTGGACAAGA GAGTTGAGTCCAAATATGGTCCCCCATGC (SEQ ID NO: 374)
7	7	Bcells	A_24_P272146				TCACTATCAGCAGCCTGCAGCCTGAAGATTTT GCAACTTACTATTGTCAACAGGCTAACA (SEQ ID NO: 375)
7	3	Bcells	A_24_P315854				ATCAGTAGACACGTCCAAGAACCAGTTCTCCC TGAAGCTGAGCTCTGTGACCGCTGCGGA (SEQ ID NO: 376)
7	4	Bcells	A_24_P33341	XM_370973	LOC388255	PREDICTED: Homo sapiens similar to Ig heavy chain V-III region VH26 precursor (LOC388255), mRNA	CCGTATCTGCAAATGAACAGCTTGAGAGCTGA GGACACGGCTGTGTATTACTGTGTGAAA (SEQ ID NO: 377
7	7	Bcells	A_24_P357847				CCATCAGCAGCCTGCAGTCTGAAGATTTTGCA GTTTATTACTGTCAGCAGTATAATAACT (SEQ ID NO: 378)
7	4	Bcells	A_24_P465799	AF063695		Homo sapiens clone BCPBLL11 immunoglobulin lambda light chain variable region mRNA, partial cds.	CTGTCAGGTGTGGGATAGTACTAGTGATCATT ATGTCTTCGGAACTGGGACCAAGGTCGC (SEQ ID NO: 379)
7	6	Bcells	A_24_P488083	HSA519285		Homo sapiens partial mRNA for IgM immunoglobulin heavy chain variable region (IGHV gene), clone ANBPM204.	CAATTCCAAGAACACGCTGTATCTGCAAGTGA ACAGCCTGAGAGTCGAGGACACGGCCCT (SEQ ID NO: 380)
7	6	Bcells	A_24_P490109				AGCAGCCTGCAGCCTGAAGATTTTGCAACCTA TTACTGTCAACAGAGTGACAACACAAGA (SEQ ID NO: 381)
7	7	Bcells	A_24_P510357	S76132		Ig V lambda II=IgG rheumatoid factor [human, hybridoma AEE111F, mRNA Partial, 315 nt].	CATCACTGGTCTCCAGGCTGAGGACGAGGCT GATTATTACTGCAGCTCATATACAAGCAG (SEQ ID NO: 382)
7	9	Bcells	A_24_P605563	S42404		Ig lambda chain=anti-Rh(D) antibody [human, mRNA Partial, 642 nt].	AAGATAGCAGCCCCGTCAAGCGGGAGTGGAG ACCACCACACCCTCCAAACAAAGCAACAA (SEQ ID NO: 383)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
7	5	Bcells	A_24_P608268				CCAGAGATGATTCCAAGAACACGGCGTATCTG CAAATGAACAGCCTGAAAACCGAGGACA (SEQ ID NO: 384)
7	5	Bcells	A_24_P626951				GACAGAGTCACCATCACTTGTCGGGCGAGTCA GGGAATTAGCAATTATTTAGCCTGGTTT (SEQ ID NO: 385)
7	3	Bcells	A_24_P66578				GCAGATTACACTCTCACCATCCGCAGCCTGCA GCCTGAAGATTTTGCAAATTATTACTGT (SEQ ID NO: 386)
7	6	Bcells	A_24_P702749				ATGCAGACTCCGTGAAGGGCCGATTCACCATC TCCAGAGACAATTCCAAGAACACGGTGT (SEQ ID NO: 387)
7	4	Bcells	A_24_P76868	HSZ74662		H.sapiens mRNA for immunoglobulin, light chain, V-J region.	TGGGCATCACCGGACTCCAGACTGGGGACGA GGCCGATTATTACTGCGGAACATGGAATA (SEQ ID NO: 388)
7	6	Bcells	A_24_P83102	NM_001013618	LOC91353	Homo sapiens similar to omega protein (LOC91353), mRNA	TCCAAGCCAACAAGGCTACACTGGTGTGTCTC ATGAATGACTTTTATCCGGGAATCTTGA (SEQ ID NO: 389)
7	3	Bcells	A_24_P852001	HSA234192		Homo sapiens mRNA for Ig heavy chain variable region, clone C2.	AGTTTGGGCTGAGCTGCCTTTTTCTTGTGGCT ATTTTAAAAGGTGTCCAGTGTGAGGTGC (SEQ ID NO: 390)
7	6	Bcells	A_32_P148118				CAGCAGCCTGCAGCCTGAAGATTTTGCAGCTT ATTACTGTCAACAGAGTGACAGTACCCC (SEQ ID NO: 391)
7	3	Bcells	A_32_P157927	AC096579		Homo sapiens BAC clone RP11-601N4 from 2, complete sequence.	GGCCACCATCAACTGCAAGTCCAGCCAGAGT GTTTTATACAGCTCCAACAATAAGAACTA (SEQ ID NO: 392)
7	6	Bcells	A_32_P159192				AGCAGCCTGCAGCCTGAAGATTTTGCAGTTTA TTACTGTCAGCAGGATTATAACTTACCT (SEQ ID NO: 393)
7	13	Bcells	A_32_P200144	XM_939003	LOC649923	PREDICTED: Homo sapiens similar to Ig gamma-2 chain C region (LOC649923), mRNA	CGTGAGGATGCTTGGCACGTACCCCGTGTAC ATACTTCCCAGGCACCCAGCATGGAAATA (SEQ ID NO: 394)
7	7	Bcells	A_32_P39440				GTGGGTCTGGGACAGAGTTCACTCTCACCATC AGCAGCCTGCAGTCTGAAGATTTTGCAG (SEQ ID NO: 395)
7	4	Bcells	A_32_P43664	NM_144646	IGJ	Homo sapiens immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides (IGJ), mRNA	TCTGTCATAAGTGTAGCAGGTCTCTGTAGCAC TGTCTTCATCACAGATATTGCTCTGGGT (SEQ ID NO: 396)
7	3	Bcells	A_32_P722809	XM_940969	LOC651751	PREDICTED: Homo sapiens similar to Ig kappa chain V-II region RPMI 6410 precursor (LOC651751), mRNA	GATTTTACACTGAAAATCAGCAGAGTGGAGGC TGAGGATGTTGGGGTTTATTACTGCATG (SEQ ID NO: 397)
8		all cell types					

