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(54) **Title**: GENE EXPRESSION PROFILES ASSOCIATED WITH CHRONIC ALLOGRAFT NEPHROPATHY

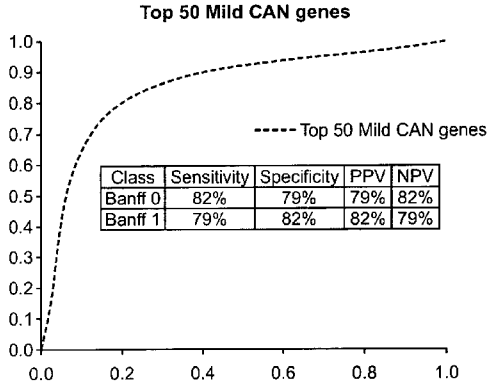


FIG. 1

(57) **Abstract**: By a genome-wide gene analysis of expression profiles of over 50,000 known or putative gene sequences in peripheral blood, the present inventors have identified a consensus set of gene expression-based molecular biomarkers associated with chronic allograft nephropathy and/or interstitial fibrosis and tubular atrophy CAN/IFTA and subtypes thereof. These genes sets are useful for diagnosis, prognosis, monitoring and/or subtyping of CAN/IFTA.

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GENE EXPRESSION PROFILES ASSOCIATED WITH CHRONIC ALLOGRAFT NEPHROPATHY

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a nonprovisional and claims the benefit of USSN 61/224,328 and 61/224,317 each filed July 9, 2009, and incorporated by reference in its entirety for all purposes.

STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[0002] The invention was made in part with funding provided by NIH grant U19A1063603. The US Government has certain rights in the invention.

BACKGROUND OF THE INVENTION

[0003] Kidney transplantation offers a significant improvement in life expectancy and quality of life for patients with end stage renal disease[1]. Unfortunately, a chronic, progressive allograft dysfunction of uncertain etiology continues to be a primary cause of graft loss[2,3]. There has been some evolution of terminology for describing the histological basis of this chronic, progressive nephropathy, which is still commonly referred to as chronic allograft nephropathy (CAN) and more recently as interstitial fibrosis and tubular atrophy (IFTA)[4-6]. In current practice CAN refers to a clinical entity of a chronic progressive loss of kidney transplant function associated with a rising serum creatinine and a falling creatinine clearance. In current practice, IFTA refers to the histological findings based on review of a kidney transplant biopsy. Immunologic factors linked to CAN/IFTA are acute, sub-clinical and CAN/IFTA, HLA mismatching and circulating donor-specific anti-HLA antibodies[7,8]. Non-immunologic factors include hypertension, chronic toxicity of calcineurin inhibitors, hyperfiltration and diabetes mellitus[9-12]. The unifying mechanism is thought to be a progressive cycle of vascular and tissue injury, incomplete repair, compensatory hypertrophy, progressive interstitial fibrosis and nephron loss[13]. Moreover, increasing evidence is suggesting that the primary mechanism of CAN/IFTA is a chronic immunological injury mediated by a combination of T cell and antibody-mediated immunity, in other words, chronic rejection.

[0004] As early as two years post kidney transplant, protocol biopsies have shown that more than 50% of recipients have mild CAN/IFTA[2,15,16] and by 10 years over 50% of kidney transplant recipients have severe CAN/IFTA that is associated with diminishing graft function[2]. Traditional kidney function measurements like serum creatinine and glomerular filtration rates used to predict CAN/IFTA have poor predictive values[17] and a diagnosis requires a transplant biopsy[18,19]. Predicting graft outcomes strictly based on the kidney biopsy is difficult and this invasive procedure has significant costs and risks for patients. Thus, there is a pressing medical need to identify minimally invasive biomarkers that are able to identify early stages of CAN/IFTA at a time that changes in therapy may alter outcomes.

[0005] Rapidly evolving technologies for genomics have created new opportunities to develop minimally invasive biomarkers. Recent studies, including our own, have reported genes that are differentially expressed at the mRNA level in kidney biopsies in the presence of CAN/IFTA[16,20,21]. The limitation of these studies is that they require an invasive transplant biopsy. Others have reported analyzing urine and peripheral blood using RT-qPCR or proteomics to identify small numbers of potential biomarkers for CAN/IFTA, though none is validated for clinical use[22,23].

BRIEF SUMMARY OF THE INVENTION

[0006] The invention provides methods of prognosing, diagnosing or monitoring chronic allograft nephropathy and/or interstitial fibrosis and tubular atrophy (CAN/IFTA). The methods entail (a) determining expression levels in a subject of at least 5 genes selected from the genes in Table A, B, C, D, E, F, G, H, I and/or J ; and (b) prognosing diagnosing or monitoring CAN/IFTA in a subject from the expression levels. Optionally, for each of the at least five genes, step (b) comprises comparing the expression level of the gene in the subject to one or more reference expression levels of the gene associated with CAN/IFTA or lack of CAN/IFTA. Optionally, step (b) further comprises for each of the at least five genes assigning the expression level of the gene in the subject a value or other designation providing an indication whether the subject has or is at risk of CAN/IFTA. Optionally, the expression level of each of the at least five genes is assigned a value on a normalized scale of values associated with a range of expression levels in kidney transplant patients with and without CAN/IFTA. Optionally, the expression level of each of the at least five genes is assigned a value or other designation providing an indication that the subject has is at risk of CAN/IFTA, lacks and is not at risk of CAN/IFTA, or that the expression level is uninformative. Optionally, step (b) further comprises, combining the values or designations for each of the genes to provide a combined value or designation providing an indication

whether the subject has or is at risk of CAN/IFTA. Optionally, the method is repeated at different times on the subject.

[0007] In some methods, the subject is receiving a drug, and a change in the combined value or designation over time provides an indication of the effectiveness of the drug. Optionally, the subject has undergone a kidney transplant within 1-10 years of performing step (a). Optionally, step (a) is performed on a blood sample of the subject. Optionally, the blood sample is a plasma sample. Optionally, step (a) is performed on at least ten, 20, 40 , or 100 genes from Table A, B, C, D, E, F, G, H, I and/or J.

[0008] Some methods further comprise changing the treatment regime of the patient responsive to the prognosing, diagnosing or monitoring step. In some methods, the subject has received a drug before performing the methods, and the change comprises administering an additional drug or administering a higher dose of the same drug. Some methods, further comprise performing an additional procedure, such as a kidney biopsy, to detect CAN/IFTA or risk thereof if the determining step provides an indication the subject has or is at risk of CAN/IFTA.

In some methods, the at least five genes are from Table A, B, C and/or D expression levels are determined at the mRNA level. In some methods, the at least five genes are from Tables E, F, G, H, I, and/or J and expression levels are determined at the protein level. In some methods, step (b) is performed by a computer. In some methods, the at least five genes are selected from Tables C and D. In some methods, the at least five genes are selected from Table C. In some methods, the at least five genes are selected from Table D. In some methods, the at least five genes are selected from Table E and F or H and I and expression levels are determined at the protein level.

[0009] The invention further provides an array, comprising a support or supports bearing a plurality of nucleic acid probes complementary to a plurality of mRNAs fewer than 5000 in number, wherein the plurality of mRNAs includes mRNAs expressed by at least five genes selected from Tables A, B, C, D. Optionally, the plurality of mRNAs are fewer than 1000, or 100 in number. Optionally a plurality of nucleic acid probes are attached to a planar support or to beads. Optionally, the at least five genes are selected from Table C and D. Optionally, the at least five genes are selected from Table C. Optionally, the at least five genes are selected from Table D.

[0010] The invention further provides an array, comprising a support or supports bearing a plurality of ligands that specifically bind to a plurality of proteins fewer than 5000 in number, wherein the plurality of proteins includes at least five proteins selected from Tables E, F, G, H, I and/or J. Optionally, the plurality of proteins are fewer than 1000 or 100 in number.

Optionally, the plurality of ligands are attached to a planar support or to beads. Optionally, the at least five proteins are selected from Tables E and F and/or I and J. Optionally, the ligands are different antibodies, wherein the different antibodies bind to different proteins of the plurality of proteins.

[0011] The invention further provides a method of expression analysis, comprising determining expression levels of up to 5000 genes in a sample from a subject having a kidney transplant, wherein the genes include at least 5 genes selected from Table A, B, C, D, E, F, G, H, I and/or J. Optionally, the expression levels of up to 1000 or 100 genes are determined. The expression levels can be determined at the mRNA or protein level. The levels can be determined by, for example, quantitative PCR or hybridization to an array.

[0012] The invention further provides methods of screening a compound for activity in inhibiting or treating CAN/IFTA. The methods entail (a) administering the compound to a subject having or at risk of CAN/IFTA; (b) determining expression levels of at least five genes in the subject selected from Table A, B, C, D, E, F, G, H, I, and/or J and species variants thereof before and after administering the drug to the subject, and (c) determining whether the compound has activity in inhibiting or treating CAN/IFTA from a change in expression levels of the genes after administering the compound. Optionally, step (c) comprises for each of the at least five changes assigning a value or designation depending on whether the change in the expression level of the gene relative to one or more reference levels indicating presence or absence of CAN/IFTA. Optionally, the method further comprises determining a combined value or designation for the at least five genes from the values or designations determined for each gene. Optionally, the subject is human or a nonhuman animal model of CAN/IFTA.

The invention further provides methods of subtyping CAN/IFTA. The methods entail (a) determining expression levels in a subject of at least 5 genes selected from the genes in Tables A, B, C, D ; E, F, G, H, I and/or J; and (b) determining a subtype of CAN/IFTA from the expression levels. The subtype can be selected from the group consisting of stage 0, 1, 2, or 3 of CAN/IFTA. Optionally, the subtype is stage 0, stage 1 or stage 2 and/or 3. In some methods for each of the at least five genes, step (b) comprises comparing the expression level of the gene in the subject to one or more reference expression levels of the gene associated with the subtype of CAN/IFTA or lack of CAN/IFTA. Some methods further comprise for each of the at least five genes assigning the expression level of the gene in the subject a value or other designation providing an indication whether the subject has or is at risk of the subtype of CAN/IFTA. In some methods, the expression level of each of the at least five genes is assigned a value on a normalized scale of values associated with a range of

expression levels in kidney transplant patients with the subtype and without CAN/IFTA. In some methods, the expression level of each of the at least five genes is assigned a value or other designation providing an indication that the subject has or is at risk of the subtype of CAN/IFTA, lacks and is not at risk of the subtype of CAN/IFTA, or that the expression level is uninformative. In some methods, step (b) further comprises, combining the values or designations for each of the genes to provide a combined value or designation providing an indication whether the subject has or is at risk of the subtype of CAN/IFTA. Some methods are repeated at different times on the subject. In some methods, the subject is receiving a drug, and a change in the combined value or designation over time provides an indication of the effectiveness of the drug. In some methods, the subject has undergone a kidney transplant within 1-10 years of performing step (a). Some methods are performed on a blood sample of the subject, such as a plasma or whole blood sample. Some methods are performed on at least ten, 20, 40 or 100 genes selected from Tables A, B, C, D, E, F, G, H, I and/or J. Some methods further comprise changing the treatment regime of the patient responsive to the whether the subtype is present. In some methods, the subject has received a drug before performing the methods, and the change comprises administering an additional drug or administering a higher dose of the same drug. Some methods further comprise performing an additional procedure, such as a kidney biopsy, to detect CAN/IFTA or risk thereof if the determining step provides an indication the subject has or is at risk of the subtype of CAN/IFTA. Expression levels can be determined at the mRNA or protein level. In some methods, step (b) is performed by a computer. In some methods, the at least five genes are selected from Table C. In some methods, the at least five genes are selected from Table D. In some methods, the at least five genes are selected from Table E and expression levels are determined at the protein level . In some methods, the at least five genes are selected from Table F and the expression levels are determined at the protein level. In some methods, the at least five genes are selected from Table H and the expression levels are determined at the protein level. In some methods, the at least five genes are selected from Table I and the expression levels are determined at the protein level.

BRIEF DESCRIPTION OF THE DRAWINGS

[0013] Figure 1: Class prediction analysis of Banff 0 vs. Banff 1 (mild CAN/IFTA) based on Diagonal Linear Discriminant Analysis for the top 50 Banff 0 vs. Banff 1 consensus genes ranked by p values. A) depicts the Receiver Operating Characteristic (ROC) curves and provides the Sensitivity, Specificity, Positive Predictive Value (PPV) and Negative Predictive Value (NPV);

[0014] **Figure 2:** Class prediction analysis of Banff 0 vs. Banff 2,3 (moderate to severe CAN/IFTA) based on Diagonal Linear Discriminant Analysis for the top 50 Banff 0 vs. Banff 2,3 consensus genes ranked by p values. A) depicts the Receiver Operating Characteristic (ROC) curves and provides the Sensitivity, Specificity, Positive Predictive Value (PPV) and Negative Predictive Value (NPV); B) depicts the heat map classifying Banff 0 vs. Banff 2,3 using the top 50 consensus genes where (red) is up-regulated and (green) is down-regulated.

DEFINITIONS

[0015] The term Chronic Allograft Nephropathy/Interstitial Fibrosis and Tubular Atrophy (CAN/IFTA) refers to a progressive, chronic, kidney tissue injury that eventually causes a progressive, chronic deterioration of kidney transplant function. The histological changes of CAN/IFTA can be found in protocol kidney transplant biopsies as early as 6 months post transplant and frequently the clinical changes of progressive kidney transplant dysfunction evolve subsequently over the next year or several years (e.g., six months to ten years). CAN/IFTA is usually a consequence of combined immunological injury (e.g. chronic rejection) and non-immunological damage (e.g. hypertensive nephrosclerosis, or nephrotoxicity of immunosuppressants like cyclosporine A), taking place months or years after transplantation and ultimately leading to histologically detectable fibrosis and sclerosis of the transplant and progressive loss of kidney function. Chronic rejection of a transplanted kidney is increasingly thought to be the major mechanism of CAN/IFTA mediated through both T cell mediated immunity and antibodies directed at antigens expressed in the kidney transplant. The hybrid term, CAN/IFTA includes histological changes and/or functional deterioration of the kidneys or both. In some patients, the present methods can provide an indication of histological changes before detectable functional deterioration of the kidneys has occurred, thereby allowing early therapeutic intervention.

[0016] Transplantation is the transfer of tissues, cells or an organ from a donor into a recipient. If the donor and recipient as the same person, the graft is referred to as an autograft and as is usually the case between different individuals of the same species an allograft. Transfer of tissue between species is referred to as a xenograft.

[0017] A biopsy is a specimen obtained from a living patient for diagnostic evaluation. Kidney biopsies can be obtained with a needle.

[0018] An average value can refer to any of a mean, median or mode.

[0019] A gene expression level is associated with a particular phenotype e.g., presence of CAN/IFTA or a subtype thereof if the gene is differentially expressed in a patient having the phenotype relative to a patient lacking the phenotype to a statistically significant extent. Unless otherwise apparent from the context a gene expression level can be measured at the mRNA and/or protein level.

[0020] A target nucleic acids is a nucleic acid (often derived from a biological sample), to which a polynucleotide probe is designed to specifically hybridize. The probe can detect presence, absence and/or amount of the target. The term can refer to the specific subsequence of a larger nucleic acid to which the probe is directed or to the overall sequence (*e.g.*, c DNA or mRNA) whose expression level it is desired to detect.

[0021] The term subject or patient can include human or non-human animals. Thus, the methods and described herein are applicable to both human and veterinary disease and animal models. Preferred subjects are "patients," *i.e.*, living humans that are receiving medical care for a disease or condition. This includes persons with no defined illness who are being investigated for signs of pathology.

[0022] Diagnosis refers to methods of estimating or determining whether or not a patient is suffering from a given disease or condition or severity of the condition. Diagnosis does not require ability to determine the presence or absence of a particular disease with 100% accuracy, or even that a given course or outcome is more likely to occur than not. Instead, the "diagnosis" refers to an increased probability that a certain disease or condition is present in the subject compared to the probability before the diagnostic test was performed.

[0023] Similarly, a prognosis signals an increased probability that a given course or outcome will occur in a patient relative to the probability before the prognostic test.

[0024] A probe or polynucleotide probe is an nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation, thus forming a duplex structure. The probe binds or hybridizes to a "probe binding site." A probe can include natural (*i.e.*, A, G, C, or T) or modified bases (e.g., 7-deazaguanosine, inosine.). A probe can be an oligonucleotide which is a single-stranded DNA. Polynucleotide probes can be synthesized or produced from naturally occurring polynucleotides. In addition, the bases in a probe can be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes can include, for example, peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester

linkages (see, *e.g.*, Nielsen *et al.*, *Science* 254, 1497-1500 (1991)). Some probes can have leading and/or trailing sequences of noncomplementarity flanking a region of complementarity.

[0025] A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The probe is typically perfectly complementary to a portion (subsequence) of a target sequence. The term "mismatch probe" refer to probes whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence.

[0026] The term "isolated," "purified" or "substantially pure" means an object species (*e.g.*, a nucleic acid sequence described herein or a polypeptide encoded thereby) has been at least partially separated from the components with which it is naturally associated.

[0027] Differential expression refers to a statistically significant difference in expression levels of a gene between two populations of samples (e.g., samples with and without CAN/IFTA). The expression levels can differ for example by at least a factor of 1.5 or 2 between such populations of samples. Differential expression includes genes that are expressed in one population and are not expressed (at least at detectable levels) in the other populations. Unique expression refers to detectable expression in one population and undetectable expression (i.e., insignificantly different from background) in the other population using the same technique (e.g., as in the present example for detection).

[0028] Control populations for comparison with populations undergoing CAN/IFTA are usually referred to as being without CAN/IFTA. Unless otherwise indicated, such a control population also means subjects without acute kidney rejection.

[0029] Hybridization reactions are preferably performed under stringent conditions in which probes or primers hybridize to their intended target with which they have perfect complementarity and not to or at least to a reduced extent to other targets. An example of stringent hybridization conditions are hybridization in 6×sodium chloride/sodium citrate (SSC) at about 45° C., followed by one or more washes in 0.2×SSC, 0.1% SDS at 50° C, 55° C, 60° C, and even more or 65° C.

[0030] Statistical significance means $p < 0.05$ or < 0.01 or even < 0.001 level.

DETAILED DESCRIPTION OF THE INVENTION

I. General

[0031] By a genome-wide gene analysis of expression profiles of over 50,000 known or putative gene sequences in peripheral blood, the present inventors have identified consensus sets of gene expression-based molecular biomarkers associated with CAN/IFTA. A set of 393 genes has differential expression levels between mild chronic allograft nephropathy (CAN/IFTA) and non-rejected transplants. A set of 63 genes have differential expression between moderate or severe CAN/IFTA and non-rejected transplants. Additional set of protein markers showing differential or unique expression between CAN/IFTA and non rejected transplants are also provided.

II. Genes in profiles

[0032] Table A lists 393 genes whose expression changes significantly between kidney transplant patients undergoing mild CAN/IFTA, Banff stage 1 compared with patients not undergoing such rejection (Banff stage 0) one year post transplant. The columns in the table have the following meanings: column 1 is a number assigned to a gene, column 2 is a measure of the statistical significance of change in gene expression between the above populations, , column 3 is a mean expression level of a gene in kidney transplant patients undergoing chronic rejection (normalized as described below), column 4 is mean expression level of the gene in kidney transplant patients not undergoing CAN/IFTA (similarly normalized), column 5 is a ratio of the expression levels, column 6 is an Affymetrix number indicating a set of probes suitable for measuring expression of the gene, column 7 is a gene name (recognized names of HUGO or similar bodies are used when available), and column 8 is a further description of the gene. Table B provides similar information for 62 genes that show differential expression between kidney transplant patients undergoing moderate or severe CAN/IFTA (Banff stage 2 or 3) with kidney transplant patients not undergoing CAN/IFTA. Tables C and D provide subsets of 50 preferred genes from Tables A and B respectively.

[0033] Table E provides 117 genes and corresponding proteins for which the proteins is uniquely expressed in patients not undergoing CAN/IFTA and not at detectable levels in patients undergoing CAN/IFTA level 1. Column 1 is a sequential number for a gene/protein, column 2 is a protein symbol, column 3 is a gene symbol, and column 4 is a gene name. Table F provides similar information about 143 proteins uniquely expressed in patients undergoing CAN/IFTA and not at detectable levels in kidney transplant patients without

CAN/IFTA. Table G provides similar information regarding 188 proteins that are differentially expressed between CAN/IFTA levels 0 and 1. The right hand column of the table indicates the degree of differential expression with positive numbers being upregulated in Banff stage 1 patients. Table H provides similar information to Table E for 28 genes uniquely expressed in kidney transplant patients not undergoing CAN/ITFA and not at detectable levels in patients undergoing CAN/IFTA level 2 or 3. Table I provides similar information to Table F for 510 proteins uniquely expressed in CAN/IFTA level 2 or 3 and not detectable in kidney transplant patients not undergoing CAN/IFTA. Table J provides similar information to Table G for 284 proteins differentially expressed between kidney transplant patients at CAN/IFTA level 0 versus level 2 or 3. If a gene symbol or gene name is not available, the protein symbol should be understood as referring to both the genes.

[0034] The genes referred to in the above tables are human genes. In some methods, species variants or homologs of these genes are used in a non-human animal model. Species variants are the genes in different species having greatest sequence identity and similarity in functional properties to one another. Many species variants of the above human genes are listed in the Swiss-Prot database.

[0035] Raw gene expression levels are comparable between different genes in the same sample but not necessarily between different samples. As noted above, values given for gene expression levels can be normalized so that values for particular genes are comparable within and between the populations being analyzed. The normalization eliminates or at least reduces to acceptable levels any sample to sample differences arising from factors other than CAN/IFTA (e.g. differences in overall transcription levels of patients due to general state of health and differences in sample preparation or nucleic acid amplification between samples). The normalization effectively applies a correction factor to the measured expression levels from a given array such that a profile of many expression levels in the array are the same between different patient samples. Software for normalizing overall expression patterns between different samples is both commercially and publically available (e.g., XRAY from Biotique Systems or BRB ArrayTools from the National Cancer Institute). After applying appropriate normalizing factors to the measured expression value of a particular gene in different samples, an average value of the expression level is determined for the samples in a population. The average values between different populations are then compared to determine whether expression level has changed significantly between the populations. The changes in expression level indicated for a given gene represent the relative expression level of that gene in samples from a population of individuals with a defined condition (e.g.,

transplant patients with CAN/IFTA of specified Banff stage) relative to samples from a control population (kidney transplant patients not undergoing CAN/IFTA). Similar principles apply in normalizing gene expression levels at the mRNA and protein levels. Comparisons between populations are made at the same level (e.g., mRNA levels in one population are compared with mRNA levels in another population or protein levels in one population with protein levels in another population).

III. Subject population

[0036] The methods are particularly useful on human subjects who have undergone a kidney transplant although can also be used on subjects who have gone other types of transplant (e.g., heart, liver, lungs, stem cell) or on non-humans who have undergone kidney or other transplant. Gene expression levels in such subjects can be measured, for example, within, three months, six months, one year, two years, five years or ten years after a kidney transplant. In some methods, gene expression levels are determined at regular intervals, e.g., every 3 months, 6 months or every year posttransplant, either indefinitely, or until evidence of CAN/IFTA is observed, in which case the frequency of monitoring is sometimes increased. In some methods, baseline values of expression levels are determined in a subject before a kidney transplant in combination with determining expression levels at one or more time points thereafter. In other methods, a measurement is initiated responsive to some other indication of potential kidney impairment, such as a rise in levels of creatinine or BUN or a decrease in glomerular filtration rate. Similar methods can be practiced in non-human species, in which cases, the expression levels measured are the species equivalent of the human genes referenced above.

IV. Chronic allograft nephropathy (CAN/IFTA) and its subtypes

[0037] The methods are particularly useful for detecting CAN/IFTA. CAN/IFTA can be further classified by histological analysis of kidney transplant biopsies based on the Banff 2007 schema and the following four subtypes or stages are recognized indicating severity: 0 (no CAN/IFTA), 1 (mild CAN/IFTA), 2 (moderate CAN/IFTA) and 3 (severe CAN/IFTA) [4]. An alternative and complementary histology grading schema is the Chronic Allograft Damage Index (CADI) score and this score is often provided by pathologists with the Banff classification score as supplemental information (for example, see Yilmaz et al, J Am Soc

Nephrol 2003 14: 773-779). There is also a Banff 2007 classification for acute rejection [4]. Acute rejection is characterized histologically by an active, inflammatory/immune cell infiltration comprised of various numbers of T cells and B cells as well as sometimes plasma cells, eosinophils, neutrophils and macrophages.

V. Methods of measuring profiles

[0038] The preferred sample type for analysis is a blood sample, which refers to whole blood or fractions thereof, such as plasma, or lymphocytes. Other samples that can be analyzed include urine, feces, saliva, and a kidney biopsy. The samples are typically isolated from a subject, particularly as a peripheral blood sample, and not returned to the subject. The analytes of interests in the samples can be analyzed with or without further processing of the sample, such as purification and amplification. Samples not requiring biopsy to obtain, particularly peripheral blood, are preferred.

[0039] Expression profiles are preferably measured at the nucleic acid level, meaning that levels of mRNA or nucleic acid derived therefrom (e.g., cDNA or cRNA). An expression profile refers to the expression levels of a plurality of genes in a sample. A nucleic derived from mRNA means a nucleic acid synthesized using mRNA as a template. Methods of isolation and amplification of mRNA are well known as described for example WO 97/10365, WO 97/27317, Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I. Theory and Nucleic Acid Preparation, (P. Tijssen, ed.) Elsevier, N.Y. (1993). If mRNA or a nucleic acid therefrom is amplified, the amplification is performed under conditions that approximately preserve the relative proportions of mRNA in the original samples, such that the levels of the amplified nucleic acids can be used to establish phenotypic associations representative of the mRNAs.

[0040] A variety of approaches are available for determining mRNA levels including probe arrays and quantitative PCR. A number of distinct array formats are available. Some arrays, such as an Affymetrix GeneChip® array, have different probes occupying discrete known areas of a contiguous support. Other arrays, such as arrays from Illumina, have different probes attached to different particles or beads. In such arrays, the identity of which probe is attached to which particle or beads is usually determinable from an encoding system. The probes can be oligonucleotides. In such case, typically several match probes are included with perfect complementarity to a given target mRNA together, optionally together with mismatch probes differing from the match probes are a known number of oligonucleotides

(Lockhart, et al., Nature Biotechnology 14:1675-1680 (1996); and Lipschutz, et al., Nature Genetics Supplement 21: 20-24, 1999). Other arrays including full length cDNA sequences with perfect or near perfect complementarity to a particular cDNA (Schena et al. (Science 270:467-470 (1995); and DeRisi et al. (Nature Genetics 14:457-460 (1996)). Such arrays can also include various control probes, such as a probe complementarity with a house keeping gene likely to be expressed in most samples. Regardless of the specifics of array design, an array contains one or more probes either perfectly complementary to a particular target mRNA or sufficiently complementarity to the target mRNA to distinguish it from other mRNAs in the sample, and the presence of such a target mRNA can be determined from the hybridization signal of such probes, optionally by comparison with mismatch or other control probes included in the array. Typically, the target bears a fluorescent label, in which case hybridization intensity can be determined by, for example, a scanning confocal microscope in photon counting mode. Appropriate scanning devices are described by e.g., U.S. 5,578,832, and U.S. 5,631,734. The intensity of labeling of probes hybridizing to a particular mRNA or its amplification product provides a raw measure of expression level.

[0041] In other methods, expression levels are determined by so-called "real time amplification" methods also known as quantitative PCR or Taqman (see, e.g., U.S. Pat Nos. 5,210,015 to Gelfand, 5,538,848 to Livak, et al., and 5,863,736 to Haaland, as well as Heid, C.A., et al., Genome Research, 6:986-994 (1996); Gibson, U.E.M, et al., Genome Research 6:995-1001 (1996); Holland, P. M., et al., Proc. Natl. Acad. Sci. USA 88:7276-7280, (1991); and Livak, K.J., et al., PCR Methods and Applications 357-362 (1995)). The basis for this method of monitoring the formation of amplification product is to measure continuously PCR product accumulation using a dual-labeled fluorogenic oligonucleotide probe. The probe used in such assays is typically a short (ca. 20-25 bases) polynucleotide that is labeled with two different fluorescent dyes. The 5' terminus of the probe is typically attached to a reporter dye and the 3' terminus is attached to a quenching dye The probe is designed to have at least substantial sequence complementarity with a site on the target mRNA or nucleic acid derived from. Upstream and downstream PCR primers that bind to flanking regions of the locus are also added to the reaction mixture. When the probe is intact, energy transfer between the two fluorophors occurs and the quencher quenches emission from the reporter. During the extension phase of PCR, the probe is cleaved by the 5' nuclease activity of a nucleic acid polymerase such as Taq polymerase, thereby releasing the reporter from the polynucleotide-quencher and resulting in an increase of reporter emission intensity which can be measured by an appropriate detector. The recorded values can then be used to calculate the increase in

normalized reporter emission intensity on a continuous basis and ultimately quantify the amount of the mRNA being amplified. mRNA levels can also be measured without amplification by hybridization to a probe, for example, using a branched nucleic acid probe, such as a QuantiGene® Reagent System from Panomics.

[0042] Alternatively or additionally, expression levels of genes can be determined at the protein level, meaning that levels of proteins encoded by the genes discussed above are measured. Several methods and devices are well known for determining levels of proteins including immunoassays such as described in e.g., U.S. Patents 6,143,576; 6,113,855; 6,019,944; 5,985,579; 5,947,124; 5,939,272; 5,922,615; 5,885,527; 5,851,776; 5,824,799; 5,679,526; 5,525,524; and 5,480,792. These assays include various sandwich, competitive, or non-competitive assay formats, to generate a signal that is related to the presence or amount of an protein analyte of interest. Any suitable immunoassay may be utilized, for example, lateral flow, enzyme-linked immunoassays (ELISA), radioimmunoassays (RIAs), competitive binding assays, and the like. Numerous formats for antibody arrays have been described proposed employing antibodies. Such arrays typically include different antibodies having specificity for different proteins intended to be detected. For example, usually at least one hundred different antibodies are used to detect one hundred different protein targets, each antibody being specific for one target. Other ligands having specificity for a particular protein target can also be used, such as the synthetic antibodies disclosed in WO/2008/048970. Other compounds with a desired binding specificity can be selected from random libraries of peptides or small molecules. US Patent No. 5,922,615 describes a device that utilizes multiple discrete zones of immobilized antibodies on membranes to detect multiple target antigens in an array. US Patent Nos. 5,458,852, 6,019,944, US 6,143,576. Microtiter plates or automation can be used to facilitate detection of large numbers of different proteins. Protein levels can also be determined by mass spectrometry as described in the examples.

