

GENE EXPRESSION SIGNATURES IN BLOOD LEUKOCYTES PERMIT DIFFERENTIAL DIAGNOSIS OF ACUTE INFECTIONS

TECHNICAL FIELD OF THE INVENTION

The present invention relates in general to the field of diagnostics for infectious diseases, and more particularly, to a system, method and apparatus for the diagnosis, prognosis and tracking of acute and chronic infectious diseases.

LENGTHY TABLE

The patent application includes 11 Supplemental Tables.

BACKGROUND OF THE INVENTION

Without limiting the scope of the invention, its background is described in connection with diagnostic methods for the detection, evaluation, tracking and prognosis of infectious diseases.

Acute infections represent a major cause of mortality in the world [1], especially among children. Concomitantly, the ability to identify infectious agents remains inadequate, particularly if the organism is not present in the blood (or other available tissue). Even if leukocytes are elevated as a result of the infection this will not permit discrimination between gram positive and gram negative bacteria and/or viruses. These diagnostic obstacles might delay initiation of appropriate therapy which can result in unnecessary morbidity and even death [2]. Furthermore, recent outbreaks caused by emerging pathogens [1, 3] and the increased risk of biothreat foster the need for improved diagnosis of infectious diseases.

Different classes of pathogens trigger specific pattern-recognition receptors (PRRs) differentially expressed on leukocytes [4, 5]. Leukocytes are components of the innate immune system (granulocytes, natural killer cells), the adaptive immune system (T and B lymphocytes), or both (monocytes and dendritic cells). Blood represents both a reservoir and a migration compartment for these cells that might have been exposed to infectious agents, allergens, tumors, transplants or autoimmune reactions. Therefore, blood leukocytes constitute an accessible source of clinically relevant information, and a comprehensive molecular phenotype of these cells can be obtained using gene expression microarrays. Gene expression technology has already brought new perspectives in the diagnosis and prognosis

of cancer [6-8], and the analysis of gene expression signatures in blood leukocytes has led to a better understanding of mechanisms of disease onset and responses to treatment [9-11].

SUMMARY OF THE INVENTION

The present invention includes systems and methods for analyzing samples for the prognosis
5 and diagnosis of infectious diseases using multiple variable gene expression analysis. The gene expression differences that remain can be attributed with a high degree of confidence to the unmatched variation. The gene expression differences thus identified can be used, for example, to diagnose host response to an infectious disease, identify physiological states, identify, track and monitor immune cell activation, design drugs, and monitor therapies.

10 In one embodiment, the present invention includes a method of identifying the immune response of a human subject predisposed to infectious agents, e.g., viral, bacterial, helminthic, parasitic, fungal, etc., by determining the expression level of a biomarker.

Additional examples of biomarkers include genes related to an infectious agent or disease caused thereby and combinations thereof. The biomarkers may be screened by quantitating
15 the mRNA, protein or both mRNA and protein level of the biomarker. When the biomarker is mRNA level, it may be quantitated by a method selected from polymerase chain reaction, real time polymerase chain reaction, reverse transcriptase polymerase chain reaction, hybridization, probe hybridization, and gene expression array. The screening method may also include detection of polymorphisms in the biomarker. Alternatively, the screening step
20 may be accomplished using at least one technique selected from the group consisting of polymerase chain reaction, heteroduplex analysis, single strand conformational polymorphism analysis, ligase chain reaction, comparative genome hybridization, Southern blotting, Northern blotting, Western blotting, enzyme-linked immunosorbent assay, fluorescent resonance energy-transfer and sequencing. For use with the present invention
25 the sample may be any of a number of immune cells, e.g., leukocytes or sub-components thereof.

Another embodiment includes a method for diagnosing a host response to an infectious disease from a tissue sample, which includes obtaining a gene expression profile from immune tissue sample, wherein expression of the two or more of the following genes is
30 measured, e.g., Supplemental Tables 1 to 11 and combinations thereof. The Lengthy Tables filed concurrently herewith are fully incorporated herein by reference. In one example of the

present invention, the gene expression profile or transcriptome value vector may include any of the genes listed in the Tables 1, 4, 5 and Supplementary Tables 1 to 11, and combinations thereof, that form part of the present disclosure, e.g., certain genes may form part of the transcriptome vector(s) that are used to differentiate between genes more highly correlated with an infection with Influenza versus bacteria, e.g., those involved in a response to a virus (e.g., *cig5*; *DNAPTP6*; *IFI27*; *IFI35*; *IFI44*; *OAS1*); an immune response (e.g., *BST2*; *G1P2*; *LY6E*; *MX1*); anti-apoptosis (e.g., *SON*); cell growth and/or maintenance (e.g., *TRIM14*); and miscellaneous genes (e.g., *APOBEC3C*; *C1orf29*; *FLJ20035*; *FLJ38348*; *HSXIAPAF1*; *KIAA0152*; *PHACTR2*; and *USP18*). For the differentiation of genes more highly correlated with an infection with a bacteria versus Influenza, it is possible to look at genes involved with translational elongation (e.g., *EEF1G*); the regulation of translational initiation (e.g., *EIF3S5*; *EIF3S7*; *EIF4B*); protein biosynthesis (e.g., *QARS*; *RPL31*; *RPL4*); the regulation of transcription (e.g., *PFDN5*); cell adhesion (e.g., *CD44*); metabolism (e.g., *HADHA*; *PCBP2*); and miscellaneous genes, such as *dJ507I15.1*. The tissue used for the source of biomarker, e.g., RNA, may be blood. In one specific embodiment, the gene profiles are obtained and compared between groups of patients, rather than between patients and controls.

Another embodiment includes a method for diagnosing a host response to a specific infectious disease from a tissue sample, which includes obtaining a gene expression profile or transcriptome from an immune tissue sample, wherein expression of the two or more of the following genes may be used to differentiate between an *S. aureus* infection and an *E. coli* infection, e.g., signal transduction genes (e.g., *CXCL1*; *JAG1*; *RGS2*); metabolism (e.g., *GAPD*); *PIIB*; *PSMA7*; *MMP9*; *p44S10*; protein targeting (e.g., *TRAM2*); intracellular protein transport (e.g., *SEC24C*); and miscellaneous genes (e.g., *ACTG1*; *CGI-96*; *MGC2963*; and *STAU*). Conversely, there may be genes that are most often found to correlate with an *E. coli* infection and not an *S. aureus* infection, e.g., intracellular signaling (e.g., *RASA1*; *SNX4*); regulation of translational initiation (e.g., *AF1Q*); regulation of transcription (e.g., *SMAD2*); cell adhesion (e.g., *JUP*); metabolism (e.g., *PP*; *MAN1C1*); and miscellaneous genes (e.g., *FLJ10287*; *FLJ20152*; *LRRN3*; *SGPP1*; *UBAP2L*). The tissue used for the source of biomarker, e.g., RNA, may be blood. The gene profiles are obtained and compared between groups of patients, rather than between patients and controls.

The method of the present invention wherein the step of determining expression levels is performed by measuring amounts of mRNA expressed by the set of genes and/or measuring

amounts of protein expressed by the set of genes. The step of determining expression levels may be performed using an oligonucleotide array, e.g., by isolating the one or more biomarkers that are nucleic acids from the sample and hybridizing them with known nucleic acids on a solid support. The step of determining expression levels may also be performed

5 using cDNA which is made using mRNA collected from the human cells as a template. In some embodiments, a detectable label may be used to label the biomarker and/or the target for biomarker binding (e.g., an antibody) that is used to determine expression levels. The step of screening may be accomplished by quantitating the mRNA, protein or both mRNA and protein level of the biomarker. Often, the biomarker may be detected at the mRNA level

10 and may be quantitated by a method selected from the group consisting of polymerase chain reaction, real time polymerase chain reaction, reverse transcriptase polymerase chain reaction, hybridization, probe hybridization, and gene expression array. It may also be useful to screen by detection of a polymorphism in the biomarker. Other ways for determining the level of expression may be accomplished using at least one technique

15 selected from the group consisting of polymerase chain reaction, heteroduplex analysis, single strand conformational polymorphism analysis, ligase chain reaction, comparative genome hybridization, Southern blotting, Northern blotting, Western blotting, enzyme-linked immunosorbent assay, fluorescent resonance energy-transfer and sequencing. The sample will often be blood, however, any of a number of cells may be used as well, e.g.,

20 leukocytes, biopsy cells, cells in fluids or secretions and the like. In some embodiments, the biomarker may be proteins extracted from blood.

Yet another embodiment of the present invention includes a method of identifying a human subject suspected of having an infectious disease by determining the expression level of a biomarker having one or more of the following genes for the listed target: genes

25 overexpressed as a result of a bacterial versus a viral infection: Translational elongation; EEF1G; Regulation of translational initiation; EIF3S5; EIF3S7; EIF4B; Protein biosynthesis; QARS; RPL31; RPL4; Regulation of transcription; PF3N5; Cell adhesion; CD44; Metabolism; HADHA; PCBP2; Miscellaneous; dJ507115.1. The step of determining expression levels is performed by measuring amounts of mRNA expressed by the set of

30 genes or even by measuring amounts of protein expressed by the set of genes.

Yet another method of identifying a human subject suspected of having an infectious disease wherein overexpression of the following genes is indicative of *S. aureus* infection: Signal Transduction; CXCL1; JAG1; RGS2; Metabolism; GAPD; PPIB; PSMA7; MMP9; p44S10;

Protein Targeting; TRAM2; Intracellular Protein Transport; SEC24C; Miscellaneous; ACTG1; CGI-96; MGC2963; STAU.

Yet another method of identifying a human subject suspected of having an infectious disease wherein overexpression of the following genes is indicative of *E. coli* infection: Intracellular
5 signaling; RASA1; SNX4; Regulation of translational initiation; AF1Q; Regulation of transcription; SMAD2; Cell adhesion ; JUP; Metabolism; PP; MAN1C1; Miscellaneous; FLJ10287; FLJ20152; LRRN3; LRRN3; SGPP1; UBAP2L.

Yet another method of the present invention includes a computer implemented method for determining the genotype of a sample by, obtaining a plurality of sample probe intensities;
10 diagnosing an infectious disease based upon the sample probe intensities; calculating linear correlation coefficient between the sample probe intensities and reference probe intensities; and accepting the tentative genotype as the genotype of the sample if the linear correlation coefficient is greater than a threshold value. In certain embodiment the threshold value may be between about 0.7 to about 1 or more, however, certain threshold values includes is at
15 least 0.8; at least 0.9 and/or at least 0.95. The probe intensities may be selected from a gene expression profile from the tissue sample wherein expression of the two or more of the following genes is measured for the listed target:

S. aureus: Signal Transduction; CXCL1; JAG1; RGS2; Metabolism; GAPD; PPIB; PSMA7; MMP9; p44S10; Protein Targeting; TRAM2; Intracellular Protein Transport; SEC24C;
20 Miscellaneous; ACTG1; CGI-96; MGC2963; STAU; and combinations thereof;

E. coli: Intracellular signaling; RASA1; SNX4; Regulation of translational initiation; AF1Q; Regulation of transcription; SMAD2; Cell adhesion ; JUP; Metabolism; PP; MAN1C1; Miscellaneous; FLJ10287; FLJ20152; LRRN3; LRRN3; SGPP1; UBAP2L; and combinations thereof; and

25 Influenza: Response to virus; cig5; DNAPTP6; IFI27; IFI35; IFI44; IFI44; OAS1; Immune response; BST2; G1P2; LY6E; MX1; Anti-apoptosis; SON; Cell growth and/or maintenance; TRIM14; Miscellaneous; APOBEC3C; C1orf29; FLJ20035; FLJ38348; HSXIAPAF1; KIAA0152; PHACTR2; USP18; ZBP1; and combinations thereof.

Another embodiment of the present invention is a computer readable medium that includes
30 computer-executable instructions for performing the method for determining the genotype of a sample comprising: obtaining a plurality of sample probe intensities; diagnosing an

infectious disease based upon the sample probe intensities for six or more genes selected those genes listed in Tables 1, 4, 5 and/or Supplemental Tables 1 to 11 and combinations thereof; and calculating a linear correlation coefficient between the sample probe intensities and reference probe intensities; and accepting the tentative genotype as the genotype of the sample if the linear correlation coefficient is greater than a threshold value.