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
8			A_23_P148473	NM_000206	IL2RG	Homo sapiens interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG), mRNA	CTTTCCTGTTTGCATTGGAAGCCGTGGTTATC TCTGTTGGCTCCATGGGATTGATTATCA (SEQ ID NO: 398)
8			A_23_P21057	NM_052838	SEPT1	Homo sapiens septin 1 (SEPT1), mRNA	ATTTCCTGAACCTGCGACGGATGCTGGTGCAG ACACACCTGCAGGACCTGAAAGAGGTGA (SEQ ID NO: 399)
8			A_23_P213424	NM_003633	ENC1	Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA	GTTGGAGGATACTTTGGCATTCAGCGATGCAA GACTTTGGACTGCTACGATCCAACATTA (SEQ ID NO: 400)
8			A_23_P25069	XM_927026	LOC440080	PREDICTED: Homo sapiens similar to cDNA sequence BC048546, transcript variant 2 (LOC440080), mRNA	TTTACTCCAACCATGTCATCCATTGAAGAGCTT GAAAACAAGGGCCAAGTGATGAAGACT (SEQ ID NO: 401)
8			A_23_P26810	NM_000546	TP53	Homo sapiens tumor protein p53 (Li-Fraumeni syndrome) (TP53), mRNA	CTGTGAGGGATGTTTGGGAGATGTAAGAAATG TTCTTGCAGTTAAGGGTTAGTTTACAAT (SEQ ID NO: 402)
8			A_23_P301925	MIHSXX		H.sapiens mitochondrial genome.	CTACGTTGTAGCCCACTTCCACTATGTCCTATC AATAGGAGCTGTATTTGCCATCATAGG (SEQ ID NO: 403)
8			A_23_P315252	HUMMTCG		Human mitochondrion, complete genome.	CATCGCTGGGTCAATAGTACTTGCCGCAGTAC TCTTAAAACTAGGCGGCTATGGTATAAT (SEQ ID NO: 404)
8			A_23_P337726	MIHSXX		H.sapiens mitochondrial genome.	CATGGCCATCCCCTTATGAGCGGGCACAGTG ATTATAGGCTTTCGCTCTAAGATTAAAAA (SEQ ID NO: 405)
8			A_23_P402751	MTHSCOXII		Homo sapiens mitochondrial coxII mRNA for cytochrome C oxidase II subunit.	GACTCCTTGACGTTGACAATCGAGTAGTACTC CCGATTGAAGCCCCCATTCGTATAATAA (SEQ ID NO: 406)
8			A_23_P70095	NM_001025158	CD74	Homo sapiens CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74), transcript variant 3, mRNA	AAGATCAGAAGCCAGTCATGGATGACCAGCG CGACCTTATCTCCAACAATGAGCAACTGC (SEQ ID NO: 407)
8			A_23_P86943	NM_003139	SRPR	Homo sapiens signal recognition particle receptor ('docking protein') (SRPR), mRNA	GCTAGGCTGGAGTGATTTGTTACAAATGAGCA AAAGATGAGTCCTTGCTTCCCTCAGAAA (SEQ ID NO: 408)
8			A_23_P98884	NM_005785	RNF41	Homo sapiens ring finger protein 41 (RNF41), transcript variant 1, mRNA	TTCCAGATGAGCTCTTCTTTCCTACAAGTTTTC ATAATTAGGGAATGCCAGGGTTTAGGG (SEQ ID NO: 409)
8			A_24_P202319	NM_005173	ATP2A3	Homo sapiens ATPase, Ca++ transporting, ubiquitous (ATP2A3), transcript variant 1, mRNA	CAACTTCTACCAGCTGAGGAACTTCCTGAAGT GCTCCGAAGACAACCCGCTCTTTGCCGG (SEQ ID NO: 410)
8			A_24_P204334				CTAGCCATGGCCATCCCCTTAAGCGGGGTGAT TATAGGCTTTCGCTCTAAGATTAAAAAT (SEQ ID NO: 411)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
8			A_24_P350200				AAGGCCACCACACACCACCTGTCCAGAAAGG CCTTCGATACGGGATAATCCTATTTATTA (SEQ ID NO: 412)
8			A_24_P381224	NM_032431	SYVN1	Homo sapiens synovial apoptosis inhibitor 1, synoviolin (SYVN1), transcript variant 1, mRNA	AAGTTTAGAATTGGAATTACTTCCTTACTAGTG TCTTTTGGCTTAAATTTTGTCTTTTGA (SEQ ID NO: 413)
8			A_24_P416728	NM_001130	AES	Homo sapiens amino-terminal enhancer of split (AES), transcript variant 2, mRNA	ACGGCTTGAACATCGAGATGCACAAACAGGCT GAGATCGTCAAAAGGCTGAACGGGATTT (SEQ ID NO: 414)
8			A_24_P551842				CTCCGATCCGTCCCTAAACAAACTAGGAGGCG TCCTTTGCCCTATTATATCCATCCTCAT (SEQ ID NO: 415)
8			A_24_P700170	NM_014225	PPP2R1A	Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), mRNA	ACGGCTGAACATCATCTCTAACCTGGACTGTG TGAACGAGGTGATTGGCATCCGGTCAGC (SEQ ID NO: 416)
8			A_24_P710024				TTAGCATCATCCCTCTACTATTTTTTAGCCAAA TCAACAACAACCTATTTTAGCTGTTCC (SEQ ID NO: 417)
8			A_24_P713185				AATATGACTAGCTTACACAATAGCTCACATAGT ACAGATACTCTTTACGGACTCCACTTA (SEQ ID NO: 418)
8			A_24_P910169				TTACATGGGTTTTCATGATCAGCCGCGAAACT GAGAACGTCAGGTCAGCGAGGAGATTGG (SEQ ID NO: 419)
9		B cells					
9	5	Bcells	A_23_P10356	NM_021777	ADAM28	Homo sapiens ADAM metallopeptidase domain 28 (ADAM28), transcript variant 3, mRNA	CTTAGAAGCTTCGAACTCAAAATCATGGAAAG GTTTTAAGATTTGAGGTTGGTTTTAGGG (SEQ ID NO: 420)
9	9	Bcells	A_23_P113572	NM_001770	CD19	Homo sapiens CD19 antigen (CD19), mRNA	TACATGCCAGTGACACTTCCAGTCCCCTTTGT ATTCCTTAAATAAACTCAATGAGCTCTT (SEQ ID NO: 421)
9	6	Bcells	A_23_P116371	NM_021950	MS4A1	Homo sapiens membrane-spanning 4-domains, subfamily A, member 1 (MS4A1), transcript variant 3, mRNA	GAGCTCACACACCATATATTAACATATACAACT GTGAACCAGCTAATCCCTCTGAGAAAA (SEQ ID NO: 422)
9	6	Bcells	A_23_P121657	NM_005114	HS3ST1	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA	GGCAGAACATTTGACTGGCACTGATTTGCAAT AAGCTAAGCTCAGAAACTTTCCTACTGT (SEQ ID NO: 423)
9			A_23_P125618	NM_000808	GABRA3	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 3 (GABRA3), mRNA	TGCATGCCTGCCCACTGAAGTTTGGAAGCTAT GCCTATACAACAGCTGAAGTGGTTTATT (SEQ ID NO: 424)
9	4	Bcells	A_23_P149368	NM_052938	FCRL1	Homo sapiens Fc receptor-like 1 (FCRL1), mRNA	AAACAAGATGGAATAAAAGAAATTGGGATCTT GGGTTGGAGGGACAGTGAAGCTTAGAGC (SEQ ID NO: 425)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
9			A_23_P151166	NM_032369	MGC15619	Homo sapiens hypothetical protein MGC15619 (MGC15619), mRNA	TCTAGAAAAGTCTCTTATTTTCAAGCTGTTCTA AATAGCTTCGTCTCAGTTTCCCCAAAA (SEQ ID NO: 426)
9	9	Bcells	A_23_P160751	NM_030764	FCRL2	Homo sapiens Fc receptor-like 2 (FCRL2), transcript variant 2, mRNA	GAGGAATCAGAAGGGAAGATCAACAGCAAGG ATGGGGCATCATTAAGACTTGCTATAAAA (SEQ ID NO: 427)
9	4	Bcells	A_23_P207201	NM_000626	CD79B	Homo sapiens CD79B antigen (immunoglobulin-associated beta) (CD79B), transcript variant 1, mRNA	CGCTGAAGGATGGTATCATCATGATCCAGACG CTGCTGATCATCCTCTTCATCATCGTGC (SEQ ID NO: 428)
9	7	Bcells	A_23_P209055	NM_001771	CD22	Homo sapiens CD22 antigen (CD22), mRNA	GCCTCAGGCACAAGAAAATGTGGACTATGTGA TCCTCAAACATTGACACTGGATGGGCTG (SEQ ID NO: 429)
9	4	Bcells	A_23_P250245	NM_001782	CD72	Homo sapiens CD72 antigen (CD72), mRNA	TGCTCAAAGCTCAAAATGTAACAAGGTACATAA AACTTGGTCATGGTGGACACTGGAGTC (SEQ ID NO: 430)
9			A_23_P307382	NM_080552	SLC32A1	Homo sapiens solute carrier family 32 (GABA vesicular transporter), member 1 (SLC32A1), mRNA	CCAGCTTGCCTGCCGGTTTTCAGGAATCTAAA CTCTCATCTTGTGCAATTTATCAGGTGT (SEQ ID NO: 431)
9	5	Bcells	A_23_P31725	NM_001715	BLK	Homo sapiens B lymphoid tyrosine kinase (BLK), mRNA	TCGCACGGTCATCCGGAGTACTAAGCCCCAGT AAGGTGTTCAGGACTGGTAAGCGACTGT (SEQ ID NO: 432)
9	5	Bcells	A_23_P357717	NM_021966	TCL1A	Homo sapiens T-cell leukemia/lymphoma 1A (TCL1A), mRNA	TTTCCCCCCTTTATAGATGGTCACGCACCTGG GTGTTACAAAGTTGTATGTGGCATGAAT (SEQ ID NO: 433)
9			A_23_P398294	NM_003959	HIP1R	Homo sapiens huntingtin interacting protein 1 related (HIP1R), mRNA	GTTAGCATTTCCTCCTGAAGTGTTCTGTTGGC AATAAAATGCACTTTGACTGTTTGTTGT (SEQ ID NO: 434)
9			A_23_P76402	NM_024549	FLJ21127	Homo sapiens tectonic (FLJ21127), mRNA	GCTTTGGTTATAGAAGTGAAGTGGACTAAATA CGGATCCCTGCTGAATCCACAGGCCAAA (SEQ ID NO: 435)
9	2	Bcells	A_23_P904	NM_024603	C1orf165	Homo sapiens chromosome 1 open reading frame 165 (C1orf165), mRNA	CATCGTCAGAGAGTGTTTGTATGACAGAATAG CACAAGAAACTGTGGATGAAACTGAAAT (SEQ ID NO: 436)
9	4	Bcells	A_24_P203056	NM_001024808	BCL7A	Homo sapiens B-cell CLL/lymphoma 7A (BCL7A), transcript variant 2, mRNA	TCGCCAAGAACCTGGTTAGAGGCATAAAGACC TTTTTTCACCGTTACCTAATTTTTTCCC (SEQ ID NO: 437)
9	4	Bcells	A_24_P252945	NM_001716	BLR1	Homo sapiens Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C-X-C motif) receptor 5) (BLR1), transcript variant 1, mRNA	TTTTCTTTTTAATAAAAAGGCACCTATAAAACA GGTCAATACAGTACAGGCAGCACAGAG (SEQ ID NO: 438)
9			A_24_P254106				AACACTATTGTAGGTAGTGATATGTGTGTTAG GAAAAAAATAAGGCCGAGAGAGGGGAGT (SEQ ID NO: 439)
9			A_24_P305067	NM_024015	HOXB4	Homo sapiens homeo box B4 (HOXB4), mRNA	GATCAACTCAAACTATGTCGACCCCAAGTTCC CTCCATGCGAGGAATATTCACAGAGCGA (SEQ ID NO: 440)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
9	3	Bcells	A_24_P324838	HSIGCMUDE		Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions).	AGATGGTGCAGTGGTTAGAGCTGAGGCTTATC CCACAGAGAACCCTGGCGCCTTGGTCAA (SEQ ID NO: 441)
9	4	Bcells	A_24_P413126	NM_020182	TMEPAI	Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA	AAGAAACTGCTTGTTGTGTATCAGTAATCATTA GTGGCAATGATGACATTCTGAAAAGCT (SEQ ID NO: 442)
9	8	Bcells	A_24_P417352	HSIGCMUS		Human C mu gene for IgM heavy chain exons CH1 4, secretory.	TGACCACCTATGACAGCGTGACCATCTCCTGG ACCCGCCAGAATGGCGAAGCTGTGAAAA (SEQ ID NO: 443)
9	8	Bcells	A_24_P621701	HS250D10		Human DNA sequence from clone CTA-250D10 on chromosome 22	TGGTAAGTTTCTCTCTCTTTAGAGACTCCACAA TAAAGTTTTCAACATGGTAAGGTTTTC (SEQ ID NO: 444)
9	7	Bcells	A_24_P64344	NM_013314	BLNK	Homo sapiens B-cell linker (BLNK), mRNA	TAAGCGAGTATATAATATTCCTGTGCGATTTAT TGAAGCAACAAAACAATATGCCTTGGG (SEQ ID NO: 445)
9			A_24_P916364	AC007172		Homo sapiens chromosome 9, clone hRPK.538_E_7, complete sequence.	GGGTGAATGTTTGAAAATCATGAATCAGCCAC CATTATTAATTGAAGAGCTGGGAATACC (SEQ ID NO: 446)
9	7	Bcells	A_24_P940348	NM_173544	BCNP1	Homo sapiens B-cell novel protein 1 (BCNP1), mRNA	AGACAAGCTTTTACCGACTTCCTCTGCTTGCC AGCAAAGTCATCTGCTAACTGGATATTG (SEQ ID NO: 447)
9			A_24_P95723	NM_014792	KIAA0125	Homo sapiens KIAA0125 (KIAA0125), mRNA	CCATTTTAAAGATGGCTACTTAGGACCATATG GATGTTGTACTGATGTCATTTGACCACG (SEQ ID NO: 448)
9			A_32_P107002	NM_001012391	LOC400509	Homo sapiens similar to FLJ12363 protein (LOC400509), mRNA	TGTGAAAAGCATCGATGATGAAGATGTGGATG AAAACGAAGATGACGTGTATGGAAACTC (SEQ ID NO: 449)
9	3	Bcells	A_32_P13337	AC006230		Homo sapiens chromosome 4 clone C0287J14 map 4p16, complete sequence.	ATCCTCCATGGTATCTGAATCCCAGAATCCTA CAATCCTGCATGGTATCTGAAACATACT (SEQ ID NO: 450)
9	3	Bcells	A_32_P137819	AL450344		Human DNA sequence from clone RP11-136K14 on chromosome 6 Contains three novel genes, the 5' end of a novel gene (contains FLJ31738 and KIAA1209) and a CpG island, complete sequence.	CTGCAGATCTTTATTACTGGCAAGAAAGTCCC AGAAGTTCTTTTCTCTAACTTATGACTA (SEQ ID NO: 451)
9	4	Bcells	A_32_P356316	NM_002119	HLA-DOA	Homo sapiens major histocompatibility complex, class II, DO alpha (HLA-DOA), mRNA	TGGAAAGGTGTTTCTCTCATCTCTGTCCTAAG GCTTGATAAAGTCATTAAAATTGTGTTC (SEQ ID NO: 452)
9	3	Bcells	A_32_P57013	NM_018014	BCL11A	Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 2, mRNA	ATAATACAAAGATGGCGCAGGGAAGATGAATT GTGGGAGAGCCGTCATGGCTTTTTTTTA (SEQ ID NO: 453)
9			A_32_P64016				CTCTGAGGCTAAGATTACTGGTGTACTCATTG GGACCAGTTTGGTCTCAGTGACTGAAAA (SEQ ID NO: 454)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
9	9	Bcells	A_32_P71876	AL356276		Human DNA sequence from clone RP11-367J7 on chromosome 1	GAAGTTTGAACTTCTTTGTATTGTATGATCATC CCTTTACCTTAATACTCACATGAAATG (SEQ ID NO: 455)
9			A_32_P8813				GACGGGACATCATGCTGGGCAACACAGCTAA AATGCGGGTGAAGACCAGATTTCTTGCAC (SEQ ID NO: 456)
10		all cell types					
10			A_23_P117480	CNS06C82		Human chromosome 14 DNA sequence BAC C-2335L22 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence.	ATTGTCGGCATCTTCCATGCTCTGAGTCAGTT AGCATTTACAGTGAATCTGCCCTTCTGT (SEQ ID NO: 457)
10			A_23_P153827	NM_005934	MLLT1	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1 (MLLT1), mRNA	TACACCGGAGGCTGATGGCGCTGCGGGAGCG CAACGTGCTGCAGCAGATTGTGAATCTGA (SEQ ID NO: 458)
10			A_23_P170464	NM_031297	DKFZP761H1710	Homo sapiens hypothetical protein DKFZp761H1710 (DKFZP761H1710), mRNA	TGGCCCCAGAGGATGAGGTCATTGTGAATCAG TACGTGATTCGGCCTGGCCCCTCGGCCT (SEQ ID NO: 459)
10			A_23_P258887	NM_012190	ALDH1L1	Homo sapiens aldehyde dehydrogenase 1 family, member L1 (ALDH1L1), mRNA	TTCGGGCCTGTCATGATCATCTCTCGGTTTGC TGATGGGGACTTGGATGCCGTGCTGTCT (SEQ ID NO: 460)
10			A_23_P30805	NM_003541	HIST1H4K	Homo sapiens histone 1, H4k (HIST1H4K), mRNA	AAGCGCCAGGGCCGCACCCTCTACGGTTTCG GTGGTTGAGCGTCCCTTTCTATCAATAAA (SEQ ID NO: 461)
10			A_23_P390504	NM_001453	FOXC1	Homo sapiens forkhead box C1 (FOXC1), mRNA	CCTTCCAGCCAGTCTCTGTACCGCACGTCCGG AGCTTTCGTCTACGACTGTAGCAAGTTT (SEQ ID NO: 462)
10			A_23_P407695	NM_147161	ACOT11	Homo sapiens acyl-CoA thioesterase 11 (ACOT11), transcript variant 2, mRNA	AGCGGACCTCAGGGCGGAGGCTTCCCACGG GGAGGCAGGAAGAAATAAAGGTCTTTGGCT (SEQ ID NO: 463)
10			A_23_P432506	NM_152757	FLJ30313	Homo sapiens hypothetical protein FLJ30313 (FLJ30313), mRNA	GTGGGGAGGGTTTCTTGGGTTTCTTGAAGCCA GTATTTCCCATAGTATCTTACGTCCCAG (SEQ ID NO: 464)
10			A_23_P46894	NM_020549	CHAT	Homo sapiens choline acetyltransferase (CHAT), transcript variant M, mRNA	TAGCCTCCTCGGCAGAAAAACTTCAACGAATA GTAAAGAACCTTGACTTCATTGTCTATA (SEQ ID NO: 465)
10			A_23_P57089	NM_020182	TMEPAI	Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA	GCCGGGCTGGGGCTGCGTAGGTGAAAAGGCA GAACACTCCGCGCTTCTTAGAAGAGGAGT (SEQ ID NO: 466)
10			A_23_P69652	NM_080819	GPR78	Homo sapiens G protein-coupled receptor 78 (GPR78), mRNA	GCTCGTGCCCTTCGTCACCGTGAACGCCCAG TGGGGCATCCTCAGCAAGTGCCTGACCTA (SEQ ID NO: 467)
10			A_23_P75283	NM_006744	RBP4	Homo sapiens retinol binding protein 4, plasma (RBP4), mRNA	TCAGTTCCCATAAAACCTTCATTACACATAAAG ATACACGTGGGGGTCAGTGAATCTGCT (SEQ ID NO: 468)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
10			A_23_P93217	NM_006672	SLC22A7	Homo sapiens solute carrier family 22 (organic anion transporter), member 7 (SLC22A7), transcript variant 1, mRNA	AGTGAACTTCTCCTATTACGGCCTGAGTCTGG ATGTGTCGGGGCTGGGGCTGAACGTGTA (SEQ ID NO: 469)