[0043] The selection of genes for determination of expression levels depends on the particular application (e.g., analysis of CAN/IFTA in general or one of the subtypes described above). In general, the genes are selected from one of the tables indicated above as appropriate for the application. In some methods, expression levels of at least 2, 3, 4, 5, 10, 20, 25, 50, 100, 150, 250 (e.g. 100-250) genes shown in any of Table A, B, C or D are determined. In some methods, expression levels of at least 2, 3, 4, 5, 10, 20, 25, 50, 100, 150, 250 or all genes shown in Table A are determined and/or expression levels of 2, 3, 4, 5, 10, 20, 25, 50 or all genes shown in Table B are determined. In some methods, expression

levels of at least 2, 3, 4, 5, 10, 20, 25, or all 50 genes in Table C and at least 2, 3, 4, 5, 10, 20, 25, or all 50 genes in Table D are determined. In some methods, expression levels of 2, 3, 4, 5, 10, 20, 25, 50 or all genes shown in Tables 2, 3, 4, 5 and/or 6 are determined (genes for which both mRNAs and proteins are differentially expressed). In some methods, all genes are from the same table (i.e., all genes with differential expression associated with mild CAN/IFTA). In some methods, genes from different tables (i.e., including genes associated with mild CAN/IFTA and moderate/severe CAN/IFTA) are tested. In some methods, genes are selected such that genes from several different pathways are represented (e.g., at least one gene from at least 2, 3, 5, or 10 pathways, such as those described in the Examples). The genes within a pathway tend to be expressed in a co-ordinated expression whereas genes from different pathways tend to be expressed more independently. Thus, changes in expression based on the aggregate changes of genes from different pathways can have greater statistical significance than aggregate changes of genes within a pathway.

[0044] In some methods, expression levels of at least 2, 3, 4, 5, 10, 20, 25, 50, 100, or150 proteins or corresponding genes shown in any of Tables E, F, G, H, I and/or J are determined. In some methods, expression levels of at least 2, 3, 4, 5, 10, 20, 25, 50, 100, 150 or all proteins or genes shown in Table E, F, and/or G are determined and/or expression levels of 2, 3, 4, 5, 10, 20, 25, 50 or all proteins or genes shown in Tables H, I and/or J are determined. In some methods, proteins or genes are selected from the same table (e.g., proteins uniquely expressed in Banff stage 1, or corresponding genes). In some methods, proteins or genes are selected from two tables (e.g., proteins uniquely expressed in Banff stage 0 (or corresponding genes) and proteins uniquely expressed in Banff stage 1 (or corresponding genes). In some methods, proteins or genes are selected from three tables (e.g., proteins uniquely expressed in Banff stage 0 or corresponding genes, proteins uniquely expressed in Banff stage 1 and corresponding genes, and proteins differentially expressed between Banff stages 1 and 0. Analogous selections of proteins can be made from Tables H-J for purposes of distinguishing Banff stages 0 and 2/3. In some methods, proteins or corresponding genes are selected such that proteins from several different pathways are represented (e.g., at least one gene from at least 2, 3, 5, or 10 pathways, such as those described in the Examples).

[0045] Expression levels of the present genes and/or proteins can be combined with or without determination of expression levels of any other genes or proteins of interest (e.g., genes or proteins associated with rejection of kidneys or other organs in WO 2007/104537, WO 2009/060035), Anglicheau et al., PNAS 106, 5330-5335 (2009)) and references, 16, 20,

21, 22, 23, 25, 26, 37 and 39. In some methods, the gene is not DPYD or IRS2 or the method includes determining the expression level of at least 5, 10, 25 or 50 genes other than DPYD and IRS2.

[0046] Regardless of the format adopted, the present methods can (but need not) be practiced by detection expression levels of a relatively small number of genes or proteins compared with the whole genome level expression analysis described in the Examples. In some methods, the total number of genes whose expression levels are determined is less than 5000, 1000, 500, 200, 100, 50, 25, 10, 5 or 3. In some methods, the total number of genes whose expression level is determined is 100-1500, 100-250, 500-1500 or 750-1250. In some methods, the total number of proteins whose expression levels are determined is less than 5000, 1000, 500, 200, 100, 50, 25, 10, 5 or 3. In some methods, the total number of proteins whose expression level is determined is 100-1500, 100-250, 500-1500 or 750-1250. Correspondingly, when an array form is used for detection of expression levels, the array includes probes or probes sets for less than 5000, 1000, 500, 200, 100, 50, 25, 10, 5 or 3 genes. Thus, for example, an Affymetrix GeneChip® expression monitoring array contains a set if about 20-50 oligonucleotide probes (half match and half-mismatch) for monitoring each gene of interest. Such an array design would include less than 5000, 1000, 500, 200, 100, 50, 25, 10, 5 or 3 such probes sets for detecting less than 5000, 1000, 500, 200, 100, 50, 25, 10, 5 or 3 genes. By further example, an alternative array including one cDNA for each gene whose expression level is to be detected would contain less than 5000, 1000, 500, 200, 100, 50, 25, 10, 5 or 3 such cDNAs for analyzing less than 5000, 1000, 500, 200, 100, 50, 25, 10, 5 or 3 genes. By further example, an array containing a different antibody for each protein to be detected would containing less than 5000, 1000, 500, 200, 100, 50, 25, 10, 5 or 3 different antibodies for analyzing less than 5000, 1000, 500, 200, 100, 50, 25, 10, 5 or 3 gene products.

VI. Analysis of Expression Levels

[0047] Analysis of expression levels initially provides a measurement of the expression level of each of several individual genes. The expression level can be absolute in terms of a concentration of an expression product, or relative in terms of a relative concentration of an expression product of interest to another expression product in the sample. For example, relative expression levels of genes can be expressed with respect to the expression level of a house-keeping gene in the sample. Relative expression levels can also be determined by simultaneously analyzing differentially labeled samples hybridized to the same array.

Expression levels can also be expressed in arbitrary units, for example, related to signal intensity.

[0048] The individual expression levels, whether absolute or relative, can be converted into values or other designations providing an indication of presence or risk of CAN/IFTA by comparison with one or more reference points. The principles are first discussed with respect to CAN/IFTA without regarding to subtype. However, the same principles apply for analysis of subtypes except that the gene sets used may be different. For example, mild CAN/IFTA can be determined using genes or proteins from Tables A, C, E, F and/or G. Mid to severe CAN/IFTA can be determine using genes or proteins from Tables B, D, H, I and/or J. Genes or proteins from any of the tables can be used in analyzing CAN/IFTA without regard to subtype. Preferably, genes in both Tables A/C and B/D or proteins occurring in at least one of Tables E-G and at least one of Tables H-J are used for such analysis. Genes or proteins are found in both Banff 1 and Banff 2,3 CAN/IFTA but not found in Banff 0 are also useful in distinguishing the presence of CAN/IFTA in a patient. A combination of genes and/or proteins associated with mild CAN/IFTA and genes and/or proteins associated with mid to severe CAN/IFTA can be used.

[0049] The reference points can include a measure of an average expression level of a gene in subjects having had a kidney transplant without CAN/IFTA, and/or an average value of expression levels in subjects having had a kidney transplant with CAN/IFTA. The reference points can also include a scale of values found in kidney transplant patients including patients having and not having CAN/IFTA. The reference points can also or alternatively include a reference value in the subject before kidney transplant, or a reference value in a population of a patients who have not undergone kidney transplant. Such reference points can be expressed in terms of absolute or relative concentrations of gene products as for measured values in a sample.

[0050] For comparison between a measured expression level and reference level(s), the measured level sometimes needs to be normalized for comparison with the reference level(s) or vice versa. The normalization serves to eliminate or at least minimize changes in expression level unrelated to CAN/IFTA (e.g., from differences in overall health of the patient or sample preparation). Normalization can be performed by determining what factor is needed to equalize a profile of expression levels measured from different genes in a sample with expression levels of these genes in a set of reference samples from which the reference levels were determined. Commercial software is available for performing such normalizations between different sets of expression levels.

[0051] Comparison of the measured expression level of a gene with one or more of the above reference points provides a value (i.e., numerical) or other designation (e.g., symbol or word(s)) of presence or susceptibility to CAN/IFTA. In some methods, a binary system is used; that is a measured expression level of a gene is assigned a value or other designation indicating presence or susceptibility to CAN/IFTA or lack thereof without regard to degree. For example, the expression level can be assigned a value of 1 to indicate presence or susceptibility to CAN/IFTA and -1 to indicate absence or lack of susceptibility to CAN/IFTA. Such assignment can be based on whether the measured expression level is closer to an average level in kidney transplant patients having or not having CAN/IFTA. In other methods, a ternary system is used in which an expression level is assigned a value or other designation indicating presence or susceptibility to CAN/IFTA or lack thereof or that the expression level is uninformative. Such assignment can be based on whether the expression level is closer to the average level in kidney transplant patient undergoing CAN/IFTA, closer to an average level in kidney transplant patients lacking CAN/IFTA or intermediate between such levels. For example, the expression level can be assigned a value of +1, -1 or 0 depending on whether it is closer to the average level in patients undergoing CAN/IFTA, is closer to the average level in patients not undergoing CAN/IFTA or is intermediate. In other methods, a particular expression level is assigned a value on a scale, where the upper level is a measure of the highest expression level found in kidney transplant patients and the lowest level of the scale is a measure of the lowest expression level found in kidney transplant patients at a defined time point at which patients may be susceptible to CAN/IFTA (e.g., one year post transplant). Preferably, such a scale is normalized scale (e.g., from 0-1) such that the same scale can be used for different genes. Optionally, the value of a measured expression level on such a scale is indicated as being positive or negative depending on whether the upper level of the scale associates with presence or susceptibility to CAN/IFTA or lack thereof. It does not matter whether a positive or negative sign is used for chronic ejection or lack thereof as long as the usage is consistent for different genes.

[0052] Values or other designation can also be assigned based on a change in expression level of a gene relative to a previous measurement of the expression level of gene in the same patient. Here as elsewhere expression level of a gene can be measured at the protein or nucleic acid level. Such a change can be characterized as being toward, away from or neutral with respect to average expression levels of the gene in kidney transplant patients undergoing or not undergoing CAN/IFTA. For example, a gene whose expression level changes toward an average expression level in kidney transplant patients undergoing CAN/IFTA can be

assigned a value of 1 and a gene whose express level changes way from an average expression level in kidney transplant patients undergoing CAN/IFTA and toward an average expression level in kidney transplant patients not undergoing CAN/IFTA can be assigned a value -1. Of course, more sophisticated systems of assigning values are possible based on the magnitude of changes in expression of a gene in a patient.

[0053] Having determined values or other designations of expression levels of individual genes providing an indication of presence or susceptibility to chronic ejection or lack thereof, the values or designations are combined to provide an aggregate value for all of the genes being analyzed. If each gene is assigned a score of +1 if its expression level indicates presence or susceptibility to CAN/IFTA and -1 if its expression level indicates absence or lack of susceptibility to CAN/IFTA and optionally zero if uninformative, the different values can be combined by addition. The same approach can be used if each gene is assigned a value on the same normalized scale and assigned as being positive or negative depending whether the upper point of the scale is associate with presence or susceptibility to CAN/IFTA or lack thereof. Other methods of combining values for individual markers of disease into a composite value that can be used as a single marker are described in US20040126767 and WO/2004/059293.

VII. Subtyping

[0054] CAN/IFTA can be classified into three subtypes, mild, mid and severe by the Banff scheme. These subtypes differ by histology and severity. The subtypes can be distinguished by the same principles and strategy as just discussed for presence or absence of CAN/IFTA, except that the set of genes whose expression levels is determined may be different for presence and absence of CAN/IFTA overall and each of the subtypes as indicated above. In some methods, one first analyzes CAN/IFTA independent of subtype and then looks at profiles of one or more sets of genes characteristic of one of the above subtypes. In some methods, detection of CAN/IFTA and subtypes are performed simultaneously, for example, by including probes for the sets of genes required for each analysis on the same array. In other methods, analysis of multiple subtypes is performed sequentially or simultaneously and analysis of overall CAN/IFTA is performed by aggregating the results from the different subtypes.

[0055] The principles for subtyping are closely analogous to those for analyzing CAN/IFTA independent of subtype. For example, to analyze whether mild CAN/IFTA is present, one determines expression levels of a set of genes whose expression levels are

characterized of this subtype (Tables A, C, E, F and/or G). The measured expression levels are then compared with one or more reference levels of the genes. The reference levels can, for example, represent an average expression level of a gene in kidney transplant patients undergoing mild CAN/IFTA with borderline phenotype and an average expression level of the gene in kidney transplant patients not undergoing any kidney rejection, an average expression level of the gene in kidney transplant patients undergoing CAN/IFTA of a different subtype, or an earlier measurement of expression level of the gene in the same patient. The same principles are used for analyzing combined moderate/severe CAN/IFTA except that the set of genes is selected from Tables B, D, H, I and/or J and the reference levels represent an average expression level of a gene in transplant patients undergoing CAN/IFTA with Banff subtype 2 or 3 , an average expression level of the gene in kidney transplant patients not undergoing kidney rejection of any kind, an average expression level of the gene in kidney transplant patients undergoing CAN/IFTA of a different subtype, or an earlier measurement of expression level of the gene in the same patient.

[0056] If subtyping is performed for both mild CAN/IFTA and moderate/severe CAN/IFTA, the aggregate of the results also indicates overall CAN/IFTA. For example, if the patient is assigned a value or other designation indicating absence or relatively low risk of developing mild CAN/IFTA and a value or other designation indicating absence or relatively low risk of developing moderate/severe CAN/IFTA, then the patient is also indicated as having absence of overall CAN/IFTA and/or a relatively low risk of developing the same. Conversely, if the patient is assigned a value or other designation indicating presence or enhanced risk to either mild CAN/IFTA or mid/severe CAN/IFTA, or both, the patients is also indicated as having presence or enhanced risk of overall CAN/IFTA.

VIII. Diagnosis, Prognosis and Monitoring

[0057] The above described methods can provide a value or other designation for a patient which indicates whether the aggregate measured expression levels in a patient is more like kidney transplant patients with or without CAN/IFTA or a subtype thereof. Such a value provides an indication that the patient either has or is at enhanced risk of CAN/IFTA or a subtype thereof, or conversely does not have or is at reduced risk of CAN/IFTA or a subtype thereof. Risk is a relative term in which risk of one patient is compared with risk of other patients either qualitatively or quantitatively. For example, the a value of one patient can be compared with a scale of values for a population of patients having undergone kidney transplant to determine whether the patient's risk relative to that of other patients. In general, diagnosis is the determination of the present condition of a patient (e.g., presence or absence

of CAN/IFTA) and prognosis is developing future course of the patient (e.g., risk of developing CAN/IFTA in the future or likelihood of improvement in response to treatment); however, the analyses contemplated by these terms may overlap or even be the same. For example, the present methods alone do not necessarily distinguish between presence and enhanced risk of CAN/IFTA or a subtype thereof. However, these possibilities can be distinguished by additional testing.

[0058] If a patient is indicated as having or being at enhanced risk of CAN/IFTA or a subtype thereof, the physician can subject the patient to additional testing including performing a kidney biopsy or performing other analyses such as creatinine, BUN or glomerular filtration rate at increased frequency. Additionally or alternatively, the physician can change the treatment regime being administered to the patient. A change in treatment regime can include administering an additional or different drug, or administering a higher dosage or frequency of a drug already being administered to the patient. Many different drugs are available for treating rejection, such as immunosuppressive drugs used to treat transplant rejection calcineurin inhibitors (e.g., cyclosporine, tacrolimus), mTOR inhibitors (e.g., sirolimus and everolimus), anti-proliferatives (e.g., azathioprine, mycophenolic acid), corticosteroids (e.g., prednisolone and hydrocortisone) and antibodies (e.g., basiliximab, daclizumab, Orthoclone, anti-thymocyte globulin and anti-lymphocyte globulin). Conversely, if the value or other designation of aggregate expression levels of a patient indicates the patient does not have or is at reduced risk of CAN/IFTA, the physician need not order further diagnostic procedures, particularly not invasive ones such as biopsy. Further, the physician can continue an existing treatment regime, or even decrease the dose or frequency of an administered drug.

[0059] In some methods, expression levels are determined at intervals in a particular patient (i.e., monitoring). Such methods can provide a series of values changing over time indicating whether the aggregate expression levels in a particular patient are more like the expression levels in patients undergoing CAN/IFTA or not undergoing CAN/IFTA. Movement in value toward or away from CAN/IFTA or a subtype can provide an indication whether an existing immunosuppressive regime is working, whether the immunosuppressive regime should be changed or whether a biopsy or increased monitoring by markers such as creatinine or glomerular filtration rate should be performed.

[0060] Information from subtyping analysis can provide further guidance in whether to perform additional diagnostic measures and/or change the immunosuppressive regime administered to a subject. For example, presence or risk of subtype 2 or 3 is more suggestive

of performing an additional diagnostic procedure (e.g., biopsy) and/or increasing the rigor of an immunosuppressive regime that is the presence or risk of subtype 1.

IX. Drug Screening

[0061] The expression profiles associated with CAN/IFTA (including subtypes) or lack thereof provided by the invention are useful in screening drugs, either in clinical trials or in animal models of CAN/IFTA. A clinical trial can be performed on a drug in similar fashion to the monitoring of a individual patient described above, except that drug is administered in parallel to a population of kidney transplant patients, usually in comparison with a control population administered a placebo.

[0062] The changes in expression levels of genes can be analyzed in individual patients and across a treated or control population. Analysis at the level of an individual patient provides an indication of the overall status of the patient at the end of the trial (i.e., whether gene expression profile indicates presence or enhanced susceptibility to CAN/IFTA) and/or an indication whether that profile has changed toward or away from such indication in the course of the trial. Results for individual patients can be aggregated for a population allowing comparison between treated and control population.

[0063] Similar trials can be performed in non-human animal models of chronic kidney disease, e.g., the mouse model of Mannon et al., Kidney International (1999) 55, 1935–1944 In this case, the expression levels of genes detected are the species variants or homologs of the human genes referenced above in whatever species of non-human animal on which tests are being conducted. Although the average expression levels of human genes determined in human kidney transplant patients undergoing or not undergoing CAN/IFTA are not necessarily directly comparable to those of homolog genes in an animal model, the human values can nevertheless be used to provide an indication whether a change in expression level of a non-human homolog is in a direction toward or away from CAN/IFTA or susceptibility thereto. The expression profile of individual animals in a trial can provide an indication of the status of the animal at the end of the trial with respect to presence or susceptibility to CAN/IFTA and/or change in such status during the trial. Results from individual animals can be aggregated across a population and treated and control populations compared. Average changes in the expression levels of genes can then be compared between the two populations.

X. Computer implemented methods

[0064] Expression levels can be analyzed and associated with status of a subject (e.g., presence or susceptibility to chronic kidney infection) in a digital computer. Optionally, such a computer is directly linked to a scanner or the like receiving experimentally determined signals related to expression levels. Alternatively, expression levels can be input by other means. The computer can be programmed to convert raw signals into expression levels (absolute or relative), compare measured expression levels with one or more reference expression levels, or a scale of such values, as described above. The computer can also be programmed to assign values or other designations to expression levels based on the comparison with one or more reference expression levels, and to aggregate such values or designations for multiple genes in an expression profile. The computer can also be programmed to output a value or other designation providing an indication of presence or susceptibility to CAN/IFTA as well as any of the raw or intermediate data used in determining such a value or designation.

[0065] A typically computer (see US 6,785,613 Figs. 4 and 5) includes a bus which interconnects major subsystems such as a central processor, a system memory, an input/output controller, an external device such as a printer via a parallel port, a display screen via a display adapter, a serial port, a keyboard, a fixed disk drive and a floppy disk drive operative to receive a floppy disk. Many other devices can be connected such as a scanner via I/O controller, a mouse connected to serial port or a network interface. The computer contains computer readable media holding codes to allow the computer to perform a variety of functions. These functions include controlling automated apparatus, receiving input and delivering output as described above. The automated apparatus can include a robotic arm for delivering reagents for determining expression levels, as well as small vessels, e.g., microtiter wells for performing the expression analysis.

EXAMPLES

Materials and Methods:

[0066] **Patient Populations:** Test Set 1 comprised 42 kidney transplant patients randomized to either cyclosporine or de novo rapamycin at the Cleveland Clinic, whose clinical courses have been previously, described [15,16,24]. Density gradient-purified peripheral blood lymphocytes (PBL) were collected at the time of protocol two-year biopsies.

Test Set 2 comprised 35 patients from 3 clinical centers (St. Vincent's Medical Center, Scripps Clinic, and Cleveland Clinic). All patients were on FK506. Whole blood was collected directly into PaxGene Tubes (PreAnalytix) at the time of biopsies for suspected CAN/IFTA or protocol one-year biopsies. All the studies in this manuscript were covered by Human Subjects Research Protocols approved by each Center's Institutional Review Board and by the IRB of The Scripps Research Institute as the parent institution. Informed consent was obtained from all study subjects in the study.

[0067] Pathology: Banff IF/TA grades based on tubulointerstitial features were determined for all patients by kidney biopsies: grade 0 (no evidence CAN/IFTA), 1 (mild CAN/IFTA), and 2 (moderate CAN/IFTA) and 3 (severe CAN/IFTA). We merged patients with Banff 2 and Banff 3 IF/TA to increase numbers. Diagnosis was done first by local pathologists and reviewed in a blinded fashion. C4d staining was only available in the more recently acquired Test Set 2.

[0068] Gene expression profiling and analysis: RNA was extracted from Test Set 1 using Trizol (Invitrogen) and in Test Set 2 using Paxgene Blood RNA system (PreAnalytix) and globin transcripts were reduced using GlobinClear (Ambion). Biotinylated cRNA was prepared using Ambion MessageAmp Biotin II (Ambion) and hybridized to Affymetrix Human Genome U133 Plus 2.0 GeneChips. Normalized signals that were generated using a quantile normalization strategy (RMAExpress[25]) were used for class comparisons (ANOVA) and class predictions (BRB Array Tools; linus.nci.nih.gov/BRB-ArrayTools.html). We chose the Diagonal Linear Discriminant Analysis (DLDA) method for class predictions, which is based on maximum likelihood discriminant rules that give consistently good results with our data set and others[26]. Receiver Operating Characteristics (ROC) analysis was done using JROCFIT (rad.jhmi.edu/jeng/javarad/roc/JROCFITi.html). Heatmaps were generated using Cluster and Treeview[27] and functional analysis was performed using Gene Ontology (GO) (geneontology.org/) and Ingenuity Pathway Analysis (IPA). Consensus analysis was designed to identify true classifiers in the two independently collected data sets. Variability between the two test sets within each class (i.e. Banff 1/Test Set 1 vs. Banff 1/Test Set 2) was eliminated by removing all genes with a Student's t-test p-value of <0.05 after which the remaining genes were used to identify consensus candidates by class comparisons. All the microarray data for this study is available for review at the private GEO accession site ncbi.nlm.nih.gov/geo/query/acc.cgi?token=vbgvzkwuggqiqpy&acc=GSE12187.

[0069] **Shotgun LC/MS/MS proteomics:** All protein samples were prepared from density gradient-purified PBL. Individual patient samples were pooled within each Test Set (3 samples/pool) based on Banff classifications and pools were run in triplicates. Total protein was proteolytically digested with trypsin and samples run using Multidimensional Protein Identification Tool (MudPIT) protocol as previously described[28] using an LTQ XL mass spectrometer (ThermoFisher). Raw data were searched against the EBI-IPI_human_12_01_2006 database supplemented with a decoy database where each entry of the original protein contains its reversed sequence. Database searching used SEQUEST (v27)[29] and outcomes were filtered using DTASelect[30]. Relative quantifications were done using spectral counts normalized to the median of the total spectral counts[31]. Pair-wise comparisons between CAN/IFTA biopsy classes were done by differentially expressed proteins (Student's t-test, $p \leq 0.05$) and as all-or-none/unique events.

Results:

Study Population

[0070] Recipients in both Test Sets were sex and age matched (Table 1). The only significant differences in Test Set 1 were Donor age between Banff 0 and Banff 1 groups. In Test Set 2 there were significant differences in induction therapy between Banff 0 and Banff 1 and between Banff 0 and the Banff 2,3; time to biopsy between Banff 0 and Banff 1 and between Banff 0 and the Banff 2,3; and steroid use between Banff 0 and Banff 1 and between Banff 0 and Banff 2,3. Only the Banff 2,3 group in Test Set 2 had a significantly higher serum creatinine compared to the Banff 0, thus, renal function levels per se were not a major determinant of the gene profiles. The higher creatinine levels in the Banff 2,3 group of Test Set 2 most likely reflect the fact that this group was "biopsy for cause," whereas Test Set 1 were all protocol biopsies done regardless of any renal function change. However, by design, the two Test Sets differed significantly in recipient age, HLA mismatch, induction therapy, clinical center, immunosuppression, serum creatinines, and time to biopsy.

Gene expression profiling of mild CAN/IFTA

[0071] We performed ANOVA-based class comparisons between Banff 0 (no histological evidence of CAN/IFTA) and Banff 1 (mild CAN/IFTA). At p-values <0.005, 1066 genes (1307 probe sets) were differentially expressed. Annotation of function by Gene Ontology (GO) shows 8 categories comprised of >25 genes each including 58 genes linked to immunity and inflammation. The percentage of genes in each category was immune/inflammatory 5%, apoptosis, 4%, cell adhesion 3%, signal transduction 5%, regulation of transcription 6%,

protein phosphorylation 3%, cell cycle 3%, metabolism 11%, other functions 40%, unknown functions 20%. IPA shows that these 1066 genes fall into 27 networks with >15 genes per network. The top network was immune response and two additional networks in the top 10 were also immune response with 27 and 22 focus genes, respectively. The top canonical pathway was Toll-like Receptor Signaling followed by SAPK/JNK, Apoptosis, Notch and Death Receptor and Interferon Signaling. Finding 1066 significantly differentially expressed genes is a first indication that PBL transcript profiling is capable of classifying subjects defined by CAN/IFTA biopsy histology. Class prediction using DLDA demonstrates 90% mean correct classification[32,33]. Supervised hierarchical clustering shows misclassification of only 2 samples.

[0072] Based on gene expression profiles of the whole blood samples in Test Set 2, there were 1429 genes (1591 probe sets) differentially expressed at p-values <0.005. GO annotation of gene functions revealed the same groups as PBL including 50 immune response genes. The percentage of genes in each category was immune/inflammatory 4%, apoptosis, 2%, cell adhesion 2%, signal transduction 8%, regulation of transcription 6%, protein phosphorylation 1%, cell cycle 1%, metabolism 4%, other functions 35%, unknown functions 37%. IPA reveals 30 networks with ≥15 genes per network. The top canonical pathways were: B Cell Receptor, Toll-like Receptor, Death Receptor, Chemokine, Glucocorticoid Receptor, and IL-4 Signaling. DLDA demonstrates 88% mean correct classification. Supervised hierarchical clustering shows misclassification of only 1 sample.

[0073] A consensus analysis for Banff 0 vs. Banff 1 was performed with these two independently collected data sets by a class comparison at p-values <0.005 and identified 393 genes (424 probe sets) significantly differentially expressed in both data sets. This "consensus" gene list represents the intersection of these two significantly different test sets classifying mild CAN/IFTA by blood transcription profiling. We then combined all the samples of both Test Sets (n=55) and performed class predictions using the top 50 differentially expressed, consensus genes ranked by p values to obtain a class prediction accuracy of 80% depicted as a ROC curve (Figure 1). A heat map classifying Banff 0 vs. Banff 1 using the 50 genes shows there are large "blocks" of up- or down-regulated genes that classify the Banff 0 vs. Banff 1 (mild CAN/IFTA). However, signatures of multiple genes are advantageous to achieve high class predictive accuracies in heterogeneous clinical populations that are the reality of transplantation medicine. We took the top 10 and top 3 genes from our consensus set for mild CAN/IFTA and performed class prediction using the DLDA method. The top 10 had a predictive accuracy of 80%, sensitivity of 85% and

specificity of 77%, whereas the top 3 genes had a predictive accuracy of 80%, sensitivity of 74% and specificity of 86%.

Gene expression profiling of moderate/severe CAN/IFTA

[0074] Class comparisons between Banff 0 and Banff 2,3 identified genes differentially expressed between patients without CAN/IFTA and those with moderate to severe CAN/IFTA. In Test Set 1, 172 genes were differentially expressed ($p<0.005$) and classified the samples by DLDA with 78% accuracy. In Test Set 2 there were 545 differentially expressed genes. DLDA classified 95% of the samples accurately. The percentage of genes in each category for sets 1 and 2 was immune/inflammatory 4%, 3%, apoptosis, 2%, 3%, cell adhesion 2%, 3%, signal transduction 8%, 7%, regulation of transcription 6%, 8%, protein phosphorylation 1%, 3%, cell cycle 1%, 1%, metabolism 4%, 6% other functions 33%, 30%, unknown functions 37%, 36%. A consensus analysis was done as already described to yield 62 differentially expressed genes ($p<0.005$) shared for both Test Sets of moderate/severe CAN/IFTA ($n=49$). The ROC curve for the top 50 genes from this consensus gene set shows a class prediction accuracy of 92% (Figure 2).

Proteomic expression of mild and moderate/severe CAN/IFTA

[0075] To investigate using proteomics to define blood cell biomarkers for CAN/IFTA, we performed shotgun tandem mass spectrometry. All samples represented purified PBL obtained at the same time as biopsies. We did not use the whole blood samples from Test Set 2 because high quality protein preparations cannot be obtained from PaxGene tubes. Differential protein expression was performed using a relative quantification strategy based on normalized spectral counts [31]. We identified 206 differentially expressed proteins ($p<0.05$) for Banff 0 vs. Banff 1 (mild CAN/IFTA). In addition, we identified 135 proteins unique to Banff 0 and 167 proteins unique to Banff 1. Class comparisons for Banff 0 vs. Banff 2,3 (moderate/severe CAN/IFTA) yielded 282 differentially expressed proteins ($p<0.05$) and 509 proteins unique to Banff 2,3. We found 95 proteins differentially expressed in mild and moderate/severe CAN/IFTA as compared to Banff 0, representing candidate protein markers for any stage of CAN/IFTA. In parallel, 94 proteins were differentially expressed only in mild CAN/IFTA and these were linked to cell death, cell signaling, and post-translational protein modifications. The 168 proteins differentially expressed only in moderate/severe CAN/IFTA were linked to cellular morphology, growth and proliferation and signaling via ERK/MAPK, acute phase responses, IGF1 and PPARa/RXRa.

[0076] There were 135 proteins unique to mild CAN/IFTA and 322 proteins unique to moderate/severe CAN/IFTA. Both mild and moderate/severe CAN/IFTA had immune and inflammation related proteins (20 and 37, respectively) but many of these proteins are not mapped to the same functional pathways (e.g. calcium signaling in mild CAN/IFTA and apoptosis, NK cell and PTEN signaling for moderate/severe CAN/IFTA). In other cases, such as signaling via T and B cell receptors, IL4 and JAK/STAT, the same canonical pathways were found but different unique proteins were identified.

[0077] Using only the differentially expressed proteins, DLDA obtained a 64% mean correct classification of mild CAN/IFTA and an 83% correct classification for moderate/severe CAN/IFTA. In contrast, the unique proteins identified only in the blood of patients with biopsy-documented mild (n=135) or moderate/severe CAN/IFTA (n=322), represent candidate biomarkers with a 100% class prediction value in this data set.