Another embodiment of the present invention is a system for identifying a host immune response to an infectious disease that includes a microarray for the detection of gene expression, wherein the microarray comprises four or more biomarker selected from selected those genes listed in Table 4, Table 5, and Supplemental Tables 1 to 11 and combinations thereof; wherein the gene expression data obtained from the microarray correlates to the host immune response to an infectious disease with a threshold value.

Another embodiment of the present invention is a system for diagnosing an infectious disease by obtaining gene expression data from a microarray; and determining the expression four or more biomarkers selected from the group consisting of four or more genes selected from Tables 1, 4 and/or 5, wherein the gene expression data obtained from the microarray correlates to a host immune response to the infectious disease with a threshold value of at least 0.8. For use with the system of the present invention, the biomarkers may be selected from 5, 6, 7, 8, 9, 10, 11, 12 or 13 genes or gene modules and from one or more of the Supplementary Tables, and combinations thereof, incorporated herein by reference.

Another embodiment is a prognostic gene array that is a customized gene array that includes a combination of genes that are representative of one or more transcriptional modules, wherein the transcriptome of a patient that is contacted with the customized gene array is prognostic of SLE. The array may be used to monitor the patient's response to therapy for SLE. The array may also be used to distinguish between an autoimmune disease, a viral infection a bacterial infection, cancer and transplant rejection. For certain direct measurement purposes the array may even be organized into two or more transcriptional modules that may be visually scanned and the extent of expression analyzed optically, e.g., with the naked eye and/or with image processing equipment. For example, the array may be organized into three transcriptional modules with one or more submodules selected from 5, 6, 7, 8, 9, 10, 11, 12 or 13 genes or gene modules and from one or more of the Supplementary Tables, and combinations thereof, wherein probes that bind specifically to

one or more of the genes are selected from within the three or more modules and are indicative of an infectious disease or other condition, as disclosed herein.

Another embodiment of the present invention includes a method for selecting patients for a clinical trial by obtaining the transcriptome of a prospective patient; comparing the transcriptome to one or more transcriptional modules that are indicative of a disease or condition that is to be treated in the clinical trial; and determining the likelihood that a patient is a good candidate for the clinical trial based on the presence, absence or level of one or more genes that are expressed in the patient's transcriptome within one or more transcriptional modules that are correlated with success in a clinical trial. For use with the method, each module may include a vector that correlates with a sum of the proportion of transcripts in a sample; a vector wherein one or more diseases or conditions are associated with the one or more vectors; a vector that correlates to the expression level of one or more genes within each module and/or a vector that includes modules for the detection, characterization, diagnosis, prognosis and/or monitoring of normal versus patients infected with an infectious disease or a congenital, degenerative, acquired or other disease.

BRIEF DESCRIPTION OF THE DRAWINGS

For a more complete understanding of the features and advantages of the present invention, reference is now made to the detailed description of the invention along with the accompanying figures and in which:

Figure 1 shows that it is possible to differentiate between patients with influenza A virus infection from patients with bacterial infections. Figure 1a shows the hierarchical clustering of 854 genes obtained from Mann-Whitney rank test comparison ($p < 0.01$) between two groups: influenza A (Inf A, 11 samples, green rectangle) and bacterial infections (red rectangle) with *Escherichia coli* (*E.coli*, 6 samples) or *Streptococcus pneumoniae* (*S.pn*, 6 samples). Transformed expression levels are indicated by color scale, with red representing relatively high expression and blue indicating relatively low expression compared to the median expression for each gene across all donors. The black bar indicates interferon-inducible genes (IFN), and the blue bar indicates genes involved in protein biosynthesis. Genes are listed in Supplementary Table 2. Figure 1b shows the results from a supervised learning algorithm was used to identify 35 genes presenting the highest capacity to discriminate the two classes (Table 1 and Supplementary Table 3). Leave-one-out cross-validation of the training set with 35 genes classified the samples with 91% accuracy. The

predicted class is indicated by light colored solid rectangles (green for influenza A and red for bacteria). Two patients with bacterial infections were misclassified. Figure 1c shows a summary of the 35 classifier genes thus identified were tested on an independent set of patients (open rectangles), including 7 new patients with influenza A (green), 23 with *E. coli* (red) and 7 with *S. pneumoniae* infections. The 37 samples in this test set were classified with 95% accuracy (predicted class is indicated by light colored rectangles). One patient was misclassified and one patient was indeterminate in class prediction (gray box). Figure 1d shows the 35 classifier genes identified in 7b that were tested on an independent set of patients (open squares), including 7 new patients with influenza A (Inf A), and 31 with *S. aureus* infections. The 38 samples were classified with 87% accuracy.

Figure 2 shows the expression levels of the 35 classifier genes discriminating patients with Influenza A infection from patients with bacterial infections. Scaled gene expression values (Average Difference intensity) are plotted for the 35 classifier genes represented in Figure 7b that discriminate between samples from patients with influenza A (11 samples, green squares) and bacterial infections (6 samples with *E. coli* and 6 samples with *S. pneumoniae*, red diamonds). Each plot represents one sample, lines represent median expression.

Figure 3a to 3e shows that it is possible to differentiate between patients with *S. aureus* infections from patients with *E. coli* infections. Figure 9a shows the hierarchical clustering of 211 genes obtained from Mann-Whitney rank test comparison ($p < 0.01$) between two groups: *Staphylococcus aureus* (*S. aureus*, 10 samples, red rectangle) and *Escherichia coli* (*E. coli* 10 samples, blue rectangle) infections. Transformed expression levels are indicated by color scale, with red representing relative high expression and blue indicating relative low expression compared to the median expression for each gene across all donors. Genes are listed in Supplementary Table 4. Figure 3b shows the results from a supervised learning algorithm was used to identify 30 genes presenting the highest capacity to discriminate the two classes (see also Supplementary Table 6). Leave-one-out cross-validation of the training set with 30 classifier genes grouped the samples with 95% accuracy. Figure 3c shows that the 30 classifier genes thus identified were tested on an independent set of patients (open rectangles), including 21 new patients with *S. aureus* and 19 with *E. coli* infections. The 40 samples in this test set were predicted with 85% accuracy (predicted class is indicated by light colored rectangles). Of these 40 samples, only 2 were misclassified, while the class of four other samples could not be determined (open rectangles).

Figure 3d and 3e show the validation of differentially expressed genes by real-time RT-PCR. Figure 3d shows the levels of expression of 9 genes were measured by real-time RT-PCR in samples obtained from patients with *S. aureus* (Sa) or *E. coli* (Ec) infections (fold change in gene expression over healthy controls, log transformed except for RGS2, FCAR and ALOX). Each plot represents one sample, lines represent median expression. Figure 9e shows the correlation between expression values obtained by real-time RT-PCR analysis (abscissa) and microarray analysis (ordinate - normalized to the expression in the sample from the same healthy control to which real-time RT-PCR data were normalized; log scale). See Supplementary Table 5 for details.

Figure 4a to 4e show the expression levels of the 30 classifier genes discriminating patients with *E. coli* infections from patients with *S. aureus* infections. Scaled gene expression values (Average Difference intensity) are plotted for the 30 classifier genes represented in Figure 3b that discriminate between samples from patients with *E. coli* (10 samples, blue squares) and *S. aureus* infections (10 samples, red diamonds). Each plot represents one sample, lines represent median expression. Figures 4b to 4e show that the present invention may be used to discern between patients with bacterial infections. Figure 4b shows hierarchical clustering of 242 genes obtained from Mann-Whitney rank test comparison ($p < 0.01$) between groups of patients with *E. coli* infections (11 samples) or *S. pneumoniae* infections (11 samples). Transformed expression levels are indicated by color scale, with red representing relative high expression and blue indicating relative low expression compared to the median expression for each gene across all donors. Genes are listed in Supplementary Table 7. Figure 4c shows the results from a supervised learning algorithm was used to identify genes representing the highest capacity to discriminate the two classes. Leave-one-out cross-validation of the training set with 45 predictor genes classified the samples with 85 % (20/22) accuracy. Classifier genes are listed in Supplementary Table 8. Figure 4d shows the results from an unsupervised hierarchical clustering of 127 genes obtained from Mann-Whitney rank test comparison ($p < 0.01$) between groups of patients with *S. aureus* infection (12 samples) or *S. pneumoniae* infection (11 samples). Transformed expression levels are indicated by color scale, with red representing relative high expression and blue indicating relative low expression compared to the median expression for each gene across all donors. Genes are listed in Supplementary Table 9 Figure 4e shows a supervised learning algorithm was used to identify genes presenting the highest capacity to discriminate the two classes.

Leave-one-out cross-validation of the training set with 30 genes classified the samples with 83% (19/23) accuracy. Classifier genes are listed in Supplementary Table 10.

Figure 5 shows the distinctive patterns of gene expression in circulating leukocytes obtained from patients with acute respiratory infections. Figure 5a shows uses the 30 classifier genes found to discriminate *S. aureus* from *E. coli* (Venn diagram, right: Sa from Ec; Figure 2 and Supplementary Table 6), to identify 30 genes that distinguish *S. aureus* from *S. pneumoniae* (Venn diagram, left: Sa from Sp; Figure 5a and Supplementary Table 10) and 45 genes that distinguish *E. coli* from *S. pneumoniae* (Venn diagram, bottom: Ec from Sp; Supplementary Figure 5b and Supplementary Table 8). Only 3 genes were shared between either of these groups. In Figure 5b the three groups of genes found to discriminate samples from patients with bacterial infections shown in Figure 5a were merged (102 unique genes, Venn diagram, left) and compared to the classifier genes used to discriminate influenza A from bacterial infections (35 genes, Venn diagram, right; Figure 5b and Supplementary Table 3). No genes were shared between these two groups. Figure 5c shows the 137 classifier genes that discriminate Influenza A from bacterial infections and the three groups of patients with different bacterial infections were merged and used to generate discriminatory patterns of expression among 27 patients with respiratory infections and 7 healthy volunteers. Values were normalized to the median expression of each gene across all donors. Clustering of conditions partitioned samples into four major groups. Four samples belonging to the influenza A group and one from the *S. aureus* formed a distinct subgroup characterized by a mixed signature (*).

Figure 6 shows an analysis of significance patterns for infectious disease monitoring. Gene expression levels measured in each group of patients were compared to results obtained in control groups formed by healthy volunteers (Mann Whitney U test). Selection criteria were then applied to p-values generated for patients with Influenza A (FLU) or Systemic Lupus Erythematosus (SLE). Left column: over-expressed genes; Right column: under-expressed genes; Upper row: significantly changed in both FLU and SLE ($p < 0.01$); Middle row: significantly changed in SLE ($p < 0.01$), not FLU ($p > 0.5$); Bottom row: significantly changed in FLU ($p < 0.01$), not SLE ($p > 0.5$). Genes were arranged by hierarchical clustering of p-values. Color scale: Green indicates low p-values, yellow and white high p-values. Blue branches of the dendrograms indicate disease-specific signatures (C1-C4; see Supplementary Table 11 for details).

Figure 7 shows gene vectors that may be used for mapping transcriptional changes at the module-levels identifies disease-specific patterns.

Figure 8 shows the microarray scores for the assessment of disease severity in patients with acute infections.

- 5 Figures 9a to 9c summarize independent confirmation and validation across microarray platforms.

DETAILED DESCRIPTION OF THE INVENTION

While the making and using of various embodiments of the present invention are discussed in detail below, it should be appreciated that the present invention provides many applicable
10 inventive concepts that can be embodied in a wide variety of specific contexts. The specific embodiments discussed herein are merely illustrative of specific ways to make and use the invention and do not delimit the scope of the invention.

To facilitate the understanding of this invention, a number of terms are defined below. Terms defined herein have meanings as commonly understood by a person of ordinary skill
15 in the areas relevant to the present invention. Terms such as “a”, “an” and “the” are not intended to refer to only a singular entity, but include the general class of which a specific example may be used for illustration. The terminology herein is used to describe specific embodiments of the invention, but their usage does not delimit the invention, except as outlined in the claims. Unless defined otherwise, all technical and scientific terms used
20 herein have the meaning commonly understood by a person skilled in the art to which this invention belongs. The following references provide one of skill with a general definition of many of the terms used in this invention: Singleton, et al., Dictionary Of Microbiology And Molecular Biology (2d ed. 1994); The Cambridge Dictionary Of Science And Technology (Walker ed., 1988); The Glossary Of Genetics, 5th Ed., R. Rieger et al. (eds.), Springer
25 Verlag (1991); and Hale & Marham, The Harper Collins Dictionary Of Biology (1991).