10			A_24_P187539				ACGAATATGCGTTCGACAAGCCGGTCCCGAAA GACATGGTCATCTGGAATCGTGAACGGG (SEQ ID NO: 470)
10			A_24_P297539	NM_007019	UBE2C	Homo sapiens ubiquitin-conjugating enzyme E2C (UBE2C), transcript variant 1, mRNA	TTGTCTTTTAAATTAAGCCTCGGTTGAGCCCTT GTATATTAAATAAATGCATTTTTGTCC (SEQ ID NO: 471)
10			A_24_P302172	NM_000959	PTGFR	Homo sapiens prostaglandin F receptor (FP) (PTGFR), mRNA	CCCATTCAAATTGTCCTAGGTCTATCAGAAATT AGGGAAGGTAGTCCTGCTTTATAATAG (SEQ ID NO: 472)
10			A_24_P322229	NM_033315	RASL10B	Homo sapiens RAS-like, family 10, member B (RASL10B), mRNA	TGGGGGAAGGGTCGTGGGTGGGGAATTTATC ACCAACATCCATTGTAGGGGGAATCTATG (SEQ ID NO: 473)
10			A_24_P396489	HSM807143		Homo sapiens mRNA; cDNA DKFZp686E15252 (from clone DKFZp686E15252).	AGCTTTGCTTTGCAAAGATTGATGACAGACTG GTTCCTCAGAGGCCTAGGCTACCCGTCA (SEQ ID NO: 474)
10			A_24_P418176	NM_001007238	HRES1	Homo sapiens HTLV-1 related endogenous sequence (HRES1), mRNA	GCGGGCTGGGCGCTCTGGCGGTGTGCGCTG AGGTGGGCAGAGCGGCAGGTGGGGGCGTTG (SEQ ID NO: 475)
10			A_24_P636974	NM_001013665	LOC399744	Homo sapiens hypothetical LOC399744 (LOC399744), mRNA	GTGGGAGGGGCCGGTGTGAGGCAAGGCTCA CGCTGACCTCTCTCGGCGTGGGAGGGGCCG (SEQ ID NO: 476)
10			A_24_P741378	AC027682		Homo sapiens chromosome 16 clone CTD-2012K14, complete sequence.	CACAGAAACATACAAGGAAGGCACCCCCGCTC TGTGGGCGAGACAAAGCAGCAATCCTCT (SEQ ID NO: 477)
10			A_24_P810084	AC016394		Homo sapiens chromosome 10 clone RP11-152N13, complete sequence.	GGAATTGGCTCTTCCTATTTCCCTACTTCATGA AAACTCCAGTAGAAGACCTTAGAACCT (SEQ ID NO: 478)
10			A_24_P8298	AC026740		Homo sapiens chromosome 5 clone CTD-2589H19, complete sequence.	TTTAAACACACGTGGTCCCCCGTCTAGAAGCC TCTGCATTTAAGCACACGTGGTCCCCCG (SEQ ID NO: 479)
10			A_32_P138032	NM_006365	C1orf61	Homo sapiens chromosome 1 open reading frame 61 (C1orf61), mRNA	ATGGCTAAGTTGGGAGACCAAAAAGAAGAATG TACTTCATCTGGTTGGGCTGGATTCCCT (SEQ ID NO: 480)
10			A_32_P187571	NM_004588	SCN2B	Homo sapiens sodium channel, voltage-gated, type II, beta (SCN2B), mRNA	TGTGACTCGACTGCTGGGATGTATCTGCTTTT GGGAGCAGACTGAGTTTCTTTTGCAATT (SEQ ID NO: 481)
10			A_32_P219148	NM_001013725	LOC441268	Homo sapiens hypothetical gene supported by BC044942 (LOC441268), mRNA	TCCCCGTCCACGTTACCGCATTCAGAGCTTGG GTCACCTGGACACTGAACTCAGGTGAAT (SEQ ID NO: 482)
10			A_32_P222149	XM_499058	LOC442512	PREDICTED: Homo sapiens similar to U2 small nuclear ribonucleoprotein A (U2 snRNP-A) (LOC442512), mRNA	TACAGAGCAGTCGCCGGGCAGTTGAAGATCA GCTAAAGATATGTGGCCACAGGAGGGATG (SEQ ID NO: 483)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
10			A_32_P52386	AC004080		Homo sapiens PAC clone RP1-170O19 from 7p15-p21, complete sequence.	AAATGTGGCGCTCTCGCCAAGAAAAAGCTTGGGGACTGAATTCTTGAGATTTATGGTGCA (SEQ ID NO: 484)
10			A_32_P71710	NM_000577	IL1RN	Homo sapiens interleukin 1 receptor antagonist (IL1RN), transcript variant 3, mRNA	AAGATTTTATTGTAAAACAGAGCTGAAGTCACAGGAAGTAGGGAACTTTGCACCCAACAT (SEQ ID NO: 485)
11		all cell types					
11			A_23_P128974	NM_006399	BATF	Homo sapiens basic leucine zipper transcription factor, ATF-like (BATF), mRNA	TATTAAGAAAGATGCTCAAGTCCCATGGCACAGAGCAAGGCGGGCAGGGAACGGTTATTT (SEQ ID NO: 486)
11			A_23_P218731	NM_005111	CRYZL1	Homo sapiens crystallin, zeta (quinone reductase)-like 1 (CRYZL1), transcript variant 1, mRNA	AAGATGATGAACCAGCTGTAAAACTACAACTACTACCACATAAACATGATATCATCACAC (SEQ ID NO: 487)
11			A_23_P42514	NM_030939	C6orf62	Homo sapiens chromosome 6 open reading frame 62 (C6orf62), mRNA	TCCTTTGGAGTAAAACTAGTGCTTACCAGTTTCCAATTGTATTTAGCTTCTGGTTGGAAT (SEQ ID NO: 488)
11			A_23_P92967	NM_004531	MOCS2	Homo sapiens molybdenum cofactor synthesis 2 (MOCS2), transcript variant 3, mRNA	AAGCATATCTACCCATGGCGGAAAATGAAGTCAGAAAGATTTGTAGTGACATTAGGCAGA (SEQ ID NO: 489)
11			A_32_P160615	AC016554		Homo sapiens chromosome 5 clone CTC-340H12, complete sequence.	ACTGCAATGAACACATATACATATACATCCAAACATTCCTCCATTCGTCTATTAATCTGC (SEQ ID NO: 490)
11			A_32_P37461				CATCAACTGGTAAACAAAAAACTGTGAGAACGGATCCTGAATCTTGCGCTTACCAGGGGA (SEQ ID NO: 491)
12		all cell types					
12			A_23_P100711	NM_000304	PMP22	Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA	TGTGCCTCCAAGGACTGTCTGGCAATGACTTGTATTGGCCACCAACTGTAGATGTATATA (SEQ ID NO: 492)
12			A_23_P135730	NM_145295	ZNF627	Homo sapiens zinc finger protein 627 (ZNF627), mRNA	ACTCCCCTAGTCTGTAGACGGAATTGGCATACGGTCTAATTTGTGTAGTAAGCACCTTTG (SEQ ID NO: 493)
12			A_23_P307968	NM_022124	CDH23	Homo sapiens cadherin-like 23 (CDH23), transcript variant 1, mRNA	CCATCTGACGCTACAGTCACCACGACCTTCAATATCCTGGTTATTGACATCAATGACAAT (SEQ ID NO: 494)
12			A_23_P411162	NM_003894	PER2	Homo sapiens period homolog 2 (Drosophila) (PER2), transcript variant 2, mRNA	TCCTCCTGAAAAGAGAATTTTTACAACCACCCATACACCAAATTGTTTGTTCCAGGATGT (SEQ ID NO: 495)
12			A_23_P63343	NM_006786	UTS2	Homo sapiens urotensin 2 (UTS2), transcript variant 2, mRNA	AGAATCTGGAAACCATACAAGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTC (SEQ ID NO: 496)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
12			A_23_P64879	NM_004982	KCNJ8	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 8 (KCNJ8), mRNA	CTTCCCTCATGGTACCAAAGGTGCAATTTATG ACTCCAGAAGGAAATCAAAACACATCGG (SEQ ID NO: 497)
12			A_24_P45620	NM_006786	UTS2	Homo sapiens urotensin 2 (UTS2), transcript variant 2, mRNA	AGAAAGTTTCAGGATTTCTCTGGACAAGATCC TAACATTTTACTGAGTCATCTTTTGGCC (SEQ ID NO: 498)
12			A_24_P614702	AC091320		Homo sapiens BAC clone RP11-447A2 from 7, complete sequence.	CCTTCCTCATTTTGGAACTTAAGGTTGTGTACA GAACAGTCTTACAATGACAGTGTTTAG (SEQ ID NO: 499)
12			A_32_P31144				TTCTATACCTCTAAGCTGTTCTTTTCTGAACCA TGAATCGGGAGAATTATTGTCACTCAT (SEQ ID NO: 500)
12			A_32_P427222	XM_291007	LOC339766	PREDICTED: Homo sapiens hypothetical protein LOC339766 (LOC339766), mRNA	TCTCTACCGCTTCTTGCTAGAAACAATGGCCT ATGTTAAAAATAACTTGTCAAGAATCAG (SEQ ID NO: 501)
13		Red Blood cells					
13			A_23_P109322	NM_006198	PCP4	Homo sapiens Purkinje cell protein 4 (PCP4), mRNA	CCCTCCTAGTCCACCTGAAAACACCAAATTCA ACCATCATCTGTCAAGAAATTAAAAGAA (SEQ ID NO: 502)
13	3	RBC	A_23_P11408	NM_001002758	PRY2	Homo sapiens PTPN13-like, Y-linked 2 (PRY2), mRNA	ACCTCCTTCTCTTCTGGACATGTCCAGGAGTG GCCGTTGCTACAAGTCACCTGGTGCTAC (SEQ ID NO: 503)
13			A_23_P135568	AC026315		Homo sapiens 3 BAC RP11-114D6 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	AGCAAGATATCCTCCTCATGGTCCCTTTAGCT CTCAAAAGCAATGAAATCCTCCTGTTCT (SEQ ID NO: 504)
13			A_23_P161474	NM_018518	MCM10	Homo sapiens MCM10 minichromosome maintenance deficient 10 (S. cerevisiae) (MCM10), transcript variant 2, mRNA	CCTCCTGTGACTCTGGAAAGCAAAGGATTGGC TGTGTATTGTCCATTGATTCCTGATTGA (SEQ ID NO: 505)
13			A_23_P204998	NM_005766	FARP1	Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, mRNA	TCCTCCTGCAACTGTGGTTTGAAACTGCGCAT TCTCTAGTAGTATATATCGTGCCTGTCT (SEQ ID NO: 506)
13	3	RBC	A_23_P205637	NM_015163	TRIM9	Homo sapiens tripartite motif-containing 9 (TRIM9), transcript variant 1, mRNA	CCTCCTCGACTTAAATAGAAAAAACTTGACATT TTTTATCAACGATGAACAACAAGGTCC (SEQ ID NO: 507)
13			A_23_P215549	NM_000940	PON3	Homo sapiens paraoxonase 3 (PON3), mRNA	GCACCTCTGTGGCTTCTGTGTACCATGGGAAA ATTCTCATAGGCACCGTATTTCACAAAA (SEQ ID NO: 508)
13			A_23_P254626	NM_003919	SGCE	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA	ACTGGTCCTTTTTCTAATACTTGCTTATATCAT GTGCTGCCGACGGGAAGGCGTGGAAAA (SEQ ID NO: 509)
13			A_23_P26582	NM_020988	GNAO1	Homo sapiens guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O (GNAO1), transcript variant 1, mRNA	TTGTACTGACCTCTTGTCCTGTATAGCAACCTA TTTGACTGCTTCACGGACTCTTTGCTG (SEQ ID NO: 510)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
13			A_23_P303803	NM_152474	C19orf18	Homo sapiens chromosome 19 open reading frame 18 (C19orf18), mRNA	CAGCTCGAGTCACTTTATAAGAACCTCAGGAT ACCGTTATTAGGAGATGAAGAAGAGGGC (SEQ ID NO: 511)
13			A_23_P309278	NM_173158	NR4A1	Homo sapiens nuclear receptor subfamily 4, group A, member 1 (NR4A1), transcript variant 3, mRNA	CTCCCTTGCCACCCAAATGTTAGAAAAATAGCT GTGAACAGAGAGCGCTTTTGTCTGCAA (SEQ ID NO: 512)
13			A_23_P326844	NM_174913	C14orf21	Homo sapiens chromosome 14 open reading frame 21 (C14orf21), mRNA	ACTCCTGGTCTTGTACTTCGAAGTCTGGGTGC CTTGACGGGACCACAGCTTCTGTCCCTT (SEQ ID NO: 513)
13			A_23_P44648	NM_030955	ADAMTS12	Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA	CAGACCTCCAGAATTCAAAAAATGCAACCAGC AGGCCTGCAAGAAAAGTGCCGATTTACT (SEQ ID NO: 514)
13			A_23_P68234	NM_006794	GPR75	Homo sapiens G protein-coupled receptor 75 (GPR75), mRNA	ATCCTCCCATCATGAAACAAACTCTGCCTACAT GTTATCTCCAAAGCCACAGAAGAAATT (SEQ ID NO: 515)
13			A_23_P78795	NM_001009813	MEIS3	Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse) (MEIS3), transcript variant 2, mRNA	CCTCCCAGACCAGAATAATATGTGGATTCGAG ACCATGAGGATAGTGGGTCTGTACATTT (SEQ ID NO: 516)
13			A_23_P80122	NM_004627	WRB	Homo sapiens tryptophan rich basic protein (WRB), mRNA	CCTGGTAGCCTTTCCTACTAGAGTAGCAGGTG GTGTTGGAATTACCTGTTGGATTTTAGT (SEQ ID NO: 517)
13			A_24_P126587	NM_181489	ZNF445	Homo sapiens zinc finger protein 445 (ZNF445), mRNA	GCTCCTACAGGAGATGACCTCCAGAGTAAAAC AAACAAATTCATCTTAAATCAGGAACCT (SEQ ID NO: 518)
13			A_24_P136299	AC103975		Homo sapiens chromosome 15, clone RP11-1001M11, complete sequence.	TCAATTGCTTCCTCCTCAATCTGGCAGCCACT GACCTGCAGTTTGTGCTAACGCTGCCCT (SEQ ID NO: 519)
13			A_24_P200250	HSU37055		Human hepatocyte growth factor-like protein gene, complete cds.	CCTTCCATTAGCAACTACTCTGTACCACCCTTC CCAAGAGTATGTCTGGAGGACTAGTGT (SEQ ID NO: 520)
13			A_24_P312594	AL133215		Human DNA sequence from clone RP11-108L7 on chromosome 10	TTCTTCCCTCCATACATTTGCTTCCAAGTGAAT TTGCATAAGCAGTGCTCAGACTGCACC (SEQ ID NO: 521)
13			A_24_P31875	NM_152577	ZNF645	Homo sapiens zinc finger protein 645 (ZNF645), mRNA	CTCCTTCAACCCTACATGGTCGATCACATCATT CACACCAGAGAAGACATAGACGGTATT (SEQ ID NO: 522)
13	2	RBC	A_24_P341116	NM_207378	SERPINA13	Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 13 (SERPINA13), mRNA	CTTCCTGGTGATGACTTTCCACACGGAAACAG GAAGCATGCTTTTTCTGGAGAAGATTGT (SEQ ID NO: 523)
13			A_24_P365349	AC008440		Homo sapiens chromosome 19 clone CTC-331H23, complete sequence.	CCTGGCTCTGTTATTTACCGTGTATCATATGTA AATATCGACAGAAACTTCAATAAACTT (SEQ ID NO: 524)
13			A_24_P409451	NM_018651	ZNF167	Homo sapiens zinc finger protein 167 (ZNF167), transcript variant 1, mRNA	AAGAACTATCCTCCTGTCTGCGAAATCTTCCG GCTACACTTCAGGCAATTGTGTTACCAC (SEQ ID NO: 525)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
13	4	RBC	A_24_P59735	BC041372		Homo sapiens similar to seven in absentia 2, mRNA (cDNA clone IMAGE:5273845), partial cds.	TCCTGGTTTTTGAGACTCAACCACTTTGAAAGC ATTTGTGTAGCATCACAGGTGCTCCAG (SEQ ID NO: 526)
13			A_24_P607751	HSU91328		Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.	CCTTCTTGGGTCAGTTAGGCCATTGGTTTCTTT TTAAAGGTTTTCAAATTTATTTGCATC (SEQ ID NO: 527)
13			A_24_P666035	AC055716		Homo sapiens 12 BAC RP11-641A6 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	AGTTGTACTGTCAAGGGGCAGCATTTCTGGTA TTTCTATAATAAATTTTTCTGTGATCTC (SEQ ID NO: 528)
13			A_24_P915376	NM_006757	TNNT3	Homo sapiens troponin T type 3 (skeletal, fast) (TNNT3), mRNA	AGAAACCGAGACCCAAACTCACTGCTCCTAAG ATCCCAGAAGGGGAGAAAGTGGACTTCG (SEQ ID NO: 529)
13			A_24_P920555	NM_198486	RPL7L1	Homo sapiens ribosomal protein L7-like 1 (RPL7L1), mRNA	GGCATTCACTGATCCCAGCAGGTCTCCATCTA TTTGTACCAGCCTCCTCTATTCCTCCCA (SEQ ID NO: 530)
13			A_24_P927404	AC084033		Homo sapiens 12q BAC RP11-58A17 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	GCCCTTTTTTGTCACTCACTGTTGTGACAGATC CTCCGATTTCTTACATAAGTTATGCAG (SEQ ID NO: 531)
13			A_32_P114483	NM_153344	C6orf141	Homo sapiens chromosome 6 open reading frame 141 (C6orf141), mRNA	GAGCCCAACTACCCTTCTGTCTTTCAACGAGA AAAGCGAATTTCTGGCAGGCGTGTAGCC (SEQ ID NO: 532)
13	3	RBC	A_32_P133106	AP005433		Homo sapiens genomic DNA, chromosome 18 clone:RP11-945C19, complete sequence.	CTAATGGACTAGATTGCTGACCTTTTAATACCT TTGGTTTTCATTGAACATACAATCACC (SEQ ID NO: 533)
13			A_32_P181638	NM_007073	BVES	Homo sapiens blood vessel epicardial substance (BVES), transcript variant A, mRNA	AATCCTGGTTTCCTAACCTCCTCTTGTAGTAAT TCTCAACTCAACTCAAAGTCCCAAGAA (SEQ ID NO: 534)
13			A_32_P354945	AC011503		Homo sapiens chromosome 19 clone CTB-92J24, complete sequence.	CCCTCCTGATGATGAAGGACCTGTCATTGGAG AATCGACCAAAACTGACAGTGATAACTT (SEQ ID NO: 535)
13	2	RBC	A_32_P5057	AC010798		Homo sapiens, clone RP11-470B24, complete sequence.	CCCTGAACCTACATAGACATTTTATATCAGCAT ACAGAAAAGTAAAATCCTCCTTCAGTC (SEQ ID NO: 536)
13			A_32_P51005	BX629352		Human DNA sequence from clone WI2-80267E6 on chromosome 9, complete sequence.	ATTCCTTTCTGGTCTCCATCCTCTCTGTAGATA TGTAGATCTCTTTGAAACGAAGTAAGC (SEQ ID NO: 537)
13			A_32_P524904				GGCTGAGCACTCTGTGCTGAAAACCTTTGAAC CTCACGGTGTCCTGATGAAGGAAGCAGA (SEQ ID NO: 538)
14		Red Blood cells					