[0078] We compiled the matches between proteins identified by mass spectrometry and mRNA transcripts identified using microarrays. The premise is that protein/transcript matches are a form of candidate biomarker validation based on two independent technologies. There were 11 matches for the 393 consensus genes for mild CAN/IFTA, 32 matches for the 1066 genes for mild CAN/IFTA in Test Set 1 and 40 matches for the 1429 genes for mild CAN/IFTA in Test Set 2. There were no matches for the 62 consensus genes for moderate/severe CAN/IFTA but 9 matches in the 172 genes for moderate/severe CAN/IFTA in Test Set 1 and 9 matches in the 545 genes for moderate/severe CAN/IFTA in Test Set 2. All protein/transcript matches are listed in Tables 2-6.

Discussion

[0079] The primary objective of this study (also reported as [40]) was the discovery of biomarkers in the peripheral blood of kidney transplant patients with biopsy-documented interstitial fibrosis and tubular atrophy (IF/TA) and no known cause, which we refer to here as Chronic Allograft Nephropathy (CAN/IFTA)[14]. To this end, we integrated the results of two, independently collected sets of patient samples that were significantly different in multiple clinical elements. Thus, the selection of biomarker candidates was not significantly influenced by the time of biopsy (ranging from 1 to 6 years post-transplant), the specific immunosuppressive protocols (use of different calcineurin inhibitors vs. sirolimus) or the technology used to purify the mRNA transcripts (density gradient-separated cells vs. whole blood). This experimental design was chosen for its advantages in defining a consensus set of robust candidate biomarkers for CAN/IFTA suitable for clinical use.

[0080] Using more closely matched sets of patient samples, for example, patients only 2 years post-transplant or only one source of blood cell RNA such as the PaxGene tubes might have resulted in higher total numbers of differentially expressed candidate mRNA transcripts and proteins. However, classifications for CAN/IFTA based on the consensus mRNA candidates described here for these otherwise very heterogeneous clinical data sets are 80% for mild CAN/IFTA and 92% for moderate/severe CAN/IFTA. By contrast, the widely used prostate specific antigen (PSA) biomarker, tested in an equally heterogenous human population, was originally introduced with a predictive value of 28-35%[34] because there was no other minimally invasive option for early detection of prostate cancer at that time, which is true for CAN/IFTA today.

[0081] We obtain very reasonable predictive accuracy, sensitivity and specificity with 150, 100 and 50 total genes per signature. There are now several technology platforms perfectly suitable for point of clinical service implementation that can measure 100 genes or more cost effectively and within hours. In clinical practice, the differentially expressed genes and proteins can be used for serial, prospective measurements of the signature at regular intervals for the life of the kidney transplant. The absence of a positive CAN/IFTA signature at any point in time will indicate adequate immunosuppression or over-immunosuppression. Careful reductions in immunosuppressive drug doses can then be used with repeat monitoring of the signature to establish the optimal drug combination and level for each patient to prevent CAN/IFTA and ensure the long term safety of the therapy.

[0082] Biomarker discovery has been reported using peripheral blood profiling for acute rejection in heart transplantation[35,36]. Peripheral blood studies of kidney transplant patients with "operational tolerance" included 22 patients with biopsy-documented CAN/IFTA[37]. Two of the genes (DPYD, IRS2) reported to distinguish "operational tolerance" are identified in our consensus sets. Our earlier study of 42 kidney biopsies showed that gene expression profiles of CAN/IFTA had significant up-regulation of immune/inflammation, fibrosis and tissue remodeling genes[16]. However, only 5 genes from these CAN/IFTA biopsies were identified in the current peripheral blood consensus sets. A study of 11 CAN/IFTA biopsies identified 3 genes linked to immunity and fibrosis that were tested by quantitative PCR in urine and peripheral blood with good correlations in urine but none in peripheral blood[38]. Therefore, gene biomarkers identified in peripheral blood are mostly distinct from those identified in tissue.

[0083] Although practice of the invention is not dependent on an understanding of mechanism, we propose that the peripheral blood represents a fully functional and distinct

compartment of the immune system that actively serves to traffic and modulate all the components of effector immunity. Although the tissue injury that causes the progression of CAN/IFTA is occurring in the kidney, we believe that a significant determinant of the phenotype of the host immune response, either acceptance of the graft or CAN/IFTA, is actually established and subsequently regulated within the peripheral blood compartment, lymph nodes and spleen.

[0084] Urine based proteomics have been used to report biomarkers for acute rejection using SELDI-TOF mass spectroscopy[23,39] but to our knowledge this is the first study to identify blood cell-based proteomic markers for transplantation using tandem mass spectroscopy. We have identified several hundred proteins that are significantly differentially expressed in peripheral blood of patients with CAN/IFTA as a function of histology grade, mild to moderate/severe. The group of uniquely identified proteins potentially represents the highest value biomarker candidates giving 100% accuracy in our tests. Integrating proteomics with gene expression, we identified over 80 protein/transcript matches for CAN/IFTA providing candidate validation based on two independent technologies. However, genes in which differential expression is found only at the gene or protein level but not both also allow accurate analyses.

[0085] Although the invention has been described with reference to the presently preferred embodiments, it should be understood that various modifications can be made without departing from the invention. Unless otherwise apparent from the context any step, element, embodiment, feature or aspect of the invention can be used with any other.

[0086] All publications (including GenBank Accession numbers, UniProtKB/Swiss-Prot accession numbers and the like), patents and patent applications cited are herein incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent and patent application was specifically and individually indicated to be incorporated by reference in its entirety for all purposes. In the event of any variance in sequences associated with Genbank, Unigene, International Protein Index, Entrez, UniProtKB/Swiss-Prot accession numbers and the like, the application refers to the sequences associated with the cited accession numbers as of July 9, 2009.

References

1. Meier-Kriesche (2001) J Am Soc Nephrol 12: 1293-1296.
2. Nankivell (2003) N Engl J Med 349: 2326-2333.

3. Pascual (2002) N Engl J Med 346: 580-590.
4. Solez (2008) Am J Transplant 8: 753-760.
5. Racusen (1999) Kidney Int 55: 713-723.
6. Solez K, (2007) Am J Transplant 7: 518-526.
7. Banasik M, Klinger M (2006) Ann Transplant 11: 7-10.
8. Yates (2006) Transpl Immunol 16: 148-157.
9. Calne (1978) Lancet 2: 1323-1327.
10. de Mattos (2000) Am J Kidney Dis 35: 333-346.
11. Jevnikar (2008) Clin J Am Soc Nephrol 3 Suppl 2: S56-67.
12. Pascual. (1998) Immunol Today 19: 514-519.
13. Nankivell (2006) Transplantation 81: 643-654.
14. Colvin RB (2003) N Engl J Med 349: 2288-2290.
15. Flechner (2007) Transplantation 83: 883-892.
16. Flechner (2004) Am J Transplant 4: 1776-1785.
17. Yilmaz (2007) Transpl Int 20: 608-615.
18. Lachenbruch (2004) Am J Transplant 4: 451-457.
19. Pascual (1999) Transplantation 67: 737-741.
20. Kurian (2005) Current Opinion in Organ Transplantation 10: 193-197.
21. Kurian (2007) Int Immunopharmacol 7: 1948-1960.
22. Oetting (2006) Am J Kidney Dis 47: 898-904.
23. Schaub (2005) Am J Transplant 5: 729-738.
24. Flechner (2004) Am J Transplant 4: 1475-1489.
25. Bolstad (2003) Bioinformatics 19: 185-193.
26. Dudoit (2002) Journal of the American Statistical Association 97: 77-87.
27. Eisen (1998) Proc Natl Acad Sci U S A 95: 14863-14868.
28. Washburn (2001) Nat Biotechnol 19: 242-247.
29. Sadygov (2002) J Proteome Res 1: 211-215.
30. Tabb (2002) J Proteome Res 1: 21-26.
31. Liu (2004) Anal Chem 76: 4193-4201.
32. Guo (2007) Biostatistics 8: 86-100.
33. Huang (2006) Pediatr Blood Cancer 46: 728-738.
34. Woolf (1995) N Engl J Med 333: 1401-1405.
35. Deng (2006) Am J Transplant 6: 150-160.
36. Horwitz (2004) Circulation 110: 3815-3821.
37. Brouard (2007) Proc Natl Acad Sci U S A 104: 15448-15453.
38. Mas (2007) Transplantation 83: 448-457.
39. Clarke (2003) Ann Surg 237: 660-664; discussion 664-665.
40. Kurian et al., PLoS One. 2009 Jul 10;4(7):e6212

Table 1: Clinical Characteristics of the Study Populations.

	Test Set 1				Test Set 2				Test Set 1 vs. Test Set 2
	Banff 0	Banff 1	Banff 2,3	Significance	Banff 0	Banff 1	Banff 2,3	Significance	Significance
Number	18	15	9	NA	8	14	13	NA	NS
Recipient age	42.61±12.8	48.47±11.6	45.67±17.5	NS	56.88±12.2	51.36±12.6	49.08±12.9	NS	Banff0 =0.01
Recipient gender (% female)	38.9	20	44.4	NS	62.5	35.7	53.8	NS	NS
Recipient race African American	22.22	13.33	11.11	NS	0	14.3	7.7	NS	NS
Pre tx diabetes	16.7	26.7	22.2	NS	25	14.3	7.7	NS	NS
PRA >20% (%)	5.6	6.7	11.1	NS	12.5	7.1	15.4	NS	NS
HLA mismatch	3.06±1.7	2.66±1.6	2.67±2.2	NS	3.43+2.4	4.33+1.4	3.58+1.6	NS	Banff1=0.008
Deceased donor	55.6	73.3	77.8	NS	75	71.4	46.2	NS	NS
% re-transplant	0	0	0	_	0	14.3	15.4	NS	NS
Donor age	32.39±15.7	42.33±11.8	37.11±12.1	Banff0 vs. Banff1 p=0.05	31.25±19.3	41.54±17.7	44.62±13.4	NS	NS
Donor gender female	50	53.3	33.3	NS	12.5	57	53.8	NS	NS
Donor race African American	16.7	13.3	11.1	NS	0	7.1	7.7	NS	NS
Induction	100	100	100	NS	75	21.4	23.1	Banff0 vs. Banff1 p=0.026; Banff0 vs. Banff2,3	Banff1=0.0001 Banff2,3=0.0005

	Test Set 1				Test Set 2				Test Set 1 vs. Test Set 2
	Banff 0	**Banff 1**	**Banff 2,3**	**Significance**	**Banff 0**	**Banff 1**	**Banff 2,3**	**Significance**	**Significance**
								p=0.032	
Serum Creatinine	1.32±0.38	1.45±0.51	1.84±0.77	NS	1.70+1.3	2.41+0.7	3.09+1.2	Banff0 vs. Banff2,3 p=0.025	Banff1=0.0002 Banff2,3=0.007
Time to Biopsy	755±101	710±109	659±133	NS	420±309	1664±1364	2398±1120	Banff0 vs. Banff1 p=0.005; Banff0 vs. Banff2,3 p=0.00002	Banff0=0.05 Banff1=0.02 Banff2,3=0.0001
CNI	38.9	60	77.8	NS	100	100	84.6	NS	Banff0=0.007
MMF	100	93.3	88.9	NS	75	78.6	76.9	NS	NS
Steroids	100	100	100	NS	37.5	100	92.3	Banff0 vs. Banff1 p=0.0002; Banff0 vs. Banff2,3 p=0.0022	Banff1=0.0009
C4d+ staining*	ND	ND	ND	NA	NA	2	3	NS	NA

ND - Not Done
NA - Not Applicable
NS - Not Significant

TABLE A

Differentially expressed consensus genes for mild CAN for both Test
Mild CAN = CAN Banff Class 1; No evidence of CAN = CAN Banff Class 0
Probesets with positive fold changes are upregulated in mild CAN

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
1	0.000002	27.9	19.3	-1.45	203796_s_at	BCL7A	B-cell CLL/lymphoma 7A
2	2.1E-06	11.6	16.7	1.44	233650_at	CEP63	centrosomal protein 63kDa
3	3.2E-06	50.5	40.1	-1.26	1552892_at	TNFRSF13C	tumor necrosis factor receptor superfamily, member 13C
4	5.9E-06	19.2	33.6	1.75	1565597_at	EST1	Homo sapiens, clone IMAGE:4275461, mRNA
5	8.3E-06	15.1	23.5	1.56	241752_at	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1
6	1.25E-05	803.7	1050.5	1.31	213702_x_at	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1
7	1.61E-05	224.8	174.8	-1.29	223259_at	ORMDL3	ORM1-like 3 (S. cerevisiae)
8	1.84E-05	135.4	189.9	1.40	204054_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
9	1.86E-05	26	46	1.77	239012_at	IBRDC2	IBR domain containing 2
10	2.39E-05	1182	1724.7	1.46	200975_at	PPT1	Palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile)
11	0.000024	174.3	363.5	2.09	206584_at	LY96	Lymphocyte antigen 96
12	3.35E-05	9	7.6	-1.18	228044_at	C13orf21	Chromosome 13 open reading frame 21
13	4.41E-05	250.1	327.6	1.31	225492_at	EST2	---
14	4.53E-05	7828	10660.2	1.36	202917_s_at	S100A8	S100 calcium binding protein A8
15	0.000047	374.1	724.5	1.94	223501_at	TNFSF13B	Tumor necrosis factor (ligand) superfamily, member

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
							13b
16	4.75E-05	112.7	204	1.81	222496_s_at	FLJ20273	RNA-binding protein
17	5.11E-05	22.4	38.8	1.73	224996_at	EST3	CDNA FLJ39064 fis, clone NT2RP7014583
18	5.13E-05	21.6	17.5	-1.23	244863_at	EST4	Transcribed locus
19	0.000052	7.5	9	1.20	238791_at	ZNF100	Zinc finger protein 100
20	5.66E-05	85.2	123.8	1.45	218177_at	CHMP1B	Chromatin modifying protein 1B
21	5.67E-05	203.3	336.4	1.65	226208_at	ZSWIM6	Zinc finger, SWIM-type containing 6
22	7.26E-05	180.8	237.2	1.31	203778_at	MANBA	Mannosidase, beta A, lysosomal
23	0.000089	86.6	123.4	1.42	238903_at	LOC137886	Hypothetical protein LOC137886
24	0.000094	19.7	14.5	-1.36	214308_s_at	HGD	Homogentisate 1,2-dioxygenase (homogentisate oxidase)
25	0.000103	492.9	744.6	1.51	211368_s_at	CASP1	Caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
26	0.000103	132.8	184.8	1.39	227017_at	ERICH1	Glutamate-rich 1
27	0.000107	10.3	15.5	1.50	228624_at	TMEM144	Transmembrane protein 144
28	0.000108	128.7	170.2	1.32	232149_s_at	NSMAF	Neutral sphingomyelinase (N-SMase) activation associated factor
29	0.000112	26.4	35.2	1.33	243287_s_at	OSTM1	Osteopetrosis associated transmembrane protein 1
30	0.000116	59.5	134.7	2.26	1552773_at	CLEC4D	C-type lectin domain family 4, member D
31	0.000121	2887.4	3972.4	1.38	202902_s_at	CTSS	Cathepsin S
32	0.000125	142.4	229	1.61	211744_s_at	CD58	CD58 molecule
33	0.000133	35.6	26.9	-1.32	243507_s_at	C20orf196	Chromosome 20 open reading frame 196
34	0.000137	101.9	77.4	-1.32	228832_at	FLJ20021	Hypothetical LOC90024
35	0.000149	1057.6	1433.5	1.36	202727_s_at	IFNGR1	Interferon gamma receptor 1
36	0.000169	40.5	55.5	1.37	213952_s_at	ALOX5	*Arachidonate* 5-*lipoxygenase*
37	0.000174	364.6	288.1	-1.27	219045_at	RHOF	Ras homolog gene family, member F (in filopodia)
38	0.000175	666	974.1	1.46	212268_at	SERPINB1	Serpin peptidase inhibitor, clade B (ovalbumin),

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
							member 1
39	0.00018	80.3	119.4	1.49	203276_at	LMNB1	Lamin B1
40	0.00019	347.2	814.1	2.34	219666_at	MS4A6A	Membrane-spanning 4-domains, subfamily A, member 6A
41	0.000204	54.9	110.9	2.02	204860_s_at	NAIP /// NAIP1B	NLR family, apoptosis inhibitory protein /// neuronal apoptosis inhibitory protein (centromeric)
42	0.000212	3812.4	4958.6	1.30	202388_at	RGS2	Regulator of G-protein signaling 2, 24kDa
43	0.000226	24.5	43.9	1.79	1553514_a_at	VNN3	Vanin 3
44	0.000239	84.6	108.3	1.28	218364_at	LRRFIP2	Leucine rich repeat (in FLII) interacting protein 2
45	0.000242	15.5	21.5	1.39	218888_s_at	NETO2	Neuropilin (NRP) and tolloid (TLL)-like 2
46	0.000258	64.6	87.8	1.36	204108_at	NFYA	Nuclear transcription factor Y, alpha
47	0.000273	35.6	50.1	1.41	213935_at	ABHD5	Abhydrolase domain containing 5
48	0.000278	54	75.5	1.40	208883_at	UBR5	Ubiquitin protein ligase E3 component n-recognin 5
49	0.000282	334.9	425	1.27	222148_s_at	RHOT1	Ras homolog gene family, member T1
50	0.000284	564.8	712.6	1.26	227266_s_at	FYB	FYN binding protein (FYB-120/130)
51	0.000287	75.4	138.6	1.84	204714_s_at	F5	Coagulation factor V (proaccelerin, labile factor)
52	0.000302	6.3	5.6	-1.13	229777_at	CLRN3	Clarin 3
53	0.000302	16.9	19.2	1.14	241073_at	EST5	Transcribed locus
54	0.000309	29.8	52.7	1.77	1558549_s_at	VNN1	Vanin 1
55	0.000319	584.3	710	1.22	201007_at	HADHB	Hydroxyacyl-Coenzyme A dehydrogenase/2-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
56	0.000323	9	7.8	-1.15	241171_at	EST6	Transcribed locus
57	0.000328	18.4	33.5	1.82	239759_at	EST7	Transcribed locus
58	0.000368	44.5	76.4	1.72	209684_at	RIN2	Ras and Rab interactor 2
59	0.000369	22.6	18.4	-1.23	240654_at	EST8	Transcribed locus
60	0.00037	356	693	1.95	217738_at	PBEF1	Pre-B-cell colony enhancing factor 1

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
61	0.000377	48.8	73.7	1.51	228540_at	QKI	Quaking homolog, KH domain RNA binding (mouse)
62	0.000386	24.1	20	-1.21	221261_x_at	MAGED4 /// MAGED4B	Melanoma antigen family D, 4B///melanoma antigen family D, 4
63	0.000393	8.3	9.9	1.19	1562458_at	UBE2W	Ubiquitin-conjugating enzyme E2W (putative)
64	0.000399	28.9	40.2	1.39	227403_at	PIGX	Phosphatidylinositol glycan anchor biosynthesis, class X
65	0.000406	21.6	27.6	1.28	226827_at	TMEM165	Transmembrane protein 165
66	0.000418	61.4	54.1	-1.13	1568691_at	EST9	CDNA clone IMAGE:3613441
67	0.000444	31	51.9	1.67	230343_at	EST10	Transcribed locus
68	0.000445	10.3	8.2	-1.26	212650_at	EHBP1	EH domain binding protein 1
69	0.000448	168.6	306.1	1.82	238066_at	RBP7	Retinol binding protein 7, cellular
70	0.000451	69.6	97.7	1.40	213292_s_at	SNX13	Sorting nexin 13
71	0.000463	38.7	63.7	1.65	228362_s_at	FAM26F	Family with sequence similarity 26, member F
72	0.000477	30	23.6	-1.27	236139_at	EST11	Transcribed locus
73	0.000486	15.4	20.2	1.31	220775_s_at	UEVLD	UEV and lactate/malate dehydrogenase domains
74	0.000493	55.2	46.9	-1.18	221189_s_at	TARS2	Threonyl-tRNA synthetase 2, mitochondrial (putative)
75	0.000497	24.5	20	-1.23	210150_s_at	LAMA5	Laminin, alpha 5
76	0.000509	49.3	41.2	-1.20	211304_x_at	KCNJ5	Potassium inwardly-rectifying channel, subfamily J, member 5
77	0.000524	5.4	4.7	-1.15	233609_at	PTPRK	Protein tyrosine phosphatase, receptor type, K
78	0.000538	12.2	17.6	1.44	202422_s_at	ACSL4	Acyl-CoA synthetase long-chain family member 4
79	0.000539	360.3	442.2	1.23	225284_at	DNAJC3 /// LOC144871	DnaJ (Hsp40) homolog, subfamily C, member 3///hypothetical protein LOC144871
80	0.000549	10.4	8.7	-1.20	204983_s_at	GPC4	Glypican 4
81	0.000555	15.5	13.4	-1.16	231318_at	C15orf51	Chromosome 15 open reading frame 51
82	0.000564	59.4	83.9	1.41	208158_s_at	OSBPL1A	Oxysterol binding protein-like 1A
83	0.000571	9.2	8.1	-1.14	205542_at	STEAP1	Six transmembrane epithelial antigen of the prostate 1

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
84	0.000573	186.9	235.8	1.26	218905_at	INTS8	Integrator complex subunit 8
85	0.000588	100.3	177.5	1.77	212820_at	DMXL2	Dmx-like 2
86	0.000594	160.5	341.8	2.13	215049_x_at	CD163	CD163 molecule
87	0.000595	20.8	34.4	1.65	206674_at	FLT3	Fms-related tyrosine kinase 3
88	0.000595	52.3	40.2	-1.30	233487_s_at	LRRC8A	Leucine rich repeat containing 8 family, member A
89	0.000607	17.5	21.1	1.21	33197_at	MYO7A	Myosin VIIA
90	0.000642	26.5	23.5	-1.13	203793_x_at	PCGF2	Polycomb group ring finger 2
91	0.000648	9.1	8.2	-1.11	1566935_at	TYRO3P	TYRO3P protein tyrosine kinase pseudogene
92	0.000663	10.8	15.2	1.41	203767_s_at	STS	Steroid sulfatase (microsomal), isozyme S
93	0.000668	303.5	421.8	1.39	226136_at	GLIPR1	GLI pathogenesis-related 1 (glioma)
94	0.00067	52.1	81.1	1.56	216252_x_at	FAS	Fas (TNF receptor superfamily, member 6)
95	0.000694	244.7	420.5	1.72	221724_s_at	CLEC4A	C-type lectin domain family 4, member A
96	0.000696	11.6	13.1	1.13	230419_at	FLJ37644	Hypothetical gene supported by AK094963
97	0.000701	26.8	33.2	1.24	225778_at	FUT1	Fucosyltransferase I (galactoside 2-alpha-L-fucosyltransferase, H blood group)
98	0.000702	14.8	10.3	-1.44	216063_at	HBBP1	Hemoglobin, beta pseudogene 1
99	0.000745	6.9	6.2	-1.11	207516_at	CHRNB4	Cholinergic receptor, nicotinic, beta 4
100	0.000749	21.8	17.3	-1.26	216910_at	XPNPEP2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound
101	0.00075	14.7	12.5	-1.18	1555655_at	OR10A4	Olfactory receptor, family 10, subfamily A, member 4
102	0.000755	266.1	339	1.27	225606_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)
103	0.000768	17	14.8	-1.15	207967_at	VPS45	Vacuolar protein sorting 45 homolog (S. cerevisiae)
104	0.000775	253.9	336.8	1.33	219079_at	CYB5R4	Cytochrome b5 reductase 4
105	0.000803	94.6	134.1	1.42	222498_at	AZI2	5-azacytidine induced 2
106	0.00081	570.4	686.2	1.20	210817_s_at	CALCOCO2	Calcium binding and coiled-coil domain 2
107	0.00082	344.4	494.4	1.44	211404_s_at	APLP2	Amyloid beta (A4) precursor-like protein 2
108	0.000824	9.6	16.4	1.71	1562481_at	EST12	---

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
109	0.000834	78.3	105.7	1.35	203693_s_at	E2F3	E2F transcription factor 3
110	0.00084	23.2	33.6	1.45	205841_at	JAK2	Janus kinase 3 (a protein tyrosine kinase)
111	0.000847	10.2	9.1	-1.12	1553504_at	MRGPRX4	MAS-related GPR, member X4
112	0.00085	140.6	212.9	1.51	203139_at	DAPK1	Death-associated protein kinase 1
113	0.000864	186.1	235.2	1.26	226850_at	SUMF1	Sulfatase modifying factor 1
114	0.000896	4.9	5.4	1.10	230684_at	GTPBP10	GTP-binding protein 10 (putative)
115	0.000907	34.8	21.7	-1.60	228802_at	RBPMS2	RNA binding protein with multiple splicing 2
116	0.000969	7.6	6.8	-1.12	204596_s_at	STC1	Stanniocalcin 1
117	0.000972	45.3	57	1.26	228061_at	CCDC126	Coiled-coil domain containing 126
118	0.000979	31.4	22.6	-1.39	244876_at	EST13	---
119	0.000992	12.4	10.7	-1.16	233015_at	MBNL1	Muscleblind-like (Drosophila)
120	0.001033	21.6	14.5	-1.49	234284_at	GNG8	Guanine nucleotide binding protein (G protein), gamma 8
121	0.001036	38.2	24.8	-1.54	1560262_at	EST14	Homo sapiens, clone IMAGE:5751523, mRNA
122	0.001037	5.4	4.8	-1.13	1562902_at	EST15	Homo sapiens, clone IMAGE: 5176738, mRNA
123	0.001045	1215.1	2084.9	1.72	205863_at	S100A12	S100 calcium binding protein A12
124	0.001057	37.8	31.9	-1.18	222302_at	EST16	---
125	0.001065	44.9	51.1	1.14	212932_at	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)
126	0.001066	36.3	49.6	1.37	233924_s_at	EXOC6	Exocyst complex component 6
127	0.001087	34.5	41.5	1.20	230209_at	EST17	CDNA FLI36477 fis, clone THYMU2017158
128	0.001103	498.4	419.3	-1.19	41047_at	C9orf16	Chromosome 9 open reading frame 16
129	0.001136	57.1	40.8	-1.40	200884_at	CKB	Creatine kinase, brain
130	0.001137	177	245.9	1.39	219157_at	KLHL2	Kelch-like 2, Mayven (Drosophila)
131	0.001153	7.3	6.4	-1.14	207818_s_at	HTR7	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)
132	0.001162	13.3	16.1	1.21	234977_at	ZADH2	Zinc binding alcohol dehydrogenase, domain containing 2

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
133	0.001164	4.6	4.3	-1.07	238391_at	EST18	Transcribed locus
134	0.001173	125.2	160.3	1.28	222759_at	SUV420H1	Suppressor of variegation 4-20 homolog 1 (Drosophila)
135	0.001197	16.5	13.5	-1.22	233962_at	C20orf120	Chromosome 20 open reading frame 120
136	0.001212	183	250.9	1.37	204526_s_at	TBC1D8	TBC1 domain family, member 8 (with GRAM domain)
137	0.001214	39.9	31.5	-1.27	235417_at	SPOCD1	SPOC domain containing 1
138	0.001228	67.2	87.8	1.31	1552472_a_at	CENTB2	Centaurin, beta 2
139	0.001232	423	513.3	1.21	200768_s_at	MAT2A	Methionine adenosyltransferase II, alpha
140	0.001246	17	14.7	-1.16	229536_at	REC8	REC8 *homolog (yeast)*
141	0.001283	1790.8	2281.3	1.27	204220_at	GMFG	Glia maturation factor, gamma
142	0.001291	41.6	35.4	-1.18	234958_at	EST19	Clone HQ0352 PRO0352
143	0.001294	1519.9	1803	1.19	207168_s_at	H2AFY	H2A histone family, member Y
144	0.001329	9.9	8.3	-1.19	1557235_at	EST20	CDNA FLI44051 fis, clone TESTI4033433
145	0.001329	7.7	6.8	-1.13	207120_at	ZNF667	Zinc finger protein 667
146	0.001348	12	15.3	1.28	226688_at	C3orf23	Chromosome 3 open reading frame 23
147	0.001363	201.6	311.2	1.54	224374_s_at	EMILIN2	Elastin microfibril interfacer 2
148	0.001364	79.4	48.9	-1.62	244523_at	MMD	Monocyte to macrophage differentiation-associated
149	0.001415	10.4	9.1	-1.14	226533_at	HINT3	Histidine triad nucleotide binding protein 3
150	0.001421	505.7	358.5	-1.41	202074_s_at	OPTN	Optineurin
151	0.001438	10.9	9.6	-1.14	234372_at	LOC644728	Similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (38 kDa 8FA-dependent ADP-ribosylation substrate) (BARS-38)
152	0.001448	239.8	331.7	1.38	202192_s_at	GAS7	Growth arrest-specific 7
153	0.001464	16.6	20.7	1.25	1559052_s_at	PAK2	p21 (CDKN1A)-activated kinase 2
154	0.001472	32.5	47.6	1.46	223304_at	SLC37A3	Solute carrier family 37 (glycerol-3-phosphate transporter), member 3
155	0.001491	43.1	58.5	1.36	213582_at	ATP11A	ATPase, Class VI, type 11A
156	0.001507	6.5	5.8	-1.12	233770_at	EST21	CDNA FLI12077 fis, clone HEMBB1002453

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
157	0.001515	14.1	12.7	-1.11	234627_at	FLJ21408	Hypothetical gene supported by AK025061
158	0.00152	815.3	1047.6	1.28	209007_s_at	C1orf63	Chromosome 1 open reading frame 63
159	0.00153	15.6	11.2	-1.39	214502_at	HIST1H2BJ	Histone cluster 1, H2bj
160	0.001533	206.6	140.7	-1.47	202124_s_at	TRAK2	Trafficking protein, kinesin binding 2
161	0.001538	16.1	12.9	-1.25	223709_s_at	WNT10A	Wingless-type MMTV integration site family, member 10A
162	0.001544	143.1	194.3	1.36	219132_at	PELI2	Pellino homolog 2 (Drosophila)
163	0.001561	556.9	684.6	1.23	217492_s_at	LOC731292 /// PTEN /// PTENP1	Phosphatase and tensin homolog (mutated in multiple advanced cancers 1) ///phosphatase and tensin homolog (mutated in multiple advanced cancers 1), pseudogene 1///similar to Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN (Phosphatase and tensin homolog) (Mutated in multiple advanced cancers1)
164	0.001562	7.4	6.7	-1.10	241226_at	EST22	Transcribed locus
165	0.001565	12.1	10.6	-1.14	231965_at	FAM113A	Family with sequence similarity 113, member A
166	0.00157	39.4	69.3	1.76	207605_x_at	ZNF117	Zinc finger protein 117
167	0.001602	22.4	19.4	-1.15	232249_at	FMNL3	Formin-like 3
168	0.001612	81.2	116	1.43	205698_s_at	MAP2K6	Mitogen-activated protein kinase kinase 6
169	0.001613	110.4	140.3	1.27	229798_s_at	EST23	---
170	0.00162	21	17.7	-1.19	219554_at	RHCG	Rh family, C glycoprotein
171	0.001625	7	6.1	-1.15	244690_at	EST24	Transcribed locus
172	0.00163	343.7	497.4	1.45	225919_s_at	C9orf72	Chromosome 9 open reading frame 72
173	0.001642	74.3	101.7	1.37	213792_s_at	INSR	Insulin receptor
174	0.001677	23.1	26.8	1.16	208328_s_at	MEF2A	Myocyte enhancer factor 2A
175	0.00168	6.9	6.2	-1.11	207362_at	SLC30A4	Solute carrier family 30 (zinc transporter), member 4
176	0.001709	17.5	15.4	-1.14	206521_s_at	GTF2A1	General transcription factor IIA, 1, 19/37kDa