Various biochemical and molecular biology methods are well known in the art. For example, methods of isolation and purification of nucleic acids are described in detail in 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
30 Acid Preparation, (P. Tijssen, ed.) Elsevier, N.Y. (1993); Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid

Probes, Part 1. Theory and Nucleic Acid Preparation, (P. Tijssen, ed.) Elsevier, N.Y. (1993); and Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, N.Y., (1989); and Current Protocols in Molecular Biology, (Ausubel, F. M. et al., eds.) John Wiley & Sons, Inc., New York (1987-1999), including supplements such as supplement 46
 5 (April 1999).

BIOINFORMATICS DEFINITIONS

As used herein, an “object” refers to any item or information of interest (generally textual, including noun, verb, adjective, adverb, phrase, sentence, symbol, numeric characters, etc.). Therefore, an object is anything that can form a relationship and anything that can be
 10 obtained, identified, and/or searched from a source. “Objects” include, but are not limited to, an entity of interest such as gene, protein, disease, phenotype, mechanism, drug, etc. In some aspects, an object may be data, as further described below.

As used herein, a “relationship” refers to the co-occurrence of objects within the same unit (e.g., a phrase, sentence, two or more lines of text, a paragraph, a section of a webpage, a
 15 page, a magazine, paper, book, etc.). It may be text, symbols, numbers and combinations, thereof

As used herein, “meta data content” refers to information as to the organization of text in a data source. Meta data can comprise standard metadata such as Dublin Core metadata or can be collection-specific. Examples of metadata formats include, but are not limited to,
 20 Machine Readable Catalog (MARC) records used for library catalogs, Resource Description Format (RDF) and the Extensible Markup Language (XML). Meta objects may be generated manually or through automated information extraction algorithms.

As used herein, an “engine” refers to a program that performs a core or essential function for other programs. For example, an engine may be a central program in an operating system or
 25 application program that coordinates the overall operation of other programs. The term “engine” may also refer to a program containing an algorithm that can be changed. For example, a knowledge discovery engine may be designed so that its approach to identifying relationships can be changed to reflect new rules of identifying and ranking relationships.

As used herein, “statistical analysis” refers to a technique based on counting the number of
 30 occurrences of each term (word, word root, word stem, n-gram, phrase, etc.). In collections unrestricted as to subject, the same phrase used in different contexts may represent different

concepts. Statistical analysis of phrase co-occurrence can help to resolve word sense ambiguity. “Syntactic analysis” can be used to further decrease ambiguity by part-of-speech analysis. As used herein, one or more of such analyses are referred to more generally as “lexical analysis.” “Artificial intelligence (AI)” refers to methods by which a non-human device, such as a computer, performs tasks that humans would deem noteworthy or “intelligent.” Examples include identifying pictures, understanding spoken words or written text, and solving problems.

As used herein, the term “database” refers to repositories for raw or compiled data, even if various informational facets can be found within the data fields. A database is typically organized so its contents can be accessed, managed, and updated (e.g., the database is dynamic). The term “database” and “source” are also used interchangeably in the present invention, because primary sources of data and information are databases. However, a “source database” or “source data” refers in general to data, e.g., unstructured text and/or structured data, that are input into the system for identifying objects and determining relationships. A source database may or may not be a relational database. However, a system database usually includes a relational database or some equivalent type of database which stores values relating to relationships between objects.

As used herein, a “system database” and “relational database” are used interchangeably and refer to one or more collections of data organized as a set of tables containing data fitted into predefined categories. For example, a database table may comprise one or more categories defined by columns (e.g. attributes), while rows of the database may contain a unique object for the categories defined by the columns. Thus, an object such as the identity of a gene might have columns for its presence, absence and/or level of expression of the gene. A row of a relational database may also be referred to as a “set” and is generally defined by the values of its columns. A “domain” in the context of a relational database is a range of valid values a field such as a column may include.

As used herein, a “domain of knowledge” refers to an area of study over which the system is operative, for example, all biomedical data. It should be pointed out that there is advantage to combining data from several domains, for example, biomedical data and engineering data, for this diverse data can sometimes link things that cannot be put together for a normal person that is only familiar with one area or research/study (one domain). A “distributed

database” refers to a database that may be dispersed or replicated among different points in a network.

Terms such “data” and “information” are often used interchangeably, as are “information” and “knowledge.” As used herein, “data” is the most fundamental unit that is an empirical measurement or set of measurements. Data is compiled to contribute to information, but it is fundamentally independent of it. Information, by contrast, is derived from interests, e.g., data (the unit) may be gathered on ethnicity, gender, height, weight and diet for the purpose of finding variables correlated with risk of cardiovascular disease. However, the same data could be used to develop a formula or to create “information” about dietary preferences, i.e., likelihood that certain products in a supermarket have a higher likelihood of selling.

As used herein, “information” refers to a data set that may include numbers, letters, sets of numbers, sets of letters, or conclusions resulting or derived from a set of data. “Data” is then a measurement or statistic and the fundamental unit of information. “Information” may also include other types of data such as words, symbols, text, such as unstructured free text, code, etc. “Knowledge” is loosely defined as a set of information that gives sufficient understanding of a system to model cause and effect. To extend the previous example, information on demographics, gender and prior purchases may be used to develop a regional marketing strategy for food sales while information on nationality could be used by buyers as a guideline for importation of products. It is important to note that there are no strict boundaries between data, information, and knowledge; the three terms are, at times, considered to be equivalent. In general, data comes from examining, information comes from correlating, and knowledge comes from modeling.

As used herein, “a program” or “computer program” refers generally to a syntactic unit that conforms to the rules of a particular programming language and that is composed of declarations and statements or instructions, divisible into, “code segments” needed to solve or execute a certain function, task, or problem. A programming language is generally an artificial language for expressing programs.

As used herein, a “system” or a “computer system” generally refers to one or more computers, peripheral equipment, and software that perform data processing. A “user” or “system operator” in general includes a person, that uses a computer network accessed through a “user device” (e.g., a computer, a wireless device, etc) for the purpose of data processing and information exchange. A “computer” is generally a functional unit that can

perform substantial computations, including numerous arithmetic operations and logic operations without human intervention.

As used herein, “application software” or an “application program” refers generally to software or a program that is specific to the solution of an application problem. An
 5 “application problem” is generally a problem submitted by an end user and requiring information processing for its solution.

As used herein, a “natural language” refers to a language whose rules are based on current usage without being specifically prescribed, e.g., English, Spanish or Chinese. As used herein, an “artificial language” refers to a language whose rules are explicitly established
 10 prior to its use, e.g., computer-programming languages such as C, C++, Java, BASIC, FORTRAN, or COBOL.

As used herein, “statistical relevance” refers to using one or more of the ranking schemes (O/E ratio, strength, etc.), where a relationship is determined to be statistically relevant if it occurs significantly more frequently than would be expected by random chance.

15 As used herein, the terms “coordinately regulated genes” or “transcriptional modules” are used interchangeably to refer to grouped, gene expression profiles (e.g., signal values associated with a specific gene sequence) of specific genes. A value may be assigned to the combination of one or more “coordinately regulated genes” to provide a “transcriptome value vector” or “transcriptome vector” that may be expressed as a single value. For
 20 example, the value may be provided numerically, plotted in a spider chart, plotted with various intensities, color(s), values or as a contours, e.g., an elevation plot. Each transcriptional module may correlate with one or more pieces of data, e.g., a literature search portion and actual empirical gene expression value data obtained from a gene microarray. The set of genes that is selected into a transcriptional modules is based on the analysis of
 25 gene expression data (module extraction algorithm described above). Additional steps are taught by Chaussabel, D. & Sher, A. Mining microarray expression data by literature profiling. *Genome Biol* 3, RESEARCH0055 (2002), (<http://genomebiology.com/2002/3/10/research/0055>) relevant portions incorporated herein by reference and expression data obtained from a disease or condition of interest, e.g.,
 30 Systemic Lupus erythematosus, arthritis, lymphoma, carcinoma, melanoma, acute infection, autoimmune disorders, autoinflammatory disorders, etc.).

The Table below lists examples of keywords that were used to develop the literature search portion or contribution to the transcription modules. The skilled artisan will recognize that other terms may easily be selected for other conditions, e.g., specific cancers, specific infectious disease, transplantation, etc. For example, genes and signals for those genes associated with T cell activation are described hereinbelow as Module ID “M 2.8” in which certain keywords (e.g., Lymphoma, T-cell, CD4, CD8, TCR, Thymus, Lymphoid, IL2) were used to identify key T-cell associated genes, e.g., T-cell surface markers (CD5, CD6, CD7, CD26, CD28, CD96); molecules expressed by lymphoid lineage cells (lymphotoxin beta, IL2-inducible T-cell kinase, TCF7; and T-cell differentiation protein mal, GATA3, STAT5B). Next, the complete module is developed by correlating data from a patient population for these genes (regardless of platform, presence/absence and/or up or downregulation) to generate the transcriptional module. In some cases, the gene profile does not match (at this time) any particular clustering of genes for these disease conditions and data, however, certain physiological pathways (e.g., cAMP signaling, zinc-finger proteins, cell surface markers, etc.) are found within the “Underdetermined” modules. In fact, the gene expression data set may be used to extract genes that have coordinated expression prior to matching to the keyword search, i.e., either data set may be correlated prior to cross-referencing with the second data set.

Table 1. Examples of Genes within Distinct Modules

Module I.D.	Number of probe sets	Keyword selection	Assessment
M 1.1	76	Ig, Immunoglobulin, Bone, Marrow, PreB, IgM, Mu.	Plasma cells. Includes genes coding for Immunoglobulin chains (e.g. IGHM, IGHJ, IGLL1, IGKC, IGHID) and the plasma cell marker CD38.
M 1.2	130	Platelet, Adhesion, Aggregation, Endothelial, Vascular	Platelets. Includes genes coding for platelet glycoproteins (ITGA2B, ITGB3, GP6, GPIA/B), and platelet-derived immune mediators such as PPPB (pro-platelet basic protein) and PF4 (platelet factor 4).
M 1.3	80	Immunoreceptor, BCR, B-cell, IgG	B-cells. Includes genes coding for B-cell surface markers (CD72, CD79A/B, CD19, CD22) and other B-cell associated molecules: Early B-cell factor (EBF), B-cell linker (BLNK) and B lymphoid tyrosine kinase (BLK).
M 1.4	132	Replication, Repression, Repair, CREB, Lymphoid, TNF-alpha	Undetermined. This set includes regulators and targets of cAMP signaling pathway (JUND, ATF4, CREM, PDE4, NR4A2, VIL2), as well as repressors of TNF-alpha mediated NF-KB activation (CYLD, ASK, TNFAIP3).
M 1.5	142	Monocytes, Dendritic, MHC, Costimulatory, TLR4, MYD88	Myeloid lineage. Includes molecules expressed by cells of the myeloid lineage (CD86, CD163, FCGR2A), some of which being involved in pathogen recognition (CD14, TLR2, MYD88). This set also includes TNF family members (TNFR2, BAFF).
M 1.6	141	Zinc, Finger, P53, RAS	Undetermined. This set includes genes coding for signaling molecules, e.g. the zinc finger containing