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
14			A_23_P153351	NM_000713	BLVRB	Homo sapiens biliverdin reductase B (flavin reductase (NADPH)) (BLVRB), mRNA	CAAGGTGCCCCCACGACTGCAGGCTGTGACT GATGACCACATCCGGATGCACAAGGTGCT (SEQ ID NO: 539)
14	7	RBC	A_23_P207842	NM_000964	RARA	Homo sapiens retinoic acid receptor, alpha (RARA), transcript variant 1, mRNA	AGTTCTCCTCCTCAGCCTTTTCCTCCTCAGTTT TCTCTTTAAAACTGTGAAGTACTAACT (SEQ ID NO: 540)
14	3	RBC	A_23_P210465	NM_002638	PI3	Homo sapiens peptidase inhibitor 3, skin-derived (SKALP) (PI3), mRNA	TCCTGCCCCATTATCTTGATCCGGTGCGCCAT GTTGAATCCCCCTAACCGCTGCTTGAAA (SEQ ID NO: 541)
14	2	RBC	A_23_P23850	NM_021080	DAB1	Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA	CTCCCTCACCTGTACCTCAGAGGCCTTCTCCA GTTACTTCAACAAAGTCGGGGTGGCACA (SEQ ID NO: 542)
14			A_23_P251898	NM_152743	C7orf27	Homo sapiens chromosome 7 open reading frame 27 (C7orf27), mRNA	GGCGCAGAAGTCTTGTGACCTCCTTCTCTTCC TGAGGGACAAGATTGCTTCCTACAGCAG (SEQ ID NO: 543)
14	6	RBC	A_23_P332392	NM_152479	TTC9B	Homo sapiens tetratricopeptide repeat domain 9B (TTC9B), mRNA	ACCTCCCCTGCAGACACCAATGTGCTCCGCTA CATCCAGCTGACTCAGCTGAAGATGAAT (SEQ ID NO: 544)
14	2	RBC	A_23_P338168	NM_019085	FBXL19	Homo sapiens F-box and leucine-rich repeat protein 19 (FBXL19), mRNA	TCCTTCCCCCTGACCCTGACTCCTTGAACGTC ACTGAAAACGGCAGCTATTGCAAGGAGT (SEQ ID NO: 545)
14			A_23_P362893	NM_021961	TEAD1	Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA	TTTTTTCTCCTTCCCCTTTCTTTAAGAGAGGCT GACAGATCTAGGTGTCAATCAATTGGA (SEQ ID NO: 546)
14	5	RBC	A_23_P377717	NM_002516	NOVA2	Homo sapiens neuro-oncological ventral antigen 2 (NOVA2), mRNA	CCTCCCCTTCTGGTAGTCATAGGCAGGATTGA GTGACGGTTGGGAAGGGGGCTCAGAAGC (SEQ ID NO: 547)
14			A_23_P39265	NM_014400	LYPD3	Homo sapiens LY6/PLAUR domain containing 3 (LYPD3), mRNA	TCCCCTACTCCCCGCATCTTTGGGGAATCGGT TCCCCATATGTCTTCCTTACTAGACTGT (SEQ ID NO: 548)
14	5	RBC	A_23_P62361	NM_014235	UBL4A	Homo sapiens ubiquitin-like 4A (UBL4A), mRNA	GCTTCCTGCACCCTGAAGTGACTGAGACAATG GAGAAGGGCTTCTCCAAATAGAATTCTC (SEQ ID NO: 549)
14	3	RBC	A_23_P67332	NM_007121	NR1H2	Homo sapiens nuclear receptor subfamily 1, group H, member 2 (NR1H2), mRNA	ACCACCCTCCAGCAGATAGACGCCGGCACCC CTTCCTCTTCCTAGGGTGGAAGGGGCCCT (SEQ ID NO: 550)
14	4	RBC	A_23_P79323	NM_003936	CDK5R2	Homo sapiens cyclin-dependent kinase 5, regulatory subunit 2 (p39) (CDK5R2), mRNA	TCCCTTCAGCCCATTCCCCCTCGGTTTTATCC ATTTCCTTGCCTCCTTTTTGTGTCTTCA (SEQ ID NO: 551)
14			A_23_P81717	NM_024919	FRMD1	Homo sapiens FERM domain containing 1 (FRMD1), mRNA	AGGTTCCTCCCAGACCTGAATCCCTCTCTGCA ACTCCTGTTTGCAAGCGCTGGGCCTGCC (SEQ ID NO: 552)
14	2	RBC	A_24_P102343	NM_017957	EPN3	Homo sapiens epsin 3 (EPN3), mRNA	TCCCTCAGCTTCCTCCTTGGTCAACCTTGACT CGTTGGTCAAGGCACCCCAGGTTGCAAA (SEQ ID NO: 553)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
14			A_24_P233078	NM_021093	PYY2	Homo sapiens peptide YY, 2 (seminalplasmin) (PYY2), mRNA	GCCCACCTCATTTACATGTTCACTCCCGACCC TGGAAACCCGGATTTCGCCTCCGGACAG (SEQ ID NO: 554)
14	4	RBC	A_24_P256083	HS526I14		Human DNA sequence from clone RP3-526I14 on chromosome 22, complete sequence.	ATTTTCACCTCCCCTGGTCCATGCTCAGGAAG TCTGGTCACCCTGGCAAACTGCACCTGA (SEQ ID NO: 555)
14	3	RBC	A_24_P318990	HSZ85332		H.sapiens Ig lambda light chain variable region gene (22-21SWIA31) rearranged; Ig-Light-Lambda; VLambda.	TCTGACACCTCAGCCTCCCTGGCCATCACTGG ACTCCAGGCTGAAGATGAGGCTGATTAT (SEQ ID NO: 556)
14	4	RBC	A_24_P365523	NM_021784	FOXA2	Homo sapiens forkhead box A2 (FOXA2), transcript variant 1, mRNA	CCTCCTACTACCAGGGGGTGTACTCCCGGCC CATTATGAACTCCTCTTAAGAAGACGACG (SEQ ID NO: 557)
14			A_24_P493646	AP002776		Homo sapiens genomic DNA, chromosome 11 clone:RP11-126P21, complete sequence.	TCGCCACGCCAGCCCCTTTCCTCAGAACGCC GAGGCCTCAGGAGCGTGTGCGCGCCGGGA (SEQ ID NO: 558)
14	2	RBC	A_24_P911718	AF240580		Homo sapiens clone 17ptel_2111ctg_drft sequence.	CTTCCTTCCCTAGGATCTCAGCACCCTTTTAGA TCCCGTGCAGATTGTCTTTCTGTTAAA (SEQ ID NO: 559)
14			A_24_P920188	AY236488		Homo sapiens unidentified genomic region, partial sequence.	CTCCTTCCCCATCTTCTGGTAACACAACCTTTA TTTATTTGTGGGGAACCTATTCCCTGT (SEQ ID NO: 560)
14	6	RBC	A_32_P48536	2772567		7n93b04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571927 3', mRNA sequence	AATTGCCATGCTGCCCACCTCCCGAAGTGTTA GGAGGTAACATCTCATCGTCTCATCGCA (SEQ ID NO: 561)
15		all cell types					
15			A_23_P101121	NM_031303	KATNAL2	Homo sapiens katanin p60 subunit A-like 2 (KATNAL2), mRNA	TCAGAAGATCTCGTATTTGTCTTAGCAGCTTCT AACCTGCCGTGGTAAGAGACCAAGAGA (SEQ ID NO: 562)
15			A_23_P120243	NM_024501	HOXD1	Homo sapiens homeobox D1 (HOXD1), mRNA	TTTTTTCTTTAAAAAAGCGGTTTCTACCTCTCTA TGTGCCTGAGTGATGATACAATCGCT (SEQ ID NO: 563)
15			A_23_P132845	NM_004366	CLCN2	Homo sapiens chloride channel 2 (CLCN2), mRNA	TGGGAGTGGACCATGCTTATGTCACCAGTATT GGCAGACTCATTGGAATCGTTACTCTAA (SEQ ID NO: 564)
15			A_23_P15765	NM_018996	TNRC6C	Homo sapiens trinucleotide repeat containing 6C (TNRC6C), mRNA	GACATTGTGTTTGCAACATGGGCCTCTTATCA CATTCCACCTGAATCTGACTCAAGGCAA (SEQ ID NO: 565)
15			A_23_P313623	NM_015198	COBL	Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA	GTCTACAGGCCAAAATGCGCACAGTTGATTTT CGGTGTGTTCCTGTATAACGGCTTGAAA (SEQ ID NO: 566)
15			A_23_P319466	NM_020377	CYSLTR2	Homo sapiens cysteinyl leukotriene receptor 2 (CYSLTR2), mRNA	GGCAAATAGCAAAAGTTGTTGCACTCCTGAAA TTCTATTAACATTTCCGCAGAAGATGAG (SEQ ID NO: 567)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
15			A_23_P369994	NM_004734	DCAMKL1	Homo sapiens doublecortin and CaM kinase-like 1 (DCAMKL1), mRNA	AAATGTTTTTACCGTAGCCCTCATCTAACTTAC ACGTGGTGCATATTAAAATAAGCAGAG (SEQ ID NO: 568)
15			A_23_P39294	AC011533		Homo sapiens chromosome 19 clone LLNLR-240E6, complete sequence.	CTCCCAGCAGAGTCATCACTACCTTTGGGGCC GCAGGATCACCCAGCTTGGAACTAGATA (SEQ ID NO: 569)
15			A_23_P399797	AC009014		Homo sapiens chromosome 5 clone P1_748D6, complete sequence.	ACAACTGCCCAGAGTGTAATTCCCACCGATAA GCGCGGATCCTTATCTTTGAAACACAAA (SEQ ID NO: 570)
15			A_23_P413923	NM_022160	DMRTA1	Homo sapiens DMRT-like family A1 (DMRTA1), mRNA	CTGTACTTCAGACCAAATCAGGACAATCCGTA ATGTATATGCCCATTCTCTCTTTCTGGA (SEQ ID NO: 571)
15			A_23_P45560	NM_000273	GPR143	Homo sapiens G protein-coupled receptor 143 (GPR143), mRNA	ATATTCCTCAGACTCAACAATTCTTGTTCTTTA GAACTGTGTTCTCACCTTCCCAACACT (SEQ ID NO: 572)
15			A_23_P502413	NM_002974	SERPINB4	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 4 (SERPINB4), mRNA	TCCTCTTCTATGGCAGATTCTCATCCCCATAGA TGCAATTAGTCTGTCACTCCATTTAGA (SEQ ID NO: 573)
15			A_23_P81103	NM_003013	SFRP2	Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA	ATAACCTACATCAACCGAGATACCAAAATCATC CTGGAGACCAAGAGCAAGACCATTTAC (SEQ ID NO: 574)
15			A_24_P20091	NM_153041	FLJ32955	Homo sapiens hypothetical protein FLJ32955 (FLJ32955), mRNA	CACAAATTCCTCACTCATCTTGCAGAAGCTCC CAGTTTTCAATATTCTCCTAAATGCTGT (SEQ ID NO: 575)
15			A_24_P252780	NM_198514	NHLRC2	Homo sapiens NHL repeat containing 2 (NHLRC2), mRNA	GTTCCTAGTAGAAAAACAGAAGACATTACCCA AACTACCTAAATCTGCTCCAAGCATTAG (SEQ ID NO: 576)
15			A_24_P382187	NM_001552	IGFBP4	Homo sapiens insulin-like growth factor binding protein 4 (IGFBP4), mRNA	GAAAAATCTCATTCCCAGAGTCAGAGGAGAAG AGACATGTACCTTGACCATCGTCCTTCC (SEQ ID NO: 577)
15			A_24_P410605	BC080541		Homo sapiens receptor tyrosine kinase-like orphan receptor 1, mRNA (cDNA clone IMAGE:5477978), complete cds.	GACATCCCAGCTTGCGGTAAATAGAAGTCATT GCCCCTAATGTATTCAATCATCTTTAAA (SEQ ID NO: 578)
15			A_24_P499215	NM_001005751	LOC387680	Homo sapiens similar to KIAA0592 protein (LOC387680), mRNA	TCAAAGACAAGAGAAAGCAAAAGCCTCCAAGC TCTCCAAAAAGAAAGCATCTGCCCTGTT (SEQ ID NO: 579)
15			A_24_P744957	AL353653		Human DNA sequence from clone RP11-244L4 on chromosome 20 Contains ESTs, STSs and GSSs, complete sequence.	AGACACAGGATGTTCCTGTTGGTCCAGATACT TGAGCTAAAAGGTGATGGATACCTGGAT (SEQ ID NO: 580)
15			A_24_P82155	NM_182703	ANKDD1A	Homo sapiens ankyrin repeat and death domain containing 1A (ANKDD1A), mRNA	CTACTTCCCAAAATAGTATTTCTCTCAGCAGAT ATTTCTTTGGTACTACCATGTATTGTG (SEQ ID NO: 581)
15			A_24_P91165	NM_000723	CACNB1	Homo sapiens calcium channel, voltage-dependent, beta 1 subunit (CACNB1), transcript variant 1, mRNA	TACTTCAAAGGCTCATCAAGTCCCGAGGAAAG TCTCAGTCCAAACACCTCAATGTCCAAA (SEQ ID NO: 582)