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
177	0.001735	100.2	142	1.42	218027_at	MRPL15	Mitochondrial ribosomal protein L15
178	0.001737	19.6	22.8	1.16	224198_at	ELA1	Elastase 1, pancreatic
179	0.001741	69.6	97.1	1.40	212572_at	STK38L	Serine/threonine kinase 38 like
180	0.001743	22.3	18.6	-1.20	206993_at	ATP5S	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)
181	0.001788	45.4	36.5	-1.24	203479_s_at	OTUD4	OTU domain containing 4
182	0.001835	13.4	11	-1.22	232820_s_at	FAM112A	Family with sequence similarity 112, member A
183	0.001854	7.2	6.6	-1.09	1558621_at	CABLES1	Cdk5 and Abl enzyme substrate 1
184	0.001854	59.1	49.6	-1.19	220765_s_at	LIMS2	LIM and senescent cell antigen-like domains 2
185	0.001859	24.3	20.6	-1.18	205477_s_at	AMBP	Alpha-1-microglobulin/bikunin precursor
186	0.00189	102.8	59	0.57	207826_s_at	ID3	Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
187	0.001892	10.5	17.8	1.70	209992_at	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2
188	0.001928	207.8	151.9	-1.37	201841_s_at	HSPB1	Heat shock 27kDa protein 1
189	0.001936	61.4	83.5	1.36	210768_x_at	TMCO1	Transmembrane and coiled-coil domains 1
190	0.001951	43.1	63.6	1.48	242794_at	MAML3	Mastermind-like 3 (Drosophila)
191	0.001976	58.7	79.2	1.35	213379_at	COQ2	Coenzyme Q2 homolog, prenyltransferase (yeast)
192	0.001983	425.9	650.8	1.53	202446_s_at	PLSCR1	Phospholipid scramblase 1
193	0.001984	24.7	28.7	1.16	204210_s_at	PCYT1A	Phosphate cytidylyltransferase 1, choline, alpha
194	0.001993	31.8	58.3	1.83	236898_at	EST25	Transcribed locus. strongly similar to XP_0011011634.1 similar to tripartite motif-containing 25 (Macaca mulatta)
195	0.002	8.8	7.4	-1.19	242661_x_at	ALS2CR12	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12
196	0.002013	19.4	15.4	-1.26	1558773_s_at	RANBP10	RAN binding protein 10
197	0.002032	63.6	79.5	1.25	218896_s_at	C17orf85	Chromosome 17 open reading frame 85

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
198	0.002033	27.8	37.2	1.34	220865_s_at	PDSS1	Prenyl (decaprenyl) diphosphate synthase, subunit 1
199	0.002038	214.1	282.4	1.32	224511_s_at	TXNDC17	Thioredoxin domain containing 17
200	0.002045	7.6	6.4	-1.19	243347_at	EST26	---
201	0.002054	8.1	7	-1.16	236336_at	EST27	CDNA clone IMAGE:4796690
202	0.002098	153.9	205.6	1.34	224983_at	SCARB2	Scavenger receptor class B, member 2
203	0.002099	30.1	26	-1.16	1569144_a_at	LOC653325 /// MGC59937	Similar to RIKEN cDNA 2310002J15 gene///hypothetical LOC653325
204	0.002104	15.9	13.7	-1.16	234511_at	C20orf86	Chromosome 20 open reading frame 86
205	0.002106	20.3	17.2	-1.18	237254_at	SLC5A11	Solute carrier family 5 (sodium/glucose cotransporter), member 11
206	0.002112	9.3	10.5	1.13	231310_at	EST28	Transcribed locus
207	0.002171	15.7	13	-1.21	244226_s_at	EST29	---
208	0.0022	13.3	11.4	-1.17	230957_at	PCDHB19P	Protocadherin beta 19 pseudogene
209	0.002206	10.8	9.5	-1.14	232321_at	MUC17	Mucin 17, cell surface associated
210	0.00221	27.4	19.8	-1.38	235557_at	LOC150763	Hypothetical protein LOC150763
211	0.002218	11251.4	8508.5	-1.32	214414_x_at	HBA2	Hemoglobin, alpha 2
212	0.00222	16.1	13.8	-1.17	1558118_at	DGCR5	DiGeorge syndrome critical region gene 5 (non-coding)
213	0.002223	18.1	15.9	-1.14	231994_at	CHDH	Choline dehydrogenase
214	0.002229	29.1	34.7	1.19	212710_at	CAMSAP1	Calmodulin regulated spectrin-associated protein 1
215	0.002253	94.3	73.7	-1.28	243579_at	MSI2	Musashi homolog 2 (Drosophila)
216	0.002256	446.2	305.3	-1.46	200702_s_at	DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24
217	0.002266	94.9	124.4	1.31	227046_at	SLC39A11	Solute carrier family 39 (Metal ion transporter), member 11
218	0.002294	36	31.2	-1.15	40020_at	CELSR3	Cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila)
219	0.002303	27.6	22.9	-1.21	218903_s_at	OBFC2B	Oligonucleotide/oligosaccharide-binding fold

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
							containing 2B
220	0.002329	5.5	6.7	1.22	223861_at	HORMAD1	HORMA domain containing 1
221	0.002348	508.5	692.2	1.36	201926_s_at	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
222	0.00235	1265.9	1098.5	-1.15	209075_s_at	ISCU	Iron-sulfur cluster scaffold homolog (E.coli)
223	0.002351	7.1	6	-1.18	231721_at	JAM3	Junctional adhesion molecule 3
224	0.002354	8.2	7.4	-1.11	237505_at	EST30	Transcribed locus
225	0.002368	67.4	100.4	1.49	201952_at	ALCAM	Activated leukocyte cell adhesion molecule
226	0.002389	10	8.7	-1.15	211896_s_at	DCN	Decorin
227	0.002394	40.2	31.8	-1.26	216080_s_at	FADS3	Fatty acid desaturase 3
228	0.002427	252.5	326.4	1.29	202277_at	SPTLC1	Serine palmitoyltransferase, long chain base subunit 1
229	0.002435	37.7	56.3	1.49	208488_s_at	CR1	Complement component (3b/4b) receptor 1 (Knops blood group)
230	0.002437	100.3	135.1	1.35	213868_s_at	DHRS7	Deydrogenase/reductase (SDR family) member 7
231	0.002443	314.9	419.1	1.33	225921_at	NIN	Ninein (GSK3B interacting protein)
232	0.002447	56.7	82.8	1.46	233329_s_at	KRCC1	Lysine-rich coiled-coil 1
233	0.002472	28.3	24.6	-1.15	232663_s_at	LOC390595	Similar to ubiquitin-associated protein 1 (predicted)
234	0.002474	88.9	143.5	1.61	204150_at	STAB1	Stabilin 1
235	0.002511	10	11.5	1.15	219831_at	CDKL3	Cyclin-dependent kinase-like 3
236	0.002528	69.8	101.9	1.46	216202_s_at	SPTLC2	Serine palmitoyltransferase, long chain base subunit 2
237	0.002536	28.7	24.3	-1.18	233381_at	RUFY1	RUN and FYVE domain containing 1
238	0.002552	67.7	84	1.24	222842_at	EIF2C4	Eukaryotic translation initiation factor 2C, 4
239	0.002566	13.7	10.6	-1.29	1554413_s_at	RUNDC2B /// RUNDC2C	RUN domain containing 2B///RUN domain containing 2C
240	0.002598	13.9	12.2	-1.14	202403_s_at	COL1A2	Collagen, type 1, alpha 2
241	0.002603	531.4	440.6	-1.21	210950_s_at	FDFT1	Farnesyl-diposphate farnesyltransferase 1
242	0.002605	10.1	8.5	-1.19	215742_at	EST31	CDNA FLI12157 fis, clone MAMMA1000500

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
243	0.002672	35.9	42.2	1.18	221567_at	NOL3	Nucleolar protein 3 (apoptosis repressor with CARD domain)
244	0.002691	16	12	-1.33	203151_at	MAP1A	Microtubule-associated protein 1A
245	0.002693	406.6	540.5	1.33	208864_s_at	TXN	Thioredoxin
246	0.002706	83	62.3	-1.33	201072_s_at	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
247	0.002715	77.7	63.5	-1.22	211358_s_at	CIZ1	CDKN1A interacting zinc finger protein 1
248	0.002724	11.1	13.7	1.23	205416_s_at	ATXN3	Ataxin 3
249	0.002731	27	23.9	-1.13	244694_at	LOC402665	hCG1651476
250	0.002731	94.6	135.6	1.43	212511_at	PICALM	Phosphatidylinositol binding clathrin assembly protein
251	0.002736	81.1	112.4	1.39	223978_s_at	CRLS1	Cardiolipin synthase 1
252	0.002737	12.1	10.7	-1.13	210923_at	SLC1A7	Solute carrier family 1 (glutamate transporter), member 7
253	0.002738	5.6	5.1	-1.10	204320_at	COL11A1	Collagen, type XI, alpha 1
254	0.002739	61	83.3	1.37	209666_s_at	CHUK	Conserved helix-loop-helix ubiquitous kinase
255	0.002747	29.9	24.5	-1.22	238097_at	EST32	---
256	0.002749	10.1	8.6	-1.17	205295_at	CKMT2	Creatine kinase, mitochondrial 2 (sarcomeric)
257	0.002773	240.1	331.4	1.38	1555797_a_at	ARPC5	Actin related protein 2/3 complex, subunit 5, 16kDa
258	0.002776	32.5	28.1	-1.16	235402_at	C11orf66	Chromosome 11 open reading frame 66
259	0.002793	30.8	25.5	-1.21	216562_at	EST33	---
260	0.002823	19.6	17.1	-1.15	1553967_at	ADAT3	Adenosine deaminase, tRNA-specific 3, TAD3 homolog (S. cerevisiae)
261	0.002831	883.8	1069.3	1.21	226525_at	EST34	Transcribed locus
262	0.002853	65.1	109.4	1.68	220034_at	IRAK3	Interleukin-1 receptor-associated kinase 3
263	0.002856	7.7	7.1	-1.08	1563656_at	EST35	MRNA; cDNA DKFZp586H1217 (from clone DKFZp586H1217)
264	0.002859	60.5	53.8	-1.12	233235_x_at	EST36	CDNA: FLI21443 fis, clone COL04430

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
265	0.002876	5	5.5	1.10	1558640_a_at	LOC728411	Similar to Beta-glucuronidase precursor
266	0.00288	143.4	216.8	1.51	204646_at	DPYD	Dihydropyrimidine dehydrogenase
267	0.002888	52.8	83.6	1.58	207719_x_at	CEP170	Centrosomal protein 170kDa
268	0.00289	41.3	50.9	1.23	228791_at	C15orf38	Chromosome 15 open reading frame 38
269	0.002915	17.6	15	-1.17	240705_at	CYP19A1	Cytochrome P450, family 19, subfamily A, polypeptide 1
270	0.002927	50.7	42.9	-1.18	218725_at	SLC25A22	Solute carrier family 25 (mitochondrial carrier:glutamate), member 22
271	0.002996	105.1	163.4	1.55	201328_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
272	0.002997	13.9	16.3	1.17	239332_at	EST37	Homo sapiens, clone IMAGE: 3897156, mRNA
273	0.00302	14	16.9	1.21	240394_at	EST38	Transcribed locus
274	0.003049	60.3	51.8	-1.16	1556900_at	LOC149773	Hypothetical protein LOC149773
275	0.003057	43.4	33.4	-1.30	220588_at	BCAS4	Breast carcinoma amplified sequence 4
276	0.003067	10.1	8.4	-1.20	210127_at	RAB6B	RAB6B, member RAS oncogene family
277	0.003068	5.5	4.9	-1.12	1559450_at	EST39	CDNA clone IMAGE:5286225
278	0.003109	22	36.6	1.66	1558920_at	EST40	CDNA FLI43417 fis, clone OCBBF2026025
279	0.003116	9.2	8.2	-1.12	206847_s_at	HOXA7	Homeobox A7
280	0.003117	12.9	11.3	-1.14	216303_s_at	MTMR1	Myotubularin related protein 1
281	0.003131	14	12.3	-1.14	216799_at	EST41	MRNA;cDNA DKFZp547G044 (from clone DKFZp547G044)
282	0.003131	5.8	5.3	-1.09	242130_at	EST42	Transcribed locus
283	0.003145	10.6	9.4	-1.13	1562106_at	EST43	Homo sapiens, clone IMAGE:5240933, mRNA
284	0.003147	40.2	46.9	1.17	224416_s_at	MED28	Mediator complex subunit 28
285	0.003153	441.7	716.5	1.62	203799_at	CD302	CD302 molecule
286	0.00318	23.2	19.5	-1.19	243062_at	FLCN	Folliculin
287	0.003188	15.1	19.7	1.30	239574_at	EST44	Transcribed locus

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
288	0.003189	5.7	5.2	-1.10	1559518_at	HSD17B12	Hydroxysteroid (17-beta) dehydrogenase 12
289	0.0032	27.3	38.8	1.42	207601_at	SULT1B1	Sulfotransferase family, cytosolic, 1B, member 1
290	0.003219	14.6	13	-1.12	219576_at	MAP7D3	MAP7 domain containing 3
291	0.003229	98.4	127.1	1.29	209234_at	KIF1B	Kinesin family member 1B
292	0.003234	151.4	100.7	-1.50	225775_at	TSPAN33	Tetraspanin 33
293	0.003255	10.8	12.9	1.19	238921_at	LOC641767 /// LOC644794	Hypothetical protein LOC641767///hypothetical LOC644794
294	0.003276	5.2	5.8	1.12	236262_at	MMRN2	Multimerin 2
295	0.003296	20.4	16.2	-1.26	215526_at	EST45	MRNA;cDNA DKFZp586C2020 (from clone DKFZp586C2020)
296	0.003296	14.9	13.2	-1.13	236914_at	EST46	Transcribed locus, moderately similar to XP_001137307.1 hypothetical protein (Pan troglodytes)
297	0.003306	43.6	58.4	1.34	236465_at	RNF175	Ring finger protein 175
298	0.00334	106.2	210.1	1.98	204619_s_at	VCAN	Versican
299	0.003365	15.3	12.5	-1.22	243365_s_at	AUTS2	Autism susceptibility candidate 2
300	0.003378	165.7	146	-1.13	201618_x_at	GPAA1	Glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)
301	0.003383	82.2	97.6	1.19	209445_x_at	C7orf44	Chromosome 7 open reading frame 44
302	0.003388	66.1	101.4	1.53	1552485_at	LACTB	Lactamase, beta
303	0.003393	6	5.5	-1.09	1558010_s_at	SLC1A2	Solute carrier family 1 (glial high affinity glutamate transporter), member 2
304	0.003404	8	11	1.38	225008_at	EST47	CDNA FLI39064 fis, clone NT2RP7014583
305	0.003412	13.5	11.3	-1.19	1560108_at	EST48	CDNA FLI30757 fis, clone FEBRA2000468
306	0.003423	29.3	27.2	-1.08	244055_at	EST49	Transcribed locus
307	0.003447	16.6	20	1.20	233750_s_at	C1orf25	Chromosome 1 open reading frame 25

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
308	0.00346	5.4	5	-1.08	220361_at	IQCH	IQ motif containing H
309	0.003472	110	181.2	1.65	222303_at	EST50	---
310	0.003502	58.3	80.3	1.38	230937_at	LOC285835	Hypothetical protein LOC285835
311	0.003535	39.4	52	1.32	207627_s_at	TFCP2	Transcription factor CP2
312	0.003539	20.3	17.5	-1.16	1555752_at	STH	Saitohin
313	0.003542	3088.2	3805.3	1.23	212501_at	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta
314	0.003551	6.2	5.7	-1.09	244675_at	RGS8	Regulator of G-protein signaling 8
315	0.003571	12.7	11.2	-1.13	208275_x_at	UTF1	Undifferentiated embryonic cell transcription factor 1
316	0.003572	397.4	524.7	1.32	210951_x_at	RAB27A	RAB27A, member RAS oncogene family
317	0.003582	7.8	6.7	-1.16	219840_s_at	TCL6	T-cell leukemia/lymphoma 6
318	0.003626	124.1	166.3	1.34	219256_s_at	SH3TC1	SH3 domain and tetratricopeptide repeats 1
319	0.003657	5.3	4.8	-1.10	1558778_s_at	MKL2	MKL/myocardin-like 2
320	0.00366	32.1	27.1	-1.18	218480_at	AGBL5	ATP/GTP binding protein-like 5
321	0.003672	118	176.7	1.50	204099_at	SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
322	0.003678	480.1	579	1.21	225750_at	EST51	CDNA FLI14162 fis, clone NT2RM4002504
323	0.003715	50.7	43.5	-1.17	214253_s_at	DTNB	Dystrobrevin, beta
324	0.003718	12.1	10.8	-1.12	243048_at	CECR7	Cat eye syndrome chromosome region, candidate 7
325	0.003757	9	7.9	-1.14	1556012_at	KLHDC7A	Kelch domain containing 7A
326	0.003773	17.6	23.4	1.33	215285_s_at	PHTF1	Putative homeodomain transcription factor 1
327	0.00378	64.4	81.7	1.27	231321_s_at	PHCA	Phytoceramidase, alkaline
328	0.003783	5.4	4.9	-1.10	238901_at	EST52	Full length insert cDNA clone ZE01A04
329	0.003793	25.4	21.4	-1.19	214595_at	KCNG1	Potassium voltage-gated channel, subfamily G, member 1
330	0.0038	10.5	9.4	-1.12	216470_x_at	PRSS1 /// PRSS2 /// PRSS3 ///	Protease, serine, 1 (trypsin1)///protease, serine, 2 (trypsin2)///protease, serine, 3 (mesotrypsin) trypsinogen 3

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
						TRY6	
331	0.003819	36.6	59.4	1.62	204787_at	VSIG4	V-set and immunoglobulin domain containing 4
332	0.003841	11.7	10.2	-1.15	216101_at	EST53	Full length insert cDNA clone YR67C11
333	0.003845	51	75.1	1.47	224862_at	GNAQ	Guanine nucleotide binding protein (G protein), q polypeptide
334	0.003873	17.6	23.6	1.34	234664_at	LOC284701	Hypothetical protein LOC284701
335	0.003878	16.8	14	-1.20	202796_at	SYNPO	Synaptopodin
336	0.003884	11.4	10	-1.14	238217_at	EST54	Transcribed locus
337	0.003905	559.2	823.8	1.47	209184_s_at	IRS2	Insulin receptor substrate 2
338	0.003905	5.6	5.2	-1.08	1565578_at	EST55	CDNA FLI34486 fis, clone HLUNG2004217
339	0.003909	202.6	269.2	1.33	217823_s_at	UBE2J1	Ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
340	0.003952	7	6.2	-1.13	240873_x_at	DAB2	Disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)
341	0.003967	206.9	281.1	1.36	212795_at	KIAA1033	KIAA1033
342	0.003968	36	48.9	1.36	239085_at	EST56	Transcribed locus
343	0.003972	110.8	171.2	1.55	223423_at	GPR160	G protein-coupled receptor 160
344	0.003992	12.3	10.8	-1.14	238917_s_at	MGC24039	Hypothetical protein MGC24039
345	0.003999	36.9	48.4	1.31	226395_at	LOC286170	Hypothetical protein LOC286170
346	0.004021	155.6	222.8	1.43	215000_s_at	FEZ2	Fasciculation and elongation protein zeta 2 (zygin II)
347	0.004032	196.3	235.6	1.20	203605_at	SRP54	Signal recognition particle 54kDa
348	0.004054	7.7	6.6	-1.17	242805_at	EST57	---
349	0.004085	50.4	66.2	1.31	204043_at	TCN2	Transcobalamin II; macrocytic anemia
350	0.004142	9.8	11.4	1.16	237845_at	EST58	Transcribed locus, moderately similar to XP_001103240.1 similar to kinesin family member 27 (Macaca mulatta)
351	0.004144	28.5	22.5	-1.27	1569499_at	EST59	CDNA clone IMAGE:3840913

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
352	0.004179	21.1	18.5	-1.14	217876_at	GTF3C5	General transcription factor IIIC, polypeptide 5, 63kDa
353	0.004185	9.9	15.3	1.55	223660_at	ADORA3	Adenosine A3 receptor
354	0.004186	5.8	6.3	1.09	231160_at	EST60	Transcribed locus
355	0.00419	9.7	15.7	1.62	236901_at	EST61	Transcribed locus
356	0.0042	20.9	18	-1.16	215979_s_at	SLC7A1	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
357	0.004234	1525.2	1779.3	1.17	208736_at	ARPC3	Actin related protein 2/3 complex, subunit 3, 21kDa
358	0.004238	82.6	123.2	1.49	229383_at	EST62	CDNA FLJ34016 fis, clone FCBBF2002541
359	0.004265	32	27.2	-1.18	32137_at	JAG2	Jagged 2
360	0.004278	7.6	6.9	-1.10	213249_at	FBXL7	F-box and leucine-rich repeat protein 7
361	0.004288	2770.3	3252	1.17	202803_s_at	ITGB2	Integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
362	0.004321	119	159.5	1.34	203310_at	STXBP3	Syntaxin binding protein 3
363	0.004335	798.5	1181	1.48	202295_s_at	CTSH	Cathespin H
364	0.004354	10.4	9.1	-1.14	220994_s_at	STXBP6	Syntaxin binding protein 6 (amisyn)
365	0.004355	49	90.4	1.84	212224_at	ALDH1A1	Aldehyde dehydrogenase 1 family, member A1
366	0.004381	208.3	260.9	1.25	212120_at	RHOQ	Ras homolog gene family, member Q
367	0.004435	32.8	29.9	-1.10	37586_at	ZNF142	Zinc finger protein 142
368	0.004453	285.1	404.8	1.42	219356_s_at	CHMP5	Chromatin modifying protein 5
369	0.004458	118.6	152.6	1.29	241370_at	LOC286052	Hypothetical protein LOC286052
370	0.004465	13.1	11.4	-1.15	1558476_at	C1orf165	Chromosome 1 open reading frame 165
371	0.004485	5.5	6.2	1.13	206533_at	CHRNA5	Cholinergic receptor, nicotinic, alpha 5
372	0.004489	33.2	28.8	-1.15	229979_x_at	EST63	Transcribed locus
373	0.004526	66.2	83.5	1.26	200764_s_at	CTNNA1	Catenin (cadherin-associated protein), alpha 1, 102kDa
374	0.004556	7.3	6.5	-1.12	240874_at	EST64	Transcribed locus
375	0.004558	20.4	17.2	-1.19	1556672_a_at	RBM6	RNA binding motif protein 6
376	0.004559	13.6	10.9	-1.25	236268_at	SEC22C	SEC22 vesicle trafficking protein homolog C (S.

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
							cerevisiae)
377	0.004594	68.3	57	-1.20	220968_s_at	TSPAN9	Tetraspanin 9
378	0.004616	363.3	284.7	-1.28	223042_s_at	FUNDC2	FUN14 domain containing 2
379	0.004683	6.9	9.4	1.36	226311_at	EST65	CDNA clone IMAGE:30924414
380	0.004699	5	4.7	-1.06	1570482_at	EST66	Pp14356
381	0.00476	5.9	6.6	1.12	1562274_at	EST67	MRNA; cDNA DKFZp 313I0929 (from clone DKFZp313I0929)
382	0.004769	40.5	32.8	-1.23	201792_at	AEBP1	AE binding protein 1
383	0.004776	11.7	13.7	1.17	229671_s_at	C21orf45	Chromosome 21 open reading frame 45
384	0.004783	23	15.8	-1.46	208501_at	GFI1B	Growth factor independent 1B (potential regulator of CDKN1A, translocated in CML)
385	0.004788	6.6	5.9	-1.12	206142_at	ZNF135	Zing finger protein 135
386	0.004813	6.9	6.4	-1.08	233594_at	EST68	CDNA clone IMAGE:4823221
387	0.004845	9	8	-1.13	1565407_at	LHX9	LIM homeobox 9
388	0.004861	7.1	6.3	-1.13	1559634_at	CHRM3	Cholinergic receptor, muscarinic 3
389	0.004927	23.8	36.5	1.53	236297_at	EST69	CDNA FLI45742 fis, clone KIDNE2016327
390	0.004932	29.6	33.1	1.12	215930_s_at	CTAGE5	CTAGE family, member 5
391	0.004946	101.1	128.9	1.27	209463_s_at	TAF12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa
392	0.004975	26.4	18.6	-1.42	206759_at	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23)
393	0.004988	14.3	12.3	-1.16	230950_at	EST70	Transcribed locus

TABLE B

Differentially expressed consensus genes for moderate/severe CAN/IFTA for both Test Sets

Moderate/Severe CAN/IFTA = CAN/IFTA Banff Class 2,3; No evidence of CAN/IFTA = CAN/IFTA Banff Class 0

Probesets with positive fold changes are upregulated in moderate/severe CAN

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 2,3	Ratio of geom means	Probe Set ID	Gene Symbol	Gene Title
1	0.0001775	11.1	9	-1.23	1566879_at	EST1	ATP/GTP binding protein-like 1
2	0.0003852	4.9	4.5	-1.09	241139_at	EST2	---
3	0.0004281	5.5	6.1	1.11	231591_at	BHMT	anthrax toxin receptor 2
4	0.0004852	20.5	26.2	1.28	242619_x_at	EST3	---
5	0.0005716	20.8	34.5	1.66	206674_at	FLT3	LIM homeobox 9
6	0.0005983	5.6	4.9	-1.14	204005_s_at	PAWR	---
7	0.0006361	23	39.6	1.72	220112_at	ANKRD55	---
8	0.0006841	6.6	5.9	-1.12	239312_at	EST4	Phospholipase C epsilon
9	0.0007962	21.4	28.1	1.31	205977_s_at	EPHA1	---
10	0.0008868	9.3	8.1	-1.15	210412_at	GRIN2B	olfactory receptor, family 8, subfamily G, member 1
11	0.0008881	5	4.5	-1.11	216089_at	MCFD2L	---
12	0.0009531	10	8.5	-1.18	226211_at	MEG3	PRKC, apoptosis, WT1, regulator
13	0.001086	58.7	72.7	1.24	226856_at	MUSTN1	CUG triplet repeat, RNA binding protein 1
14	0.001156	11.7	14.7	1.26	229671_s_at	C21orf45	PBX/knotted 1 homeobox 1
15	0.001212	10	11.6	1.16	219831_at	CDKL3	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa
16	0.0013123	8.7	10	1.15	233429_at	FLJ23577	matrix metallopeptidase 1 (interstitial collagenase)
17	0.0013489	14	19	1.36	210896_s_at	ASPH	IKAROS family zinc finger 1 (Ikaros)
18	0.0014846	9.7	15	1.55	236901_at	EST5	EPH receptor A1
19	0.0015437	7.7	6.8	-1.13	213994_s_at	SPON1	fms-related tyrosine kinase 3
20	0.0015498	11	9.5	-1.16	242417_at	LOC283278	cytochrome P450, family 4, subfamily B, polypeptide 1
21	0.0015652	6.3	5.6	-1.13	229777_at	CLRN3	glutamate receptor, ionotropic, N-methyl D-aspartate 2B

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensitie s in class 2: Banff 2,3	Ratio of geom means	Probe Set ID	Gene Symbol	Gene Title
22	0.0016885	311.3	218.7	-1.42	205039_s_at	IKZF1	aspartate beta-hydroxylase
23	0.0017597	18.8	22.5	1.20	204113_at	CUGBP1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
24	0.0019344	11.6	14.8	1.28	233650_at	CEP63	met proto-oncogene (hepatocyte growth factor receptor)
25	0.0019513	42.8	57	1.33	236832_at	LOC221442	spondin 1, extracellular matrix protein
26	0.0019757	21.9	18.6	-1.18	228721_at	C3orf41	---
27	0.0020356	6.9	8.9	1.29	226311_at	EST6	secretogranin III
28	0.0020555	5.5	4.6	-1.20	1566428_at	EST7	cyclin-dependent kinase-like 3
29	0.0020848	18.7	15	-1.25	229532_at	ZNF502	ankyrin repeat domain 55
30	0.0021794	10.6	12	1.13	1554615_at	EST8	heparan-alpha-glucosaminide N-acetyltransferase
31	0.0022636	5.9	5.4	-1.09	230650_at	EST9	family with sequence similarity 135, member A
32	0.0022797	76.1	62.4	-1.22	204459_at	CSTF2	maternally expressed 3 (non-protein coding)
33	0.0023808	5.3	4.8	-1.10	1570050_at	EST10	---
34	0.0023855	4.7	4.3	-1.09	1566096_x_at	EST11	musculoskeletal, embryonic nuclear protein 1
35	0.0025531	9	8	-1.13	1565407_at	LHX9	hexokinase domain containing 1
36	0.0025848	5.1	5.6	1.10	232770_at	TUSC3	---
37	0.0026131	6.4	5.6	-1.14	204475_at	MMP1	hypothetical protein LOC90784
38	0.0026527	11.3	14.3	1.27	243349_at	KIAA1324	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)
39	0.0027257	5.7	5.1	-1.12	240604_at	EXOD1	chromosome 3 open reading frame 41
40	0.0027342	6	5.6	-1.07	210096_at	CYP4B1	RNA binding protein with multiple splicing 2
41	0.0027896	39.3	22	-1.79	228390_at	EST12	hypothetical protein LOC729680
42	0.0027907	6.3	6.9	1.10	228977_at	LOC729680	nuclear receptor subfamily 2, group F, member 2
43	0.0028215	9.5	10.6	1.12	213807_x_at	MET	zinc finger protein 502
44	0.0028343	7.9	6.7	-1.18	228716_at	THRB	CDNA FLJ90800 fis, clone Y79AA1000127
45	0.0029105	6.1	10.7	1.75	1560800_at	EST13	clarin 3
46	0.0031196	12.6	14.3	1.13	1567060_at	OR8G1	---