Module I.D.	Number of probe sets	Keyword selection	Assessment
			inhibitor of activated STAT (PIAS1 and PIAS2), or the nuclear factor of activated T-cells NFATC3.
M 1.7	129	Ribosome, Translational, 40S, 60S, HLA	MHC/Ribosomal proteins. Almost exclusively formed by genes coding MHC class I molecules (HLA-A,B,C,G,E)+ Beta 2-microglobulin (B2M) or Ribosomal proteins (RPLs, RPSs).
M 1.8	154	Metabolism, Biosynthesis, Replication, Helicase	Undetermined. Includes genes encoding metabolic enzymes (GLS, NSF1, NAT1) and factors involved in DNA replication (PURA, TERF2, EIF2S1).
M 2.1	95	NK, Killer, Cytolytic, CD8, Cell-mediated, T-cell, CTL, IFN-g	Cytotoxic cells. Includes cytotoxic T-cells and NK-cells surface markers (CD8A, CD2, CD160, NKG7, KLRs), cytolytic molecules (granzyme, perforin, granulysin), chemokines (CCL5, XCL1) and CTL/NK-cell associated molecules (CTSW).
M 2.2	49	Granulocytes, Neutrophils, Defense, Myeloid, Marrow	Neutrophils. This set includes innate molecules that are found in neutrophil granules (Lactotransferrin: LTF, defensin: DEAF1, Bacterial Permeability Increasing protein: BPI, Cathelicidin antimicrobial protein: CAMP...).
M 2.3	148	Erythrocytes, Red, Anemia, Globin, Hemoglobin	Erythrocytes. Includes hemoglobin genes (HGBs) and other erythrocyte-associated genes (erythrocytic alkaline phosphatase: ANK1, Glycophorin C: GYPC, hydroxymethylbilane synthase: HMBS, erythroid associated factor: ERAF).
M 2.4	133	Ribonucleoprotein, 60S, nucleolus, Assembly, Elongation	Ribosomal proteins. Including genes encoding ribosomal proteins (RPLs, RPSs), Eukaryotic Translation Elongation factor family members (EEFs) and Nucleolar proteins (NPM1, NOAL2, NAP1L1).
M 2.5	315	Adenoma, Interstitial, Mesenchyme, Dendrite, Motor	Undetermined. This module includes genes encoding immune-related (CD40, CD80, CXCL12, IFNA5, IL4R) as well as cytoskeleton-related molecules (Myosin, Dedicator of Cytokinesis, Syndecan 2, Plexin C1, Distrobrevin).
M 2.6	165	Granulocytes, Monocytes, Myeloid, ERK, Necrosis	Myeloid lineage. Includes genes expressed in myeloid lineage cells (IGTB2/CD18, Lymphotoxin beta receptor, Myeloid related proteins 8/14 Formyl peptide receptor 1), such as Monocytes and Neutrophils.
M 2.7	71	No keywords extracted.	Undetermined. This module is largely composed of transcripts with no known function. Only 20 genes associated with literature, including a member of the chemokine-like factor superfamily (CKLFSF8).
M 2.8	141	Lymphoma, T-cell, CD4, CD8, TCR, Thymus, Lymphoid, IL2	T-cells. Includes T-cell surface markers (CD5, CD6, CD7, CD26, CD28, CD96) and molecules expressed by lymphoid lineage cells (lymphotoxin beta, IL2-inducible T-cell kinase, TCF7, T-cell differentiation protein mal, GATA3, STAT5B).
M 2.9	159	ERK, Transactivation, Cytoskeletal, MAPK, JNK	Undetermined. Includes genes encoding molecules that associate to the cytoskeleton (Actin related protein 2/3, MAPK1, MAP3K1, RAB5A). Also present are T-cell expressed genes (FAS, ITGA4/CD49D, ZNF1A1).
M 2.10	106	Myeloid, Macrophage, Dendritic, Inflammatory, Interleukin	Undetermined. Includes genes encoding for Immune-related cell surface molecules (CD36, CD86, LILRB), cytokines (IL15) and molecules involved in signaling pathways (FYB, TICAM2-Toll-like receptor pathway).
M 2.11	176	Replication, Repress, RAS,	Undetermined. Includes kinases (UIMK1, CSNK1G1, CDK6, WNK1, TAOK1, CALM2, PRKC1, ITPKB,

Module I.D.	Number of probe sets	Keyword selection	Assessment
		Autophosphorylation, Oncogenic	SRPK2, STK17B, DYRK2, PIK3R1, STK4, CLK4, PKN2) and RAS family members (G3BP, RAB14, RASA2, RAP2A, KRAS).
M 3.1	122	ISRE, Influenza, Antiviral, IFN-gamma, IFN-alpha, Interferon	Interferon-inducible. This set includes interferon-inducible genes: antiviral molecules (OAS1/2/3/L, GBP1, G1P2, EIF2AK2/PKR, MX1, PML), chemokines (CXCL10/IP-10), signaling molecules (STAT1, STA2, IRF7, ISGF3G).
M 3.2	322	TGF-beta, TNF, Inflammatory, Apoptotic, Lipopolysaccharide	Inflammation I. Includes genes encoding molecules involved in inflammatory processes (e.g. IL8, ICAM1, C5R1, CD44, PLAUR, IL1A, CXCL16), and regulators of apoptosis (MCL1, FOXO3A, RARA, BCL3/6/2A1, GADD45B).
M 3.3	276	Inflammatory, Defense, Lysosomal, Oxidative, LPS	Inflammation II. Includes molecules inducing or inducible by inflammation (IL18, ALOX5, ANPEP, AOAII, HMOX1, SERPINB1), as well as lysosomal enzymes (PPT1, CTSB/S, NEU1, ASAH1, LAMP2, CAST).
M 3.4	325	Ligase, Kinase, KIP1, Ubiquitin, Chaperone	Undetermined. Includes protein phosphatases (PPP1R12A, PTPRC, PPP1CB, PPM1B) and phosphoinositide 3-kinase (PI3K) family members (PIK3CA, PIK32A, PIP5K3).
M 3.5	22	No keyword extracted	Undetermined. Composed of only a small number of transcripts. Includes hemoglobin genes (HBA1, HBA2, HBB).
M 3.6	288	Ribosomal, T-cell, Beta-catenin	Undetermined. This set includes mitochondrial ribosomal proteins (MRPLs, MRPs), mitochondrial elongations factors (GFM1/2), Sortin Nexins (SN1/6/14) as well as lysosomal ATPases (ATP6V1C/D).
M 3.7	301	Spliceosome, Methylation, Ubiquitin	Undetermined. Includes genes encoding proteasome subunits (PSMA2/5, PSMB5/8); ubiquitin protein ligases HBP2, STUB1, as well as components of ubiquitin ligase complexes (SUGT1).
M 3.8	284	CDC, TCR, CREB, Glycosylase	Undetermined. Includes genes encoding enzymes: aminomethyltransferase, arginyltransferase, asparagines synthetase, diacylglycerol kinase, inositol phosphatases, methyltransferases, helicases...
M 3.9	260	Chromatin, Checkpoint, Replication, Transactivation	Undetermined. Includes genes encoding kinases (IBTK, PRKRII, PRKDC, PRKCI) and phosphatases (e.g. PTPLB3, PPP2CB/3CB, PTPRC, MTM1, MTMR2).

BIOLOGICAL DEFINITIONS

As used herein, the term “array” refers to a solid support or substrate with one or more peptides or nucleic acid probes attached to the support. Arrays typically have one or more different nucleic acid or peptide probes that are coupled to a surface of a substrate in different, known locations. These arrays, also described as “microarrays”, “gene-chips” or DNA chips that may have 10,000; 20,000, 30,000; or 40,000 different identifiable genes based on the known genome, e.g., the human genome. These pan-arrays are used to detect the entire “transcriptome” or transcriptional pool of genes that are expressed or found in a sample, e.g., nucleic acids that are expressed as RNA, mRNA and the like that may be

subjected to RT and/or RT-PCR to make a complementary set of DNA replicons. Arrays may be produced using mechanical synthesis methods, light directed synthesis methods and the like that incorporate a combination of non-lithographic and/or photolithographic methods and solid phase synthesis methods. Bead arrays that include 50-mer oligonucleotide probes
5 attached to 3 micrometer beads may be used that are, e.g., lodged into microwells at the surface of a glass slide or are part of a liquid phase suspension arrays (e.g., Luminex or Illumina) that are digital beadarrays in liquid phase and uses "barcoded" glass rods for detection and identification.

Various techniques for the synthesis of these nucleic acid arrays have been described, e.g.,
10 fabricated on a surface of virtually any shape or even a multiplicity of surfaces. Arrays may be peptides or nucleic acids on beads, gels, polymeric surfaces, fibers such as fiber optics, glass or any other appropriate substrate. Arrays may be packaged in such a manner as to allow for diagnostics or other manipulation of an all inclusive device, see for example, U.S. Pat. No. 6,955,788, relevant portions incorporated herein by reference.

As used herein, the term "disease" refers to a physiological state of an organism with any abnormal biological state of a cell. Disease includes, but is not limited to, an interruption, cessation or disorder of cells, tissues, body functions, systems or organs that may be inherent, inherited, caused by an infection, caused by abnormal cell function, abnormal cell division and the like. A disease that leads to a "disease state" is generally detrimental to the
20 biological system, that is, the host of the disease. With respect to the present invention, any biological state, such as an infection (e.g., viral, bacterial, fungal, helminthic, etc.), inflammation, autoinflammation, autoimmunity, anaphylaxis, allergies, premalignancy, malignancy, surgical, transplantation, physiological, and the like that is associated with a disease or disorder is considered to be a disease state. A pathological state is generally the
25 equivalent of a disease state.

Disease states may also be categorized into different levels of disease state. As used herein, the level of a disease or disease state is an arbitrary measure reflecting the progression of a disease or disease state as well as the physiological response upon, during and after treatment. Generally, a disease or disease state will progress through levels or stages,
30 wherein the affects of the disease become increasingly severe. The level of a disease state may be impacted by the physiological state of cells in the sample.

As used herein, the terms “therapy” or “therapeutic regimen” refer to those medical steps taken to alleviate or alter a disease state, e.g., a course of treatment intended to reduce or eliminate the affects or symptoms of a disease using pharmacological, surgical, dietary and/or other techniques. A therapeutic regimen may include a prescribed dosage of one or more drugs or surgery. Therapies will most often be beneficial and reduce the disease state but in many instances the effect of a therapy will have non-desirable or side-effects. The effect of therapy will also be impacted by the physiological state of the host, e.g., age, gender, genetics, weight, other disease conditions, etc.

As used herein, the term “pharmacological state” or “pharmacological status” refers to those samples that will be, are and/or were treated with one or more drugs, surgery and the like that may affect the pharmacological state of one or more nucleic acids in a sample, e.g., newly transcribed, stabilized and/or destabilized as a result of the pharmacological intervention. The pharmacological state of a sample relates to changes in the biological status before, during and/or after drug treatment and may serve a diagnostic or prognostic function, as taught herein. Some changes following drug treatment or surgery may be relevant to the disease state and/or may be unrelated side-effects of the therapy. Changes in the pharmacological state are the likely results of the duration of therapy, types and doses of drugs prescribed, degree of compliance with a given course of therapy, and/or un-prescribed drugs ingested.

As used herein, the term “biological state” refers to the state of the transcriptome (that is the entire collection of RNA transcripts) of the cellular sample isolated and purified for the analysis of changes in expression. The biological state reflects the physiological state of the cells in the sample by measuring the abundance and/or activity of cellular constituents, characterizing according to morphological phenotype or a combination of the methods for the detection of transcripts.

As used herein, the term “expression profile” refers to the relative abundance of RNA, DNA or protein abundances or activity levels. The expression profile can be a measurement for example of the transcriptional state or the translational state by any number of methods and using any of a number of gene-chips, gene arrays, beads, multiplex PCR, quantitative PCR, run-on assays, Northern blot analysis, Western blot analysis, protein expression, fluorescence activated cell sorting (FACS), enzyme linked immunosorbent assays (ELISA), chemiluminescence studies, enzymatic assays, proliferation studies or any other method,

apparatus and system for the determination and/or analysis of gene expression that are readily commercially available.

As used herein, the term “transcriptional state” of a sample includes the identities and relative abundances of the RNA species, especially mRNAs present in the sample. The entire transcriptional state of a sample, that is the combination of identity and abundance of RNA, is also referred to herein as the transcriptome. Generally, a substantial fraction of all the relative constituents of the entire set of RNA species in the sample are measured.