TABLE 1

Cluster	Ratio cell type to all cells	cell Type	Array ID	Genbank ID	Gene ID	Description	Sequence
15			A_24_P933902	AY358788		Homo sapiens clone DNA129793 AVLL5809 (UNQ5809) mRNA, complete cds.	TCGCGGTGAGACTGAACATTTCATGAGCTCAT GTTGCCTTTGACCACCATTTCTTAAGGA (SEQ ID NO: 583)
15			A_24_P934063	NM_004978	KCNC4	Homo sapiens potassium voltage-gated channel, Shaw-related subfamily, member 4 (KCNC4), transcript variant 1, mRNA	ATGGGAGATTTTCCACCAGTCCTGTGCAAACA AGGATATCTGAGTCTTTCCCAGCGAAAA (SEQ ID NO: 584)
15			A_32_P102383	HS243L18		Human DNA sequence from clone RP1-243L18 on chromosome 1p36.11-36.23 Contains the 5' end of a novel gene (KIAA1026) and a CpG island, complete sequence.	TTCTCTTGAGGGTTGAGAGAGTCTGTTTTCCT AAGAATCTGGTTCTCTCCATCAGTCTCT (SEQ ID NO: 585)
15			A_32_P146764	AC002076		Homo sapiens BAC clone GS1-345D13 from 7, complete sequence.	ATGTCTCTTTCAACCATATGATCAATCAGTTGG ACGACTTCTGGTTTTTCCTGAATAAAT (SEQ ID NO: 586)
15			A_32_P181131	NM_001005353	AK3L1	Homo sapiens adenylate kinase 3-like 1 (AK3L1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA	CTCTTCATAGCTCAGTTCTCAGTGCATACAGA GATTCAATATAGCCCCATCGCTCTCAGT (SEQ ID NO: 587)
15			A_32_P221507	BC066346		Homo sapiens cDNA clone IMAGE:4824446, partial cds.	CATAGAGCAGTTGCTCCCCATTGACACCAAGT AATTCCAGTCCACATTTGCCTTTAAGCA (SEQ ID NO: 588)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
2703	A_23_P48513	IFI27	interferon, alpha-inducible protein 27 variant a	1	ACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGG GTGAAATATACCAAATTCTGCAT (SEQ ID NO: 589)
40154	A_23_P48513	IFI27	interferon, alpha-inducible protein 27 variant a	0.999	ACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGG GTGAAATATACCAAATTCTGCAT (SEQ ID NO: 590)
32566	A_23_P48513	IFI27	interferon, alpha-inducible protein 27 variant a	0.999	ACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGG GTGAAATATACCAAATTCTGCAT (SEQ ID NO: 591)
7079	A_23_P48513	IFI27	interferon, alpha-inducible protein 27 variant a	0.999	ACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGG GTGAAATATACCAAATTCTGCAT (SEQ ID NO: 592)
508	A_23_P48513	IFI27	interferon, alpha-inducible protein 27 variant a	0.999	ACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGG GTGAAATATACCAAATTCTGCAT (SEQ ID NO: 593)
18306	A_23_P48513	IFI27	interferon, alpha-inducible protein 27 variant a	0.999	ACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGG GTGAAATATACCAAATTCTGCAT (SEQ ID NO: 594)
5149	A_23_P48513	IFI27	interferon, alpha-inducible protein 27 variant a	0.999	ACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGG GTGAAATATACCAAATTCTGCAT (SEQ ID NO: 595)
13333	A_23_P48513	IFI27	interferon, alpha-inducible protein 27 variant a	0.998	ACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGG GTGAAATATACCAAATTCTGCAT (SEQ ID NO: 596)
6656	A_24_P270460	IFI27	interferon, alpha-inducible protein 27 variant a	0.997	TGAAATATACCAAATTCTGCATCTCCAGAGGAAAATAA GAAATAAAGATGAATTGTTGCA (SEQ ID NO: 597)
16373	A_23_P48513	IFI27	interferon, alpha-inducible protein 27 variant a	0.996	ACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGG GTGAAATATACCAAATTCTGCAT (SEQ ID NO: 598)
5290	A_23_P48513	IFI27	interferon, alpha-inducible protein 27 variant a	0.996	ACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGG GTGAAATATACCAAATTCTGCAT (SEQ ID NO: 599)
27987	A_23_P819	G1P2	interferon, alpha-inducible protein	0.911	CACGGTCCTGCTGGTGGTGGACAAATGCGACGAACCT CTGAGCATCCTGGTGAGGAATAA (SEQ ID NO: 600)
27626	A_23_P45871	IFI44L	chromosome 1 ORF 29 (C1orf29)	0.893	TTGTTCGTTTTGCCTTCTGTCCTTGGAACAGTCATATCT CAAGTTCAAAGGCCAAAACCT (SEQ ID NO: 601)
11715	A_32_P132206	USP18	ubiquitin specific protease 18	0.887	AGACTTGTATACTGGCTGAATATCAGTGCTGTTTGTAA TTTTTCACTTTGAGAACCAACA (SEQ ID NO: 602)
21005	A_24_P28722	RSAD2	viperin (cig5)	0.877	ACTCTGAGTCAGTTGAAATAGGGTACCATCTAGGTCAG TTTAAGAAGAGTCAGCTCAGAG (SEQ ID NO: 603)
30386	A_24_P261929	FAM14B	family with sequence similarity 14, member B	0.868	TGCAGTCAGTGGGGGCAGCTGGACTCTCTGTGACATC TAAAGTTATCGGGGGCTTTGCTG (SEQ ID NO: 604)
36995	A_32_P99533	G1P2	interferon, alpha-inducible protein	0.864	ACCAGGATGTTCAGAGGTTCGTCGCATTTGTCCACCA CCAGCAGGACCGTGCTGCCGGGG (SEQ ID NO: 605)
36654	A_24_P361896	MT2A	metallothionein 2A	0.863	CGCTCCCAGATGTAAAGAACGCGACTTCCACAAACCT GGATTTTTTATGTACAACCCTGA (SEQ ID NO: 606)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
21017	A_24_P316965	RSAD2	viperin (cig5)	0.861	ATTCTGGATGAATATATGCGCTTTCTGAACTGTAGAAA GGGACGGAAGGACCCTTCCAAG (SEQ ID NO: 607)
12478	A_23_P64828	OAS1	2',5'-oligoadenylate synthetase 1 variant E18	0.855	CTCTGCATCTACTGGACAAAGTATTATGACTTTAAAAAC CCCATTATTGAAAAGTACCTG (SEQ ID NO: 608)
36260	A_23_P106844	MT2A	metallothionein 2A	0.854	CAACCCTGACCGTGACCGTTTGCTATATTCCTTTTTCT ATGAAATAATGTGAATGATAAT (SEQ ID NO: 609)
16580	A_23_P23074	IFI44	interferon-induced protein 44	0.852	AAGGATGTTCTAATTCTTTCTGCTCTGAGACGAATGCT ATGGGCTGCAGATGACTTCTTA (SEQ ID NO: 610)
22208	A_23_P252413	MT2A	metallothionein 2A	0.850	CTGACCGTGACCGTTTGCTATATTCCTTTTTCTATGAAA TAATGTGAATAATAATTAAAC (SEQ ID NO: 611)
20525	A_23_P201459	G1P3	interferon, alpha-inducible protein variant	0.846	AGTAGCCAGCAGCTCCCAGAACCTCTTCTTCCTTCTTG GCCTAACTCTTCCAGTTAGGAT (SEQ ID NO: 612)
43723	A_23_P105794	EPSTI1	epithelial stromal interaction 1	0.846	AGAAGAGAAGCATTTAGAGAGCATCAGCAATACAAAAC CGCTGAGTTCTTGAGCAAACTG (SEQ ID NO: 613)
16830	A_24_P316257	FLJ36208	hypothetical protein FLJ36208	0.839	TGGGGGAGCTTCCTACAAGGAGAGACTCCTGCTGCTT TGGAAAACTGAGAAAAAATAGGG (SEQ ID NO: 614)
25919	A_23_P131255	DNAPTP6	DNA polymerase-transactivated protein 6	0.836	CTGAAGATCAGAGGCTCAGTTAGCAACCTGTGTTGTA GCAGTGATGTCAGTCCATTGATT (SEQ ID NO: 615)
41211	A_32_P227059	RSAD2	upsteam 5' end of Gene	0.835	CAAAATAATCTGAAACTTTACTGGCCAAAGTGGGACTC CTTTAAAATTCCAAAACTTGCC (SEQ ID NO: 616)
41347	A_23_P384355	LOC129607	thymidylate kinase family LPS-inducible member	0.834	ACAGTGGATCTTGGAGTGGGATTTCTTGGGTAAATTAT CTTTGCCCTTTGAAATGTCTCC (SEQ ID NO:617)
36358	A_23_P47955	QAS3	2'-5' oligoadenylate synthetase 3	0.834	AGAAGGCAGAGAAAGTGAAGACCAAGTCCAGAACTGA ATCCTAAGAAATGCAGGACTGCA (SEQ ID NO: 618)
14388	A_24_P335305	OAS3	2'-5' oligoadenylate synthetase 3	0.833	TCTTTGGCAATGGCCACCCTGGTGTTGGCATATTGGC CCCACTGTAACTTTTGGGGGCTT (SEQ ID NO: 619)
19864	A_24_P943205	EPSTI1	downstream from gene	0.824	AACCAAATATCTATGTAGGCAGAGGTAACCAGGAGAG AAGCAAGACTTGCTGCCTAAAGG (SEQ ID NO: 620)
3173	A_23_P132159	USP18	ubiquitin specific protease 18	0.822	CTGTCATTTTCCATTTCCGTTCCTGGATCTACGGAGTC TTCTAAGAGATTTTGCAATGAG (SEQ ID NO:621)
23814	A_23_P139786	OASL	2'-5'-oligoadenylate synthetase-like variant	0.821	GTTTCCAGCCAGTTAGTTTTCTCTGGGAGACTTCTCTG TACATTTCTGCCATGTACTCCA (SEQ ID NO: 622)
28716	A_24_P557479	HSXIAPAF1	XIAP associated factor-1 variant 2	0.816	CAAATAAACCAACGGGAAAAAAGAAAGGTTCCAGTTTT GTCTGAAAATTCTGATTAAGCC (SEQ ID NO: 623)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
39451	A_23_P206724	MT1E	metallothionein 1E	0.816	GGCATCGGAGAAGTGCAGCTGCTGTGCCTGATGTGG GAACAGCTCTTCTCCCAGATGTAA (SEQ ID NO: 624)
632	A_23_P52266	IFIT1	interferon-induced protein variant 2	0.815	ACTTTGAGAACTCTGTGAGACAAGGTCCTTAGGCACC CAGATATCAGCCACTTTCACATT (SEQ ID NO: 625)
7680	A_23_P427703	MT1E	602705675F1 NIH_MGC_43 clone IMAGE:4842259 5'	0.813	CTGCTGTGCCTGATGTGGGGACAGACCTGCTCCCAGA TGTAAACAGAGCAACCTGCACAA (SEQ ID NO: 626)
18216	A_23_P17663	MX1	myxovirus (influenza virus) resistance 1, IFI protein p78	0.808	CAGCTTATTTCCTCATTTTTATAATGTCCCTTCACAAAC CCAGTGTTTTAGGAGCATGAG (SEQ ID NO: 627)
1309	A_23_P303242	MT1X	metallothionein 1X	0.805	TGCCAAGTGTGCCCAGGGCTGCATCTGCAAAGGGAC GTCAGACAAGTGCAGCTGCTGTGC (SEQ ID NO: 628)
13366	A_23_P414343	MT1J	metallothionein 1J	0.804	TGTGCCAAGTGTGCCCACGGCTGCATCTGCAAAGGGA CGTCGGAGAAGTGCAGCTGCTGT (SEQ ID NO: 629)
21994	A_23_P60933	MT1G	metallothionein 1G	0.804	AGCTGCTGTGCCTGATGTCGGGACAGCCCTGCTCCCA AGTACAAATAGAGTGACCCGTAA (SEQ ID NO: 630)
22827	A_23_P166797	IFRG28	28kD interferon responsive protein	0.798	CAAGCAGGATCAAGTTTGTAGAATAAACACTGGTTTCC TAGCCATCCTCTGAAAACAGTA (SEQ ID NO: 631)
34047	A_24_P317762	LY6E	lymphocyte antigen 6 complex, locus E	0.798	CTACTGCGTGACTGTGTCTGCTAGTGCCGGCATTGGG AATCTCGTGACATTTGGCCACAG (SEQ ID NO: 632)
27981	A_23_P4286	HSXIAPAF1	XIAP associated factor-1 variant 2	0.796	TTTAACACTGGCATTCCTGCCTACTTGCTGTGGTGGTC TTGTGAAAGGTGATGGGTTTTA (SEQ ID NO: 633)
41919	A_24_P917810	BRCA2 intron	BRCA2 intron	0.795	TTTGCACTATGGTAGATTTCAGGAATTTCAAAAGAAATC TGATGTCAGTGCAATTATCCG (SEQ ID NO: 634)
42276	A_23_P4283	BIRC4BP	X-linked inhibitor of apoptosis	0.791	TCAACTTGACTTCATGTTAAAAACCCTCAACAAACCAG GCGTCGAAGGAACATACCTCAA (SEQ ID NO: 635)
7108	A_23_P204087	OAS2	2'-5'-oligoadenylate synthetase 2 variant 1	0.789	TCTTCAAAGCAAAGCTCTTTACTTTCCCCTTGGTTCTCA TAACTCTGTGATCTTGCTCTC (SEQ ID NO: 636)
8777	A_23_P110196	HERC5	hect domain and RLD 5	0.787	TGTCCTGAAAGTTGGAATGAAAGAGACCCTATAAGAG CACTGACATGTTTCAGTGTCCTC (SEQ ID NO: 637)
1565	A_24_P343929	OAS2	2'-5'-oligoadenylate synthetase 2 variant 1	0.784	GGAAGGTCAATTACAACTTTGAAGATGAGACCGTGAG GAAGTTTCTACTGAGCCAGTTGC (SEQ ID NO: 638)
18175	A_23_P35412	IFIT4	IFI protein with tetratricopeptide repeats 4	0.779	ATTCGAATAAAGCTCTTGAGAAGGGACTGAATCCTCTG AATGCATACTCCGATCTCGCTG (SEQ ID NO: 639)
18624	A_23_P38346	LGP2	likely ortholog of mouse D11lgp2	0.775	CATACTGTACTCAGAATCACGACATTCCTTCCCTACCA AGGCCACTTCTATTTTTTGAGG (SEQ ID NO: 640)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
28011	A_23_P250353	HERC6	hect domain and RLD 6	0.764	TTCACCTCAGTCTCTAATTGGCTGTGAGTCAGTCTTTC ATTTACATAGGGTGTAACCATC (SEQ ID NO: 641)
24371	A_23_P37983	MT1B	metallothionein 1B	0.761	TCATCAGAGAAGTGCCGCTGCTGTGCCTGATGTTGGG AGAGCCCTGCTCCCAGACATAAA (SEQ ID NO: 642)
18869	A_24_P378019	IRF7	interferon regulatory factor variant a	0.760	CAACAGCCTCTATGACGACATCGAGTGCTTCCTTATGG AGCTGGAGCAGCCCGCCTAGAA (SEQ ID NO: 643)
11320	A_24_P125096	MT1X	metallothionein 1X	0.759	CCAGGGCTGCATCTGCAAAGGGACGTCAGACAAGTGC AGCTGCTGTGCCTGATGCCAGGA (SEQ ID NO: 644)
20855	A_23_P152782	IFI35	interferon-induced protein 35	0.758	CGGAAGTGCCTAAGTCTTTAGTTTCCAATTTGCGGATC CACTGCCCTCTGCTTGCGGGCT (SEQ ID NO: 645)
33108	A_32_P15128	OAS2	2'-5'-oligoadenylate synthetase 2 variant 1	0.755	TAAAGAGCTTTGCTTTGAAGACACAGAGGATTCCTTTT TTAGACTGGAAGGAAAAAGGAG (SEQ ID NO: 646)
40042	A_24_P30194	IFIT5	IFI protein with tetratricopeptide repeats 5	0.741	AATGTGGCTTCTCTAATGTAGTTTCTTTGATTACCGACT ACACAATTATGTACCATCACA (SEQ ID NO: 647)
7065	A_23_P132388	SCO2	SCO cytochrome oxidase deficient homolog 2	0.738	AGTCACAGTTACCGCGTGTACTACAATGCCGGCCCCA AGGATGAGGACCAGGACTACATC (SEQ ID NO: 648)
4620	A_23_P63668	IFIT5	IFI protein with tetratricopeptide repeats 5	0.731	AAGATAGATCCAGAAAATGCAGAATTCCTGACTGCTCT CTGTGAGCTCCGACTTTCCATT (SEQ ID NO: 649)
32013	A_23_P38894	FLJ11286	hypothetical protein FLJ11286	0.727	ATCCCCCCACCAGGATAAAAGTCCTGACCTTTGTTCTC TTGACGGAATAAAAGCTTGCTT (SEQ ID NO: 650)
41755	A_23_P29773	LAMP3	lysosomal-associated membrane protein 3	0.726	ACCATGTTGACTTTCCTCATGTGTTTCCTTATGACTCAG TAAGTTGGCAAGGTCCTGACT (SEQ ID NO: 651)
3171	A_23_P64343	TIMM10	translocase of inner mitochondrial membrane 10 homolog	0.725	ATGAGCGGATGGGCAAAAAGTTGACAGAGTTGTCTAT GCAGGATGAAGAGCTGATGAAGA (SEQ ID NO: 652)
35302	A_23_P39465	BST2	bone marrow stromal cell antigen 2	0.722	TGCTCGGCTTTTCGCTTGAACATTCCCTTGATCTCATC AGTTCTGAGCGGGTCATGGGGC (SEQ ID NO: 653)
28820	A_23_P370682	MGC20410	hypothetical protein BC012330	0.722	TGGAAGTTCAGTTTTGGTGTCTGCTTCAAGAGGGGGT TTTACACTCTGATTCCAGGACAA (SEQ ID NO: 654)
16269	A_23_P358944	PML	promyelocytic leukemia variant 8	0.718	GGACTGGCTATCCCAAGACCTGGCAGATGTGGCTGCT CAATAAACACTTGTTGAACCATC (SEQ ID NO: 655)
13700	A_23_P142750	PRKR	protein kinase, IFI double-stranded RNA dependent	0.717	AGAACAGATTTCTTCGCAAGACTATGGAAAGGAAGTG GACCTCTACGCTTTGGGGCTAAT (SEQ ID NO: 656)
26554	A_23_P259141	DLM-1	FLJ46548 fis, THYMU3038347, highly similar to DLM-1	0.716	ATGTTTGAGTCCCAACAAAATTCATATCAAAACATAATC CCAACTGGGTGCAGTGGCTCA (SEQ ID NO: 657)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
7372	A_32_P54553	USP41	ubiquitin specific protease 41	0.714	ATATGATCCGGATGAAGGACTCCTTGATTTGCCTTGAC TGTGCCATGGAGAGTAGCAGAA (SEQ ID NO: 658)
22061	A_24_P334361	FLJ20035	hypothetical protein FLJ20035	0.712	GTGAAAATGAAGACGACAACGTTGTCTTAGCCTTTGAA CAACTGAGTACAACTTTTTGGG (SEQ ID NO: 659)
23517	A_23_P139123	SERPING1	serine proteinase inhibitor, clade G member 1	0.710	GACAACATTTGATCCCAAGAAAACCAGAATGGAACCCT TTCACTTCAAAAACTCAGTTAT (SEQ ID NO: 660)
19683	A_32_P452655	LGALS9	lectin, galactoside-binding, soluble, 9 variant	0.708	TGACCAGAGTGTTCTCTTCAGGGGACTGGCTCCTTTC CCAGTGTCCTTAAAATAAAGAAA (SEQ ID NO: 661)
28706	A_23_P218879	TREX1	three prime repair exonuclease 1 variant 4	0.707	CAGCCTTGGAGAGAGCAGGGGTACCAAGGATCTTCCT CCAGTGAAGGACCCTGGAGCCCT (SEQ ID NO: 662)
41524	A_24_P332926	SFRS14	splicing factor, arginine/serine-rich 14	0.701	GTGTGTCTCATCCAGGAGCCAAAAGTCCATGAACCAG TTCGAATTGCCTATGACAGGCCT (SEQ ID NO: 663)
3797	A_23_P20814	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	0.697	TGAGTGGAGAAGAAACAAACATAGTGGGTATAATCATG GATCGCTTGTACCCCTGTGAAA (SEQ ID NO: 664)
40576	A_32_P134290	ZCCHC2	zinc finger, CCHC domain containing 2	0.697	AATTAATTGTTAAGCTGCAGTTGAGTTGTTCAAGTGAG AGTTTTGATAAGCCACTTATGG (SEQ ID NO: 665)
8270	A_23_P145874	C7orf6	chromosome 7 ORF 6	0.695	CATTGATATCCACTGGTCACATCATAACTGTCTATAGG GCAATAAAATCTGTGTTAAACT (SEQ ID NO: 666)
10995	A_23_P304054	LOC400653	hypothetical LOC400653	0.694	AGTTCTTTACGCTTTCTGATTGAACTGATTTGAAGTTCT TATTTCGTGTGTTGGGGAACA (SEQ ID NO: 667)
23236	A_23_P68155	MDA5	melanoma differentiation associated protein-5	0.693	CTACGTCCTGGTTGCTCACAGTGGTTCAGGAGTTATC GAACGTGAGACAGTTAATGATTT (SEQ ID NO: 668)
40635	A_23_P206441	FANCA	Fanconi anemia, complementation group A	0.685	ATGAGGGCCTCGTTTATTAAGATCTTTAAACTGCTTTAT ACACTGTCACGTGGCTTCATC (SEQ ID NO: 669)
43149	A_23_P17481	SIGLEC1	lectin-like adhesion molecule	0.681	GGAAGAGGTGATCACTCTCACACTAAGACTGAGGAAA TAAAAAAGGTTTGGTGTTTTCCT (SEQ ID NO: 670)
1523	A_24_P561165	SERPING1	serine proteinase inhibitor, clade G member 1	0.678	CGATTTTTCTTCATGACCTTAACCTGTGTGGGCTAACA GAGGACCCAGATCTTACAGGTT (SEQ ID NO: 671)
34907	A_23_P111804	ZC3HDC1	zinc finger CCCH type domain containing 1	0.677	TGATTCGGTTTCTCAGAGTCTCATGGCATCATAGTTTTT CCAGAATGACACAGTAGCCAC (SEQ ID NO: 672)
37561	A_24_P304071	IFIT2	IFI protein with tetratricopeptide repeats 2	0.673	TCTAAGAGAGAATGGAATGTATGGGAAAAGAAAGTTAC TGGAACTAATAGGACACGCTGT (SEQ ID NO: 673)
37323	A_24_P118892	IRF7	interferon regulatory factor 7 variant a	0.669	TCAGCCGGGAGCTGTGCTGGCGAGAAGGCCCAGGCA CGGACCAGACTGAGGCAGAGGCCC (SEQ ID NO: 674)
1157	A_23_P163782	MT1H	metallothionein 1H	0.668	AAGTGCAAATGCACCTCCTGCAAGAAGAGCTGCTGCT CCTGTTGCCCCCTGGGCTGTGCC (SEQ ID NO: 675)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
21378	A_23_P97064	FBXO6	F-box protein 6	0.665	CAACAGTGGAACAATGCCACATGGACAGAGGTCTCCT ACACCTTCTCAGACTACCCCCGG (SEQ ID NO: 676)
37891	A_23_P18604	LAP3	leucine aminopeptidase 3	0.660	TTCGTTTCAGTCAAGACAATGCTTAGTTCAGATACTCA AAAATGTCTTCACTCTGTCTTA (SEQ ID NO: 677)
1986	A_23_P69109	PLSCR1	phospholipid scramblase 1	0.660	GTTTAGCTCTTACACTCTATCCTTCCTAGAAAATGGTAA TTGAGATTACTCAGATATTAA (SEQ ID NO: 678)
6936	A_23_P203498	TRIM22	tripartite motif-containing 22	0.652	GTACATAAGAATCTATCACTAAGTAATGTATCCTTCAGA ATGTGTTGGTTTACCAGTGAC (SEQ ID NO: 679)
17172	A_23_P120435	WFDC3	WAP four-disulfide core domain 3 variant 4	0.652	ACCAGTCCTGCCCCCAAAACTGACCATGAACCCCAAC TGGACTGTGAGGTCTGATTCCGA (SEQ ID NO: 680)
7518	A_23_P21838	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase	0.651	TAACAGGGCCTTGCTAATCGGGTTGTCACTCAACAAAA GTGCTTTGGATTTAAGTTACTA (SEQ ID NO: 681)