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 2,3	Ratio of geom means	Probe Set ID	Gene Symbol	Gene Title
47	0.0033408	24.1	19.6	-1.23	223497_at	FAM135A	Betaine:homocysteine methyltransferase
48	0.0039416	5.3	5.9	1.11	211524_at	NFKB2	tumor suppressor candidate 3
49	0.0039539	14.2	12.3	-1.15	241261_x_at	EST14	sperm flagellar 2
50	0.003958	12.1	10.5	-1.15	243048_at	CECR7	centrosomal protein 63kDa
51	0.0040206	34.8	22.1	-1.57	228802_at	RBPMS2	---
52	0.004032	4.7	4.4	-1.07	219196_at	SCG3	*hypothetical LOC221442*
53	0.0041033	18.9	24.7	1.31	227614_at	HKDC1	---
54	0.0041799	39.2	46	1.17	204195_s_at	PKNOX1	---
55	0.0042431	25	30.2	1.21	228515_at	LOC90784	exoribonuclease 2
56	0.0042468	9.7	8.7	-1.11	1566739_at	PLCE1	---
57	0.0043315	27.7	33.5	1.21	222491_at	HGSNAT	---
58	0.0044839	7.3	8.1	1.11	1553447_at	AGBL1	---
59	0.0045669	6.7	6.2	-1.08	229092_at	EST15	hypothetical protein LOC283278
60	0.0047554	9.7	11.1	1.14	233993_at	EST16	---
61	0.004775	17.7	21	1.19	242264_at	EST17	cat eye syndrome chromosome region, candidate 7
62	0.0048752	34.1	38.1	1.12	1555536_at	ANTXR2	KIAA1324

TABLE C

Differentially expressed consensus genes for mild CAN/IFTA for both Test Sets
Mild CAN/IFTA = CAN/IFTA Banff Class 1; No evidence of CAN/IFTA = CAN/IFTA Banff Class 0

Probesets with positive fold changes are upregulated in mild CAN

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
1	0.000002	27.9	19.3	-1.45	203796_s_at	BCL7A	B-cell CLL/lymphoma 7A
2	2.1E-06	11.6	16.7	1.44	233650_at	CEP63	centrosomal protein 63kDa
3	3.2E-06	50.5	40.1	-1.26	1552892_at	TNFRSF13C	tumor necrosis factor receptor superfamily, member 13C
4	5.9E-06	19.2	33.6	1.75	1565597_at	EST1	Homo sapiens, clone IMAGE:4275461, mRNA
5	8.3E-06	15.1	23.5	1.56	241752_at	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1
6	1.25E-05	803.7	1050.5	1.31	213702_x_at	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1
7	1.61E-05	224.8	174.8	-1.29	223259_at	ORMDL3	ORM1-like 3 (S. cerevisiae)
8	1.84E-05	135.4	189.9	1.40	204054_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
9	1.86E-05	26	46	1.77	239012_at	IBRDC2	IBR domain containing 2
10	2.39E-05	1182	1724.7	1.46	200975_at	PPT1	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile)
11	0.000024	174.3	363.5	2.09	206584_at	LY96	lymphocyte antigen 96
12	3.35E-05	9	7.6	-1.18	228044_at	C13orf21	chromosome 13 open reading frame 21
13	4.41E-05	250.1	327.6	1.31	225492_at	EST2	---
14	4.53E-05	7828	10660.2	1.36	202917_s_at	S100A8	S100 calcium binding protein A8
15	0.000047	374.1	724.5	1.94	223501_at	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b
16	4.75E-05	112.7	204	1.81	222496_s_at	FLJ20273	RNA-binding protein
17	5.11E-05	22.4	38.8	1.73	224996_at	EST3	CDNA FLJ39064 fis, clone NT2RP7014583
18	5.13E-05	21.6	17.5	-1.23	244863_at	EST4	Transcribed locus
19	0.000052	7.5	9	1.20	238791_at	ZNF100	zinc finger protein 100

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
20	5.66E-05	85.2	123.8	1.45	218177_at	CHMP1B	chromatin modifying protein 1B
21	5.67E-05	203.3	336.4	1.65	226208_at	ZSWIM6	zinc finger, SWIM-type containing 6
22	7.26E-05	180.8	237.2	1.31	203778_at	MANBA	mannosidase, beta A, lysosomal
23	0.000089	86.6	123.4	1.42	238903_at	LOC137886	hypothetical protein LOC137886
24	0.000094	19.7	14.5	-1.36	214308_s_at	HGD	homogentisate 1,2-dioxygenase (homogentisate oxidase)
25	0.000103	492.9	744.6	1.51	211368_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
26	0.000103	132.8	184.8	1.39	227017_at	ERICH1	glutamate-rich 1
27	0.000107	10.3	15.5	1.50	228624_at	TMEM144	transmembrane protein 144
28	0.000108	128.7	170.2	1.32	232149_s_at	NSMAF	neutral sphingomyelinase (N-SMase) activation associated factor
29	0.000112	26.4	35.2	1.33	243287_s_at	OSTM1	osteopetrosis associated transmembrane protein 1
30	0.000116	59.5	134.7	2.26	1552773_at	CLEC4D	C-type lectin domain family 4, member D
31	0.000121	2887.4	3972.4	1.38	202902_s_at	CTSS	cathepsin S
32	0.000125	142.4	229	1.61	211744_s_at	CD58	CD58 molecule
33	0.000133	35.6	26.9	-1.32	243507_s_at	C20orf196	chromosome 20 open reading frame 196
34	0.000137	101.9	77.4	-1.32	228832_at	FLJ20021	hypothetical LOC90024
35	0.000149	1057.6	1433.5	1.36	202727_s_at	IFNGR1	interferon gamma receptor 1
36	0.000169	40.5	55.5	1.37	213952_s_at	ALOX5	Arachidonate 5-lipoxygenase
37	0.000174	364.6	288.1	-1.27	219045_at	RHOF	ras homolog gene family, member F (in filopodia)
38	0.000175	666	974.1	1.46	212268_at	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1
39	0.00018	80.3	119.4	1.49	203276_at	LMNB1	lamin B1
40	0.00019	347.2	814.1	2.34	219666_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
41	0.000204	54.9	110.9	2.02	204860_s_at	NAIP /// NAIP1B	NLR family, apoptosis inhibitory protein /// neuronal apoptosis inhibitory protein (centromeric)
42	0.000212	3812.4	4958.6	1.30	202388_at	RGS2	regulator of G-protein signaling 2, 24kDa
43	0.000226	24.5	43.9	1.79	1553514_a_at	VNN3	vanin 3
44	0.000239	84.6	108.3	1.28	218364_at	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 1	Fold Change	Probe Set ID	Gene Symbol	Gene Title
45	0.000242	15.5	21.5	1.39	218888_s_at	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2
46	0.000258	64.6	87.8	1.36	204108_at	NFYA	nuclear transcription factor Y, alpha
47	0.000273	35.6	50.1	1.41	213935_at	ABHD5	abhydrolase domain containing 5
48	0.000278	54	75.5	1.40	208883_at	UBR5	ubiquitin protein ligase E3 component n-recognin 5
49	0.000282	334.9	425	1.27	222148_s_at	RHOT1	ras homolog gene family, member T1
50	0.000284	564.8	712.6	1.26	227266_s_at	FYB	FYN binding protein (FYB-120/130)

TABLE D

Top 50 Differentially expressed consensus genes for moderate/severe CAN/IFTA for both Test Sets

Moderate/Severe CAN/IFTA = CAN/IFTA Banff Class 2,3; No evidence of CAN/IFTA = CAN/IFTA Banff Class 0

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 2,3	Ratio of geom means	Probe Set ID	Gene Symbol	Gene Title
1	0.000178	11.1	9	-1.23	1566879_at	EST1	ATP/GTP binding protein-like 1
2	0.000385	4.9	4.5	-1.09	241139_at	EST2	---
3	0.000428	5.5	6.1	1.11	231591_at	BHMT	anthrax toxin receptor 2
4	0.000485	20.5	26.2	1.28	242619_x_at	EST3	---
5	0.000572	20.8	34.5	1.66	206674_at	FLT3	LIM homeobox 9
6	0.000598	5.6	4.9	-1.14	204005_s_at	PAWR	---
7	0.000636	23	39.6	1.72	220112_at	ANKRD55	---
8	0.000684	6.6	5.9	-1.12	239312_at	EST4	Phospholipase C epsilon
9	0.000796	21.4	28.1	1.31	205977_s_at	EPHA1	---
10	0.000887	9.3	8.1	-1.15	210412_at	GRIN2B	olfactory receptor, family 8, subfamily G, member 1
11	0.000888	5	4.5	-1.11	216089_at	MCFD2L	---
12	0.000953	10	8.5	-1.18	226211_at	MEG3	PRKC, apoptosis, WT1, regulator
13	0.001086	58.7	72.7	1.24	226856_at	MUSTN1	CUG triplet repeat, RNA binding protein 1
14	0.001156	11.7	14.7	1.26	229671_s_at	C21orf45	PBX/knotted 1 homeobox 1
15	0.001212	10	11.6	1.16	219831_at	CDKL3	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa
16	0.001312	8.7	10	1.15	233429_at	FLJ23577	matrix metallopeptidase 1 (interstitial collagenase)
17	0.001349	14	19	1.36	210896_s_at	ASPH	IKAROS family zinc finger 1 (Ikaros)
18	0.001485	9.7	15	1.55	236901_at	EST5	EPH receptor A1
19	0.001544	7.7	6.8	-1.13	213994_s_at	SPON1	fms-related tyrosine kinase 3
20	0.00155	11	9.5	-1.16	242417_at	LOC283278	cytochrome P450, family 4, subfamily B, polypeptide 1
21	0.001565	6.3	5.6	-1.13	229777_at	CLRN3	glutamate receptor, ionotropic, N-methyl D-aspartate 2B

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 2,3	Ratio of geom means	Probe Set ID	Gene Symbol	Gene Title
22	0.001689	311.3	218.7	-1.42	205039_s_at	IKZF1	aspartate beta-hydroxylase
23	0.00176	18.8	22.5	1.20	204113_at	CUGBP1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
24	0.001934	11.6	14.8	1.28	233650_at	CEP63	met proto-oncogene (hepatocyte growth factor receptor)
25	0.001951	42.8	57	1.33	236832_at	LOC221442	spondin 1, extracellular matrix protein
26	0.001976	21.9	18.6	-1.18	228721_at	C3orf41	---
27	0.002036	6.9	8.9	1.29	226311_at	EST6	secretogranin III
28	0.002056	5.5	4.6	-1.20	1566428_at	EST7	cyclin-dependent kinase-like 3
29	0.002085	18.7	15	-1.25	229532_at	ZNF502	ankyrin repeat domain 55
30	0.002179	10.6	12	1.13	1554615_at	EST8	heparan-alpha-glucosaminide N-acetyltransferase
31	0.002264	5.9	5.4	-1.09	230650_at	EST9	family with sequence similarity 135, member A
32	0.00228	76.1	62.4	-1.22	204459_at	CSTF2	maternally expressed 3 (non-protein coding)
33	0.002381	5.3	4.8	-1.10	1570050_at	EST10	---
34	0.002386	4.7	4.3	-1.09	1566096_x_at	EST11	musculoskeletal, embryonic nuclear protein 1
35	0.002553	9	8	-1.13	1565407_at	LHX9	hexokinase domain containing 1
36	0.002585	5.1	5.6	1.10	232770_at	TUSC3	---
37	0.002613	6.4	5.6	-1.14	204475_at	MMP1	hypothetical protein LOC90784
38	0.002653	11.3	14.3	1.27	243349_at	KIAA1324	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)
39	0.002726	5.7	5.1	-1.12	240604_at	EXOD1	chromosome 3 open reading frame 41
40	0.002734	6	5.6	-1.07	210096_at	CYP4B1	RNA binding protein with multiple splicing 2
41	0.00279	39.3	22	-1.79	228390_at	EST12	hypothetical protein LOC729680
42	0.002791	6.3	6.9	1.10	228977_at	LOC729680	nuclear receptor subfamily 2, group F, member 2
43	0.002822	9.5	10.6	1.12	213807_x_at	MET	zinc finger protein 502
44	0.002834	7.9	6.7	-1.18	228716_at	THRB	CDNA FLJ90800 fis, clone Y79AA1000127
45	0.002911	6.1	10.7	1.75	1560800_at	EST13	clarin 3

	Parametric p-value	Geom mean of intensities in class 1: Banff 0	Geom mean of intensities in class 2: Banff 2,3	Ratio of geom means	Probe Set ID	Gene Symbol	Gene Title
46	0.00312	12.6	14.3	1.13	1567060_at	OR8G1	---
47	0.003341	24.1	19.6	-1.23	223497_at	FAM135A	Betaine:homocysteine methyltransferase
48	0.003942	5.3	5.9	1.11	211524_at	NFKB2	tumor suppressor candidate 3
49	0.003954	14.2	12.3	-1.15	241261_x_at	EST14	sperm flagellar 2
50	0.003958	12.1	10.5	-1.15	243048_at	CECR7	centrosomal protein 63kDa

TABLE E

	International Protein Index/UniGene	Symbol	Entrez Gene Name
1	Hs.103854	DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)
2	Hs.109752	C6ORF108	chromosome 6 open reading frame 108
3	Hs.110675	APOC1	apolipoprotein C-I
4	Hs.116459	MAN2A2	mannosidase, alpha, class 2A, member 2
5	Hs.117331	TREML1	triggering receptor expressed on myeloid cells-like 1
6	Hs.119177	ARF3	ADP-ribosylation factor 3
7	Hs.123198	MYO9B	myosin IXB
8	Hs.134084	M6PR	mannose-6-phosphate receptor (cation dependent)
9	Hs.151135	FN3K	fructosamine 3 kinase
10	Hs.159509	SERPINF2	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2
11	Hs.190334	RAP1A	RAP1A, member of RAS oncogene family
12	Hs.191215	CYTH1	cytohesin 1
13	Hs.202	TSPO	translocator protein (18kDa)
14	Hs.203637	PLS1	plastin 1 (I isoform)
15	Hs.226007	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)
16	Hs.24178	EML2	echinoderm microtubule associated protein like 2
17	Hs.24258	GUCY1A3	guanylate cyclase 1, soluble, alpha 3
18	Hs.24889	FMN2	formin 2
19	Hs.260750	SNX12	sorting nexin 12
20	Hs.277624	ZZEF1	zinc finger, ZZ-type with EF-hand domain 1
21	Hs.287714	RAB32	RAB32, member RAS oncogene family
22	Hs.301412	UFC1	ubiquitin-fold modifier conjugating enzyme 1
23	Hs.306327	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)
24	Hs.327527	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
25	Hs.363396	CFH	complement factor H

	International Protein Index/UniGene	Symbol	Entrez Gene Name
26	Hs.368078	DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2
27	Hs.368527	TOLLIP	toll interacting protein
28	Hs.368626	RTN1	reticulon 1
29	Hs.369840	NID2	nidogen 2 (osteonidogen)
30	Hs.376933	GUK1	guanylate kinase 1
31	Hs.38449	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2
32	Hs.390567	FYN	FYN oncogene related to SRC, FGR, YES
33	Hs.390667	GSTK1	glutathione S-transferase kappa 1
34	Hs.411312	ITGA2B (includes EG:3674)	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)
35	Hs.414795	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
36	Hs.416848	CTSW	cathepsin W
37	Hs.420529	UBE2V1	ubiquitin-conjugating enzyme E2 variant 1
38	Hs.429608	REEP5	receptor accessory protein 5
39	Hs.433068	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta
40	Hs.435291	ARHGAP6	Rho GTPase activating protein 6
41	Hs.435512	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform
42	Hs.438906	C22ORF30	chromosome 22 open reading frame 30
43	Hs.443976	CEP250	centrosomal protein 250kDa
44	Hs.458917	SCAMP2	secretory carrier membrane protein 2
45	Hs.460109	MYH11	myosin, heavy chain 11, smooth muscle
46	Hs.462379	TOM1L2	target of myb1-like 2 (chicken)
47	Hs.464813	PSMA8	proteasome (prosome, macropain) subunit, alpha type, 8
48	Hs.465295	LMAN1	lectin, mannose-binding, 1
49	Hs.466910	CDA	cytidine deaminase
50	Hs.477009	USP24	ubiquitin specific peptidase 24
51	Hs.477352	PDIA5	protein disulfide isomerase family A, member 5

	International Protein Index/UniGene	Symbol	Entrez Gene Name
52	Hs.4779	GATAD2B	GATA zinc finger domain containing 2B
53	Hs.480364	METAP1	methionyl aminopeptidase 1
54	Hs.481836	MTMR12	myotubularin related protein 12
55	Hs.481860	TARS	threonyl-tRNA synthetase
56	Hs.482873	TMED5	transmembrane emp24 protein transport domain containing 5
57	Hs.487540	RPA3	replication protein A3, 14kDa
58	Hs.49582	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A
59	Hs.501200	RGS10	regulator of G-protein signaling 10
60	Hs.502244	EIF3M	eukaryotic translation initiation factor 3, subunit M
61	Hs.50382	TJP2	tight junction protein 2 (zona occludens 2)
62	Hs.506603	APPL2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2
63	Hs.513055	WDR61	WD repeat domain 61
64	Hs.513646	IVD	isovaleryl Coenzyme A dehydrogenase
65	Hs.514012	MAP2K3	mitogen-activated protein kinase kinase 3
66	Hs.514199	VAT1	vesicle amine transport protein 1 homolog (T. californica)
67	Hs.514870	ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1
68	Hs.520048	HLA-DRA	major histocompatibility complex, class II, DR alpha
69	Hs.524518	STAT6	signal transducer and activator of transcription 6, interleukin-4 induced
70	Hs.525419	LIMA1	LIM domain and actin binding 1
71	Hs.528952	TRIM25	tripartite motif-containing 25
72	Hs.529023	ZNF532	zinc finger protein 532
73	Hs.530096	EIF3I (includes EG:8668)	eukaryotic translation initiation factor 3, subunit I
74	Hs.573495	SLC44A1	solute carrier family 44, member 1
75	Hs.578450	MESDC2	mesoderm development candidate 2
76	Hs.584790	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform
77	Hs.592771	DGKG	diacylglycerol kinase, gamma 90kDa
78	Hs.620557	ANK2	ankyrin 2, neuronal
79	Hs.631569	PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A
80	Hs.63348	EMILIN1	elastin microfibril interfacer 1

	International Protein Index/UniGene	Symbol	Entrez Gene Name
80	Hs.63348	EMILIN1	elastin microfibril interfacer 1
81	Hs.64016	PROS1	protein S (alpha)
82	Hs.647018	CLIP2	CAP-GLY domain containing linker protein 2
83	Hs.647064	RARRES2	retinoic acid receptor responder (tazarotene induced) 2
84	Hs.653263	CEP110	centrosomal protein 110kDa
85	Hs.654404	HLA-C	major histocompatibility complex, class I, C
86	Hs.654439	APOE	apolipoprotein E
87	Hs.654473	MAOB	monoamine oxidase B
88	Hs.654581	PRPS2	phosphoribosyl pyrophosphate synthetase 2
89	Hs.654634	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)
90	Hs.655207	F2	coagulation factor II (thrombin)
91	Hs.655361	HPR (includes EG:3250)	haptoglobin-related protein
92	Hs.656274	TNFAIP8	tumor necrosis factor, alpha-induced protein 8
93	Hs.656726	STRN	striatin, calmodulin binding protein
94	Hs.658434	PSIP1	PC4 and SFRS1 interacting protein 1
95	Hs.660130	CD226	CD226 molecule
96	Hs.695926	RASA1	RAS p21 protein activator (GTPase activating protein) 1
97	Hs.696074	DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15
98	Hs.696326	ANO6	anoctamin 6
99	Hs.699154	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
100	Hs.7486	ETHE1	ethylmalonic encephalopathy 1
101	Hs.7753	CALU	calumenin
102	Hs.77741	KNG1 (includes EG:3827)	kininogen 1
103	Hs.79322	QARS	glutaminyl-tRNA synthetase
104	Hs.8004	KALRN	kalirin, RhoGEF kinase
105	Hs.81934	ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain
106	Hs.90061	PGRMC1	progesterone receptor membrane component 1
107	Hs.904	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase

	International Protein Index/UniGene	Symbol	Entrez Gene Name
108	IPI00010951	EPPK1	epiplakin 1
109	IPI00011891	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit
110	IPI00165421	SERPINC1	serpin peptidase inhibitor, clade C (antithrombin), member 1
111	IPI00301271	RPN2	ribophorin II
112	IPI00382606	F7	coagulation factor VII (serum prothrombin conversion accelerator)
113	IPI00448925	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)
114	IPI00783829	IPO5	importin 5
115	IPI00787190	HLA-B	major histocompatibility complex, class I, B
116	IPI00788786	VWF	von Willebrand factor
117	IPI00797856	HPSE	heparanase

TABLE F

	International Protein Index/UniGene	Symbol	Entrez Gene Name
1	IPI00001753	MYH4	myosin, heavy chain 4, skeletal muscle
2	Hs.110837	TUBB4	tubulin, beta 4
3	Hs.132499	ARPC5L (includes EG:81873)	actin related protein 2/3 complex, subunit 5-like
4	Hs.133892	TPM1	tropomyosin 1 (alpha)
5	Hs.143046	CORO6	coronin 6
6	Hs.1437	GAA	glucosidase, alpha; acid
7	Hs.143703	EHD4	EH-domain containing 4
8	Hs.147433	PCNA	proliferating cell nuclear antigen
9	Hs.148641	CTSH	cathepsin H
10	Hs.154078	LBP	lipopolysaccharide binding protein
11	Hs.156367	RPS29	ribosomal protein S29
12	Hs.158339	SERPINB10	serpin peptidase inhibitor, clade B (ovalbumin), member 10
13	Hs.161357	PDHB (includes EG:5162)	pyruvate dehydrogenase (lipoamide) beta
14	Hs.16355	MYH10	myosin, heavy chain 10, non-muscle
15	Hs.163867	CD14	CD14 molecule
16	Hs.164144	EIF5A2	eukaryotic translation initiation factor 5A2
17	Hs.169284	PRPS1L1	phosphoribosyl pyrophosphate synthetase 1-like 1
18	Hs.169900	PABPC4	poly(A) binding protein, cytoplasmic 4 (inducible form)
19	Hs.170310	CECR1	cat eye syndrome chromosome region, candidate 1
20	Hs.171626	SKP1	S-phase kinase-associated protein 1
21	Hs.173043	MTA2	metastasis associated 1 family, member 2
22	Hs.188401	ANXA10	annexin A10
23	Hs.189409	FNBP1	formin binding protein 1
24	Hs.196437	MOBKL1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)
25	Hs.200333	APOB48R	apolipoprotein B48 receptor

	International Protein Index/UniGene	Symbol	Entrez Gene Name
26	Hs.213470	PSMB7	proteasome (prosome, macropain) subunit, beta type, 7
27	Hs.220594	CCDC58	coiled-coil domain containing 58
28	Hs.224171	ENO3	enolase 3 (beta, muscle)
29	Hs.236030	SMARCC2 (includes EG:6601)	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2
30	Hs.248746	AGXT2L2	alanine-glyoxylate aminotransferase 2-like 2
31	Hs.252549	CTSZ (includes EG:1522)	cathepsin Z
32	Hs.258314	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)
33	Hs.263812	NUDC	nuclear distribution gene C homolog (A. nidulans)
34	Hs.268963	UBAP1	ubiquitin associated protein 1
35	Hs.279640	TPR	translocated promoter region (to activated MET oncogene)
36	Hs.282901	RBM39	RNA binding motif protein 39
37	Hs.284491	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase
38	Hs.309090	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa
39	Hs.3100	KARS	lysyl-tRNA synthetase
40	Hs.31053	TBCB	tubulin folding cofactor B
41	Hs.319334	NASP	nuclear autoantigenic sperm protein (histone-binding)
42	Hs.325978	NUMA1	nuclear mitotic apparatus protein 1
43	Hs.335034	DPYD	dihydropyrimidine dehydrogenase
44	Hs.337766	RPL18A	ribosomal protein L18a
45	Hs.3439	STOML2	stomatin (EPB72)-like 2
46	Hs.356604	WNK1	WNK lysine deficient protein kinase 1
47	Hs.368077	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8
48	Hs.368203	DOCK11	dedicator of cytokinesis 11
49	Hs.368266	CLTCL1	clathrin, heavy chain-like 1
50	Hs.36927	HSPH1	heat shock 105kDa/110kDa protein 1
51	Hs.369373	SEC23B	Sec23 homolog B (S. cerevisiae)
52	Hs.375957	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
53	Hs.376933	GUK1	guanylate kinase 1

	International Protein Index/UniGene	Symbol	Entrez Gene Name
54	Hs.388664	RPL11	ribosomal protein L11
55	Hs.403436	DCI	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
56	Hs.406423	SF3B2	splicing factor 3b, subunit 2, 145kDa
57	Hs.407190	FKBP5	FK506 binding protein 5
58	Hs.408061	FABP5	fatty acid binding protein 5 (psoriasis-associated)
59	Hs.408236	TXNDC17	thioredoxin domain containing 17
60	Hs.409834	PHPT1	phosphohistidine phosphatase 1
61	Hs.412117	ANXA6	annexin A6
62	Hs.429180	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
63	Hs.432674	LARS	leucyl-tRNA synthetase
64	Hs.433222	NPC2	Niemann-Pick disease, type C2
65	Hs.434996	GIT2	G protein-coupled receptor kinase interacting ArfGAP 2
66	Hs.437385	NECAP2	NECAP endocytosis associated 2
67	Hs.440895	MYH3	myosin, heavy chain 3, skeletal muscle, embryonic
68	Hs.440932	9-Sep	septin 9
69	Hs.460002	FLJ11151	hypothetical protein FLJ11151
70	Hs.461925	RPA1	replication protein A1, 70kDa
71	Hs.465224	NARS	asparaginyl-tRNA synthetase
72	Hs.465761	ARHGEF18	rho/rac guanine nucleotide exchange factor (GEF) 18
73	Hs.465924	SDHB (includes EG:6390)	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
74	Hs.470627	LCK	lymphocyte-specific protein tyrosine kinase
75	Hs.471207	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
76	Hs.477126	ATG3	ATG3 autophagy related 3 homolog (S. cerevisiae)
77	Hs.484412	EXOC2	exocyst complex component 2
78	Hs.491440	PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
79	Hs.494496	FBP1	fructose-1,6-bisphosphatase 1
80	Hs.494595	TMOD1	tropomodulin 1
81	Hs.497599	WARS	tryptophanyl-tRNA synthetase
82	Hs.502328	CD44	CD44 molecule (Indian blood group)

	International Protein Index/UniGene	Symbol	Entrez Gene Name
83	Hs.502756	AHNAK	AHNAK nucleoprotein
84	Hs.505033	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
85	Hs.5086	RBM42	RNA binding motif protein 42
86	Hs.508738	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7
87	Hs.509736	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1
88	Hs.513726	GBP5	guanylate binding protein 5
89	Hs.514495	SRP68	signal recognition particle 68kDa
90	Hs.514581	ACTG1	actin, gamma 1
91	Hs.517307	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
92	Hs.517949	MAP4	microtubule-associated protein 4
93	Hs.518198	CSTA (includes EG:1475)	cystatin A (stefin A)
94	Hs.518662	FAM129A	family with sequence similarity 129, member A
95	Hs.521924	PUF60	poly-U binding splicing factor 60KDa
96	Hs.529989	RNASET2	ribonuclease T2
97	Hs.531176	SARS	seryl-tRNA synthetase
98	Hs.531807	ARHGAP25	Rho GTPase activating protein 25
99	Hs.534350	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1
100	Hs.534770	PKM2	pyruvate kinase, muscle
101	Hs.535581	TPM3	tropomyosin 3
102	Hs.55682	EIF3D	eukaryotic translation initiation factor 3, subunit D
103	Hs.583855	SNX6	sorting nexin 6
104	Hs.587558	NCF2	neutrophil cytosolic factor 2
105	Hs.591176	DYNLL2	dynein, light chain, LC8-type 2
106	Hs.591768	BTF3	basic transcription factor 3
107	Hs.591922	SLK	STE20-like kinase (yeast)
108	Hs.632733	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)
109	Hs.643487	ACAA1	acetyl-Coenzyme A acyltransferase 1
110	Hs.649475	RPL24	ribosomal protein L24

	International Protein Index/UniGene	Symbol	Entrez Gene Name
111	Hs.654404	HLA-C	major histocompatibility complex, class I, C
112	Hs.654408	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
113	Hs.654429	SEC24C (includes EG:9632)	SEC24 family, member C (S. cerevisiae)
114	Hs.654521	WIPF1	WAS/WASL interacting protein family, member 1
115	Hs.654543	TUBB2A	tubulin, beta 2A
116	Hs.654597	ACAP2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2
117	Hs.655196	HP	haptoglobin
118	Hs.656726	STRN	striatin, calmodulin binding protein
119	Hs.656870	SLC25A24	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24
120	Hs.687055	PARP14	poly (ADP-ribose) polymerase family, member 14
121	Hs.68714	SFRS1	splicing factor, arginine/serine-rich 1
122	Hs.690634	HSPA1L	heat shock 70kDa protein 1-like
123	Hs.69293	HEXB	hexosaminidase B (beta polypeptide)
124	Hs.695973	HNRNPK	heterogeneous nuclear ribonucleoprotein K
125	Hs.699408	CLINT1	clathrin interactor 1
126	Hs.699441	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2
127	Hs.73839	RNASE3	ribonuclease, RNase A family, 3 (eosinophil cationic protein)
128	Hs.74368	CKAP4	cytoskeleton-associated protein 4
129	Hs.77254	CBX1	chromobox homolog 1 (HP1 beta homolog Drosophila)
130	Hs.77897	SF3A3	splicing factor 3a, subunit 3, 60kDa
131	Hs.78880	ILVBL	ilvB (bacterial acetolactate synthase)-like
132	Hs.79110	NCL	nucleolin
133	Hs.8360	C11ORF54	chromosome 11 open reading frame 54
134	Hs.83753	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1
135	Hs.861	MAPK3	mitogen-activated protein kinase 3
136	Hs.99936	KRT10	keratin 10
137	IPI00074489	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa
138	IPI00384938	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)

	International Protein Index/UniGene	Symbol	Entrez Gene Name
139	IPI00396421	KIAA0776	KIAA0776
140	IPI00401105	RPS25	ribosomal protein S25
141	IPI00413108	RPSA (includes EG:3921)	ribosomal protein SA
142	IPI00456853	FAM21C	family with sequence similarity 21, member C
143	IPI00465022	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1