As used herein, the terms “transcriptional vectors,” “expression vectors,” and “genomic vectors” (used interchangeably) refers to transcriptional expression data that reflects the “proportion of differentially expressed genes.” For example, for each module the proportion of transcripts differentially expressed between at least two groups (e.g., healthy subjects vs patients). This vector is derived from the comparison of two groups of samples. The first analytical step is used for the selection of disease-specific sets of transcripts within each module. Next, there is the “expression level.” The group comparison for a given disease provides the list of differentially expressed transcripts for each module. It was found that different diseases yield different subsets of modular transcripts. With this expression level it is then possible to calculate vectors for each module(s) for a single sample by averaging expression values of disease-specific subsets of genes identified as being differentially expressed. This approach permits the generation of maps of modular expression vectors for a single sample, e.g., those described in the module maps disclosed herein. These vector module maps represent an averaged expression level for each module (instead of a proportion of differentially expressed genes) that can be derived for each sample. These composite “expression vectors” are formed through successive rounds of selection: 1) of the modules that were significantly changed across study groups and 2) of the genes within these modules which are significantly changed across study groups. Expression levels are subsequently derived by averaging the values obtained for the subset of transcripts forming each vector. Patient profiles can then be represented by plotting expression levels obtained for each of these vectors on a graph (e.g. on a radar plot). Therefore a set of vectors results from two round of selection, first at the module level, and then at the gene level. Vector expression values are composite by construction as they derive from the average expression values of the transcript forming the vector.

Using the present invention it is possible to identify and distinguish diseases not only at the module-level, but also at the gene-level; i.e., two diseases can have the same vector (identical proportion of differentially expressed transcripts, identical “polarity”), but the gene composition of the expression vector can still be disease-specific. This disease-specific
5 customization permits the user to optimize the performance of a given set of markers by increasing its specificity.

Using modules as a foundation grounds expression vectors to coherent functional and transcriptional units containing minimized amounts of noise. Furthermore, the present invention takes advantage of composite transcriptional markers. As used herein, the term
10 “composite transcriptional markers” refers to the average expression values of multiple genes (subsets of modules) as compared to using individual genes as markers (and the composition of these markers can be disease-specific). The composite transcriptional markers approach is unique because the user can develop multivariate microarray scores to assess disease severity in patients with, e.g., a viral, bacterial or other infectious disease, or
15 to derive expression vectors disclosed herein. The fact that expression vectors are composite (i.e. formed by a combination of transcripts) further contributes to the stability of these markers. Most importantly, it has been found that using the composite modular transcriptional markers of the present invention the results found herein are reproducible across microarray platform, thereby providing greater reliability for regulatory approval.
20 Indeed, vector expression values proved remarkably robust, as indicated by the excellent reproducibility obtained across microarray platforms; as well as the validation results obtained in an independent set of pediatric lupus patients. These results are of importance since improving the reliability of microarray data is a prerequisite for the widespread use of this technology in clinical practice (see, e.g., FDA MAQC program, which aims at
25 establishing reproducibility across array platforms.).

Gene expression monitoring systems for use with the present invention may include customized gene arrays with a limited and/or basic number of genes that are specific and/or customized for the one or more target diseases. Unlike the general, pan-genome arrays that are in customary use, the present invention provides for not only the use of these general
30 pan-arrays for retrospective gene and genome analysis without the need to use a specific platform, but more importantly, it provides for the development of customized arrays that provide an optimal gene set for analysis without the need for the thousands of other, non-relevant genes. One distinct advantage of the optimized arrays and modules of the present

invention over the existing art is a reduction in the financial costs (e.g., cost per assay, materials, equipment, time, personnel, training, etc.), and more importantly, the environmental cost of manufacturing pan-arrays where the vast majority of the data is irrelevant. The modules of the present invention allow for the first time the design of simple, custom arrays that provide optimal data with the least number of probes while maximizing the signal to noise ratio. By eliminating the total number of genes for analysis, it is possible to, e.g., eliminate the need to manufacture thousands of expensive platinum masks for photolithography during the manufacture of pan-genetic chips that provide vast amounts of irrelevant data. Using the present invention it is possible to completely avoid the need for microarrays if the limited probe set(s) of the present invention are used with, e.g., digital optical chemistry arrays, ball bead arrays, beads (e.g., Luminex), multiplex PCR, quantitative PCR, run-on assays, Northern blot analysis, or even, for protein analysis, e.g., Western blot analysis, 2-D and 3-D gel protein expression, MALDI, MALDI-TOF, fluorescence activated cell sorting (FACS) (cell surface or intracellular), enzyme linked immunosorbent assays (ELISA), chemiluminescence studies, enzymatic assays, proliferation studies or any other method, apparatus and system for the determination and/or analysis of gene expression that are readily commercially available.

The “molecular fingerprinting system” of the present invention may be used to facilitate and conduct a comparative analysis of expression in different cells or tissues, different subpopulations of the same cells or tissues, different physiological states of the same cells or tissue, different developmental stages of the same cells or tissue, or different cell populations of the same tissue against other diseases and/or normal cell controls. In some cases, the normal or wild-type expression data may be from samples analyzed at or about the same time or it may be expression data obtained or culled from existing gene array expression databases, e.g., public databases such as the NCBI Gene Expression Omnibus database.

As used herein, the term “differentially expressed” refers to the measurement of a cellular constituent (e.g., nucleic acid, protein, enzymatic activity and the like) that varies in two or more samples, e.g., between a disease sample and a normal sample. The cellular constituent may be on or off (present or absent), upregulated relative to a reference or downregulated relative to the reference. For use with gene-chips or gene-arrays, differential gene expression of nucleic acids, e.g., mRNA or other RNAs (miRNA, siRNA, hnRNA, rRNA, tRNA, etc.) may be used to distinguish between cell types or nucleic acids. Most commonly, the measurement of the transcriptional state of a cell is accomplished by quantitative reverse

transcriptase (RT) and/or quantitative reverse transcriptase-polymerase chain reaction (RT-PCR), genomic expression analysis, post-translational analysis, modifications to genomic DNA, translocations, in situ hybridization and the like.

For some disease states it is possible to identify cellular or morphological differences, especially at early levels of the disease state. The present invention avoids the need to identify those specific mutations or one or more genes by looking at modules of genes of the cells themselves or, more importantly, of the cellular RNA expression of genes from immune effector cells that are acting within their regular physiologic context, that is, during immune activation, immune tolerance or even immune anergy. While a genetic mutation may result in a dramatic change in the expression levels of a group of genes, biological systems often compensate for changes by altering the expression of other genes. As a result of these internal compensation responses, many perturbations may have minimal effects on observable phenotypes of the system but profound effects to the composition of cellular constituents. Likewise, the actual copies of a gene transcript may not increase or decrease, however, the longevity or half-life of the transcript may be affected leading to greatly increases protein production. The present invention eliminates the need of detecting the actual message by, in one embodiment, looking at effector cells (e.g., leukocytes, lymphocytes and/or sub-populations thereof) rather than single messages and/or mutations.

The skilled artisan will appreciate readily that samples may be obtained from a variety of sources including, e.g., single cells, a collection of cells, tissue, cell culture and the like. In certain cases, it may even be possible to isolate sufficient RNA from cells found in, e.g., urine, blood, saliva, tissue or biopsy samples and the like. In certain circumstances, enough cells and/or RNA may be obtained from: mucosal secretion, feces, tears, blood plasma, peritoneal fluid, interstitial fluid, intradural, cerebrospinal fluid, sweat or other bodily fluids. The nucleic acid source, e.g., from tissue or cell sources, may include a tissue biopsy sample, one or more sorted cell populations, cell culture, cell clones, transformed cells, biopsies or a single cell. The tissue source may include, e.g., brain, liver, heart, kidney, lung, spleen, retina, bone, neural, lymph node, endocrine gland, reproductive organ, blood, nerve, vascular tissue, and olfactory epithelium.

The present invention includes the following basic components, which may be used alone or in combination, namely, one or more data mining algorithms; one or more module-level analytical processes; the characterization of blood leukocyte transcriptional modules; the use

of aggregated modular data in multivariate analyses for the molecular diagnostic/prognostic of human diseases; and/or visualization of module-level data and results. Using the present invention it is also possible to develop and analyze composite transcriptional markers, which may be further aggregated into a single multivariate score.

- 5 The present inventors have recognized that current microarray-based research is facing significant challenges with the analysis of data that are notoriously “noisy,” that is, data that is difficult to interpret and does not compare well across laboratories and platforms. A widely accepted approach for the analysis of microarray data begins with the identification of subsets of genes differentially expressed between study groups. Next, the users try
10 subsequently to “make sense” out of resulting gene lists using pattern discovery algorithms and existing scientific knowledge.

Rather than deal with the great variability across platforms, the present inventors have developed a strategy that emphasized the selection of biologically relevant genes at an early stage of the analysis. Briefly, the method includes the identification of the transcriptional
15 components characterizing a given biological system for which an improved data mining algorithm was developed to analyze and extract groups of coordinately expressed genes, or transcriptional modules, from large collections of data.

The biomarker discovery strategy described herein is particularly well adapted for the exploitation of microarray data acquired on a global scale. Starting from ~44,000 transcripts
20 a set of 28 modules was defined that are composed of nearly 5000 transcripts. Sets of disease-specific composite expression vectors were then derived. Vector expression values (expression vectors) proved remarkably robust, as indicated by the excellent reproducibility obtained across microarray platforms. This finding is notable, since improving the reliability of microarray data is a prerequisite for the widespread use of this technology in clinical
25 practice. Finally, expression vectors can in turn be combined to obtain unique multivariate scores, therefore delivering results in a form that is compatible with mainstream clinical practice. Interestingly, multivariate scores recapitulate global patterns of change rather than changes in individual markers. The development of such “global biomarkers” can be used for both diagnostic and pharmacogenomics fields.

- 30 In one example, twenty-eight transcriptional modules regrouping 4742 probe sets were obtained from 239 blood leukocyte transcriptional profiles. Functional convergence among genes forming these modules was demonstrated through literature profiling. The second step

consisted of studying perturbations of transcriptional systems on a modular basis. To illustrate this concept, leukocyte transcriptional profiles obtained from healthy volunteers and patients were obtained, compared and analyzed. Further validation of this gene fingerprinting strategy was obtained through the analysis of a published microarray dataset.

- 5 Remarkably, the modular transcriptional apparatus, system and methods of the present invention using pre-existing data showed a high degree of reproducibility across two commercial microarray platforms.

The present invention includes the implementation of a widely applicable, two-step microarray data mining strategy designed for the modular analysis of transcriptional
10 systems. This novel approach was used to characterize transcriptional signatures of blood leukocytes, which constitutes the most accessible source of clinically relevant information.

As demonstrated herein, it is possible to determine, differential and/or distinguish between two disease based on two vectors even if the vector is identical (+/+) for two diseases – e.g. M1.3 = 53% down for both SLE and FLU because the composition of each vector can still
15 be used to differentiate them. For example, even though the proportion and polarity of differentially expressed transcripts is identical between the two diseases for M1.3, the gene composition can still be disease-specific. The combination of gene-level and module-level analysis considerably increases resolution. Furthermore, it is possible to use 2, 3, 4, 5, 10, 15, 20, 25, 28 or more modules to differentiate diseases.

- 20 The term “gene” refers to a nucleic acid (e.g., DNA) sequence that includes coding sequences necessary for the production of a polypeptide (e.g.,), precursor, or RNA (e.g., mRNA). The polypeptide may be encoded by a full length coding sequence or by any portion of the coding sequence so long as the desired activity or functional property (e.g., enzymatic activity, ligand binding, signal transduction, immunogenicity, etc.) of the full-
25 length or fragment is retained. The term also encompasses the coding region of a structural gene and the sequences located adjacent to the coding region on both the 5’ and 3’ ends for a distance of about 2 kb or more on either end such that the gene corresponds to the length of the full-length mRNA and 5’ regulatory sequences which influence the transcriptional properties of the gene. Sequences located 5’ of the coding region and present on the mRNA
30 are referred to as 5’-untranslated sequences. The 5’-untranslated sequences usually contain the regulatory sequences. Sequences located 3’ or downstream of the coding region and present on the mRNA are referred to as 3’-untranslated sequences. The term “gene”

encompasses both cDNA and genomic forms of a gene. A genomic form or clone of a gene contains the coding region interrupted with non-coding sequences termed “introns” or “intervening regions” or “intervening sequences.” Introns are segments of a gene that are transcribed into nuclear RNA (hnRNA); introns may contain regulatory elements such as enhancers. Introns are removed or “spliced out” from the nuclear or primary transcript; introns therefore are absent in the messenger RNA (mRNA) transcript. The mRNA functions during translation to specify the sequence or order of amino acids in a nascent polypeptide.