36793	A_32_P156746	STAT2	signal transducer and activator of transcription 2	0.651	GAGATTGTCCAGAGTCCTATGACAGACCTTCAAGGTTT TAAGTTCCACAGACTTGGACTT (SEQ ID NO: 682)
22443	A_23_P209995	IL1RN	interleukin 1 receptor antagonist variant 4	0.646	TATTCCTGCATTTGTGAAATGATGGTGAAAGTAAGTGG TAGCTTTTCCCTTCTTTTTCTT (SEQ ID NO: 683)
23150	A_23_P161125	MOV10	Moloney leukemia virus 10, homolog	0.642	TCCCCGTACCGGAAACAGGTGGAGAAAATCCGTTACT GCATCACCAAACTTGACAGGGAG (SEQ ID NO: 684)
17566	A_24_P395966	ZBP1	Z-DNA binding protein 1	0.641	GTCGTCGTCCCGCAGACACACAATCCAGAAGTCACTT TCCTCGAGACATTGGTCAGCCCA (SEQ ID NO: 685)
8222	A_23_P250358	HERC6	hect domain and RLD 6	0.639	CCTTACACCTAAATAATACAAGAGATTAATGAATAGTG GTTAGAAGTAGTTGAGGGAGAG (SEQ ID NO: 686)
41451	A_24_P172481	TRIM22	tripartite motif-containing 22	0.639	TGCCCCTTAAAAGATTGAAGAAAGAGAAACTTGTCAAC TCATATCCACGTTATCTAGCAA (SEQ ID NO: 687)
18011	A_24_P7040	IFITM3	interferon induced transmembrane protein 3	0.636	CGCCAAGCATGTGAACATCTGGGCCCTGACTGTGGGC ATCCTCATGACCATTCTGCTCAT (SEQ ID NO: 688)
15599	A_24_P117410	LOC113730	hypothetical protein BC009980	0.635	GCTCAGGGAAGGGGCTGGGATCGGAACTTCCTGCTCT TGTTTCTGGACAACTTTCCCCTT (SEQ ID NO: 689)
2072	A_23_P75741	UBE2L6	ubiquitin-conjugating enzyme E2L 6 variant 2	0.628	AATAGACCGAATATCAGGGAGCCCCTGCGGATGGACC TCGCTGACCTGCTGACACAGAAT (SEQ ID NO: 690)
37424	A_23_P71148	BLVRA	biliverdin reductase A	0.627	AGGTGATGTAGCACTTCCAAGATGGCACCAGCATTTG GTTCTTCTCAAGAGTTGACCATT (SEQ ID NO: 691)
28056	A_24_P45446	GBP4	guanylate binding protein 4	0.627	AGGGGACACAGGCTTCTTAAAACAACCCGGCTTCCTC ACCCTATGTCCTTTATTTACAAA (SEQ ID NO: 692)
44249	A_23_P101025	LGALS9	lectin, galactoside-binding, soluble, 9 variant	0.622	CCCAGCCTTTCCAACCGTGCCTGGGATCTGGGCTTTA ATGCAGAGGCCATGTCCTTATCT (SEQ ID NO: 693)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
24243	A_23_P91802	ECGF1	endothelial cell growth factor 1	0.619	CCGCCTGGGGGTGGGCGCAGAGCTGCTGGTCGACGT GGGTCAGAGGCTGCGCCGTGGGAC (SEQ ID NO: 694)
3378	A_24_P394246	SCOTIN	scotin	0.618	TTCTCTTCCTCACCTGAAATTATGCTTCCTAAAATCTCA AGCCAAACTCAAAGAATGGGG (SEQ ID NO: 695)
17300	A_23_P428248	STI2	TPR domain containing STI2	0.617	GCCATCAACCTACTGAAGTTGTGTGGAGGGATGGAAA GTGGGTCAGTGGAGAAGGGATTC (SEQ ID NO: 696)
9338	A_23_P24004	IFIT2	IFI protein with tetratricopeptide repeats 2	0.615	AGCTGACCCAGCATCAGCCACACTCTGGGTTGGAAAA TGTTTGCCTGTTGGAATTAATTT (SEQ ID NO: 697)
28969	A_23_P42353	ETV7	ets variant gene 7	0.611	TGAGCCCTACATCAAGTGGGAAGACAAGGACGCCAAG ATCTTCCGAGTTGTGGATCCAAA (SEQ ID NO: 698)
18692	A_23_P70660	C6orf37	chromosome 6 ORF 37	0.610	GCTATCCGGGTGTTAGCTGACCAAAATGTCATTCCTAA TGTGGCTAATGTCACTTGCTAT (SEQ ID NO: 699)
13508	A_23_P212475	SCOTIN	scotin	0.610	ATCTGTTGTGTTTCTGAGTCTAGGGTCTGTACACTTGT TTATAATAAATGCAATCGTTTG (SEQ ID NO: 700)
43198	A_23_P216655	TRIM14	tripartite motif-containing 14 variant 1	0.609	ATAGCCAGAAAGCGGCAGTTTCAGTCCATATCAATTGT GTGACCAGGGCTAGTCACTTTT (SEQ ID NO: 701)
8567	A_23_P72737	IFITM1	interferon induced transmembrane protein 1	0.594	ATACAGCAGTTTATACCCACACACCTGTCTACAGTGTC ATTCAATAAAGTGCACGTGCTT (SEQ ID NO: 702)
24307	A_24_P161018	PARP14	poly (ADP-ribose) polymerase family, member 14	0.593	AAATATTAACATTTCCCTGGACCATAAGAGACCTTTGAT TAAGGTTTTGGGAATTAGCAG (SEQ ID NO: 703)
15588	A_23_P140207	PCK2	phosphoenolpyruvate carboxykinase 2	0.589	AGGACATAGCACCCTCATCTGGGAATAGGGAAGGCAC CTTGCAGAAAATATGAGCAATTT (SEQ ID NO: 704)
31781	A_32_P38003	EIF2AK2	downstream from gene	0.589	AAACTGTGAGGCAAATAAAATGCTTCTCAAATCTGTGT GGCTCTTATGGGGTTAATTTGA (SEQ ID NO: 705)
27401	A_23_P206441	FANCA	Fanconi anemia, complementation group A (FANCA) 5503	0.587	ATGAGGGCCTCGTTTATTAAGATCTTTAAACTGCTTTAT ACACTGTCACGTGGCTTCATC (SEQ ID NO: 706)
39922	A_23_P400378	GPBAR1	G protein-coupled bile acid receptor 1	0.586	TGTCGACCTGGACTTGAACTAAAGGAAGGGCCTCTGC TGACTCCTACCAGAGCATCCGTC (SEQ ID NO: 707)
4393	A_32_P107372	LOC400760	similar to Interferon-induced guanylate-binding protein 1	0.585	GGTACTGAGCAGAGTCTTAGGTAAAAGTCTTGGGAAA TATTTGGGCATTGGTCTGGCCAA (SEQ ID NO: 708)
41600	A_23_P206441	FANCA	Fanconi anemia, complementation group A	0.580	ATGAGGGCCTCGTTTATTAAGATCTTTAAACTGCTTTAT ACACTGTCACGTGGCTTCATC (SEQ ID NO: 709)
24950	A_23_P121011	AXUD1	AXIN1 up-regulated 1	0.580	GCGTGATGTTCCTTAGCCCAAAGACGGTGAGACAGGG CTGAAATCAGGTGGCTTCTGCCA (SEQ ID NO: 710)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
37768	A_23_P206441	FANCA	Fanconi anemia, complementation group A	0.577	ATGAGGGCCTCGTTTATTAAGATCTTTAAACTGCTTTAT ACACTGTCACGTGGCTTCATC (SEQ ID NO: 711)
26191	A_24_P419286	DNAH3	dynein, axonemal, heavy polypeptide 3	0.576	CCCAGAAGATCGTTGCGACCTACCGCCTGTGCTCGGA ACAACTGTCCTCTCAGCATCATT (SEQ ID NO: 712)
10783	A_23_P206441	FANCA	Fanconi anemia, complementation group A	0.576	ATGAGGGCCTCGTTTATTAAGATCTTTAAACTGCTTTAT ACACTGTCACGTGGCTTCATC (SEQ ID NO: 713)
24951	A_23_P15174	MT1F	metallothionein 1F	0.573	TGCCAGGACAACCTTTCTCCCAGATGTAAACAGAGAG ACATGTACAAACCTGGATTTTTT (SEQ ID NO: 714)
30864	A_24_P148717	CCR1	chemokine (C-C motif) receptor 1	0.569	CTTTTCAAGTTGGGTGATATGTTGGTAGATTCTAATGG CTTTATTGCAGCGATTAATAAC (SEQ ID NO: 715)
38267	A_23_P106226	C14orf123	chromosome 14 ORF 123	0.567	CTGAGTGGGTATCCTGATAAATCTGGGCTTGTCTTCCT AATGCTACCTTTGTTGGTCCTT (SEQ ID NO: 716)
40688	A_24_P274270	STAT1	signal transducer and activator of transcription 1 variant beta	0.567	TTGAACCCTACACGAAGAAAGAACTTTCTGCTGTTACT TTCCCTGACATCATTCGCAATT (SEQ ID NO: 717)
13093	A_23_P206441	FANCA	Fanconi anemia, complementation group A	0.565	ATGAGGGCCTCGTTTATTAAGATCTTTAAACTGCTTTAT ACACTGTCACGTGGCTTCATC (SEQ ID NO: 718)
30444	A_24_P344711	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	0.565	TCCCATAGAAGTTCCCTCCCTTTGAAATTAATATATAAT GTATAAATTCTGCACTGAGCC (SEQ ID NO: 719)
42135	A_23_P125624	ACATE2	ortholog of acyl-Coenzyme A thioesterase 2, mitochondrial	0.565	TGAAGACCTGATCGAGTGTATTGATTTTAGTATTGCTT CGTGTCCTCCACACAGGAGGAG (SEQ ID NO: 720)
32604	A_24_P941912	BBAP	rhysin 2	0.564	TTTATAATAACCGTAGCCCACATTGTAGTAGTTTTTCAG CTCTTTACTAAGTCCCACCAA (SEQ ID NO: 721)
31047	A_24_P207139	PML	promyelocytic leukemia variant 1	0.564	ACAGTGAATTTTGATGCATTTAAAATAAGATTCTGATGC CAGACTGTTAAAACAGGCGCT (SEQ ID NO: 722)
30304	A_23_P65174	PHF11	PHD finger protein 11	0.564	TATGAAGAAATCGGGAGTGCACTTTTTGACTGTAGATT GTTCGAAGACACATTTGTAAAT (SEQ ID NO: 723)
9201	A_23_P355244	FLJ20073	FLJ20073 protein (FLJ20073) 6853	0.564	TCACTGGAGGAAGATTTTCCCTTGCTTCTGCATAAAAT TTTAACTCCATAACTTATAAGC (SEQ ID NO: 724)
41835	A_23_P69383	BAL	B aggressive lymphoma gene	0.561	TTTTTAGTGGCATGCAGGCTATACCTCAGTATTTGTGG ACATGCACCCAGGAATATGTAC (SEQ ID NO: 725)
13417	A_23_P306148	PML	promyelocytic leukemia variant 11	0.560	AGGCAGAGGAACGCGTTGTGGTGATCAGCAGCTCGG AAGACTCAGATGCCGAAAACTCGT (SEQ ID NO: 726)
37690	A_23_P123672	TDRD7	tudor domain containing 7	0.560	AAATCTTAACTCTGCTACATGGCTCTGACTGCTGTGGG GGATTGAAAAGAATATGCTTAT (SEQ ID NO: 727)
22106	A_23_P6263	LOC442209	FLJ16669 fis, clone THYMU3000306	0.555	TCTGGGTCAAATTCTTCTTTTGTATGTCCAGTCTCCTG CACAGCACCTGCAGCATTGTAA (SEQ ID NO: 728)
33663	A_23_P12044	FLJ10199	hypothetical protein FLJ10199	0.554	GCCTGATGAACGTAGGCACGTGATGCGTAATAGTCTT CAATGGTACACTTAACTAGTCTC (SEQ ID NO: 729)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
18942	A_23_P206441	FANCA	Fanconi anemia, complementation group A	0.549	ATGAGGGCCTCGTTTATTAAGATCTTTAAACTGCTTTAT ACACTGTCACGTGGCTTCATC (SEQ ID NO: 730)
22341	A_23_P423331	NTNG2	netrin G2	0.549	AACTATTTTTGTTTGTATTCACTGTCCCCTGCAAGGGG GACGGGGCGGGAGCACTGGTCA (SEQ ID NO: 731)
39663	A_24_P868905	LOC391020	similar to IFI transmembrane protein 3	0.544	ATCCTCATGAGCATTCTGCTCATCTTCATCCCAGTGTT GATCTTTCAAGTCTATCAATAG (SEQ ID NO: 732)
22603	A_32_P92415	PARP14	poly (ADP-ribose) polymerase family, member 14	0.543	GAAGGGTTTCACAATGAAGATGTGTAGCAGGCGTTAT CCCATTGTTATCACTGGGCAGAA (SEQ ID NO: 733)
12663	A_23_P154488	PNPT1	polyribonucleotide nucleotidyltransferase 1	0.543	AAATTCAGGTGAAATACTTTGGACGTGACCCAGCCGAT GGAAGAATGAGGCTTTCTCGAA (SEQ ID NO: 734)
38515	A_24_P15702	EST	highly conserved region	0.542	CCAATGCAGACAAACCACCCCTTTTTGTTGGGAAAGG AATTACCTTTGACAGTGGTGGTA (SEQ ID NO: 735)
37436	A_32_P53603	EST	space dust	0.542	CTTTTATGTGGTTCCTGCCCCTGAGAATAAAGAAGCCC CAGCGTGGCTGCGAGGCACCAT (SEQ ID NO:736)
19668	A_23_P116557	LGALS9	lectin, galactoside-binding, soluble, 9 variant	0.542	AGTGTGGATCTTGTGTGAAGCTCACTGCCTCAAGGTG GCCGTGGATGGTCAGCACCTGTT (SEQ ID NO: 737)
31202	A_23_P87545	IFITM3	interferon induced transmembrane protein 3	0.541	GGGCCCTGATTCTGGGCATCCTCATGACCATTCTGCT CATCGTCATCCCAGTGCTGATCT (SEQ ID NO: 738)
39745	A_23_P55564	ZCCHC2	zinc finger, CCHC domain containing 2	0.540	GACATCTGACGTAGAGACCTGCGAATGGATCTGAGAT GAGTAGTAACGCAGGTTGTCCGG (SEQ ID NO: 739)
31706	A_24_P350124	KIAA1618	KIAA1618	0.540	GCAGATTCTGAGAACAATAACTCCACAATGGCGTCGG CCTCGGAGGGTGAAATGGAGTGT (SEQ ID NO: 740)
31855	A_24_P344087	REC8L1	REC8-like 1	0.539	TCCTGGTGCTCTCAGCGCAACAGATTCTTCACGTGAAA CAAGAAAAGCCATATGGTCGCC (SEQ ID NO: 741)
27231	A_23_P75811	SLC3A2	solute carrier family 3 member 2	0.538	ATCCTGAGCCTACTCGAATCCAACAAAGACTTGCTGTT GACTAGCTCATACCTGTCTGAT (SEQ ID NO: 742)
35807	A_23_P138856	DRAP1	DR1-associated protein 1 (negative cofactor 2 alpha)	0.537	CTTCTGCCCCCCAGACCATAGCCCCTTTTAGTTGGTTT TAGTTGCTCTGGGGGGAGGAGA (SEQ ID NO: 743)
14385	A_24_P16124	IFITM4P	IFI transmembrane protein 4 pseudogene, chromosome 6	0.536	GGGATTCATAGCATTCACCTACTCCCTGAAGTCTAGG GACAGGAAGATGGTTGGAGACCT (SEQ ID NO: 744)
14104	A_23_P62890	GBP1	guanylate binding protein 1, interferon-inducible	0.536	CAAAGATGCATTTACCTCTGTATCAACTCAGGAAATCT CATAAGCTGGTACCACTCAGGA (SEQ ID NO: 745)
21955	A_24_P197964	TRIM14	tripartite motif-containing 14 variant 4	0.536	AAATTGCTTGCAGATATTTTTAAATGACAGCAATTTTCT AATATTTGGTTTAATAAAATG (SEQ ID NO: 746)
23148	A_23_P153372	HSH2D	hematopoietic SH2 domain containing	0.536	GAATCCGAGCCCTTTTCCCATATCATCTGTTTGTTCTG TTGTCTAAAAGCACACTGCAAG (SEQ ID NO: 747)
11424	A_23_P206441	FANCA	Fanconi anemia, complementation group A	0.532	ATGAGGGCCTCGTTTATTAAGATCTTTAAACTGCTTTAT ACACTGTCACGTGGCTTCATC (SEQ ID NO: 748)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
8658	A_23_P202964	PORIMIN	pro-oncosis receptor inducing membrane injury gene	0.531	TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAG CTTTGTTGGTGGTATTGTATTA (SEQ ID NO: 749)
34298	A_24_P259276	LOC254359	hypothetical protein LOC254359	0.531	ACTCAGTAAGGAAGTCGGGTTGGACCTTAACATCTGC ATTGGACAACTCCACCCCTTCCT (SEQ ID NO: 750)
26056	A_23_P98167	UNC93B1	unc-93 homolog B1	0.531	TCGCCGGCCTCAGTTTACCACGTCTGAGGTCGGGGG GACCCCCTCCGAGTCCCGCGCTGT (SEQ ID NO: 751)
43514	A_32_P157846	FLJ31401	FLJ34941 fis, clone NT2RP7007480	0.529	ACAGTTGTTTTGTCTTCAAGCCACTGACTTCTGGAATTT GCAGATTTTGCAATCCATGCA (SEQ ID NO: 752)
23132	A_24_P50543	LOC400368	hypothetical gene supported by BC031266	0.527	AAATCAGCCTCCATCAGTATCACTGCAGTTATATATGA TGTATGCCTTATTGCTCAAGAC (SEQ ID NO: 753)
22246	A_23_P214080	EGR1	early growth response 1	0.526	AAACAAAGTGACTGTTTGGCTTATAAACACATTGAATG CGCTTTATTGCCCATGGGATAT (SEQ ID NO: 754)
3490	A_23_P206441	FANCA	Fanconi anemia, complementation group A	0.523	ATGAGGGCCTCGTTTATTAAGATCTTTAAACTGCTTTAT ACACTGTCACGTGGCTTCATC (SEQ ID NO: 755)
2659	A_23_P50108	KNTC2	kinetochore associated 2	0.520	AAAGTGGGAAATAACTTGCAACGTCTGTTAGAGATGGT TGCTACACATGTTGGGTCTGTA (SEQ ID NO: 756)
21328	A_24_P382319	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1	0.519	CCATGCTGTGCTGTGTTATTTAATTTTTCCTGGCTAAGA TCATGTCTGAATTATGTATGA (SEQ ID NO: 757)
33919	A_23_P255104	LHFPL2	lipoma HMGIC fusion partner-like 2	0.518	CCAAAAGAGTTAAAGGCACGACTGGGATTTCTTCTGA GACTGTGGTGAAACTCCTTCCAA (SEQ ID NO: 758)
27245	A_24_P43588	MAD2L1BP	MAD2L1 binding protein variant 1	0.518	CCATAAACTGACTGTGACCCTGTCATGTGGCAGACCTT CCATCCGAACCACGGCTTGGGA (SEQ ID NO: 759)
33581	A_23_P502520	IL4I1	interleukin 4 induced 1 variant 2	0.517	CCAGTTATCTCTCCAAAACACGACCCACACGAGGACC TCGCATTAAAGTATTTTCGGAAA (SEQ ID NO: 760)
8566	A_24_P54879	SCARB2	scavenger receptor class B, member 2	0.516	AGTGATGTACCTCAATGAGAGTGTTCACATTGATAAAG AGACGGCGAGTCGACTGAAGTC (SEQ ID NO: 761)
16203	A_24_P175188	FLJ20073	FLJ20073 protein	0.515	TGCCAATGTACTGGCAGATTAACATACAACCTATGTTT TGAACAAAAACAACCAGCGATA (SEQ ID NO: 762)
11370	A_23_P34915	ATF3	activating transcription factor 3	0.513	GATGTCAATAGCATTGTTTTTGTCATGTAGCTGTTTTAA GAAATCTGGCCCAGGGTGTTT (SEQ ID NO: 763)
26089	A_23_P75769	MS4A4A	membrane-spanning 4-domains, subfamily A, member 4 variant 2	0.511	CACCAAAAGATCAACAGACAAATGCTCCAGAAATCTAT GCTGACTGTGACACAAGAGCCT (SEQ ID NO: 764)
7745	A_23_P166459	LGALS1	lectin, galactoside-binding, soluble, 1	0.511	CCAGATGGATACGAATTCAAGTTCCCCAACCGCCTCA ACCTGGAGGCCATCAACTACATG (SEQ ID NO: 765)
12417	A_32_P71710	IL1RN	interleukin 1 receptor antagonist variant 4	0.510	AAGATTTTATTGTAAAACAGAGCTGAAGTCACAGGAAG TAGGGAACTTTGCACCCAACAT (SEQ ID NO: 766)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
35164	A_23_P376488	TNF	tumor necrosis factor, superfamily member 2	0.509	GGGGTATCCTGGGGGACCCAATGTAGGAGCTGCCTT GGCTCAGACATGTTTTCCGTGAAA (SEQ ID NO: 767)
37407	A_23_P135123	FRMD3	FERM domain containing 3	0.509	CTGGTCTGAAGGGTCACGGGGCTGTCAACAGGTGTTC CTTACTCATAATTGATTATTCAA (SEQ ID NO: 768)
32481	A_23_P59005	TAP1	transporter 1, ATP-binding cassette, sub-family B	0.507	TCCAGGATGAGTTACTTGAAATTTGCCTTGAGTGTGTT ACCTCCTTTCCAAGCTCCTCGT (SEQ ID NO: 769)
27197	A_24_P254933	ATXN2	ataxin 2	0.506	CCGACCATGTCCTGGTCCCTGTTCAACACCCACTTCAT GAATGCTGCCTGGGCTTCATAG (SEQ ID NO: 770)
29912	A_24_P326957	WDR23	WD repeat domain 23 variant 1	0.506	TGGGTCTTTAGGGTAGGACAGGCTGTGGTATGAGAGG CAGGAGTCTCCACAAGGCTTCAT (SEQ ID NO: 771)
26767	A_23_P356526	TRIM5	tripartite motif-containing 5 variant delta	0.506	GAAGCCAGAAACTTTTCCAAAAAATCAAAGGAGAGTGT TTCGAGCTCCTGATCTGAAAGG (SEQ ID NO: 772)
41790	A_23_P165636	CAPG	capping protein (actin filament), gelsolin-like	0.506	CTGCTTGCTTCTCTGGCTGCCTGGTCAGTGCAGAGGT GCCCCCTGCAGATGTTCAATAAA (SEQ ID NO: 773)
38573	A_24_P127641	LOC441109	hypothetical gene supported by AL713721	0.503	TATATCGTAGGTGGCTTTAATACGTGTTATTTGCTCATC TGTATTTCTTACTCTTTGCAC (SEQ ID NO: 774)
40160	A_23_P88234	C14orf122	chromosome 14 ORF 122	0.503	GATAAGAACTTAGTGATGTGGAGGGACTGGGAAGAGT CACGGCAGATGGTGGGAGCTCTA (SEQ ID NO: 775)
9098	A_24_P383523	SAMD4	sterile alpha motif domain containing 4	0.501	CCATCTTCAGGGTTGCACAGAATCCTCCAAGATACTTT GCAGCCTTTTTTCCCCCTGGTC (SEQ ID NO: 776)
16598	A_24_P242391	MPZL1	myelin protein zero-like 1 variant 2	-0.501	GTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTA GAACATATCCTCAGCAAGAAAC (SEQ ID NO: 777)
39617	A_32_P109516	LOC389089	LOC389089	-0.507	TCCGTTTTTACAGCATTCTCGACCTGTGATTCTTGGTG GGGGAAACTAGTTATGTGGATA (SEQ ID NO: 778)
36575	A_23_P417282	MGC18216	hypothetical protein MGC18216, clone IMAGE:4156235	-0.507	AAATCAAACCAGAAGGCGGGATGGAATGGATGCACCG CAAATAATGCATTTTCTGAGTTT (SEQ ID NO: 779)
34695	A_23_P403284	OTX1	orthodenticle homolog 1	-0.517	TTAGTTGCTGTTGGTTGGTTGAACTGAACATATCTTGT CTTAGCACCCAGGAAACAGAAC (SEQ ID NO: 780)
33205	A_24_P467358	EEF1G	eukaryotic translation elongation factor 1 gamma	-0.526	CTGGATGCTTACTTGAAGACGAGGACTTTTCTGGTGG GCGAACGAGTGACATTGGCTGAC (SEQ ID NO: 781)
25932	A_24_P87763	EEF2	eukaryotic translation elongation factor 2	-0.527	CATGTTTGTGGTCAAGGCCTATCTGCCCGTCAACGAG TCCTTTGGCTTCACCGCTGACCT (SEQ ID NO: 782)
14152	A_23_P124252	CAMK1D	calcium/calmodulin-dependent protein kinase ID	-0.528	TCCTGTTTGCCAGGCGCTTTCTATACTTAATCCCATGT CATGCGACCCTAGGACTTTTTT (SEQ ID NO: 783)
35180	A_24_P177653	LOC340947	similar to bA508N22.1 (HSPC025)	-0.528	CATGAGTATTGATGAGAGCATTCACCTCCAGCGGTGG GATAAATACAGCAACAAGATGCT (SEQ ID NO: 784)