TABLE G

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
1	Hs.180062	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	1.74748
2	IPI00001539	ACAA2	acetyl-Coenzyme A acyltransferase 2	2.53112
3	Hs.412117	ANXA6	annexin A6	1.99146
4	Hs.90093	HSPA4	heat shock 70kDa protein 4	2.72271
5	Hs.130316	DBN1	drebrin 1	-2.19867
6	IPI00003438	DNAJC8	DnaJ (Hsp40) homolog, subfamily C, member 8	2.74556
7	Hs.186350	RPL4	ribosomal protein L4	1.80696
8	Hs.175437	EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	1.37195
9	Hs.2178	HIST2H2BE	histone cluster 2, H2be	1.73893
10	Hs.524630	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	2.17574
11	Hs.411695	HK3	hexokinase 3 (white cell)	2.79458
12	Hs.489284	ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	1.87474
13	Hs.514934	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1	1.77014
14	Hs.431279	NSF	N-ethylmaleimide-sensitive factor	4.20439
15	Hs.155975	PTPRCAP	protein tyrosine phosphatase, receptor type, C-associated protein	-1.77658
16	Hs.458272	MPO	myeloperoxidase	1.71345
17	Hs.433615	TUBB2C	tubulin, beta 2C	-1.76403
18	Hs.184233	HSPA9	heat shock 70kDa protein 9 (mortalin)	6.35072
19	Hs.295917	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	2.24142
20	Hs.521640	RAD23B	RAD23 homolog B (S. cerevisiae)	1.96378
21	Hs.699880	RPS10	ribosomal protein S10	3.17111
22	Hs.546285	RPLP0 (includes EG:6175)	ribosomal protein, large, P0	2.03495
23	Hs.389649	EIF4A3 (includes EG:9775)	eukaryotic translation initiation factor 4A, isoform 3	1.89742
24	Hs.511251	SQRDL (includes	sulfide quinone reductase-like (yeast)	2.33602

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
		EG:58472)		
25	Hs.26010	PFKP	phosphofructokinase, platelet	-2.73727
26	Hs.78888	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	2.47829
27	Hs.405144	SFRS3	splicing factor, arginine/serine-rich 3	4.47655
28	Hs.413812	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	2.76246
29	Hs.558351	KIF2A	kinesin heavy chain member 2A	-1.41796
30	Hs.355934	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	2.45856
31	Hs.464336	P4HB	prolyl 4-hydroxylase, beta polypeptide	2.20506
32	Hs.131151	PSMD9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	-1.67257
33	Hs.247362	DDAH2	dimethylarginine dimethylaminohydrolase 2	1.98084
34	Hs.356654	PSMC1	proteasome (prosome, macropain) 26S subunit, ATPase, 1	2.36445
35	Hs.527105	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	5.14561
36	Hs.472838	STK4	serine/threonine kinase 4	1.65603
37	Hs.373763	HNRNPR	heterogeneous nuclear ribonucleoprotein R	3.23939
38	Hs.440898	FCN1	ficolin (collagen/fibrinogen domain containing) 1	3.12337
39	Hs.178551	RPL8	ribosomal protein L8	2.39479
40	Hs.644646	KIF5B	kinesin family member 5B	-1.81795
41	Hs.153837	MNDA	myeloid cell nuclear differentiation antigen	2.21411
42	Hs.627414	RPS18	ribosomal protein S18	2.94127
43	Hs.546287	RPS7	ribosomal protein S7	1.83705
44	Hs.497788	EPRS	glutamyl-prolyl-tRNA synthetase	1.99658
45	Hs.511743	TUBB3	tubulin, beta 3	-1.48195
46	Hs.270291	ACTN4	actinin, alpha 4	2.09181
47	Hs.119251	UQCRC1	ubiquinol-cytochrome c reductase core protein I	2.05968
48	Hs.699298	CDV3	CDV3 homolog (mouse)	1.35707
49	Hs.111779	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	-3.78710

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
50	Hs.651923	CNN2	calponin 2	2.25485
51	Hs.465511	GZMM	granzyme M (lymphocyte met-ase 1)	2.38354
52	Hs.2853	PCBP1 (includes EG:5093)	poly(rC) binding protein 1	1.65937
53	Hs.690198	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	1.59084
54	Hs.271510	GSR	glutathione reductase	2.59620
55	Hs.406277	SF3A1	splicing factor 3a, subunit 1, 120kDa	2.92334
56	Hs.571177	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	3.05703
57	Hs.695941	HK1	hexokinase 1	1.48167
58	Hs.250758	PSMC3	proteasome (prosome, macropain) 26S subunit, ATPase, 3	1.90255
59	Hs.707	KRT2	keratin 2	3.19828
60	Hs.594444	LMNA	lamin A/C	2.42545
61	Hs.2490	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.18090
62	Hs.75307	H1FX	H1 histone family, member X	2.60755
63	Hs.534639	HADHB	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	2.04804
64	Hs.30054	F5	coagulation factor V (proaccelerin, labile factor)	-2.31510
65	Hs.533040	PDLIM7	PDZ and LIM domain 7 (enigma)	-2.15116
66	Hs.665429	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	2.97738
67	Hs.695185	NAP1L1	nucleosome assembly protein 1-like 1	-1.56121
68	Hs.75841	ERP29	endoplasmic reticulum protein 29	3.53236
69	Hs.523302	PRDX3	peroxiredoxin 3	1.71589
70	IPI00024989	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase	2.22172
71	Hs.430606	CS	citrate synthase	-2.53628
72	Hs.520973	HSPB1	heat shock 27kDa protein 1	1.89406
73	Hs.118958	STX11	syntaxin 11	-1.57367
74	Hs.610830	PRKCSH	protein kinase C substrate 80K-H	2.25450

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
75	Hs.14601	HCLS1	hematopoietic cell-specific Lyn substrate 1	2.13579
76	Hs.632828	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2 (H')	3.09381
77	Hs.694128	RPS14	ribosomal protein S14	2.10304
78	Hs.356624	NID1	nidogen 1	-4.10930
79	Hs.12084	TUFM	Tu translation elongation factor, mitochondrial	1.77413
80	Hs.95990	PKLR	pyruvate kinase, liver and RBC	2.55932
81	Hs.654614	HSPA6	heat shock 70kDa protein 6 (HSP70B')	1.28057
82	Hs.471441	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	3.18295
83	Hs.7744	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	2.82524
84	Hs.480073	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	2.72172
85	Hs.98791	ACTR1B (includes EG:10120)	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	3.00772
86	IPI00029625	FLOT2	flotillin 2	3.53456
87	Hs.11355	TMPO	thymopoietin	3.65290
88	Hs.571841	RPL7	ribosomal protein L7	1.81095
89	Hs.699271	STAT1	signal transducer and activator of transcription 1, 91kDa	2.36973
90	Hs.529451	DIAPH1	diaphanous homolog 1 (Drosophila)	1.44181
91	Hs.516032	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	4.43165
92	Hs.503043	CPT1A	carnitine palmitoyltransferase 1A (liver)	-1.45507
93	Hs.475074	PARVB	parvin, beta	-1.93236
94	Hs.655396	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	1.89081
95	Hs.122523	SND1	staphylococcal nuclease and tudor domain containing 1	2.96927
96	Hs.444075	UBASH3B	ubiquitin associated and SH3 domain containing, B	-1.85814
97	Hs.473144	CASS4	Cas scaffolding protein family member 4	-2.58235
98	Hs.436186	CAST	calpastatin	1.48337
99	Hs.465808	HNRNPM	heterogeneous nuclear ribonucleoprotein M	2.64995

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
100	Hs.506759	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-1.44671
101	Hs.535581	TPM3	tropomyosin 3	2.05422
102	Hs.654720	KIAA1967	KIAA1967	3.42772
103	Hs.515517	RPL18	ribosomal protein L18	3.72595
104	Hs.438429	RPS19	ribosomal protein S19	4.78644
105	IPI00216134	TPM1	tropomyosin 1 (alpha)	-1.36995
106	Hs.128548	WDR1	WD repeat domain 1	4.48437
107	Hs.519320	VDAC1	voltage-dependent anion channel 1	1.94443
108	Hs.512675	RPS8	ribosomal protein S8	3.35144
109	IPI00216633	EPB49	erythrocyte membrane protein band 4.9 (dematin)	-1.84863
110	Hs.496622	PLS3	plastin 3 (T isoform)	3.79198
111	Hs.654438	ANK1	ankyrin 1, erythrocytic	2.45336
112	Hs.417303	SPTB	spectrin, beta, erythrocytic	1.95917
113	Hs.89497	LMNB1	lamin B1	2.53206
114	Hs.172631	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	6.14877
115	Hs.652308	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	1.36675
116	Hs.411312	ITGA2B (includes EG:3674)	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	3.09010
117	Hs.76392	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	-1.59383
118	Hs.500756	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	1.42300
119	Hs.514196	RPL27	ribosomal protein L27	2.67384
120	Hs.445351	LGALS1	lectin, galactoside-binding, soluble, 1	2.14691
121	Hs.80828	KRT1	keratin 1	3.95879
122	Hs.654559	HNRNPL	heterogeneous nuclear ribonucleoprotein L	-3.40543
123	Hs.119825	SPTA1	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	1.66210
124	Hs.446588	RPS13	ribosomal protein S13	3.62921

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
125	Hs.433427	RPS17 (includes EG:6218)	ribosomal protein S17	4.39840
126	Hs.483305	HINT1	histidine triad nucleotide binding protein 1	-2.04047
127	Hs.476448	FLNB	filamin B, beta (actin binding protein 278)	-1.82786
128	Hs.350899	CAPN2	calpain 2, (m/II) large subunit	2.86704
129	Hs.520967	MDH2	malate dehydrogenase 2, NAD (mitochondrial)	2.20250
130	Hs.371563	RAB14	RAB14, member RAS oncogene family	1.66010
131	Hs.83722	EPS15	epidermal growth factor receptor pathway substrate 15	2.14994
132	Hs.580681	SAMHD1	SAM domain and HD domain 1	2.17687
133	Hs.88778	CBR1	carbonyl reductase 1	1.69648
134	Hs.497599	WARS	tryptophanyl-tRNA synthetase	1.58361
135	Hs.517622	UNC84B	unc-84 homolog B (C. elegans)	1.78160
136	Hs.523145	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	1.71412
137	Hs.539684	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	2.09125
138	Hs.201978	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	-1.72382
139	Hs.370770	XPO1	exportin 1 (CRM1 homolog, yeast)	2.13295
140	Hs.696016	SNX2	sorting nexin 2	1.83066
141	Hs.181301	CTSS	cathepsin S	2.66342
142	Hs.204238	LCN2	lipocalin 2	-2.88567
143	Hs.212102	PDIA6	protein disulfide isomerase family A, member 6	2.67256
144	Hs.465041	HDHD2	haloacid dehalogenase-like hydrolase domain containing 2	1.58049
145	Hs.125113	CCT8	chaperonin containing TCP1, subunit 8 (theta)	2.74083
146	Hs.218040	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	-2.86872
147	Hs.126941	FAM49B	family with sequence similarity 49, member B	2.41970
148	Hs.140452	M6PRBP1	mannose-6-phosphate receptor binding protein 1	2.45483
149	Hs.591940	APOA4	apolipoprotein A-IV	2.29544
150	Hs.519756	STK10	serine/threonine kinase 10	2.91394
151	Hs.274402	HSPA1A	heat shock 70kDa protein 1A	3.13788

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
152	Hs.571886	AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	2.51928
153	Hs.599481	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	3.52387
154	Hs.352224	EDARADD	EDAR-associated death domain	7.46803
155	Hs.534385	THOC4	THO complex 4	-1.32827
156	Hs.528668	RPL6	ribosomal protein L6	3.03691
157	Hs.368084	LRPPRC	leucine-rich PPR-motif containing	-1.71518
158	Hs.632717	MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	3.02347
159	Hs.482043	NNT	nicotinamide nucleotide transhydrogenase	2.26497
160	Hs.525600	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	2.84841
161	Hs.513530	TGFB1I1	transforming growth factor beta 1 induced transcript 1	-2.45685
162	Hs.369920	RAP1B	RAP1B, member of RAS oncogene family	-2.37368
163	Hs.148340	RPL10A (includes EG:4736)	ribosomal protein L10a	1.99620
164	Hs.200716	MECP2	methyl CpG binding protein 2 (Rett syndrome)	2.99376
165	Hs.642813	VIM	vimentin	1.75207
166	Hs.570791	LAP3	leucine aminopeptidase 3	2.49300
167	Hs.516539	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	1.70158
168	Hs.356572	RPS3A	ribosomal protein S3A	3.02357
169	Hs.518530	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	2.61046
170	Hs.37617	MYO1G	myosin IG	2.16324
171	Hs.467408	TRIM28	tripartite motif-containing 28	2.84983
172	Hs.136905	HUWE1	HECT, UBA and WWE domain containing 1	1.88641
173	IPI00464990	GP1BB	glycoprotein Ib (platelet), beta polypeptide	-1.88206
174	Hs.617193	CYCS (includes EG:54205)	cytochrome c, somatic	1.64385
175	Hs.595053	HSPD1	heat shock 60kDa protein 1 (chaperonin)	1.76318
176	Hs.534770	PKM2	pyruvate kinase, muscle	1.27869
177	Hs.166463	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor	2.79696

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
			A)	
178	Hs.2533	ALDH9A1	aldehyde dehydrogenase 9 family, member A1	1.38474
179	Hs.700575	STMN1	stathmin 1/oncoprotein 18	2.31540
180	Hs.530687	RNH1	ribonuclease/angiogenin inhibitor 1	1.64737
181	Hs.696144	TXNRD1	thioredoxin reductase 1	1.70635
182	Hs.502756	AHNAK	AHNAK nucleoprotein	6.50929
183	Hs.10842	RAN	RAN, member RAS oncogene family	2.05198
184	Hs.311609	DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	2.85922
185	Hs.533273	UBA1	ubiquitin-like modifier activating enzyme 1	1.88773
186	Hs.695946	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	-3.90341
187	IPI00646888	1-Sep	septin 1	2.21854
188	Hs.546292	RPS27A	ribosomal protein S27a	-1.51316

TABLE H

	International Protein Index/UniGene	Symbol	Entrez Gene Name
1	Hs.1012	C4BPA	complement component 4 binding protein, alpha
2	Hs.110675	APOC1	*apolipoprotein C-I*
3	Hs.116448	GLS	Glutaminase
4	Hs.191215	CYTH1	cytohesin 1
5	Hs.202	TSPO	translocator protein (18kDa)
6	Hs.203637	PLS1	plastin 1 (I isoform)
7	Hs.24889	FMN2	formin 2
8	Hs.327527	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
9	Hs.352224	EDARADD	EDAR-associated death domain
10	Hs.464813	PSMA8	proteasome (prosome, macropain) subunit, alpha type, 8
11	Hs.466910	CDA	cytidine deaminase
12	Hs.4779	GATAD2B	GATA zinc finger domain containing 2B
13	Hs.482873	TMED5	transmembrane emp24 protein transport domain containing 5
14	Hs.501200	RGS10	regulator of G-protein signaling 10
15	Hs.518750	OCIAD1	OCIA domain containing 1
16	Hs.529023	ZNF532	zinc finger protein 532
17	Hs.594444	LMNA	lamin A/C
18	Hs.620557	ANK2	ankyrin 2, neuronal
19	Hs.653263	CEP110	centrosomal protein 110kDa
20	Hs.654438	ANK1	ankyrin 1, erythrocytic
21	Hs.69771	CFB	complement factor B
22	Hs.77741	KNG1 (includes EG:3827)	kininogen 1
23	Hs.83634	HCFC1	host cell factor C1 (VP16-accessory protein)

	International Protein Index/UniGene	Symbol	Entrez Gene Name
24	IPI00010951	EPPK1	epiplakin 1
25	IPI00382606	F7	coagulation factor VII (serum prothrombin conversion accelerator)
26	IPI00641229	IGHA2	immunoglobulin heavy constant alpha 2 (A2m marker)
27	IPI00645452	TUBB	tubulin, beta
28	IPI00787190	HLA-B	major histocompatibility complex, class I, B

TABLE I

	Unigene/IPI	Symbol	Entrez Gene Name
1	Hs.406758	HIBADH	3-hydroxyisobutyrate dehydrogenase
2	Hs.656685	HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase
3	Hs.643487	ACAA1	acetyl-Coenzyme A acyltransferase 1
4	Hs.558296	ACP1	acid phosphatase 1, soluble
5	Hs.514581	ACTG1	actin, gamma 1
6	Hs.461727	ACSF3	acyl-CoA synthetase family member 3
7	Hs.464137	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl
8	Hs.512815	AP3D1	adaptor-related protein complex 3, delta 1 subunit
9	Hs.470907	AK2	adenylate kinase 2
10	Hs.525330	ARF6	ADP-ribosylation factor 6
11	Hs.62578	ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
12	Hs.418167	ALB	albumin
13	Hs.632733	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)
14	Hs.591631	AGPS	alkylglycerone phosphate synthase
15	Hs.499725	ANK3	ankyrin 3, node of Ranvier (ankyrin G)
16	Hs.696087	ANKFY1	ankyrin repeat and FYVE domain containing 1
17	Hs.412117	ANXA6	annexin A6
18	Hs.3346	ANXA9	annexin A9
19	Hs.435771	API5	apoptosis inhibitor 5
20	Hs.503165	ARAP1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1
21	Hs.465224	NARS	asparaginyl-tRNA synthetase
22	Hs.477126	ATG3	ATG3 autophagy related 3 homolog (S. cerevisiae)
23	Hs.486063	ATG5 (includes EG:9474)	ATG5 autophagy related 5 homolog (S. cerevisiae)
24	Hs.584905	ATL1	atlastin GTPase 1
25	Hs.85539	ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E
26	Hs.656515	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2
27	Hs.444957	ATP8A2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2
28	Hs.517338	ATP6V1E1	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1

	Unigene/IPI	Symbol	Entrez Gene Name
29	Hs.491737	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H
30	Hs.429294	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1
31	Hs.508423	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4
32	Hs.355983	BZW1	basic leucine zipper and W2 domains 1
33	Hs.591768	BTF3	basic transcription factor 3
34	Hs.494614	BAT2D1	BAT2 domain containing 1
35	Hs.631546	BAX	BCL2-associated X protein
36	Hs.654740	BRWD1	bromodomain and WD repeat domain containing 1
37	Hs.418533	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)
38	IPI00797310	CLSTN3	calsyntenin 3
39	Hs.524809	CLIP1	CAP-GLY domain containing linker protein 1
40	Hs.699182	CPT2	carnitine palmitoyltransferase 2
41	Hs.504096	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence
42	Hs.654616	CASP6	caspase 6, apoptosis-related cysteine peptidase
43	Hs.460232	CNOT1	CCR4-NOT transcription complex, subunit 1
44	Hs.485518	CD2AP	CD2-associated protein
45	Hs.502328	CD44	CD44 molecule (Indian blood group)
46	Hs.556638	CISD2	CDGSH iron sulfur domain 2
47	Hs.472027	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2
48	Hs.568242	CREG1	cellular repressor of E1A-stimulated genes 1
49	Hs.31819	C1ORF128	chromosome 1 open reading frame 128
50	Hs.368353	C1ORF71	chromosome 1 open reading frame 71
51	Hs.611057	C1ORF77	chromosome 1 open reading frame 77
52	Hs.462033	C1ORF93	chromosome 1 open reading frame 93
53	Hs.8360	C11ORF54	chromosome 11 open reading frame 54
54	Hs.530753	C11ORF59	chromosome 11 open reading frame 59
55	IPI00373869	C17ORF49	chromosome 17 open reading frame 49
56	Hs.368266	CLTCL1	clathrin, heavy chain-like 1
57	Hs.591506	MYCBP	c-myc binding protein
58	Hs.505652	COPZ1	coatomer protein complex, subunit zeta 1
59	Hs.655010	CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3

	Unigene/IPI	Symbol	Entrez Gene Name
60	Hs.369614	COPS2	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)
61	Hs.502917	CCS	copper chaperone for superoxide dismutase
62	Hs.460923	CBFB	core-binding factor, beta subunit
63	Hs.372286	CUL3	cullin 3
64	Hs.518198	CSTA (includes EG:1475)	cystatin A (stefin A)
65	Hs.481898	CCBL2	cysteine conjugate-beta lyase 2
66	Hs.513803	CYBA	cytochrome b-245, alpha polypeptide
67	Hs.461131	CYB5B	cytochrome b5 type B (outer mitochondrial membrane)
68	IPI00017510	COX2	cytochrome c oxidase II
69	Hs.696092	CLASP2	cytoplasmic linker associated protein 2
70	Hs.99120	DDX3Y (includes EG:8653)	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
71	Hs.75189	DAP	death-associated protein
72	Hs.368203	DOCK11	dedicator of cytokinesis 11
73	Hs.654567	DENND4A	DENN/MADD domain containing 4A
74	Hs.407618	DSG4	desmoglein 4
75	Hs.9857	DCXR	dicarbonyl/L-xylulose reductase
76	Hs.335551	DLAT	dihydrolipoamide S-acetyltransferase
77	Hs.37916	DPP7	dipeptidyl-peptidase 7
78	Hs.515210	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1
79	Hs.656476	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3
80	Hs.425801	DUSP23	dual specificity phosphatase 23
81	Hs.522413	DNM1	dynamin 1
82	Hs.529495	DYNC1LI1	dynein, cytoplasmic 1, light intermediate chain 1
83	Hs.591176	DYNLL2	dynein, light chain, LC8-type 2
84	Hs.4747	DKC1	dyskeratosis congenita 1, dyskerin
85	Hs.412103	EFHA1	EF-hand domain family, member A1
86	Hs.654553	ETFB (includes EG:2109)	electron-transfer-flavoprotein, beta polypeptide

	Unigene/IPI	Symbol	Entrez Gene Name
87	Hs.509791	ERH	enhancer of rudimentary homolog (Drosophila)
88	Hs.429879	EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase
89	Hs.419815	EGF	epidermal growth factor (beta-urogastrone)
90	Hs.477498	EEFSEC	eukaryotic elongation factor, selenocysteine-tRNA-specific
91	Hs.429180	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
92	Hs.696322	EIF2C2	eukaryotic translation initiation factor 2C, 2
93	Hs.55682	EIF3D	eukaryotic translation initiation factor 3, subunit D
94	Hs.502244	EIF3M	eukaryotic translation initiation factor 3, subunit M
95	Hs.467084	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3
96	Hs.433702	EIF5	eukaryotic translation initiation factor 5
97	Hs.483494	ETF1	eukaryotic translation termination factor 1
98	Hs.517293	F11R	F11 receptor
99	Hs.518662	FAM129A	family with sequence similarity 129, member A
100	Hs.490795	FAM62B	family with sequence similarity 62 (C2 domain containing) member B
101	Hs.335918	FDPS	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)
102	Hs.86131	FADD (includes EG:8772)	Fas (TNFRSF6)-associated via death domain
103	Hs.408061	FABP5	fatty acid binding protein 5 (psoriasis-associated)
104	Hs.433300	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
105	Hs.509343	FERMT2	fermitin family homolog 2 (Drosophila)
106	Hs.338207	FRAP1	FK506 binding protein 12-rapamycin associated protein 1
107	Hs.407190	FKBP5	FK506 binding protein 5
108	Hs.409065	FEN1	flap structure-specific endonuclease 1
109	Hs.494496	FBP1	fructose-1,6-bisphosphatase 1
110	Hs.654961	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
111	Hs.390567	FYN	FYN oncogene related to SRC, FGR, YES
112	Hs.530024	GGCT	gamma-glutamyl cyclotransferase
113	Hs.27059	GMPPA	GDP-*mannose pyrophosphorylase* A
114	Hs.567488	GMPPB	GDP-mannose pyrophosphorylase B
115	Hs.591069	GBAS	glioblastoma amplified sequence

	Unigene/IPI	Symbol	Entrez Gene Name
116	Hs.654465	GCLC	glutamate-cysteine ligase, catalytic subunit
117	Hs.390667	GSTK1	glutathione S-transferase kappa 1
118	Hs.59138	GYPC	glycophorin C (Gerbich blood group)
119	Hs.344151	GOLGA4	golgi autoantigen, golgin subfamily a, 4
120	Hs.431317	GORASP2	golgi reassembly stacking protein 2, 55kDa
121	Hs.290243	GBF1	golgi-specific brefeldin A resistant guanine nucleotide exchange factor 1
122	Hs.485449	GTPBP2	GTP binding protein 2
123	Hs.495134	GAPVD1	GTPase activating protein and VPS9 domains 1
124	Hs.591450	GBP7	guanylate binding protein 7
125	Hs.655196	HP	haptoglobin
126	Hs.531785	HS1BP3	HCLS1 binding protein 3
127	Hs.36927	HSPH1	heat shock 105kDa/110kDa protein 1
128	Hs.690634	HSPA1L	heat shock 70kDa protein 1-like
129	Hs.432648	HSPA2	heat shock 70kDa protein 2
130	Hs.509736	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1
131	Hs.525084	HECTD3	HECT domain containing 3
132	Hs.642618	HEBP1	heme binding protein 1
133	IPI00784636	HBB (includes EG:3043)	hemoglobin, beta
134	Hs.699280	HBD	hemoglobin, delta
135	Hs.502617	HNRNPCL1	heterogeneous nuclear ribonucleoprotein C-like 1
136	Hs.69293	HEXB	hexosaminidase B (beta polypeptide)
137	Hs.83634	HCFC1	host cell factor C1 (VP16-accessory protein)
138	Hs.460002	FLJ11151	hypothetical protein FLJ11151
139	Hs.78880	ILVBL	ilvB (bacterial acetolactate synthase)-like
140	IPI00384938	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)
141	Hs.699240	IPO5	importin 5
142	Hs.434102	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma
143	Hs.500546	IDE	insulin-degrading enzyme
144	Hs.513225	ITFG3	integrin alpha FG-GAP repeat containing 3
145	Hs.375957	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)

	Unigene/IPI	Symbol	Entrez Gene Name
146	Hs.431460	ICAM2	intercellular adhesion molecule 2
147	Hs.591110	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha
148	Hs.515247	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)
149	Hs.301613	JTV1	JTV1 gene
150	Hs.527919	KPNA3	karyopherin alpha 3 (importin alpha 4)
151	Hs.270043	KIAA0196	KIAA0196
152	Hs.368255	KIAA0368	KIAA0368
153	Hs.368282	KIAA0564	KIAA0564
154	IPI00396421	KIAA0776	KIAA0776
155	Hs.654497	LTBP1	latent transforming growth factor beta binding protein 1
156	Hs.478067	LXN	latexin
157	Hs.432674	LARS	leucyl-tRNA synthetase
158	Hs.700163	LY6G5B	lymphocyte antigen 6 complex, locus G5B
159	Hs.3100	KARS	lysyl-tRNA synthetase
160	Hs.654404	HLA-C	major histocompatibility complex, class I, C
161	Hs.75694	MPI	mannose phosphate isomerase
162	Hs.696082	MAPKSP1	MAPK scaffold protein 1
163	Hs.444969	MEMO1 (includes EG:51072)	mediator of cell motility 1
164	Hs.486189	MAGI3	membrane associated guanylate kinase, WW and PDZ domain containing 3
165	Hs.500842	MGEA5	meningioma expressed antigen 5 (hyaluronidase)
166	Hs.377155	MTDH	metadherin
167	Hs.516157	MAT2A	methionine adenosyltransferase II, alpha
168	Hs.252457	MVD	mevalonate (diphospho) decarboxylase
169	Hs.580782	MACF1	microtubule-actin crosslinking factor 1
170	Hs.517949	MAP4	microtubule-associated protein 4
171	Hs.515860	MAPRE3	microtubule-associated protein, RP/EB family, member 3
172	Hs.269944	MTCH2	mitochondrial carrier homolog 2 (C. elegans)
173	Hs.861	MAPK3	mitogen-activated protein kinase 3
174	Hs.507681	MAP3K7IP1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1

	Unigene/IPI	Symbol	Entrez Gene Name
175	Hs.643565	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2
176	Hs.591221	MYCBP2	MYC binding protein 2
177	Hs.91531	MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6
178	Hs.655278	MYOF	myoferlin
179	Hs.286226	MYO1C	myosin IC
180	IPI00719669	MRLC2	myosin regulatory light chain MRLC2
181	IPI00007858	MYH13	myosin, heavy chain 13, skeletal muscle
182	IPI00001753	MYH4	myosin, heavy chain 4, skeletal muscle
183	Hs.463300	MYL4	myosin, light chain 4, alkali; atrial, embryonic
184	Hs.926	MX2	myxovirus (influenza virus) resistance 2 (mouse)
185	Hs.527412	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1
186	Hs.651219	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa
187	IPI00074489	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa
188	Hs.532853	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa
189	Hs.471207	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
190	Hs.90443	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
191	Hs.464572	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa
192	Hs.473937	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa
193	Hs.655006	NCKIPSD	NCK interacting protein with SH3 domain
194	Hs.603732	NCKAP1	NCK-associated protein 1
195	Hs.467759	NBAS	neuroblastoma amplified sequence
196	Hs.524116	NRGN	neurogranin (protein kinase C substrate, RC3)
197	Hs.587558	NCF2	neutrophil cytosolic factor 2
198	Hs.493164	NAPRT1	nicotinate phosphoribosyltransferase domain containing 1
199	Hs.696107	NEK9 (includes EG:91754)	NIMA (never in mitosis gene a)- related kinase 9
200	Hs.524082	NLRX1	NLR family member X1
201	Hs.532790	NMT1	N-myristoyltransferase 1

	Unigene/IPI	Symbol	Entrez Gene Name
202	Hs.319334	NASP	nuclear autoantigenic sperm protein (histone-binding)
203	Hs.263812	NUDC	nuclear distribution gene C homolog (A. nidulans)
204	Hs.654408	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
205	Hs.325978	NUMA1	nuclear mitotic apparatus protein 1
206	Hs.79110	NCL	nucleolin
207	Hs.643487	NUP160	nucleoporin 160kDa
208	Hs.555956	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5
209	Hs.405410	OGT (includes EG:8473)	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
210	Hs.695379	OPTN	optineurin
211	Hs.430849	OSBPL8	oxysterol binding protein-like 8
212	Hs.656789	PAK3	p21 protein (Cdc42/Rac)-activated kinase 3
213	Hs.98475	PNKD (includes EG:25953)	paroxysmal nonkinesigenic dyskinesia
214	Hs.495471	PMPCA	peptidase (mitochondrial processing) alpha
215	Hs.33455	PADI2	peptidyl arginine deiminase, type II
216	IPI00745933	PPIA (includes EG:5478)	peptidylprolyl isomerase A (cyclophilin A)
217	Hs.644938	PCYT2	phosphate cytidylyltransferase 2, ethanolamine
218	Hs.372295	PITPNM1	phosphatidylinositol transfer protein, membrane-associated 1
219	Hs.272759	PITPNM2	phosphatidylinositol transfer protein, membrane-associated 2
220	Hs.75812	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
221	Hs.75160	PFKM	phosphofructokinase, muscle
222	Hs.26612	PGM2L1	phosphoglucomutase 2-like 1
223	Hs.487296	PHGDH	phosphoglycerate dehydrogenase
224	IPI00786982	PGAM5	phosphoglycerate mutase family member 5
225	Hs.409834	PHPT1	phosphohistidine phosphatase 1
226	Hs.32942	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide
227	Hs.591953	PLCB3	phospholipase C, beta 3 (phosphatidylinositol-specific)
228	Hs.413111	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)
229	Hs.517216	PEA15	phosphoprotein enriched in astrocytes 15