As used herein, the term “nucleic acid” refers to any nucleic acid containing molecule, including but not limited to, DNA, cDNA and RNA. In particular, the terms “a gene in Table X” refers to at least a portion or the full-length sequence listed in a particular table, as found hereinbelow. The gene may even be found or detected a genomic form, that is, it includes one or more intron(s). Genomic forms of a gene may also include sequences located on both the 5’ and 3’ end of the coding sequences that are present on the RNA transcript. These sequences are referred to as “flanking” sequences or regions. The 5’ flanking region may contain regulatory sequences such as promoters and enhancers that control or influence the transcription of the gene. The 3’ flanking region may contain sequences that influence the transcription termination, post-transcriptional cleavage, mRNA stability and polyadenylation.

As used herein, the term “wild-type” refers to a gene or gene product isolated from a naturally occurring source. A wild-type gene is that which is most frequently observed in a population and is thus arbitrarily designed the “normal” or “wild-type” form of the gene. In contrast, the term “modified” or “mutant” refers to a gene or gene product that displays modifications in sequence and/or functional properties (i.e., altered characteristics) when compared to the wild-type gene or gene product. It is noted that naturally occurring mutants can be isolated; these are identified by the fact that they have altered characteristics (including altered nucleic acid sequences) when compared to the wild-type gene or gene product.

As used herein, the term “polymorphism” refers to the regular and simultaneous occurrence in a single interbreeding population of two or more alleles of a gene, where the frequency of the rarer alleles is greater than can be explained by recurrent mutation alone (typically greater than 1%).

As used herein, the terms “nucleic acid molecule encoding,” “DNA sequence encoding,” and “DNA encoding” refer to the order or sequence of deoxyribonucleotides along a strand of deoxyribonucleic acid. The order of these deoxyribonucleotides determines the order of amino acids along the polypeptide protein) chain. The DNA sequence thus codes for the amino acid sequence.

As used herein, the terms “complementary” or “complementarity” are used in reference to polynucleotides (i.e., a sequence of nucleotides) related by the base-pairing rules. For example, the sequence “A-G-T,” is complementary to the sequence “T-C-A.” Complementarity may be “partial,” in which only some of the nucleic acids’ bases are matched according to the base pairing rules. Or, there may be “complete” or “total” complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection methods that depend upon binding between nucleic acids.

As used herein, the term “hybridization” is used in reference to the pairing of complementary nucleic acids. Hybridization and the strength of hybridization (i.e., the strength of the association between the nucleic acids) is impacted by such factors as the degree of complementarity between the nucleic acids, stringency of the conditions involved, the T_m of the formed hybrid, and the G:C ratio within the nucleic acids. A single molecule that contains pairing of complementary nucleic acids within its structure is said to be “self-hybridized.”

As used herein the term “stringency” is used in reference to the conditions of temperature, ionic strength, and the presence of other compounds such as organic solvents, under which nucleic acid hybridizations are conducted. Under “low stringency conditions” a nucleic acid sequence of interest will hybridize to its exact complement, sequences with single base mismatches, closely related sequences (e.g., sequences with 90% or greater homology), and sequences having only partial homology (e.g., sequences with 50-90% homology). Under “medium stringency conditions,” a nucleic acid sequence of interest will hybridize only to its exact complement, sequences with single base mismatches, and closely related sequences (e.g., 90% or greater homology). Under “high stringency conditions,” a nucleic acid sequence of interest will hybridize only to its exact complement, and (depending on conditions such a temperature) sequences with single base mismatches. In other words,

under conditions of high stringency the temperature can be raised so as to exclude hybridization to sequences with single base mismatches.

As used herein, the term "probe" refers to an oligonucleotide (i.e., a sequence of nucleotides), whether occurring naturally as in a purified restriction digest or produced synthetically, recombinantly or by PCR amplification, that is capable of hybridizing to another oligonucleotide of interest. A probe may be single-stranded or double-stranded. Probes are useful in the detection, identification and isolation of particular gene sequences. Any probe used in the present invention may be labeled with any "reporter molecule," so that it is detectable in any detection system, including, but not limited to enzyme (e.g., ELISA, as well as enzyme-based histochemical assays), fluorescent, radioactive, luminescent systems and the like. It is not intended that the present invention be limited to any particular detection system or label.

As used herein, the term "target," refers to the region of nucleic acid bounded by the primers. Thus, the "target" is sought to be sorted out from other nucleic acid sequences. A "segment" is defined as a region of nucleic acid within the target sequence.

As used herein, the term "Southern blot" refers to the analysis of DNA on agarose or acrylamide gels to fractionate the DNA according to size followed by transfer of the DNA from the gel to a solid support, such as nitrocellulose or a nylon membrane. The immobilized DNA is then probed with a labeled probe to detect DNA species complementary to the probe used. The DNA may be cleaved with restriction enzymes prior to electrophoresis. Following electrophoresis, the DNA may be partially depurinated and denatured prior to or during transfer to the solid support. Southern blots are a standard tool of molecular biologists (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, NY, pp 9.31-9.58, 1989).

As used herein, the term "Northern blot" refers to the analysis of RNA by electrophoresis of RNA on agarose gels, to fractionate the RNA according to size followed by transfer of the RNA from the gel to a solid support, such as nitrocellulose or a nylon membrane. The immobilized RNA is then probed with a labeled probe to detect RNA species complementary to the probe used. Northern blots are a standard tool of molecular biologists (Sambrook, et al., *supra*, pp 7.39-7.52, 1989).

As used herein, the term "Western blot" refers to the analysis of protein(s) (or polypeptides) immobilized onto a support such as nitrocellulose or a membrane. The proteins are run on

acrylamide gels to separate the proteins, followed by transfer of the protein from the gel to a solid support, such as nitrocellulose or a nylon membrane. The immobilized proteins are then exposed to antibodies with reactivity against an antigen of interest. The binding of the antibodies may be detected by various methods, including the use of radiolabeled antibodies.

5 As used herein, the term "polymerase chain reaction" ("PCR") refers to the method of K. B. Mullis (U.S. Pat. Nos. 4,683,195 4,683,202, and 4,965,188, hereby incorporated by reference), which describe a method for increasing the concentration of a segment of a target sequence in a mixture of genomic DNA without cloning or purification. This process for amplifying the target sequence consists of introducing a large excess of two oligonucleotide
10 primers to the DNA mixture containing the desired target sequence, followed by a precise sequence of thermal cycling in the presence of a DNA polymerase. The two primers are complementary to their respective strands of the double stranded target sequence. To effect amplification, the mixture is denatured and the primers then annealed to their complementary sequences within the target molecule. Following annealing, the primers are
15 extended with a polymerase so as to form a new pair of complementary strands. The steps of denaturation, primer annealing and polymerase extension can be repeated many times (i.e., denaturation, annealing and extension constitute one "cycle"; there can be numerous "cycles") to obtain a high concentration of an amplified segment of the desired target sequence. The length of the amplified segment of the desired target sequence is determined
20 by the relative positions of the primers with respect to each other, and therefore, this length is a controllable parameter. By virtue of the repeating aspect of the process, the method is referred to as the "polymerase chain reaction" (hereinafter "PCR"). Because the desired amplified segments of the target sequence become the predominant sequences (in terms of concentration) in the mixture, they are said to be "PCR amplified".

25 As used herein, the terms "PCR product," "PCR fragment," and "amplification product" refer to the resultant mixture of compounds after two or more cycles of the PCR steps of denaturation, annealing and extension are complete. These terms encompass the case where there has been amplification of one or more segments of one or more target sequences.

As used herein, the term "real time PCR" as used herein, refers to various PCR applications
30 in which amplification is measured during as opposed to after completion of the reaction. Reagents suitable for use in real time PCR embodiments of the present invention include but

are not limited to TaqMan probes, molecular beacons, Scorpions primers or double-stranded DNA binding dyes.

As used herein, the terms “transcriptional upregulation,” “overexpression, and “overexpressed” refers to an increase in synthesis of RNA, by RNA polymerases using a DNA template. For example, when used in reference to the methods of the present invention, the term “transcriptional upregulation” refers to an increase of about 1 fold, 2 fold, 2 to 3 fold, 3 to 10 fold, and even greater than 10 fold, in the quantity of mRNA corresponding to a gene of interest detected in a sample derived from an individual predisposed to SLE as compared to that detected in a sample derived from an individual who is not predisposed to SLE. However, the system and evaluation is sufficiently specific to require less than a 2 fold change in expression to be detected. Furthermore, the change in expression may be at the cellular level (change in expression within a single cell or cell populations) or may even be evaluated at a tissue level, where there is a change in the number of cells that are expressing the gene. Changes of gene expression in the context of the analysis of a tissue can be due to either regulation of gene activity or relative change in cellular composition. Particularly useful differences are those that are statistically significant.

Conversely, the terms “transcriptional downregulation,” “underexpression” and “underexpressed” are used interchangeably and refer to a decrease in synthesis of RNA, by RNA polymerases using a DNA template. For example, when used in reference to the methods of the present invention, the term “transcriptional downregulation” refers to a decrease of at least 1 fold, 2 fold, 2 to 3 fold, 3 to 10 fold, and even greater than 10 fold, in the quantity of mRNA corresponding to a gene of interest detected in a sample derived from an individual predisposed to SLE as compared to that detected in a sample derived from an individual who is not predisposed to such a condition or to a database of information for wild-type and/or normal control, e.g., fibromyalgia. Again, the system and evaluation is sufficiently specific to require less than a 2 fold change in expression to be detected. Particularly useful differences are those that are statistically significant.

Both transcriptional “upregulation”/overexpression and transcriptional “downregulation”/underexpression may also be indirectly monitored through measurement of the translation product or protein level corresponding to the gene of interest. The present

invention is not limited to any given mechanism related to upregulation or downregulation of transcription.

The term "eukaryotic cell" as used herein refers to a cell or organism with membrane-bound, structurally discrete nucleus and other well-developed subcellular compartments. Eukaryotes
5 include all organisms except viruses, bacteria, and bluegreen algae.

As used herein, the term "in vitro transcription" refers to a transcription reaction comprising a purified DNA template containing a promoter, ribonucleotide triphosphates, a buffer system that includes a reducing agent and cations, e.g., DTT and magnesium ions, and an appropriate RNA polymerase, which is performed outside of a living cell or organism.

10 As used herein, the term "amplification reagents" refers to those reagents (deoxyribonucleotide triphosphates, buffer, etc.), needed for amplification except for primers, nucleic acid template and the amplification enzyme. Typically, amplification reagents along with other reaction components are placed and contained in a reaction vessel (test tube, microwell, etc.).

15 As used herein, the term "diagnosis" refers to the determination of the nature of a case of disease. In some embodiments of the present invention, methods for making a diagnosis are provided which permit determination of the infectious agents or agents that are the source of the infectious disease. In certain embodiments, the analysis of the present invention may be combined with one or more of the modules of co-pending patent applications 60,748,884,
20 11,446,825 and _____, relevant portions incorporated herein by reference, for the determination of the nature of a disease condition, e.g., auto-immune diseases, auto-inflammatory diseases, cancer, transplant rejection, viral infection, bacterial infection, helminthic or parasitic infection and the like.

The present invention may be used alone or in combination with disease therapy to monitor
25 disease progression and/or patient management. For example, a patient may be tested one or more times to determine the best course of treatment, determine if the treatment is having the intended medical effect, if the patient is not a candidate for that particular therapy and combinations thereof. The skilled artisan will recognize that one or more of the expression vectors may be indicative of one or more diseases and may be affected by other conditions,
30 be they acute or chronic.

As used herein, the term “pharmacogenetic test” refers to an assay intended to study interindividual variations in DNA sequence related to, e.g., drug absorption and disposition (pharmacokinetics) or drug action (pharmacodynamics), which may include polymorphic variations in one or more genes that encode the functions of, e.g., transporters, metabolizing enzymes, receptors and other proteins.

As used herein, the term “pharmacogenomic test” refers to an assay used to study interindividual variations in whole-genome or candidate genes, e.g., single-nucleotide polymorphism (SNP) maps or haplotype markers, and the alteration of gene expression or inactivation that may be correlated with pharmacological function and therapeutic response.