Table 2

Feature	Agilent Probe	Gene	Description	Correlation - IFI27	Sequence
38227	A_23_P104318	DDIT4	DNA-damage-inducible transcript 4	-0.529	TCGTGGAGGTGGTTTGTGTATCTTACTGGTCTGAAGG GACCAAGTGTGTTTGTTGTTTGT (SEQ ID NO: 785)
3684	A_23_P57521	EIF3S6IP	eukaryotic TIF 3, subunit 6 interacting protein	-0.529	GAATTTCAGTCAGCCTCAGAGGTTGACTTCTACATTGA TAAGGACATGATCCACATCGCG (SEQ ID NO: 786)
7635	A_32_P172917	LOC389832	similar to chromosome 2 ORF 27	-0.530	AACTCAGCAGCAGCACTCCAGAATCTCCATGCCTGCA CCTGCCCAAGGATTTATTCATAG (SEQ ID NO: 787)
39387	A_32_P76399	EIF3S6IP	eukaryotic TIF 3, subunit 6 interacting protein	-0.531	AGGTTGACTTCTACATTGATAAGGACATGATCCACATC GCGGACACCAAGGTCTCCAGGC (SEQ ID NO: 788)
24015	A_23_P105138	CAT	catalase	-0.532	CTCATCACTGGATGAAGATTCTCCTGTGCTAGATGTGC AAATGCAAGCTAGTGGCTTCAA (SEQ ID NO: 789)
15339	A_24_P8371	MYBBP1A	MYB binding protein (P160) 1a	-0.536	GCTGCTGATTGTGAATCTCAGAGTCTTAAGAGAGAAG CCAAATATATTCCTCTTGTAAAT (SEQ ID NO: 790)
23589	A_24_P757154	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-0.536	ACACTTTGCATGCTGGGTCAGGGAAGATTGTGGAGAG AGGACAGTGCACCTGGTTTCCCC (SEQ ID NO: 791)
19944	A_24_P32151	MGC45871	hypothetical protein MGC45871	-0.537	AAGGAAGTAAGGTACACCTCCTTGGTCAAGTACGACT CCGAGAGGCACTTCATCGACGAC (SEQ ID NO: 792)
11244	A_24_P154037	IRS2	insulin receptor substrate 2	-0.540	GATGGTTCGTGTTCATACTGCAGCTTAAAACAAGCAAA ATACACAGATGATAATATGCTA (SEQ ID NO:793)
2728	A_32_P128258	SIGLECP3	sialic acid binding Ig-like lectin, pseudogene 3	-0.543	ACTATGTGCCAGCATTTCCGTATGTGCAGAAGTTCATC AATAGATATAGACTCAAAGAGC (SEQ ID NO: 794)
43581	A_24_P717462	LOC651628	similar to Elongation factor 1-gamma	-0.552	TGGATGAATGTGAGCAGAGTACCTTTGTGTTGGATAAA TTTCAGTGCAGGTACTCTAAGG (SEQ ID NO: 795)
24821	A_24_P136641	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	-0.552	GCTAAGGAGGAAATACCCAGACAAAATCTTTGGGACG AATGAAAATTTGTAACTCTTCTG (SEQ ID NO: 796)
26400	A_24_P588235	EIF3S6IP	eukaryotic TIF 3, subunit 6 interacting protein	-0.561	TGTGGATCATGTCCTTATCAATGTAGAAGTCAACCTCT GAGGCTGACTGAAATTCACCAT (SEQ ID NO: 797)
40567	A_23_P50081	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	-0.583	TAGCTGTTTCTCTCTTTAATCTCACGTAGCCTTTTTCAG GTTAGTACGTGTTCTTCTGTC (SEQ ID NO: 798)
10228	A_24_P299318	FAM101B	family with sequence similarity 101, member B	-0.598	ACTTAATTTGAGCGAGTACCTTTTCATTTGACACTTTTC CTGTTTCTAACCTTAGGAAAC (SEQ ID NO: 799)
6063	A_24_P856176	EST	highly conserved genomic region	-0.603	CCAGGCTGTGCAGTGGGTGAACTTTGCTGATGATAGC CAGTACCAGGGTGTTCCCACCTT (SEQ ID NO: 800)
14283	A_32_P159289	EST	EST defined by BE677474	-0.630	ACTGGCTTTTCTTTCATCTCTGGAGAGAGCTTGATTCG TCATCTTATTGCTTTGTCTGAA (SEQ ID NO: 801)
19711	A_24_P554408	EEF1G	eukaryotic translation elongation factor 1 gamma	-0.636	GGCAATGGCGTTGCTCTCAAACACACAGAATCCATCAT CACCCTCAAATGCTGGGACCTT (SEQ ID NO: 802)

TABLE 3

Patient	ABCoN ID	Sample	Date	SLEDAI	INFr	Days from 1st Sample	INFr Score
1	JHP004-01	QF1	7/26/2006	2	LOW	0	-2.813
	JHP004-02	F	10/15/2006	6	LOW	81	-1.864
2	JHP012-02	QF1	9/10/2006	0	LOW	0	-2.21
	JHP012-04	F	11/5/2006	8	LOW	56	-2.202
3	JHP017-02	QF1	11/12/2006	0	LOW	0	-2.44
	JHP017-03	F	2/4/2007	4	LOW	84	-2.07
4	JHP019-05	QF5	3/8/2007	0	LOW	0	0.255
	JHP019-06	QF1	5/16/2007	2	LOW	69	-0.219
	JHP019-07	F	8/26/2007	8	LOW	171	-0.124
5	JHP021-02	F	10/18/2006	4	HIGH	0	2.882
	JHP021-04	QF1	12/19/2006	0	HIGH	62	1.878
6	JHP023-01	QF4	8/30/2006	0	LOW	0	-1.684
	JHP023-02	F	11/15/2006	4	LOW	77	-1.404
	JHP023-03	QF1	2/14/2007	0	LOW	168	-1.959
	JHP023-04	F	5/9/2007	8	LOW	252	-1.293
7	JHP028-01	QF5	9/13/2006	4	HIGH	0	2.883
	JHP028-03	QF1	3/18/2007	4	HIGH	186	3.57
	JHP028-04	F	6/17/2007	16	HIGH	277	3.784
	JHP028-05	QF4	7/8/2007	4	HIGH	298	4.696
	JHP028-06	F	9/30/2007	16	HIGH	382	4.325
8	JHP029-01	QF1	9/13/2006	4	HIGH	0	3.463
	JHP029-03	F	3/7/2007	9	HIGH	175	3.867
9	JHP030-03	F	2/4/2007	12	LOW	0	1.392
	JHP030-09	F	6/10/2007	6	LOW	126	0.815
10	JHP033-02	QF1	12/17/2006	2	LOW	0	1.277
	JHP033-03	F	3/4/2007	12	HIGH	77	2.276
11	JHP039-02	QF1	1/24/2007	4	HIGH	0	4.707
	JHP039-03	F	3/28/2007	12	HIGH	63	4.281
12	JHP068-02	QF5	4/8/2007	0	HIGH	0	3.389
	JHP068-03	QF1	7/1/2007	0	HIGH	84	3.773
	JHP068-04	F	9/30/2007	7	HIGH	175	3.992
13	JHP072-01	F	1/14/2007	10	HIGH	0	3.178
	JHP072-02	QF5	4/15/2007	0	LOW	91	0.155
	JHP072-03	QF1	7/15/2007	0	HIGH	182	1.794
	JHP072-04	F	10/7/2007	8	HIGH	266	2.377
14	JHP074-01	QF1	1/14/2007	3	HIGH	0	3.087
	JHP074-05	F	1/13/2008	9	HIGH	364	4.226
15	JHP075-02	QF1	10/7/2007	1	LOW	0	-1.516
	JHP075-03	F	1/13/2008	11	LOW	98	-0.26

TABLE 3

Patient	ABCoN ID	Sample	Date	SLEDAI	INFr	Days from 1st Sample	INFr Score
16	JHP078-01	QF5	1/14/2007	4	HIGH	0	3.381
	JHP078-02	QF1	7/22/2007	4	HIGH	189	4.042
	JHP078-03	F	12/12/2007	10	HIGH	332	4.03
17	JHP079-02	F	2/28/2007	4	LOW	0	-2.02
	JHP079-03	QF4	4/15/2007	0	LOW	46	-2.095
	JHP079-04	F	7/15/2007	4	LOW	137	-1.931
18	JHP080-03	QF1	7/18/2007	4	HIGH	0	4.606
	JHP080-04	F	9/12/2007	8	HIGH	56	4.35
19	JHP081-01	QF5	1/17/2007	0	LOW	0	-2.31
	JHP081-02	QF1	5/16/2007	0	LOW	119	0.595
	JHP081-03	F	7/18/2007	4	LOW	182	-1.632
	JHP081-04	QQ	10/17/2007	0	LOW	273	-1.729
20	JHP100-01	QF1	5/16/2007	4	HIGH	0	3.896
	JHP100-03	F	3/26/2008	12	HIGH	315	3.88
21	JHP102-01	QF5	5/20/2007	4	HIGH	0	3.993
	JHP102-02	QF1	6/17/2007	4	HIGH	28	4.048
	JHP102-03	F	9/23/2007	8	HIGH	126	3.19
	JHP102-04	QF4	12/23/2007	0	HIGH	217	3.704
	JHP102-05	F	2/20/2008	4	HIGH	276	3.054
22	JHP104-01	QF5	6/6/2007	4	HIGH	0	4.508
	JHP104-02	QF1	9/5/2007	4	HIGH	91	3.259
	JHP104-04	F	2/27/2008	12	HIGH	266	3.59
23	JHP111-02	QQ	9/12/2007	0	HIGH	0	3.585
	JHP111-04	QF1	3/30/2008	2	HIGH	200	3.503
	JHP111-05	F	6/25/2008	6	HIGH	287	2.196
24	JHP117-02	QF1	9/30/2007	0	LOW	0	-0.932
	JHP117-03	F	12/19/2007	4	LOW	80	0.251
25	JHP120-04	QQ	11/11/2007	0	HIGH	0	3.736
	JHP120-06	QF1	4/27/2008	0	HIGH	168	2.258

CLAIMS

We claim:

1. A method of diagnosing or monitoring the status of systemic lupus erythematosus (SLE) in a subject or patient comprising:

detecting the expression of all genes of a diagnostic set in the subject or patient wherein the diagnostic set comprises two or more genes having expression correlated with the classification or status of SLE; and

diagnosing or monitoring the status of SLE in the subject or patient by applying at least one statistical method to the expression of the genes of the diagnostic set.