	Unigene/IPI	Symbol	Entrez Gene Name
230	Hs.675491	PLXNA4	plexin A4
231	Hs.632833	PLXNB3	plexin B3
232	Hs.348609	PARP10	poly (ADP-ribose) polymerase family, member 10
233	Hs.482038	PAIP1	poly(A) binding protein interacting protein 1
234	Hs.507910	PGRMC2	progesterone receptor membrane component 2
235	Hs.567410	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
236	IPI00555590	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2
237	IPI00064328	PRMT5	protein arginine methyltransferase 5
238	Hs.498570	PRKCQ	protein kinase C, theta
239	Hs.631923	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha
240	Hs.514323	PPP1R9B	protein phosphatase 1, regulatory (inhibitor) subunit 9B
241	Hs.400740	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4
242	Hs.584019	PPP6C	protein phosphatase 6, catalytic subunit
243	Hs.591549	PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)
244	Hs.439152	PCDH12	protocadherin 12
245	Hs.78524	PRUNE	prune homolog (Drosophila)
246	Hs.41735	P2RX1	purinergic receptor P2X, ligand-gated ion channel, 1
247	Hs.284491	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase
248	Hs.370781	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1
249	Hs.470633	PDK1	pyruvate dehydrogenase kinase, isozyme 1
250	Hs.534770	PKM2	pyruvate kinase, muscle
251	Hs.321541	RAB11A	RAB11A, member RAS oncogene family
252	Hs.406799	RAB18	RAB18, member RAS oncogene family
253	Hs.369017	RAB2A	RAB2A, member RAS oncogene family
254	Hs.567328	RAB5B	RAB5B, member RAS oncogene family
255	Hs.650382	RAB5C	RAB5C, member RAS oncogene family
256	Hs.591552	RAB6C	RAB6C, member RAS oncogene family
257	Hs.644420	RAB8A	RAB8A, member RAS oncogene family
258	Hs.493867	RCSD1	RCSD domain containing 1
259	Hs.461925	RPA1	replication protein A1, 70kDa
260	Hs.645283	RTN4	reticulon 4

	Unigene/IPI	Symbol	Entrez Gene Name
261	Hs.368631	ARHGAP10	Rho GTPase activating protein 10
262	Hs.531807	ARHGAP25	Rho GTPase activating protein 25
263	Hs.508738	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7
264	Hs.465761	ARHGEF18	rho/rac guanine nucleotide exchange factor (GEF) 18
265	Hs.73839	RNASE3	ribonuclease, RNase A family, 3 (eosinophil cationic protein)
266	Hs.388664	RPL11	ribosomal protein L11
267	Hs.374588	RPL17	ribosomal protein L17
268	Hs.337766	RPL18A	ribosomal protein L18a
269	IPI00741405	LOC391282	ribosomal protein L23a pseudogene 12
270	Hs.649475	RPL24	ribosomal protein L24
271	Hs.652114	RPL28	ribosomal protein L28
272	Hs.433701	RPL37A (includes EG:6168)	ribosomal protein L37a
273	IPI00796861	LOC100130892	ribosomal protein L7 pseudogene 32
274	Hs.546289	RPS12 (includes EG:6206)	ribosomal protein S12
275	Hs.370504	RPS15A	ribosomal protein S15a
276	IPI00401105	RPS25	ribosomal protein S25
277	IPI00397963	RPS27	ribosomal protein S27
278	Hs.282376	RPS4Y1	ribosomal protein S4, Y-linked 1
279	Hs.367761	RPS4Y2	ribosomal protein S4, Y-linked 2
280	Hs.408073	RPS6	ribosomal protein S6
281	IPI00413108	RPSA (includes EG:3921)	ribosomal protein SA
282	Hs.553723	RNF123 (includes EG:63891)	ring finger protein 123
283	Hs.306769	RUFY1	RUN and FYVE domain containing 1
284	Hs.272822	RUVBL1	RuvB-like 1 (E. coli)

	Unigene/IPI	Symbol	Entrez Gene Name
285	Hs.515846	RUVBL2	RuvB-like 2 (E. coli)
286	Hs.632438	SEC22B	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)
287	Hs.654429	SEC24C (includes EG:9632)	SEC24 family, member C (S. cerevisiae)
288	IPI00643835	SELP	selectin P (granule membrane protein 140kDa, antigen CD62)
289	Hs.632460	SELENBP1	selenium binding protein 1
290	Hs.283743	5-Sep	septin 5
291	Hs.440932	9-Sep	septin 9
292	Hs.435661	SPTLC2	serine palmitoyltransferase, long chain base subunit 2
293	Hs.433343	SRRM2	serine/arginine repetitive matrix 2
294	Hs.409578	STK38	serine/threonine kinase 38
295	IPI00168350	RP6-213H19.1	serine/threonine protein kinase MST4
296	Hs.368077	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8
297	Hs.531176	SARS	seryl-tRNA synthetase
298	Hs.643526	SETDB1	SET domain, bifurcated 1
299	Hs.285666	SH3PXD2B	SH3 and PX domains 2B
300	Hs.601143	SH3BP1	SH3-domain binding protein 1
301	Hs.514495	SRP68	signal recognition particle 68kDa
302	Hs.409223	SSR4	signal sequence receptor, delta (translocon-associated protein delta)
303	IPI00399212	LOC389842	similar to RanBP1
304	Hs.591680	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)
305	Hs.356549	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa
306	Hs.632166	SNRPN	small nuclear ribonucleoprotein polypeptide N
307	Hs.83753	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1
308	Hs.350927	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6
309	Hs.656870	SLC25A24	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24
310	Hs.438723	SLC27A3	solute carrier family 27 (fatty acid transporter), member 3
311	Hs.656699	SLC27A4	solute carrier family 27 (fatty acid transporter), member 4
312	Hs.502769	SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport),

	Unigene/IPI	Symbol	Entrez Gene Name
			member 2
313	Hs.469116	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), member 1
314	Hs.878	SORD	sorbitol dehydrogenase
315	Hs.505824	SAMM50	sorting and assembly machinery component 50 homolog (S. cerevisiae)
316	Hs.32706	SPTBN4	spectrin, beta, non-erythrocytic 4
317	Hs.558463	SPEN	spen homolog, transcriptional regulator (Drosophila)
318	Hs.436306	SPHKAP	SPHK1 interactor, AKAP domain containing
319	Hs.406423	SF3B2	splicing factor 3b, subunit 2, 145kDa
320	Hs.679714	SFRS1	splicing factor, arginine/serine-rich 1
321	Hs.309090	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa
322	Hs.591922	SLK	STE20-like kinase (yeast)
323	Hs.3439	STOML2	stomatin (EPB72)-like 2
324	Hs.656726	STRN	striatin, calmodulin binding protein
325	Hs.440475	SDHA (includes EG:6389)	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
326	Hs.465924	SDHB (includes EG:6390)	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
327	Hs.494827	SUSD1	sushi domain containing 1
328	Hs.83734	STX4	syntaxin 4
329	Hs.530436	STXBP3	syntaxin binding protein 3
330	Hs.643566	TAOK3	TAO kinase 3
331	IPI00642032	TXNL1	thioredoxin-like 1
332	Hs.30345	TRAP1	TNF receptor-associated protein 1
333	Hs.87968	TLR9	toll-like receptor 9
334	Hs.475733	TOP2B	topoisomerase (DNA) II beta 180kDa
335	Hs.496459	TOR1AIP1	torsin A interacting protein 1
336	Hs.34024	TNIK	TRAF2 and NCK interacting kinase
337	Hs.529618	TFRC	transferrin receptor (p90, CD71)
338	Hs.517033	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)
339	Hs.96247	TSNAX	translin-associated factor X
340	Hs.654824	TM9SF2	transmembrane 9 superfamily member 2

	Unigene/IPI	Symbol	Entrez Gene Name
341	Hs.502	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
342	IPI00018853	TPM1	tropomyosin 1 (alpha)
343	Hs.535581	TPM3	tropomyosin 3
344	Hs.497599	WARS	tryptophanyl-tRNA synthetase
345	Hs.31053	TBCB	tubulin folding cofactor B
346	Hs.279669	TUBG1	tubulin, gamma 1
347	Hs.473296	TPD52L2	tumor protein D52-like 2
348	IPI00794254	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
349	Hs.9589	UBQLN1	ubiquilin 1
350	Hs.5308	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1
351	Hs.474213	UFD1L	ubiquitin fusion degradation 1 like (yeast)
352	Hs.632370	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)
353	IPI00019932	UBE2D2	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)
354	Hs.50308	UBE2K	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)
355	IPI00216316	UROS	uroporphyrinogen III synthase
356	Hs.292689	USO1	USO1 homolog, vesicle docking protein (yeast)
357	Hs.499925	VPS26A	vacuolar protein sorting 26 homolog A (S. pombe)
358	Hs.418175	VPS28	vacuolar protein sorting 28 homolog (S. cerevisiae)
359	Hs.592009	VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)
360	Hs.631535	AKT2	v-akt murine thymoma viral oncogene homolog 2
361	Hs.632066	VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1
362	Hs.515469	VASP	vasodilator-stimulated phosphoprotein
363	Hs.66708	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)
364	Hs.505033	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
365	Hs.699154	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
366	Hs.635221	WASF3	WAS protein family, member 3
367	Hs.356604	WNK1	WNK lysine deficient protein kinase 1
368	Hs.390623	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
369	Hs.27239	ZDHHC5	zinc finger, DHHC-type containing 5
370	Hs.37003	Not Annotated	Not Annotated

	Unigene/IPI	Symbol	Entrez Gene Name
371	Hs.102696	Not Annotated	
372	Hs.10326	COPE	
373	Hs.10649	C1orf38	
374	Hs.108049	Not Annotated	Not Annotated
375	Hs.108957	Not Annotated	Not Annotated
376	Hs.111024	Not Annotated	Not Annotated
377	Hs.115242	Not Annotated	Not Annotated
378	Hs.116237	Not Annotated	Not Annotated
379	Hs.11638	ACSL5	
380	Hs.119825	Not Annotated	Not Annotated
381	Hs.124027	Not Annotated	Not Annotated
382	Hs.124126	Not Annotated	Not Annotated
383	Hs.12865	NSFL1C	
384	Hs.131255	Not Annotated	Not Annotated
385	Hs.131489	Not Annotated	Not Annotated
386	Hs.132499	Not Annotated	Not Annotated
387	Hs.132858	Not Annotated	Not Annotated
388	Hs.133512	Not Annotated	Not Annotated
389	Hs.134688	Not Annotated	Not Annotated
390	Hs.136309	Not Annotated	Not Annotated
391	Hs.138378	Not Annotated	Not Annotated
392	Hs.141125	Not Annotated	Not Annotated
393	Hs.142003	Not Annotated	Not Annotated
394	Hs.1422	FGR	
395	Hs.1437	GAA	
396	Hs.143703	EHD4	
397	Hs.144011	CYTH2	
398	Hs.144447	BRWD2	
399	Hs.146406	DEDD	
400	Hs.146602	UQCRQ	
401	Hs.149957	RPS6KA1	

	Unigene/IPI	Symbol	Entrez Gene Name
402	Hs.150206	HIST1H1A	
403	Hs.150718	JAM3 /// LOC100133502	
404	Hs.152944	VWA5A	
405	Hs.154078	LBP	
406	Hs.155975	PTPRCAP	
407	Hs.158331	RENBP	
408	Hs.15977	NDUFB9	
409	Hs.161357	PDHB	
410	Hs.162121	COPA	
411	Hs.16355	MYH10	
412	Hs.163867	CD14	
413	Hs.166011	CTNND1	
414	Hs.166551	FAM114A2	
415	Hs.166924	SEC13	
416	Hs.169284	PRPS1L1	
417	Hs.169900	PABPC4	
418	Hs.171626	SKP1	
419	Hs.173043	MTA2	
420	Hs.17614	ABCB10	
421	Hs.179309	UBQLN2	
422	Hs.18192	SRRM1	
423	Hs.182625	VAPB	
424	Hs.1872	Not Annotated	Not Annotated
425	Hs.188401	ANXA10	
426	Hs.188882	NUDT3	
427	Hs.189075	TWF1	
428	Hs.18925	CRBN	
429	Hs.189409	FNBP1	
430	Hs.190086	MRCL3	
431	Hs.191213	SNX9	

	Unigene/IPI	Symbol	Entrez Gene Name
432	Hs.194148	YES1	
433	Hs.195080	ECE1	
434	Hs.196437	MOBKL1B	
435	Hs.200804	SDCBP	
436	Hs.204041	AHSA1	
437	Hs.2057	Not Annotated	Not Annotated
438	Hs.211463	DNM2	
439	Hs.21160	ME1	
440	Hs.212088	EPHX2	
441	Hs.213389	GOLGB1	
442	Hs.213470	PSMB7	
443	Hs.214142	MTHFR	
444	Hs.220594	CCDC58	
445	Hs.224171	ENO3	
446	Hs.238839	SCYL1	
447	Hs.239818	PIK3CB	
448	Hs.24956	INF2	
449	Hs.271954	Not Annotated	Not Annotated
450	Hs.296422	Not Annotated	Not Annotated
451	Hs.301658	1554440_at	1554440_at
452	Hs.328865	Not Annotated	Not Annotated
453	Hs.351544	Not Annotated	Not Annotated
454	Hs.368359	Not Annotated	Not Annotated
455	Hs.370503	Not Annotated	Not Annotated
456	Hs.37712	AW006941	AW006941
457	Hs.43505	AF091453	
458	Hs.435775	Not Annotated	Not Annotated
459	Hs.439474	Not Annotated	Not Annotated
460	Hs.440534	Not Annotated	Not Annotated
461	Hs.460988	Not Annotated	Not Annotated
462	Hs.470544	Not Annotated	Not Annotated

	Unigene/IPI	Symbol	Entrez Gene Name
463	Hs.471528	Not Annotated	Not Annotated
464	Hs.486856	Not Annotated	Not Annotated
465	Hs.500674	Not Annotated	Not Annotated
466	Hs.590925	Not Annotated	Not Annotated
467	Hs.591005	Not Annotated	Not Annotated
468	Hs.591366	Not Annotated	Not Annotated
469	Hs.599301	Not Annotated	Not Annotated
470	Hs.632735	Not Annotated	Not Annotated
471	Hs.637017	Not Annotated	Not Annotated
472	Hs.645248	Not Annotated	Not Annotated
473	Hs.654497	Not Annotated	Not Annotated
474	Hs.659335	Not Annotated	Not Annotated
475	Hs.694210	Not Annotated	Not Annotated
476	Hs.696132	Not Annotated	Not Annotated
477	Hs.699333	Not Annotated	Not Annotated
478	Hs.699367	Not Annotated	Not Annotated
479	Hs.700648	Not Annotated	Not Annotated
480	Hs.700676	Not Annotated	Not Annotated
481	Hs.700760	Not Annotated	Not Annotated
482	IPI00011791	Not Annotated	Not Annotated
483	IPI00026138	Not Annotated	Not Annotated
484	IPI00027007	Not Annotated	Not Annotated
485	IPI00061977	Not Annotated	Not Annotated
486	IPI00140827	Not Annotated	Not Annotated
487	IPI00152990	Not Annotated	Not Annotated
488	IPI00165486	Not Annotated	
489	IPI00167258	Not Annotated	
490	IPI00176593	Not Annotated	
491	IPI00176692	Not Annotated	
492	IPI00176854	Not Annotated	
493	IPI00332493	Not Annotated	

	Unigene/IPI	Symbol	Entrez Gene Name
494	IPI00386403	Not Annotated	
495	IPI00397713	Not Annotated	
496	IPI00397808	Not Annotated	
497	IPI00398435	Not Annotated	
498	IPI00412216	Not Annotated	
499	IPI00457006	Not Annotated	
500	IPI00478310	Not Annotated	
501	IPI00556589	Not Annotated	
502	IPI00738024	Not Annotated	
503	IPI00745518	Not Annotated	
504	IPI00746177	Not Annotated	
505	IPI00788196	Not Annotated	
506	IPI00792850	Not Annotated	
507	IPI00796208	Not Annotated	
508	IPI00797737	Not Annotated	
509	IPI00807559	Not Annotated	
510	IPI00807559	Not Annotated	

TABLE J

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
1	Hs.180946	RPL5 (includes EG:6125)	ribosomal protein L5	2.991594141
2	Hs.520026	VARS	valyl-tRNA synthetase	1.788666142
3	Hs.664670	Not Annotated		1.863546477
4	IPI00001539	ACAA2	acetyl-Coenzyme A acyltransferase 2	1.778012617
5	Hs.631827	ANXA7	annexin A7	1.962977658
6	Hs.466044	PKN1	protein kinase N1	2.926215231
7	Hs.90093	HSPA4	heat shock 70kDa protein 4	2.324540439
8	Hs.185172	GNB2	guanine nucleotide binding protein (G protein), beta polypeptide 2	2.321199972

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
9	IPI00003438	DNAJC8	DnaJ (Hsp40) homolog, subfamily C, member 8	3.049698528
10	Hs.431850	MAPK1	mitogen-activated protein kinase 1	1.472676636
11	Hs.50382	TJP2	tight junction protein 2 (zona occludens 2)	2.014271952
12	Hs.180414	Not Annotated		1.683155132
13	Hs.186350	RPL4	ribosomal protein L4	2.710518039
14	Hs.699250	B2M	beta-2-microglobulin	2.103571916
15	Hs.591897	Not Annotated		2.715551514
16	Hs.489284	ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	2.034992123
17	Hs.514934	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1	2.337884511
18	Hs.431279	NSF	N-ethylmaleimide-sensitive factor	2.608040048
19	Hs.700570	APP	amyloid beta (A4) precursor protein	-2.395893698
20	Hs.279259	EPX	eosinophil peroxidase	2.005473585
21	Hs.644618	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	2.377793261
22	Hs.477155	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	1.592166761
23	Hs.75318	TUBA4A	tubulin, alpha 4a	1.410317852
24	Hs.184233	HSPA9	heat shock 70kDa protein 9 (mortalin)	3.890588764
25	Hs.521640	RAD23B	RAD23 homolog B (S. cerevisiae)	1.945040444
26	Hs.370581	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)	2.08626543
27	Hs.522969	PADI4	peptidyl arginine deiminase, type IV	-2.585597629
28	Hs.483408	Not Annotated		2.427608273
29	Hs.437594	RPLP2	ribosomal protein, large, P2	1.762376912
30	Hs.546285	RPLP0 (includes EG:6175)	ribosomal protein, large, P0	2.401809197
31	Hs.300816	RAB1B (includes EG:81876)	RAB1B, member RAS oncogene family	2.036788097
32	Hs.632535	SSB (includes EG:6741)	Sjogren syndrome antigen B (autoantigen La)	1.848049688
33	Hs.38449	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator	1.839116473

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
			inhibitor type 1), member 2	
34	Hs.374596	TPT1 (includes EG:7178)	tumor protein, translationally-controlled 1	1.916065103
35	Hs.148559	IMMT	inner membrane protein, mitochondrial (mitofilin)	2.208812239
36	Hs.405144	SFRS3	splicing factor, arginine/serine-rich 3	1.854287873
37	Hs.274309	ERAF	erythroid associated factor	-2.404141665
38	Hs.413812	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	3.007255119
39	Hs.25318	RAB27B	RAB27B, member RAS oncogene family	1.762079978
40	Hs.355934	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	2.033693659
41	Hs.464336	P4HB	prolyl 4-hydroxylase, beta polypeptide	2.058272651
42	Hs.247362	DDAH2	dimethylarginine dimethylaminohydrolase 2	2.191528732
43	Hs.527105	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	3.323650054
44	Hs.502842	CAPN1	calpain 1, (mu/I) large subunit	1.844181806
45	Hs.12970	PSMD3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	1.509756576
46	IPI00011891	Not Annotated		1.949391219
47	Hs.373763	HNRNPR	heterogeneous nuclear ribonucleoprotein R	3.183271632
48	Hs.440898	FCN1	ficolin (collagen/fibrinogen domain containing) 1	-1.921894928
49	Hs.644646	KIF5B	kinesin family member 5B	-1.435375448
50	Hs.63348	EMILIN1	elastin microfibril interfacer 1	1.663039334
51	Hs.153837	MNDA	myeloid cell nuclear differentiation antigen	1.689289277
52	Hs.656176	RBM4	RNA binding motif protein 4	1.899826892
53	Hs.77793	CSK	c-src tyrosine kinase	1.724761961
54	Hs.627414	RPS18	ribosomal protein S18	3.348251322
55	Hs.497788	EPRS	glutamyl-prolyl-tRNA synthetase	1.466442524
56	Hs.698340	Not Annotated		1.921786734
57	Hs.699298	CDV3	CDV3 homolog (mouse)	1.486895919
58	Hs.111779	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	-2.780445145

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
59	IPI00011891	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	2.713587735
60	Hs.495541	C9ORF167	chromosome 9 open reading frame 167	1.599094872
61	Hs.651923	CNN2	calponin 2	1.731782614
62	Hs.131711	DLD	dihydrolipoamide dehydrogenase	1.948923988
63	Hs.644809	Not Annotated		2.338316865
64	Hs.643072	RAB10	RAB10, member RAS oncogene family	1.911187131
65	Hs.2853	PCBP1 (includes EG:5093)	poly(rC) binding protein 1	1.878028726
66	Hs.19121	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	2.290995374
67	Hs.690198	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	2.382171241
68	Hs.271510	GSR	glutathione reductase	2.161827645
69	Hs.524161	RSU1	Ras suppressor protein 1	1.436279998
70	Hs.406277	SF3A1	splicing factor 3a, subunit 1, 120kDa	3.35665152
71	Hs.558314	CP	ceruloplasmin (ferroxidase)	-4.832439476
72	Hs.75514	NP (includes EG:4860)	nucleoside phosphorylase	1.500961251
73	Hs.501684	NAP1L4	nucleosome assembly protein 1-like 4	2.209825746
74	Hs.571177	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	2.269580549
75	Hs.695941	HK1	hexokinase 1	1.893698231
76	Hs.368149	CCT7	chaperonin containing TCP1, subunit 7 (eta)	1.433906814
77	Hs.695925	DUSP3	dual specificity phosphatase 3	2.286782204
78	Hs.75066	TSN	translin	-2.048787544
79	Hs.474751	MYH9	myosin, heavy chain 9, non-muscle	2.033216171
80	Hs.644809	Not Annotated		3.013475764
81	Hs.655207	F2	coagulation factor II (thrombin)	-2.861439244
82	Hs.143436	PLG	plasminogen	-1.893142835
83	Hs.420529	UBE2V1	ubiquitin-conjugating enzyme E2 variant 1	3.119742802
84	Hs.190028	GSTO1	glutathione S-transferase omega 1	1.353315555
85	Hs.20107	KLC1	kinesin light chain 1	1.756378314

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
86	Hs.626404	RAB11B	RAB11B, member RAS oncogene family	1.540804975
87	Hs.460109	MYH11	myosin, heavy chain 11, smooth muscle	2.332116359
88	Hs.490415	ZYX	zyxin	2.38059363
89	Hs.138860	ARHGAP1	Rho GTPase activating protein 1	1.851916091
90	Hs.646283	VISA	virus-induced signaling adapter	1.446706533
91	Hs.8004	KALRN	kalirin, RhoGEF kinase	4.58940432
92	Hs.594673	Not Annotated		1.559917838
93	Hs.707	KRT2	keratin 2	2.661810703
94	Hs.699367	Not Annotated		1.552098437
95	Hs.280342	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	1.634710854
96	Hs.73849	APOC3	apolipoprotein C-III	3.025507594
97	Hs.546255	FGG	fibrinogen gamma chain	2.194270748
98	Hs.75307	H1FX	H1 histone family, member X	2.411319459
99	Hs.632729	FAM62A	family with sequence similarity 62 (C2 domain containing), member A	1.737053335
100	Hs.120759	APOB	apolipoprotein B (including Ag(x) antigen)	-3.022308409
101	Hs.72933	PF4V1	platelet factor 4 variant 1	-1.667015899
102	Hs.507866	C13ORF15	chromosome 13 open reading frame 15	2.508431485
103	Hs.203717	FN1	fibronectin 1	-2.170422372
104	Hs.324746	AHSG	alpha-2-HS-glycoprotein	-4.302298793
105	Hs.200770	SKAP2	src kinase associated phosphoprotein 2	1.755472125
106	Hs.30054	F5	coagulation factor V (proaccelerin, labile factor)	-1.567648564
107	Hs.372208	HSPC159	galectin-related protein	1.824854702
108	Hs.505735	NACA	nascent polypeptide-associated complex alpha subunit	1.652441243
109	Hs.491351	CLTC	clathrin, heavy chain (Hc)	1.743502579
110	Hs.480042	ANXA3	annexin A3	-3.143396399
111	Hs.509226	FKBP3	FK506 binding protein 3, 25kDa	2.142363841
112	Hs.24258	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	1.848134452
113	Hs.81934	ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain	1.352453174

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
114	Hs.429608	REEP5	receptor accessory protein 5	-1.629165972
115	Hs.75841	ERP29	endoplasmic reticulum protein 29	2.32777609
116	Hs.413482	C21ORF33	chromosome 21 open reading frame 33	-1.338275818
117	Hs.502823	PRDX5	peroxiredoxin 5	1.612032187
118	Hs.523302	PRDX3	peroxiredoxin 3	1.609936792
119	Hs.408054	RPL12 (includes EG:6136)	ribosomal protein L12	2.804663051
120	IPI00024989	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase	1.567802876
121	Hs.591095	PDIA3	protein disulfide isomerase family A, member 3	1.780599508
122	Hs.430606	CS	citrate synthase	-2.357926195
123	Hs.520973	HSPB1	heat shock 27kDa protein 1	1.923931973
124	Hs.518244	RPN1	*ribophorin I*	2.112462414
125	Hs.695918	CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2	2.146454384
126	Hs.632828	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2 (H')	1.609307106
127	Hs.430425	GNB1	guanine nucleotide binding protein (G protein), beta polypeptide 1	1.915685862
128	Hs.469473	RPL31	ribosomal protein L31	1.971237465
129	Hs.381072	PPIF	peptidylprolyl isomerase F	1.919712344
130	Hs.83190	FASN	fatty acid synthase	1.596744982
131	Hs.356624	NID1	nidogen 1	-1.567370157
132	Hs.12084	TUFM	Tu translation elongation factor, mitochondrial	1.443666367
133	Hs.95990	PKLR	pyruvate kinase, liver and RBC	2.624429792
134	Hs.489040	SRI	sorcin	-1.668251058
135	Hs.192374	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	1.227206967
136	Hs.516155	CAPG	capping protein (actin filament), gelsolin-like	1.935086978
137	Hs.928	PRTN3	proteinase 3	-2.191302631
138	Hs.179986	FLOT1	flotillin 1	2.62551323
139	Hs.315137	AARS	alanyl-tRNA synthetase	2.138071963
140	Hs.275243	S100A6	S100 calcium binding protein A6	-2.091908363
141	Hs.656274	TNFAIP8	*tumor necrosis factor, alpha-induced protein 8*	1.848699684

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
142	Hs.654559	HNRNPL	heterogeneous nuclear ribonucleoprotein L	2.064236514
143	Hs.471441	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	3.189407689
144	Hs.594095	Not Annotated		1.541410846
145	Hs.7744	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	1.859664494
146	Hs.517670	TTLL12	tubulin tyrosine ligase-like family, member 12	1.548669753
147	Hs.159494	BTK	Bruton agammaglobulinemia tyrosine kinase	1.744461371
148	Hs.153961	ACTR1A	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	1.602174673
149	Hs.98791	ACTR1B (includes EG:10120)	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	2.447561282
150	IPI00029625	FLOT2	flotillin 2	2.779048389
151	Hs.232375	ACAT1	acetyl-Coenzyme A acetyltransferase 1	1.844709235
152	Hs.529451	DIAPH1	diaphanous homolog 1 (Drosophila)	1.472455435
153	Hs.477352	PDIA5	protein disulfide isomerase family A, member 5	2.417726204
154	Hs.516032	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	2.919893077
155	Hs.528007	U2AF2 (includes EG:11338)	U2 small nuclear RNA auxiliary factor 2	2.33690845
156	Hs.655340	Not Annotated		1.994399205
157	Hs.546303	Not Annotated		1.993258019
158	Hs.191346	7-Sep	septin 7	1.426720758
159	Hs.556296	Not Annotated		1.918157196
160	Hs.546407	CAND1	cullin-associated and neddylation-dissociated 1	1.355594109
161	Hs.122523	SND1	staphylococcal nuclease and tudor domain containing 1	1.764952427
162	Hs.327252	Not Annotated		1.853845796
163	IPI00154742	IGL@	immunoglobulin lambda locus	-2.322679589
164	Hs.514412	PECAM1	platelet/endothelial cell adhesion molecule	1.521872894
165	Hs.248267	MPST	mercaptopyruvate sulfurtransferase	1.802723925
166	Hs.436186	CAST	calpastatin	1.877444004

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
167	Hs.390567	FYN	FYN oncogene related to SRC, FGR, YES	1.721126996
168	IPI00168728	IGHM	immunoglobulin heavy constant mu	-1.882125059
169	Hs.558799	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3	2.424171315
170	Hs.465808	HNRNPM	heterogeneous nuclear ribonucleoprotein M	1.745065443
171	Hs.149185	CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)	1.639294303
172	IPI00179291	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	1.443429746
173	Hs.555895	TMSL3	thymosin-like 3	-2.986973706
174	Hs.126550	VPS4B	vacuolar protein sorting 4 homolog B (S. cerevisiae)	1.5707885
175	Hs.654720	KIAA1967	KIAA1967	3.861735646
176	Hs.49582	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	-1.985284505
177	Hs.63489	PTPN6	protein tyrosine phosphatase, non-receptor type 6	2.403072934
178	Hs.535581	TPM3	tropomyosin 3	-1.265339887
179	Hs.496984	MPP1	membrane protein, palmitoylated 1, 55kDa	1.825563177
180	Hs.515517	RPL18	ribosomal protein L18	3.659413318
181	Hs.438429	RPS19	ribosomal protein S19	2.504016487
182	Hs.73722	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	2.126641285
183	Hs.461047	G6PD	glucose-6-phosphate dehydrogenase	1.330805366
184	Hs.128548	WDR1	WD repeat domain 1	5.196770912
185	Hs.519320	VDAC1	voltage-dependent anion channel 1	2.440307464
186	Hs.512675	RPS8	ribosomal protein S8	2.401417871
187	Hs.494691	PFN1	profilin 1	1.824342002
188	Hs.180535	FERMT3	fermitin family homolog 3 (Drosophila)	1.933107142
189	Hs.417303	SPTB	spectrin, beta, erythrocytic	2.124657924
190	Hs.446628	Not Annotated		2.082461305
191	Hs.1869	PGM1	phosphoglucomutase 1	1.62661576
192	Hs.89497	LMNB1	lamin B1	1.892879233
193	Hs.652308	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	1.965807135