As used herein, an “expression profile” refers to the measurement of the relative abundance of a plurality of cellular constituents. Such measurements may include, e.g., RNA or protein abundances or activity levels. The expression profile can be a measurement for example of the transcriptional state or the translational state. See U.S. Pat. Nos. 6,040,138, 5,800,992, 6,020,135, 6,033,860, relevant portions incorporated herein by reference. The gene expression monitoring system, include nucleic acid probe arrays, membrane blot (such as used in hybridization analysis such as Northern, Southern, dot, and the like), or microwells, sample tubes, gels, beads or fibers (or any solid support comprising bound nucleic acids). See, e.g., U.S. Pat. Nos. 5,770,722, 5,874,219, 5,744,305, 5,677,195 and 5,445,934, relevant portions incorporated herein by reference. The gene expression monitoring system may also comprise nucleic acid probes in solution.

The gene expression monitoring system according to the present invention may be used to facilitate a comparative analysis of expression in different cells or tissues, different subpopulations of the same cells or tissues, different physiological states of the same cells or tissue, different developmental stages of the same cells or tissue, or different cell populations of the same tissue.

As used herein, the term “differentially expressed” refers to the measurement of a cellular constituent varies in two or more samples. The cellular constituent can be either up-regulated in the test sample relative to the reference or down-regulated in the test sample relative to one or more references. Differential gene expression can also be used to distinguish between cell types or nucleic acids. See U.S. Pat. No. 5,800,992, relevant portions incorporated herein by reference.

Therapy or Therapeutic Regimen: In order to alleviate or alter a disease state, a therapy or therapeutic regimen is often undertaken. A therapy or therapeutic regimen, as used herein, refers to a course of treatment intended to reduce or eliminate the affects or symptoms of a disease. A therapeutic regimen will typically comprise, but is not limited to, a prescribed dosage of one or more drugs or surgery. Therapies, ideally, will be beneficial and reduce the disease state but in many instances the effect of a therapy will have non-desirable effects as well. The effect of therapy will also be impacted by the physiological state of the sample.

As used herein, the term “pharmacological state” or “pharmacological status” refers to those samples that will be, are and/or were treated with one or more drugs, surgery and the like that may affect the pharmacological state of one or more nucleic acids in a sample, e.g., newly transcribed, stabilized or destabilized as a result of the pharmacological intervention. The pharmacological state of a sample relates to changes in the biological status before, during and/or after drug treatment and may serve a diagnostic or prognostic function, as taught herein. Some changes following drug treatment or surgery may be relevant to the disease state and/or may be unrelated side-effects of the therapy. Changes in the pharmacological state are the likely results of the duration of therapy, types and doses of drugs prescribed, degree of compliance with a given course of therapy, and/or un-prescribed drugs ingested.

Because each pathogen represents a unique combination of Pathogen Associated Molecular Patterns (PAMPs) interacting with specific pattern recognition receptors (PRRs), the present inventors determined if leukocytes isolated from the peripheral blood of patients with acute infections would carry unique transcriptional signatures, which would in turn permit pathogen discrimination. To test this hypothesis, gene expression patterns in blood leukocytes from patients with acute infections caused by four common human pathogens: (i) influenza A, an RNA virus; (ii) *Staphylococcus aureus*; and (iii) *Streptococcus pneumoniae*, two Gram-positive bacteria; and (iv) *Escherichia coli*, a Gram-negative bacterium were analyzed.

Table 2. Characteristics of 141 patients with acute infections, and 7 Healthy Controls.

Patient	Age	Ethnicity	Sex	Clinical disease	Bacteria vs Virus	<i>E. coli</i> vs <i>S. aureus</i>	Antimicrobial therapy
<i>Set 1: E. coli</i> (n=29) Median age 2m (2wks-16y)							
12	5 m	Black	M	Bacteremia	Training	Training	Ceftriaxone
13	5 m	White	F	UTI	Training	Training	Ceftriaxone
31	3 m	Hispanic	F	UTI, bacteremia	Training	Training	Gentamicin

34	16 y	White	F	Pyelonephritis	Test 1	Training	Gentamicin
48	2 m	White	M	UTI	Test 1	Test 3	Ampicillin, ceftriaxone
57	3 m	Black	F	UTI, bacteremia	Test 1	Training	Gentamicin
74	4 m	Hispanic	F	UTI, bacteremia	Training	Training	Ceftriaxone
82	2 m	Hispanic	M	UTI	Test 1	Training	Ampicillin, ceftriaxone
86	3 m	Hispanic	M	UTI	Training	Training	Ceftriaxone
118	1.5 m	White	M	UTI	Test 1	Test 3	Test 1 & 2
120	1.5 m	Hispanic	M	UTI	Test 1	Test 3	Ampicillin, ceftriaxone
133	2 m	Hispanic	M	UTI	Test 1	Test 3	Ceftriaxone
139	1 m	Hispanic	M	UTI	Test 1	Test 3	Ampicillin, ceftriaxone
148	8 y	Hispanic	F	UTI	Test 1	Training	Ceftriaxone
151	1.5 m	Hispanic	M	UTI	Test 1	Test 3	Ampicillin, gentamicin
152	2.5 m	Black	M	Bacteremia, meningitis	Training	Training	Ceftriaxone, gentamicin
154	2 m	Hispanic	M	UTI	Test 1	Test 3	Ceftriaxone
161	1.7 m	Hispanic	M	UTI	Test 1	Test 3	Ampicillin, ceftriaxone
168	3 m	White	F	UTI	Test 1	Test 3	Ceftriaxone
171	3 m	Hispanic	F	UTI	Test 1	Test 3	Ceftriaxone
175	0.5 m	Hispanic	F	UTI, bacteremia	Test 1	Test 3	Ceftriaxone
180	1 m	Hispanic	M	UTI	Test 1	Test 3	Ampicillin, gentamicin
183	1.5 m	Hispanic	M	UTI	Test 1	Test 3	Ampicillin, gentamicin, ceftriaxone
184	0.5 m	White	F	UTI, bacteremia	Test 1	Test 3	Ampicillin, gentamicin
188	1.5 m	White	M	UTI	Test 1	Test 3	Ampicillin, gentamicin, ceftriaxone
197	1.25 m	White	M	UTI	Test 1	Test 3	Ampicillin, gentamicin
219	5 m	White	F	UTI, bacteremia	Test 1	Test 3	Ceftriaxone
222	3 m	Hispanic	F	UTI, bacteremia	Test 1	Test 3	Ceftriaxone, gentamicin
229	4 m	Hispanic	F	UTI, bacteremia	Test 1	Test 3	Ceftriaxone

Set 1: S. aureus (n=32) Median age 7y (3m-18y)

5	10 y	Hispanic	M	Osteomyelitis	Test 2	Training	Cefazolin
24	3 y	Black	M	Osteomyelitis	Test 2	Test 3	Vancomycin, Rifampin
30	15 y	Black	M	Bacteremia	Test 2	Test 3	Vancomycin
40	12 y	White	M	Osteomyelitis, Bacteremia	Test 2	Test 3	Cefazolin
43	7 y	Black	M	Hip abscess, Bacteremia	Test 2	Test 3	Vancomycin, Rifampin
62	2 y	White	M	Osteomyelitis	Test 2	Training	Clindamycin
66	3 m	Black	F	Pneumonia	Test 2	Training	Vancomycin, Gentamicin
67	7 y	White	F	Osteomyelitis, Bacteremia	Test 2	Training	Vancomycin, Rifampin
69	9 mo	Hispanic	M	Lung abscess	Test 2	Training	Vancomycin, Cefazolin
70	15 m	White	F	Abscess	Test 2	Training	Vancomycin
84	18 y	Black	F	Abscess	Test 2	Test 3	Cefazolin
88	11 m	Hispanic	M	Osteomyelitis, bacteremia	Test 2	Training	Vancomycin
89	4 mo	Black	F	Abscess	Test 2	Training	Clindamycin
90	8 mo	Black	M	Septic arthritis	Test 2	Training	Oxacillin
150	9 y	Black	F	Osteomyelitis, Bacteremia	Test 2	Test 3	Vancomycin, Rifampin
179	12 y	White	M	Endocarditis, Bacteremia	Test 2	Test 3	Oxacillin, Gentamicin, Rifampin

205	7 y	Hispanic	M	Pneumonia, Bacteremia	Test 2	Test 3	Vancomycin
206	1 y	Hispanic	F	Abscess	Test 2	Test 3	Clindamycin
208	10 y	White	F	Osteomyelitis, Bacteremia, pneumonia	Test 2	Test 3	Vancomycin, Clindamycin, Rifampin
216	10 y	Hispanic	F	Osteomyelitis, Bacteremia	Test 2	Training	Vancomycin, Rifampin
220	11 y	Hispanic	M	Osteomyelitis, Bacteremia	Test 2	Test 3	Cefazolin, Rifampin
221	6 y	Black	F	Osteomyelitis, Bacteremia	Test 2	Test 3	Vancomycin, Rifampin
224	10 y	White	M	Osteomyelitis, Bacteremia	Test 2	Test 3	Oxacillin, Rifampin
241	10 m	Black	F	Pneumonia, Bacteremia	Test 2	Test 3	Vancomycin, Rifampin
242	13 m	Black	M	Abscess, Bacteremia	Test 2	Test 3	Clindamycin
258	8 y	White	F	Osteomyelitis, Bacteremia	Test 2	Test 3	Cefazolin
262	13 y	Hispanic	M	Abscess, Bacteremia	Test 2	Test 3	Clindamycin
264	13 y	Black	M	Septic arthritis	Test 2	Test 3	Vancomycin, cefazolin, gentamicin
271	13 y	Black	M	Osteomyelitis	Test 2	Test 3	Clindamycin
281	3 y	White	F	Osteomyelitis	Test 2	Test 3	Clindamycin
315	3 y	Hispanic	F	Cellulitis	Test 2	Test 3	Vancomycin
374	21m	Black	M	Septic arthritis Bacteremia			Vancomycin, Clindamycin
Set 1: <i>S. pneumoniae</i> (n=16) Median age 1.5y (2m-16y)							
9	4 m	White	M	Abscess	Training	N/A	Cefazolin
25	2 m	Hispanic	M	Meningitis	Training	N/A	Ampicillin, Ceftriaxone
41	23 m	White	F	Pneumonia, Empyema	Training	N/A	Ceftriaxone
64	10 m	White	F	Meningitis, bacteremia	Test 1	N/A	Ceftriaxone, vancomycin
96	16 m	Hispanic	M	Pneumonia, Empyema	Training	N/A	Ceftriaxone, Azithromycin
113	7 m	Hispanic	F	Septic arthritis	Training	N/A	Ceftriaxone, clindamycin
155	3 m	Hispanic	M	Meningitis	Training	N/A	Ceftriaxone, Vancomycin
261	13 y	White	M	Meningitis	Test 1	N/A	Ceftriaxone, vancomycin
268	3 y	Hispanic	M	Empyema	Test 1	N/A	Ceftriaxone, clindamycin
265	2 y	White	F	Empyema	Test 1	N/A	Ceftriaxone, vancomycin
277	16 y	White	M	Empyema	Test 1	N/A	Ceftriaxone, vancomycin
287	3 y	White	F	Pneumonia, bacteremia	Test 1	N/A	Ceftriaxone, vancomycin
289	2 y	Hispanic	M	Empyema	Test 1	N/A	Ceftriaxone, vancomycin
338	12m	White	M	Meningitis			Ceftriaxone, vancomycin
339	2.5y	White	M	Mastoiditis			Ceftriaxone
388	6m	White	M	Meningitis			Ceftriaxone, Vancomycin, Rifampin
Set 1: Influenza A (n=18) Median age 14m (3wks-36y)							
55	11 m	Hispanic	M	Respiratory distress	Training	N/A	Cefuroxime
87	19 m	White	F	Fever, Hypoxia	Training	N/A	Cefuroxime
92	1 m	Hispanic	F	Fever	Training	N/A	Ampicillin, Ceftriaxone