2. The method of claim 1 wherein the statistical method is a prediction algorithm.

3. The method of claim 2 wherein the prediction algorithm produces a number or single value indicative of the status of SLE in the subject or patient.

4. The method of claim 1 wherein the statistical method further comprises classification of the subject or patient into one of at least two classes of SLE.

5. The method of claim 4 wherein the statistical method is optimized to maximize the separation among longitudinally stable classes of SLE.

6. The method of claim 1 wherein the diagnostic set further comprises at least one gene selected from each of at least two gene clusters selected from cluster 1, cluster 2, cluster 3, cluster 4, cluster 5, cluster 6, cluster 7, cluster 8, cluster 9, cluster 10, cluster 11; cluster 12, cluster 13, cluster 14, and cluster 15 of Table 1.

7. The method of claim 4 wherein classification of the subject or patient into one of at least two classes of SLE further comprises:

detecting the expression of two or more gene whose expression correlates with the expression of the IFI27 from about 0.5 to about 1.0 and from about -0.5 to about -1.0 calculated using a Pearson correlation; and

classifying a subject or patient as having type 1 or type 2 SLE based on the expression of the two or more genes.

8. The method of claim 7 wherein one of the two or more genes is selected from Table 2.

9. The method of claim 7 wherein the classifying step uses a linear algorithm to produce an interferon response (INFr) score.

10. The method of claim 9 wherein a high INFr score is correlated with type I SLE and a low INFr score is correlated with type II SLE.

11. The method of claim 9 wherein at least one of the linear algorithm that produces an INFr score comprises IFI27 + IFI144*(1.1296) + OAS3*(1.8136).

12. The method of claim 7 wherein the Pearson correlation is selected from a range of 0.5, 0.4, 0.3, and 0.2 of these genes.

13. A method of diagnosing or monitoring the status of systemic lupus erythematosus (SLE) in a subject or patient comprising:

detecting the expression of all genes of a diagnostic set in a subject or patient wherein the diagnostic set comprises at least one gene from each of at least two gene clusters selected from cluster 1, cluster 2, cluster 3, cluster 4, cluster 5, cluster 6, cluster 7, cluster 8, cluster 9, cluster 10, cluster 11; cluster 12, cluster 13, cluster 14, and cluster 15 of Table 1; and

diagnosing or monitoring the status of SLE in the subject or patient based on expression of the genes in the diagnostic set.

14. The method of claim 1 wherein the expression of all genes in the diagnostic set is detected using a nucleic acid technology.

15. The method of claim 14 wherein the nucleic acid technology further comprises hybridization or amplification in a quantitative real-time polymerase chain reaction.

16. The method of claim 15 wherein hybridization occurs in solution or on a substrate selected from magnetic or nonmagnetic beads, chips, fibers, filters, gels, membranes, microparticles, plates, polymers, slides, capillary tubing, and wafers with surface features selected from channels, columns, pins, pores, trenches, and wells.

17. The method of claim 1 wherein detecting expression of all genes further comprises isolating RNA from a subject or patient sample.

18. The method of claim 19 wherein expression is proportional to the amount of RNA isolated from the sample.

19. The method of claim 17 wherein the sample further comprises a body fluid or tissue obtained by any sampling means.

20. The method of claim 19 wherein the body fluid is selected from ascites, bile, whole blood or a blood fraction, cerebrospinal fluid, lymph, sputum, and urine.

21. The method of claim 19 wherein the tissue sample is selected from central nervous system, joints, kidneys, liver, lungs, oral cavity, sinuses, skin, and vasculature.

22. The method of claim 19 wherein the sampling means is selected from aspiration of a body fluid, a biopsy of a tissue or an organ, drawing of peripheral blood, endoscopy, and lavage followed by aspiration.

23. The method of claim 1 wherein detecting expression comprises using at least one primer or probe set to detect the expression of each of the genes in the diagnostic set.

24. The method of claim 23 wherein the primers or probe sets are oligonucleotides selected from natural or synthetic cDNA, genomic DNA, locked nucleic acids, peptide nucleic acids, and RNA.

25. The method of claim 23, wherein the primers or probe sets comprise a diagnostic kit.

26. The method of claim 7 wherein classifying a subject or patient as type 1 SLE or type 2 SLE comprises assigning a subject or patient to a clinical trial.

27. A method of diagnosing a patient as having a longitudinally stable classification of SLE comprising:

detecting the expression of two or more genes whose expression correlates with the expression of the IFI27 from about 0.5 to about 1.0 and from about -0.5 to about -1.0 calculated using Pearson correlation; and

diagnosing the patient as having type I or type II SLE based analyzing the expression of the two or more genes using a statistical method.

28. The method of claim 1 wherein the statistical method is selected from analysis of variance, classification algorithms, classification and regression trees, Fisher's Exact Test, linear algorithm, linear discriminatory analysis, linear regression, logistic algorithm, multiple regression, nearest shrunken centroids classifier, Pearson correlation, prediction algorithm, significance analysis of microarrays, one-tailed T-tests, two-tailed T-tests, voting algorithm, and Wilcoxon's signed ranks test.

29. The method of claim 1 wherein status of SLE in a subject or patient is incipient flare or disease activity.

30. The method of claim 1 wherein status of SLE in a subject or patient comprises a response to a therapeutic agent administered to the patient.

31. The method of claim 30 wherein the therapeutic agent is selected from ACE inhibitors, aspirin, azathioprine, B7RP-1-fc, ß-blockers, brequinar sodium, campath-1H, celecoxib, chloroquine, corticosteroids, coumadin, cyclophosphamide, cyclosporin A, dehydroepiandrosterone, deoxyspergualin, dexamethasone, diclofenac, dolobid, etodolac, everolimus, FK778, feldene, fenoprofen, flurbiprofen, heparin, hydralazine, hydroxychloroquine, CTLA-4 or LFA3 immunoglobulin, ibuprofen, indomethacin, ISAtx-247, ketoprofen, ketorolac, leflunomide, meclophenamate, mefenamic acid, mepacrine, 6-mercaptopurine, meloxicam, methotrexate, mizoribine, mycophenolate mofetil, naproxen, oxaprozin, Plaquenil, NOX-100, prednisone, methyprenisone, rapamycin (sirolimus), sulindac, tacrolimus (FK506), thymoglobulin, tolmetin, tresperimus, UO126, and antibodies including but not limited to alpha lymphocyte antibodies, adalimumab, anti-CD3, anti-CD25, anti-CD52 anti-IL2R, and anti-TAC antibodies, basiliximab, daclizumab, etanercept, hu5C8, infliximab, OKT4, and natalizumab.

32. The method of claim 1 wherein status of SLE in a subject or patient comprises response to an immunosuppressant administered to a patient.

33. The method of claim 32 wherein the immunosuppressant is selected from aspirin, azathioprine, chloroquine, corticosteroids, cyclophosphamide, cyclosporin A, dehydroepiandrosterone, deoxyspergualin, dexamethasone, everolimus, fenoprofen, hydralazine, hydroxychloroquine, immunoglobulin, ibuprofen, indomethacin, leflunomide, ketoprofen, meclophenamate, mepacrine, 6-mercaptopurine, methotrexate, mizoribine, mycophenolate mofetil, naproxen, prednisone, methyprenisone, rapamycin (sirolimus), solumedrol, tacrolimus (FK506), thymoglobulin, tolmetin, tresperimus, and triamcinoline.

34. The method of claim 1 wherein diagnosing and monitoring the status of SLE further comprises screening a subject exhibiting symptoms of a rheumatic disease for SLE.

35. The method of claim 34 wherein the rheumatic disease is selected from ankylosing spondylitis, dermatomyositis, autoimmune hepatitis, hepatitis-C (hep-C), polymyalgia

rheumatica, polymyositis, rheumatoid arthritis (RA), scleroderma, systemic sclerosis, Sjogren's disease, systemic vasculitis, and Whipple's disease.

36. A method of producing a probe set for diagnosing or monitoring SLE in a subject or patient comprising:

selecting at least one gene from each of at least two of the gene clusters of Table 1 and at least two genes from Table 2; and

producing a probe set consisting of at least one oligonucleotide that detects the expression of each of the selected genes.

37. The method of claim 36 wherein the probe set is used in a diagnostic kit.

38. A method for predicting flare in a patient diagnosed with SLE comprising:

analyzing expression in a sample from the patient to produce a gene expression profile wherein

a first portion of the analysis comprises using the expression of at least one gene selected from each of at least two of the clusters 1 through 15 of Table 1 and at least one statistical method to produce a patient gene expression profile, and

a second portion of the analysis comprises using expression of at least two genes selected from Table 2 and a linear algorithm to classify the patient as having type 1 SLE or type 2 SLE; and

predicting flare by comparing the patient gene expression profile at least one reference profile.

39. The method of claim 38 wherein reference profile is selected from at least one normal subject, at least one patient classified as having type 1 SLE with quiescent status, at least one patient classified as having type 1 SLE in flare, at least one patient classified as having type 2 SLE with quiescent status, at least one patient classified as having type 2 SLE in flare.

FIGURE 1

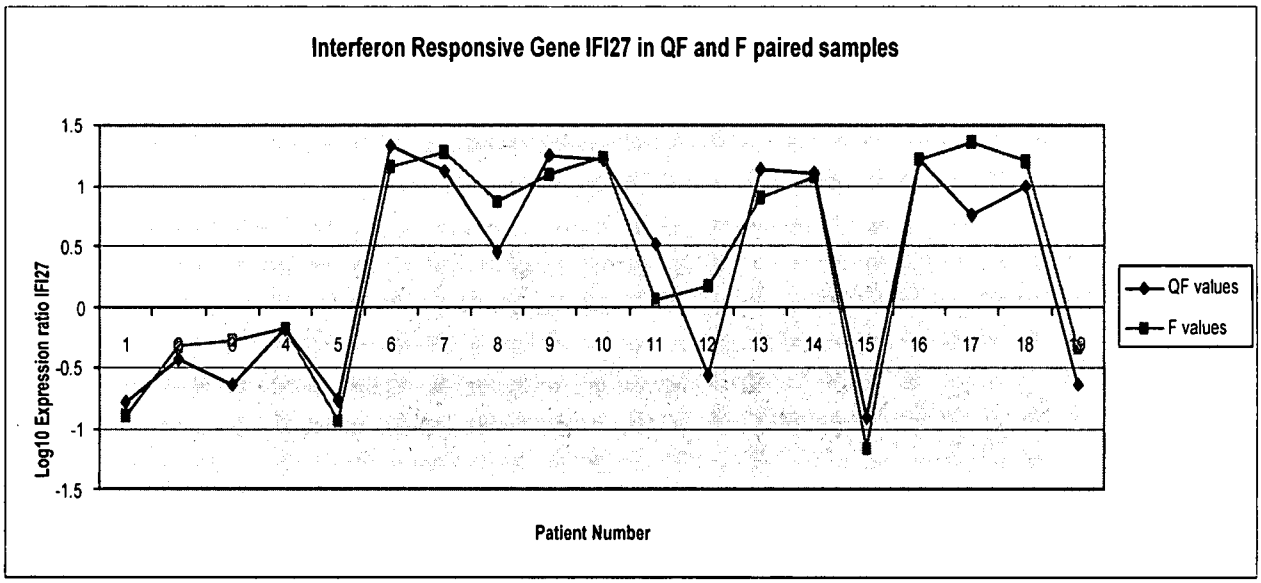

Interferon Responsive Gene IFI27 in QF and F paired samples
Log10 Expression ratio IFI27
1.5
1
0.5
0
-0.5
-1
-1.5
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
Patient Number
QF values
F values

FIGURE 2

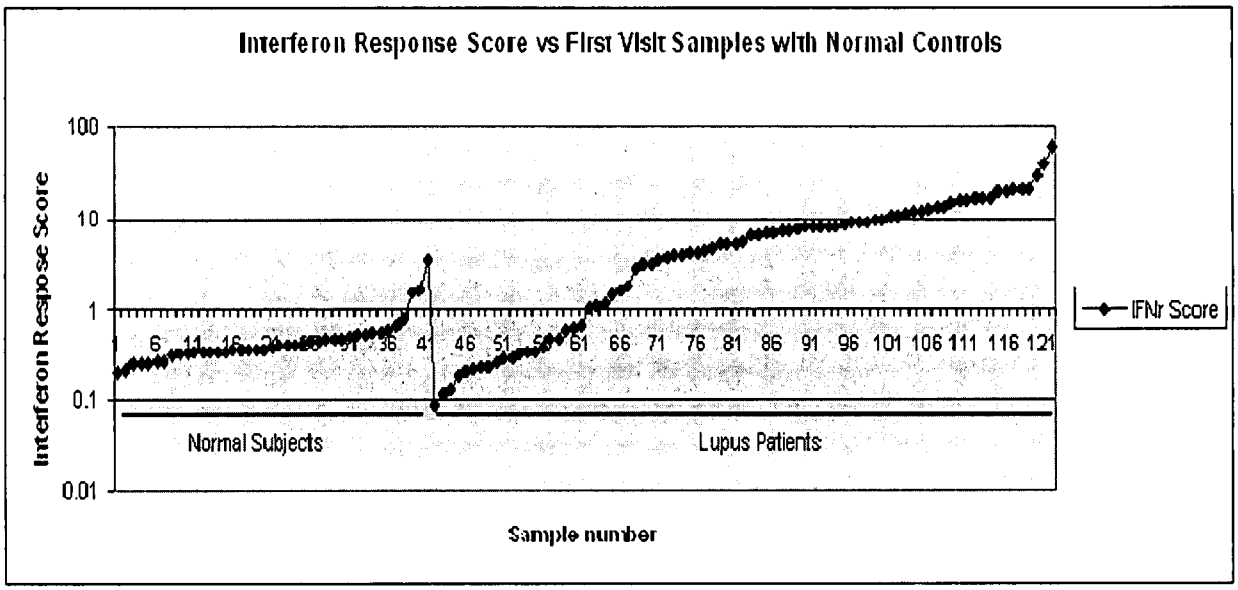
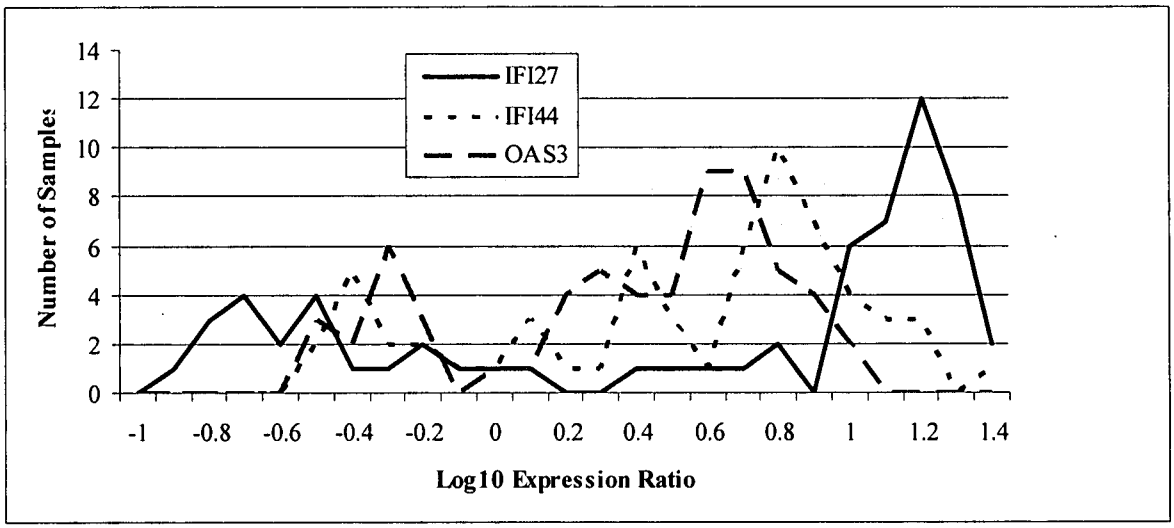

Interferon Response Score vs First Visit Samples with Normal Controls
Interferon Response Score
100
10
1
0.1
0.01
Normal Subjects
Lupus Patients
Sample number
IFNr Score

FIGURE 3


IFI27
IFI44
OAS3
Number of Samples
14
12
10
8
6
4
2
0
-1
-0.8
-0.6
-0.4
-0.2
0
0.2
0.4
0.6
0.8
1
1.2
1.4
Log10 Expression Ratio