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
194	Hs.446149	LDHB	lactate dehydrogenase B	1.507117812
195	Hs.87752	MSN	moesin	1.792183522
196	Hs.253903	STOM	stomatin	1.663466237
197	Hs.523836	GSTP1	glutathione S-transferase pi 1	3.12010713
198	Hs.573688	PRDX6	peroxiredoxin 6	1.768671919
199	Hs.80828	KRT1	keratin 1	2.488668295
200	Hs.289123	DCTN2	dynactin 2 (p50)	1.517636012
201	Hs.654554	Not Annotated		-3.221258193
202	Hs.90061	PGRMC1	progesterone receptor membrane component 1	1.645197721
203	Hs.514819	AP2B1	adaptor-related protein complex 2, beta 1 subunit	1.967752606
204	Hs.467284	RPS9	ribosomal protein S9	2.046621121
205	Hs.397609	RPS16	ribosomal protein S16	3.411967491
206	Hs.433427	RPS17 (includes EG:6218)	ribosomal protein S17	3.95408013
207	Hs.350899	CAPN2	calpain 2, (m/II) large subunit	1.680232488
208	Hs.363137	TCP1	t-complex 1	1.787923894
209	Hs.520967	MDH2	malate dehydrogenase 2, NAD (mitochondrial)	1.559612551
210	Hs.699180	VCL	vinculin	3.129938695
211	Hs.371563	RAB14	RAB14, member RAS oncogene family	2.101732978
212	Hs.83722	EPS15	epidermal growth factor receptor pathway substrate 15	1.373102908
213	Hs.277035	MGLL	monoglyceride lipase	1.805879512
214	Hs.64016	PROS1	protein S (alpha)	-2.623015853
215	Hs.584790	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	-1.810743224
216	Hs.580681	SAMHD1	SAM domain and HD domain 1	2.000782596
217	Hs.444770	SH3KBP1	SH3-domain kinase binding protein 1	2.069800255
218	Hs.88778	CBR1	carbonyl reductase 1	1.904274616
219	Hs.339278	COPB1	coatomer protein complex, subunit beta 1	1.443967836
220	Hs.592490	FH	fumarate hydratase	2.186123666

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
221	Hs.486458	ARHGAP18	Rho GTPase activating protein 18	2.274383381
222	Hs.335513	F13A1	coagulation factor XIII, A1 polypeptide	2.145284002
223	Hs.189772	CCT2	chaperonin containing TCP1, subunit 2 (beta)	1.435139731
224	Hs.539684	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	2.261012155
225	Hs.33642	ARCN1	archain 1	2.07225933
226	Hs.370770	XPO1	exportin 1 (CRM1 homolog, yeast)	2.343773987
227	Hs.573018	Not Annotated		1.456482565
228	Hs.291030	IQGAP2	IQ motif containing GTPase activating protein 2	1.646289191
229	Hs.212102	PDIA6	protein disulfide isomerase family A, member 6	2.480879671
230	Hs.499839	RPL7A	ribosomal protein L7a	1.726750017
231	Hs.465041	HDHD2	haloacid dehalogenase-like hydrolase domain containing 2	2.231113926
232	Hs.654957	PPA2	pyrophosphatase (inorganic) 2	2.076884027
233	Hs.660070	Not Annotated		2.0488303
234	Hs.125113	CCT8	chaperonin containing TCP1, subunit 8 (theta)	2.39782042
235	Hs.274402	HSPA1A	heat shock 70kDa protein 1A	2.358211938
236	Hs.75285	ITIH2	inter-alpha (globulin) inhibitor H2	-2.825741915
237	Hs.571886	AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	2.166498126
238	Hs.368794	AP1B1	adaptor-related protein complex 1, beta 1 subunit	1.872459483
239	Hs.599481	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	3.551326775
240	Hs.416848	CTSW	cathepsin W	-1.696934761
241	Hs.528668	RPL6	ribosomal protein L6	2.430141179
242	Hs.368084	LRPPRC	leucine-rich PPR-motif containing	-2.370581231
243	Hs.509736	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	2.408626383
244	Hs.632717	MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	3.625359469
245	Hs.654614	HSPA6	heat shock 70kDa protein 6 (HSP70B')	2.880497988
246	Hs.567380	FUBP1	far upstream element (FUSE) binding protein 1	2.457237888
247	Hs.525600	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	2.30575168
248	Hs.699168	TUBA1B	tubulin, alpha 1b	1.343588946

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
249	IPI00398135	Not Annotated		1.706927145
250	Hs.128420	VPS4A	vacuolar protein sorting 4 homolog A (S. cerevisiae)	2.041670779
251	Hs.591054	BID	BH3 interacting domain death agonist	1.977789146
252	Hs.200716	MECP2	methyl CpG binding protein 2 (Rett syndrome)	2.115913201
253	Hs.155247	ALDOC	aldolase C, fructose-bisphosphate	2.390316052
254	Hs.570791	LAP3	leucine aminopeptidase 3	1.7773007
255	Hs.598115	PPIA (includes EG:5478)	peptidylprolyl isomerase A (cyclophilin A)	-1.252231897
256	Hs.356572	RPS3A	ribosomal protein S3A	3.364033062
257	Hs.518530	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	1.820573252
258	Hs.98510	WDR44	WD repeat domain 44	1.715515466
259	IPI00448925	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)	-2.709398355
260	Hs.41045	UNC13D	unc-13 homolog D (C. elegans)	1.475081587
261	Hs.380956	Not Annotated		2.840678067
262	Hs.404321	GARS	glycyl-tRNA synthetase	2.140952373
263	Hs.306769	RUFY1	RUN and FYVE domain containing 1	2.531625079
264	Hs.292493	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	1.787163446
265	Hs.595053	HSPD1	heat shock 60kDa protein 1 (chaperonin)	1.255650787
266	Hs.699280	HBD	hemoglobin, delta	-2.913740187
267	Hs.655361	HPR (includes EG:3250)	haptoglobin-related protein	-4.710560337
268	Hs.534770	PKM2	pyruvate kinase, muscle	1.537311441
269	Hs.2533	ALDH9A1	aldehyde dehydrogenase 9 family, member A1	2.429592013
270	Hs.530687	RNH1	ribonuclease/angiogenin inhibitor 1	1.905230817
271	Hs.517168	TAGLN2	transgelin 2	1.822335623
272	Hs.14770	BIN2	bridging integrator 2	1.68853164
273	Hs.436439	TWF2	twinfilin, actin-binding protein, homolog 2 (Drosophila)	1.884510405
274	Hs.433068	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	1.54914478
275	Hs.502756	AHNAK	AHNAK nucleoprotein	2.893577011

	International Protein Index/UniGene	Symbol	Entrez Gene Name	Fold Change (positive numbers are upregulated in B1)
276	Hs.515876	NRBP1	nuclear receptor binding protein 1	2.746197889
277	Hs.132858	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	2.107982605
279	Hs.311609	DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	2.84761005
280	Hs.438678	TALDO1	transaldolase 1	2.691818999
282	IPI00746976	DNM1L	dynamin 1-like	1.617915807
283	Hs.270428	SUCLG1	succinate-CoA ligase, alpha subunit	2.37225264
284	Hs.471014	TLN1	talin 1	2.579118784

Table 2: Protein Transcript Matches of 393 mild CAN consensus genes

	Probe Set ID	UniGene ID	Gene Title	Gene Symbol
1	212224_at	Hs.76392	aldehyde dehydrogenase 1 family, member A1	ALDH1A1
2	209970_x_at	Hs.2490	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1
3	216799_at	Hs.24907	Coronin, actin binding protein, 2B	CORO2B
4	202902_s_at	Hs.181301	cathepsin S	CTSS
5	203276_at	Hs.89497	lamin B1	LMNB1
6	1559052_s_at	Hs.518530	p21 (CDKN1A)-activated kinase 2	PAK2
7	202803_s_at	Hs.375957	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)	ITGB2
8	224511_s_at	Hs.408236	thioredoxin-like 5 /// thioredoxin-like 5	TXNL5
9	216063_at	Hs.20205	hemoglobin, beta pseudogene 1 /// hemoglobin, beta pseudogene 1	HBBP1
10	202277_at	Hs.90458	serine palmitoyltransferase, long chain base subunit 1	SPTLC1

Table 3: Protein Transcript Matches of 1066 mild CAN Data Set 1 genes

	Probe Set ID	UniGene ID	Gene Title	Gene Symbol
1	212224_at	Hs.76392	aldehyde dehydrogenase 1 family, member A1	ALDH1A1
2	201089_at	Hs.295917	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2	ATP6V1B2
3	213312_at	Hs.70769	chromosome 6 open reading frame 162	C6orf162
4	206011_at	Hs.2490	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1
5	202902_s_at	Hs.181301	cathepsin S	CTSS
6	204714_s_at	Hs.30054	coagulation factor V (proaccelerin, labile factor)	F5
7	202957_at	Hs.14601	Hematopoietic cell-specific Lyn substrate 1	HCLS1
8	205936_s_at	Hs.411695	hexokinase 3 (white cell)	HK3

	Probe Set ID	UniGene ID	Gene Title	Gene Symbol
9	204959_at	Hs.153837	myeloid cell nuclear differentiation antigen /// myeloid cell nuclear differentiation antigen	MNDA
10	208875_s_at	Hs.518530	p21 (CDKN1A)-activated kinase 2	PAK2
11	207668_x_at	Hs.212102	protein disulfide isomerase family A, member 6	PDIA6
12	227516_at	Hs.406277	splicing factor 3a, subunit 1, 120kDa	SF3A1
13	217995_at	Hs.511251	sulfide quinone reductase-like (yeast)	SQRDL
14	220966_x_at	Hs.132499	actin related protein 2/3 complex, subunit 5-like /// actin related protein 2/3 complex, subunit 5-like	ARPC5L
15	219505_at	Hs.170310	cat eye syndrome chromosome region, candidate 1	CECR1
16	202295_s_at	Hs.148641	cathepsin H	CTSH
17	209759_s_at	Hs.403436	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	DCI
18	204646_at	Hs.335034	dihydropyrimidine dehydrogenase	DPYD
19	218610_s_at	Hs.460002	hypothetical protein FLJ11151	FLJ11151
20	209876_at	Hs.434996	G protein-coupled receptor kinase interactor 2	GIT2
21	201944_at	Hs.69293	hexosaminidase B (beta polypeptide)	HEXB
22	211023_at	Hs.161357	pyruvate dehydrogenase (lipoamide) beta	PDHB
23	202671_s_at	Hs.284491	pyridoxal (pyridoxine, vitamin B6) kinase	PDXK
24	225214_at	Hs.213470	Proteasome (prosome, macropain) subunit, beta type, 7	PSMB7
25	217983_s_at	Hs.529989	ribonuclease T2	RNASET2
26	206034_at	Hs.368077	serpin peptidase inhibitor, clade B (ovalbumin), member 8	SERPINB8
27	204981_at	Hs.50868	solute carrier family 22 (organic cation transporter), member 18	SLC22A18
28	219403_s_at	Hs.44227	heparanase	HPSE
29	232359_at	Hs.226007	Retinol dehydrogenase 11 (all-trans and 9-cis)	RDH11
30	203485_at	Hs.368626	reticulon 1	RTN1
31	221532_s_at	Hs.513055	WD repeat domain 61	WDR61
32	208857_s_at	Hs.279257	protein-L-isoaspartate (D-aspartate) O-methyltransferase	PCMT1

Table 4: Protein Transcript Matches of 1429 mild CAN Data Set 2 genes

	Probe Set ID	UniGene ID	Gene Title	Gene Symbol
1	201305_x_at	Hs.494604	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	ANP32B
2	216123_x_at	Hs.514934	Capping protein (actin filament) muscle Z-line, alpha 1	CAPZA1
3	209970_x_at	Hs.2490	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1
4	209789_at	Hs.24907	coronin, actin binding protein, 2B	CORO2B
5	237104_at	Hs.181301	Cathepsin S	CTSS
6	202428_x_at	Hs.78888	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	DBI
7	235999_at	Hs.480073	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	HNRPD
8	243593_s_at	Hs.465808	Heterogeneous nuclear ribonucleoprotein M	HNRPM
9	201841_s_at	Hs.520973	heat shock 27kDa protein 1	HSPB1
10	1566785_x_at	Hs.431279	Ribosomal protein S7	NSF
11	216253_s_at	Hs.475074	parvin, beta	PARVB
12	215628_x_at	Hs.483408	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	PPP2CA
13	200927_s_at	Hs.371563	RAB14, member RAS oncogene family	RAB14
14	213941_x_at	Hs.546287	ribosomal protein S7	RPS7
15	240855_at	Hs.417303	Spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)	SPTB
16	237875_at	Hs.519756	Serine/threonine kinase 10	STK10
17	238749_at	Hs.258314	Brain and reproductive organ-expressed (TNFRSF1A modulator)	BRE
18	1565868_at	Hs.502328	CD44 antigen (homing function and Indian blood group system)	CD44
18	1565868_at	Hs.502328	CD44 antigen (homing function and Indian blood group system)	CD44
19	226875_at	Hs.368203	dedicator of cytokinesis 11	DOCK11
20	208000_at	Hs.86161	GPI anchored molecule like protein	GML
21	243147_x_at	Hs.432674	Leucyl-tRNA synthetase	LARS
22	226253_at	Hs.143774	leucine rich repeat containing 45	LRRC45
23	229851_s_at	Hs.8360	PTD012 protein	PTD012

	Probe Set ID	UniGene ID	Gene Title	Gene Symbol
24	208720_s_at	Hs.282901	RNA-binding region (RNP1, RRM) containing 2	RNPC2
25	201742_x_at	Hs.68714	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	SFRS1
26	215274_at	Hs.369271	solute carrier family 12 (sodium/chloride transporters), member 3	SLC12A3
27	231324_at	Hs.534350	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	SMARCB1
28	215416_s_at	Hs.3439	stomatin (EPB72)-like 2	STOML2
29	206116_s_at	Hs.133892	tropomyosin 1 (alpha)	TPM1
30	224511_s_at	Hs.408236	thioredoxin-like 5 /// thioredoxin-like 5	TXNL5
31	201266_at	Hs.337766	thioredoxin reductase 1	TXNRD1
32	243160_at	Hs.363396	Complement factor H	CFH
33	218218_at	Hs.506603	DIP13 beta	DIP13B
34	221942_s_at	Hs.24258	guanylate cyclase 1, soluble, alpha 3	GUCY1A3
35	232169_x_at	Hs.90443	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	NDUFS8
36	205190_at	Hs.203637	plastin 1 (I isoform)	PLS1
37	202429_s_at	Hs.435512	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)	PPP3CA
38	1555340_x_at	Hs.190334	RAP1A, member of RAS oncogene family	RAP1A
39	1569073_x_at	Hs.327527	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	SMARCA4
40	212577_at	Hs.8118	structural maintenance of chromosomes flexible hinge domain containing 1	SMCHD1

Table 5: Protein Transcript Matches of 545 moderate/severe CAN Data Set 1 genes

	Probe Set ID	UniGene ID	Gene Title	Gene Symbol
1	223598_at	Hs.521640	RAD23 homolog B (S. cerevisiae)	RAD23B
2	208000_at	Hs.86161	GPI anchored molecule like protein	GML

	Probe Set ID	UniGene ID	Gene Title	Gene Symbol
3	1557724_a_at	Hs.407190	hypothetical protein LOC285847	LOC285847
4	236356_at	Hs.471207	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	NDUFS1
5	238688_at	Hs.133892	Tropomyosin 1 (alpha)	TPM1
6	218090_s_at	Hs.144447	bromodomain and WD repeat domain containing 2	BRWD2
7	200898_s_at	Hs.500842	meningioma expressed antigen 5 (hyaluronidase)	MGEA5
8	201569_s_at	Hs.505824	sorting and assembly machinery component 50 homolog (S. cerevisiae)	SAMM50
9	1560854_s_at	Hs.50216	zinc finger protein 588	ZNF588

Table 6: Protein Transcript Matches of 172 moderate/severe CAN Data Set 2 genes

	Probe Set ID	UniGene ID	Gene Title	Gene Symbol
1	216251_s_at	Hs.517670	KIAA0153 protein	KIAA0153
2	204959_at	Hs.153837	myeloid cell nuclear differentiation antigen /// myeloid cell nuclear differentiation antigen	MNDA
3	227770_at	Hs.128420	Vacuolar protein sorting 4A (yeast)	VPS4A
4	231324_at	Hs.534350	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	SMARCB1
5	209029_at	Hs.530823	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	COPS7A
6	218326_s_at	Hs.502176	leucine-rich repeat-containing G protein-coupled receptor 4	LGR4
7	1568619_s_at	Hs.530899	Hypothetical protein LOC162073	LOC162073
8	204994_at	Hs.926	myxovirus (influenza virus) resistance 2 (mouse)	MX2
9	205325_at	Hs.334688	phytanoyl-CoA hydroxylase interacting protein	PHYHIP

WHAT IS CLAIMED IS:

1. A method of prognosing, diagnosing or monitoring chronic allograft nephropathy and/or interstitial fibrosis and tubular atrophy (CAN/IFTA), comprising

(a) determining expression levels in a subject of at least 5 genes selected from the genes in Table A, B, C, D, E, F, G, H, I and/or J; and

(b) prognosing, diagnosing or monitoring CAN/IFTA in a subject from the expression levels.

2. The method of claim 1, wherein for each of the at least five genes, step (b) comprises comparing the expression level of the gene in the subject to one or more reference expression levels of the gene associated with CAN/IFTA or lack of CAN/IFTA.

3. The method of claim 2, wherein step (b) further comprises for each of the at least five genes assigning the expression level of the gene in the subject a value or other designation providing an indication whether the subject has or is at risk of CAN/IFTA.

4. The method of claim 3, wherein the expression level of each of the at least five genes is assigned a value on a normalized scale of values associated with a range of expression levels in kidney transplant patients with and without CAN/IFTA.

5. The method of claim 3, wherein the expression level of each of the at least five genes is assigned a value or other designation providing an indication that the subject has is at risk of CAN/IFTA, lacks and is not at risk of CAN/IFTA, or that the expression level is uninformative.

6. The method of claim 3, wherein step (b) further comprises, combining the values or designations for each of the genes to provide a combined value or designation providing an indication whether the subject has or is at risk of CAN/IFTA.

7. The method of claim 6, wherein the method is repeated at different times on the subject.

8. The method of claim 6, wherein the subject is receiving a drug, and a change in the combined value or designation over time provides an indication of the effectiveness of the drug.

9. The method of claim 1, wherein the subject has undergone a kidney transplant within 1-10 years of performing step (a).

10. The method of claim 1, wherein step (a) is performed on a blood sample of the subject.

11. The method of claim 1, wherein step (a) is performed on at least ten genes from Table A, B, C, D, E, F, G, H, I and/or J.

12. The method of claim 1, wherein step (a) is performed on at least twenty genes from Table A, B, C, D, E, F, G, H, I and/or J.

13. The method of claim 1, wherein step (a) is performed on at least 40 genes from Table A, B, C, D, E, F, G, H, I and/or J.

14. The method of claim 1, wherein step (a) is performed on at least 100 genes from Table A, B, C, D, E, F, G, H, I and/or J.

15. The method of claim 1, further comprising changing the treatment regime of the patient responsive to the prognosing, diagnosing or monitoring step.

16. The method of claim 15, wherein the subject has received a drug before performing the methods, and the change comprises administering an additional drug or administering a higher dose of the same drug.

17. The method of claim 1, further comprising performing an additional procedure to detect CAN/IFTA or risk thereof if the determining step provides an indication the subject has or is at risk of CAN/IFTA.

18. The method of claim 17, wherein the additional procedure is a kidney biopsy.

19. The method of claim 1, wherein the at least five genes are from Table A, B, C and/or D expression levels are determined at the mRNA level.

20. The method of claim 1, wherein the at least five genes are from Tables E, F, G, H, I, and/or J and expression levels are determined at the protein level.

21. The method of claim 1, wherein step (b) is performed by a computer.

22. The method of claim 1, wherein the at least five genes are selected from Tables C and D.

23. The method of claim 1, wherein the at least five genes are selected from Table C.

24. The method of claim 1, wherein the at least five genes are selected from Table D.

25. The method of claim 1, wherein the at least five genes are selected from Table E and F or H and I and expression levels are determined at the protein level.

26. An array, comprising a support or supports bearing a plurality of nucleic acid probes complementary to a plurality of mRNAs fewer than 5000 in number, wherein the plurality of mRNAs includes mRNAs expressed by at least five genes selected from Table A, B, C, D.

27. The array of claim 26, wherein the plurality of mRNAs are fewer than 1000 in number.

28. The array of claim 26, wherein the plurality of mRNAs are fewer than 100 in number.

29. The array of claim 26, wherein the plurality of nucleic acid probes are attached to a planar support.

30. The array of claim 26, wherein the plurality of nucleic acid probes are attached to beads.

31. The array of claim 26, wherein the at least five genes are selected from Table C and D

32. The array of claim 26, wherein the at least five genes are selected from Table C.

33. The array of claim 26, wherein the at least five genes are selected from Table D.

34. An array, comprising a support or supports bearing a plurality of ligands that specifically bind to a plurality of proteins fewer than 5000 in number, wherein the plurality of proteins includes atleast five proteins selected from Table E, F, G, H, I and/or J.

35. The array of claim 34, wherein the plurality of proteins are fewer than 1000 in number.

36. The array of claim 34, wherein the plurality of proteins are fewer than 100 in number.

37. The array of claim 34,wherein the plurality of ligands are attached to a planar support.

38 The array of claim 34, wherein the plurality of ligands are attached to beads.

39. The array of claim 34 wherein the at least five proteins are selected from Tables E and F and/or I and J.

40 The array of claim 34 wherein the ligands are different antibodies, wherein the different antibodies bind to different proteins of the plurality of proteins.

41 A method of expression analysis, comprising

determining expression levels of up to 5000 genes in a sample from a subject having a kidney transplant, wherein the genes include at least 5 genes selected from Table A, B, C, D, E, F, G, H, I and/or J.

42 The method of claim 41 wherein the expression levels of up to 1000 genes are determined.

43 The method of claim 41 wherein the expression levels of up to 100 genes are determined.

44 The method of claim 41 wherein the expression levels are determined at the mRNA level.

45 The method of claim 41 wherein the expression levels are determined at the protein level.

46 The method of claim 41 wherein the expression levels are determined by quantitative PCR.

47 The method of claim 41, wherein the expression levels are determined by hybridization to an array.

48. A method of screening a compound for activity in inhibiting or treating CAN/IFTA, comprising

(a) administering the compound to a subject having or at risk of CAN/IFTA;

(b) determining expression levels of at least five genes in the subject selected from Table A, B, C, D, E, F, G, H, I, and/or J and species variants thereof before and after administering the drug to the subject,

(c) determining whether the compound has activity in inhibiting or treating CAN/IFTA from a change in expression levels of the genes after administering the compound.

49. The method of claim 48, wherein step (c) comprising for each of the at least five changes assigning a value or designation depending on whether the change in the expression level of the gene relative to one or more reference levels indicating presence or absence of CAN/IFTA.

50. The method of claim 48, further comprising determining a combined value or designation for the at least five genes from the values or designations determined for each gene.

51. The method of claim 48, wherein the subject is human.

52. The method of claim 48, wherein the subject is a nonhuman animal model of CAN/IFTA.

53. A method of subtyping a CAN/IFTA, comprising

(a) determining expression levels in a subject of at least 5 genes selected from the genes in Tables A, B, C, D ; E, F, G, H, I and/or J; and

(b) determining a subtype of CAN/IFTA from the expression levels.

54. The method of claim 53, wherein the subtype is selected from the group consisting of stage 0, 1, 2, or 3 of CAN/IFTA.

55. The method of claim 53, wherein the subtype is stage 0, stage 1 or stage 2 and/or 3.

56. The method of claim 53, wherein for each of the at least five genes, step (b) comprises comparing the expression level of the gene in the subject to one or more

reference expression levels of the gene associated with the subtype of CAN/IFTA or lack of CAN/IFTA.

57. The method of claim 53, wherein step (b) further comprises for each of the at least five genes assigning the expression level of the gene in the subject a value or other designation providing an indication whether the subject has or is at risk of the subtype of CAN/IFTA.

58. The method of claim 57, wherein the expression level of each of the at least five genes is assigned a value on a normalized scale of values associated with a range of expression levels in kidney transplant patients with the subtype and without CAN/IFTA.

59. The method of claim 57, wherein the expression level of each of the at least five genes is assigned a value or other designation providing an indication that the subject has or is at risk of the subtype of CAN/IFTA, lacks and is not at risk of the subtype of CAN/IFTA, or that the expression level is uninformative.

60. The method of claim 57, wherein step (b) further comprises, combining the values or designations for each of the genes to provide a combined value or designation providing an indication whether the subject has or is at risk of the subtype of CAN/IFTA.

61. The method of claim 60, wherein the method is repeated at different times on the subject.

62. The method of claim 61, wherein the subject is receiving a drug, and a change in the combined value or designation over time provides an indication of the effectiveness of the drug.

63. The method of claim 53, wherein the subject has undergone a kidney transplant within 1-10 years of performing step (a).

64 The method of claim 53, wherein step (a) is performed on a blood sample of the subject.

65 The method of claim 64, wherein the blood sample is a plasma sample.

66 The method of claim 53, wherein step (a) is performed on at least ten genes selected from Table A, B, C, D, E, F, G, H, I and/or J.

67 The method of claim 53, wherein step (a) is performed on at least twenty genes selected from Table A, B, C, D, E, F, G, H, I and/or J.

68 The method of claim 53, wherein step (a) is performed on at least 40 genes selected from Table A, B, C, D, E, F, G, H, I and/or J.

69. The method of claim 53, wherein step (a) is performed on at least 100 genes selected from Table A, B, C, D, E, F, G, H, I and/or J.

70. The method of claim 53, further comprising changing the treatment regime of the patient responsive to the whether the subtype is present.

71. The method of claim 70, wherein the subject has received a drug before performing the methods, and the change comprises administering an additional drug or administering a higher dose of the same drug.

72. The method of claim 53, further comprising performing an additional procedure to detect CAN/IFTA or risk thereof if the determining step provides an indication the subject has or is at risk of the subtype of CAN/IFTA.

73. The method of claim 72, wherein the additional procedure is a kidney biopsy.

74. The method of claim 53, wherein the expression levels are determined at the mRNA level.

75. The method of claim 53, wherein the expression levels are determined at the protein level.

76. The method of claim 53, wherein step (b) is performed by a computer.

77. The method of claim 53, wherein the at least five genes are selected from Table C.

78. The method of claim 53, wherein the at least five genes are selected from Table D.

79. The method of claim 53, wherein the at least five genes are selected from Table E and expression levels are determined at the protein level .

80. The method of claim 53, wherein the at least five genes are selected from Table F and the expression levels are determined at the protein level .

81. The method of claim 53, wherein the at least five genes are selected from Table H and the expression levels are determined at the protein level.

82. The method of claim 53, wherein the at least five genes are selected from Table I and the expression levels are determined at the protein level.

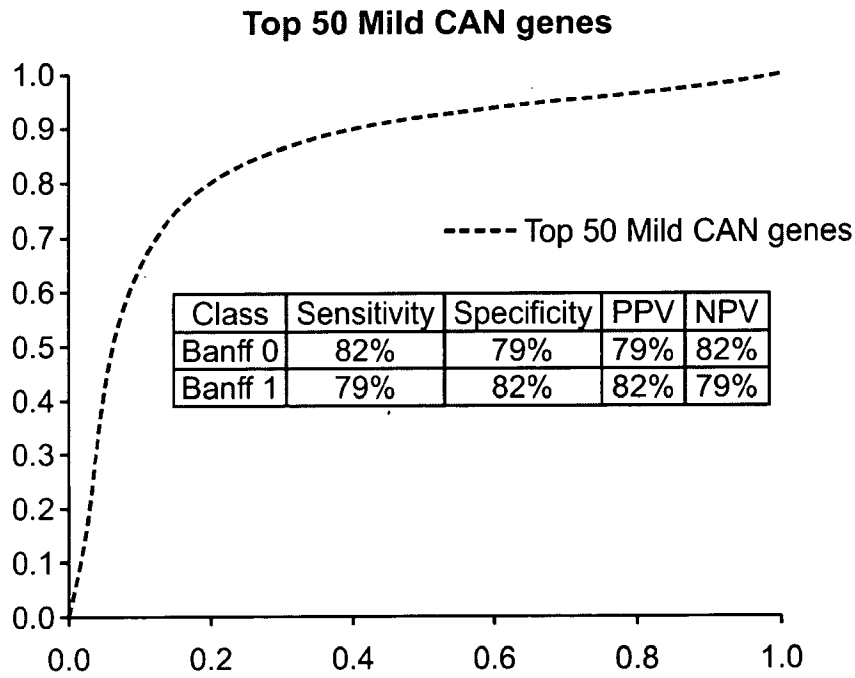

Top 50 Mild CAN genes
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.2
0.4
0.6
0.8
1.0
----- Top 50 Mild CAN genes
Class | Sensitivity | Specificity | PPV | NPV
Banff 0 | 82% | 79% | 79% | 82%
Banff 1 | 79% | 82% | 82% | 79%

FIG. 1

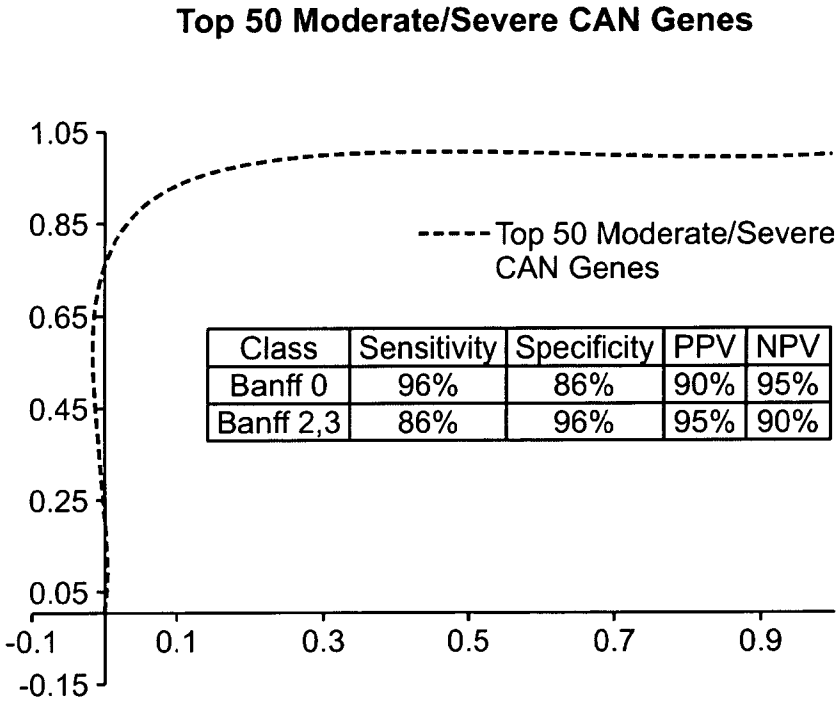

Top 50 Moderate/Severe CAN Genes
1.05
0.85
0.65
0.45
0.25
0.05
-0.1
-0.15
0.1
0.3
0.5
0.7
0.9
-----Top 50 Moderate/Severe CAN Genes
Class | Sensitivity | Specificity | PPV | NPV
Banff 0 | 96% | 86% | 90% | 95%
Banff 2,3 | 86% | 96% | 95% | 90%

FIG. 2