95	4 y	Hispanic	M	Fever	Test 1 & 2	N/A	None
101	4 m	Hispanic	M	Fever, URI	Training	N/A	Cefuroxime, Oseltamivir
104	17 m	Hispanic	M	Seizures, Fever, Respiratory failure	Training	N/A	Ceftriaxone
105	4 y	Hispanic	F	Fever, Encephalopathy	Test 1 & 2	N/A	Ceftriaxone, Aciclovir, Oseltamivir
107	1.5 m	Asian	M	Fever, Lethargy	Training	N/A	Ampicillin, Ceftriaxone
108	5 m	Hispanic	M	Fever	Training	N/A	Ceftriaxone
112	1 m	Hispanic	M	Fever, URI	Test 1 & 2	N/A	Ampicillin, Gentamycin
114	18 m	Black	F	Respiratory distress, fever	Training	N/A	Cefuroxime, Oseltamivir
115	20 m	White	M	Seizures	Training	N/A	Amoxicillin
116	2 y	White	M	Fever, URI	Test 1 & 2	N/A	Cefuroxime, Clindamycin
117	24 y	White	F	Fever	Test 1 & 2	N/A	None
128	11 m	Hispanic	F	Fever, Hypoxia	Training	N/A	Cefuroxime
132	6 m	White	M	Respiratory distress, fever	Training	N/A	Oxacillin, Tobramycin
259	3 m	Hispanic	F	Pneumonia	Test 1 & 2	N/A	None
266	36 y	White	F	Fever, cough	Test 1 & 2	N/A	None
Patient	Age	Ethnicity	Sex	Clinical disease	Analysis	Platform	Antimicrobial therapy
<i>Set 2: Influenza (n= 18) Median age= 11m (2 wk-13y)</i>							
311	0.1y	Hispanic	M	Influenza B Fever, URI	Fig. 6c	Illumina Sentrix Hu6	Ampicillin + Ceftriaxone
320	0.04y	Hispanic	F	Influenza B Fever, URI	Fig. 6c	Illumina Sentrix Hu6	Ampicillin+ Gentamicin
517	0.5y	Hispanic	F	Influenza A Pneumonia	Fig. 6a Fig. 6b	Affymetrix U133plus2	None
519	0.13y	Hispanic	F	Influenza A Fever	Fig. 6c	Illumina Sentrix Hu6	None
524	6y	Hispanic	M	Influenza A Fever	Fig. 6a	Affymetrix U133plus2	None
527	0.13y	Black	M	Influenza A Fever	Fig. 6c	Illumina Sentrix Hu6	Ampicillin + Ceftriaxone
530	0.38y	Hispanic	M	Influenza A Fever, Seizure	Fig. 6c	Illumina Sentrix Hu6	None
532	0.08y	Hispanic	F	Influenza A Fever, Cough	Fig. 6a Fig. 6b	Affymetrix U133plus2	Ampicillin + Gentamicin
533	11y	Caucasian	M	Influenza B Fever, Cough	Fig. 6a Fig. 6b	Affymetrix U133plus2	None
536	2y	Hispanic	F	Influenza A Fever, Cough	Fig. 6a Fig. 6b	Affymetrix U133plus2	None

540	0.08y	Hispanic	M	Influenza A Fever, Cough	Fig. 6a Fig. 6b	Affymetrix U133plus2	Ampicillin+ Gentamicin
542	0.04y	Hispanic	F	Influenza A Fever	Fig. 6c	Illumina Sentrix Hu6	Ampicillin+ Gentamicin
547	1.33y	Black	F	Influenza A Encephalitis	Fig. 6a	Affymetrix U133plus2	Ceftriaxone + Oseltamivir
549	13y	Hispanic	F	Influenza B Fever, Syncope	Fig. 6a	Affymetrix U133plus2	Ceftriaxone + Vancomycin + Oseltamivir
553	1.5y	Caucasian	F	Influenza A Fever, URI	Fig. 6a Fig. 6b	Affymetrix U133plus2	Oseltamivir
556	3.5y	Caucasian	F	Influenza A Fever, Seizure	Fig. 6c	Illumina Sentrix Hu6	Ceftriaxone + Oseltamivir
560	10y	Black	F	Influenza B Encephalitis	Fig. 6c	Illumina Sentrix Hu6	Acyclovir
567	2y	Hispanic	F	Influenza B Fever, URI	Fig. 6a Fig. 6b	Affymetrix U133plus2	None
<i>Set 2: S. aureus (n= 19) Median age = 7.5y (0.08-14y)</i>							
305	4.5y	Hispanic	F	MSSA Bacteremia, Suppurative Arthritis, Osteomyelitis	Fig. 6a	Affymetrix U133plus2	Cefazolin
308	12y	Black	F	MSSA Disseminated with Pneumonia	Fig. 6a Fig. 6b	Affymetrix U133plus2	Oxacillin + Clindamycin
369	14y	Black	M	MRSA Disseminated	Fig. 6a	Affymetrix U133plus2	Vancomycin, Rifampin
372	14y	Caucasian	M	MRSA Bacteremia, Osteomyelitis	Fig. 6a	Affymetrix U133plus2	Vancomycin, Rifampin
374	1.75	Black	M	MRSA Bacteremia, Suppurative Arthritis	Fig. 6a	Affymetrix U133plus2	Vancomycin
380	7.5y	Black	M	MRSA Osteomyelitis, Suppurative Arthritis	Fig. 6a	Affymetrix U133plus2	Clindamycin
458	12y	Black	M	MRSA	Fig. 6c	Illumina Sentrix Hu6	Vancomycin + Rifampin + Linezolid

				Disseminated			
459	10y	Caucasian	F	MSSA Osteomyelitis, Suppurative Arthritis	Fig. 6c	Illumina Sentrix Hu6	Oxacillin + Rifampin
465	13y	Caucasian	M	MRSA Osteomyelitis, Suppurative Arthritis, Bacteremia	Fig. 6c	Illumina Sentrix Hu6	Vancomycin
466	0.5y	Black	M	MRSA SST Abscess	Fig. 6c	Illumina Sentrix Hu6	Clindamycin
472	0.08y	Caucasian	M	MSSA SST Abscess	Fig. 6c	Illumina Sentrix Hu6	Cefazolin
475	1.33y	Black	M	MSSA Suppurative Arthritis	Fig. 6c	Illumina Sentrix Hu6	Nafcillin
477	6y	Black	M	MRSA Bacteremia, Suppurative Arthritis	Fig. 6c	Illumina Sentrix Hu6	Clindamycin + Rifampin
480	12y	Caucasian	M	MSSA Bacteremia	Fig. 6c	Illumina Sentrix Hu6	Clindamycin + Doxycycline
489	1.08y	Caucasian	M	MRSA SST Abscess	Fig. 6c	Illumina Sentrix Hu6	Clindamycin
522	9.5y	Black	F	MRSA Bacteremia, Osteomyelitis	Fig. 6c	Illumina Sentrix Hu6	Vancomycin + Rifampin
529	1.75	Black	M	MRSA Bacteremia, Pneumonia	Fig. 6c	Illumina Sentrix Hu6	Vancomycin + Rifampin
535	0.58y	Other	F	MSSA Suppurative arthritis	Fig. 6c	Illumina Sentrix Hu6	Cefazolin
537	9y	Black	F	MSSA Bacteremia, Osteomyelitis, Suppurative Arthritis	Fig. 6c	Illumina Sentrix Hu6	Oxacillin
Set 2: <i>S. pneumoniae</i> (n=9) Median age=2.5y (1.3-16y)							
96	1.33y	Hispanic	M	Pneumonia, Empyema	Fig. 6a Fig. 6b	Affymetrix U133plus2	Ceftriaxone + Azithromycin
265	2.2y	Caucasian	F	Pneumonia,	Fig. 6a	Affymetrix	Ceftriaxone +

				Empyema	Fig. 6b	U133plus2	Vancomycin
268	3y	Hispanic	M	Pneumonia, Empyema	Fig. 6a Fig. 6b	Affymetrix U133plus2	Ceftriaxone
277	16y	Caucasian	M	Pneumonia, Empyema	Fig. 6a Fig. 6b	Affymetrix U133plus2	Ceftriaxone + Clindamycin
287	3.2y	Caucasian	F	Pneumonia, Bacteremia	Fig. 6a Fig. 6b	Affymetrix U133plus2	Ceftriaxone
289	2.5y	Hispanic	M	Pneumonia, Empyema	Fig. 6a Fig. 6b	Affymetrix U133plus2	Ceftriaxone
471	2y	Caucasian	F	Bacteremia, Meningitis	Fig. 6c	Illumina Sentrix Hu6	Vancomycin + Ceftriaxone
473	2.5y	Hispanic	M	Bacteremia, Pneumonia	Fig. 6c	Illumina Sentrix Hu6	Ceftriaxone
523	3y	Hispanic	M	Suppurative Arthritis	Fig. 6c	Illumina Sentrix Hu6	Cefazolin

Table 3. SLE Patient demographics

SLE patients (n=11) 13y (9-17y)				
SLE 87	11y	White	F	N/A
SLE 85	16y	Black	F	N/A
SLE 79	10y	Hispanic	F	N/A
SLE 76	15y	Black	F	N/A
SLE 66	17y	Hispanic	F	N/A
SLE 57	12y	Black	M	N/A
SLE 48	14y	White	F	N/A
SLE 45	9y	Black	F	N/A
SLE 107	14y	Black	F	N/A
SLE 27	13y	Black	F	N/A
SLE 19	9y	Black	M	N/A
Healthy controls (n=17) 4.5y (4m-17y)				
INF 20N	11m	Hispanic	M	Healthy
INF 19N	4m	Hispanic	M	Healthy
INF 27N	10m	White	M	Healthy
INF 25N	11m	Hispanic	F	Healthy
INF 204	2y	White	M	Healthy
INF 7N	19m	Black	F	Healthy
INF 391	18m	White	F	Healthy
INF 392	10m	Black	M	Healthy
H 162	15y	Black	F	Healthy
HJM	13y	Hispanic	F	Healthy
HJC	8y	Hispanic	M	Healthy
HBW	14y	White	F	Healthy
H45	12y	Black	F	Healthy
H42	9y	Hispanic	M	Healthy
H36	7y	White	F	Healthy
H28	11y	Hispanic	F	Healthy

H37 8y White F Healthy

Table 4. List of the 35 classifier genes distinguishing influenza A from bacterial infections. Genes are grouped functionally based on ontologies and levels of significance are shown. Full details are available in Supplementary Table 3.

Influenza>Bacteria		Bacteria>Influenza	
Response to virus		Translational elongation	
cig5	1.46E-05	EEF1G	4.52E-06
DNATP6	4.52E-06	EEF1G	2.35E-06
IFI27	4.52E-06	Regulation of translational initiation	
IFI35	0.00033	EIF3S5	9.34E-08
IFI44	0.00023	EIF3S7	2.35E-07
IFI44	0.00015	EIF4B	1.16E-06
OAS1	6.52E-05	Protein biosynthesis	
Immune response		QARS	5.41E-07
BST2	4.08E-05	RPL31	4.52E-06
G1P2	0.000101	RPL4	2.35E-07
LY6E	8.28E-06	Regulation of transcription	
MX1	6.52E-05	PFDN5	5.41E-07
Anti-apoptosis		Cell adhesion	
SON	0.00067	CD44	2.35E-07
Cell growth and/or maintenance		Metabolism	
TRIM14	4.08E-05	HADHA	4.08E-05
Miscellaneous		PCBP2	9.34E-08
APOBEC3C	2.35E-07	Miscellaneous	
C1orf29	0.00015	dJ507115.1	6.52E-05
FLJ20035	4.08E-05		
FLJ38348	0.00128		
HSXIAPAF1	4.52E-06		
KIAA0152	2.48E-05		
PHACTR2	9.34E-08		
USP18	1.46E-05		
ZBP1	5.41E-07		

5 Table 5. List of the 30 classifier genes distinguishing *S. aureus* from *E. coli* infections. Genes are grouped functionally based on ontologies and levels of significance are shown. Full details are available in Supplementary Table 6.

<i>S. aureus</i> > <i>E. coli</i>		<i>E. coli</i> > <i>S. aureus</i>	
Signal Transduction		Intracellular signaling	
CXCL1	0.00106	RASA1	1.20E-05
JAG1	0.00158	SNX4	4.92E-05
RGS2	0.00027	Regulation of translational initiation	
Metabolism		AF1Q	0.00106
GAPD	0.00044	Regulation of transcription	

PPIB	0.00044	SMAD2	0.00044
PSMA7	0.00106	Cell adhesion	
MMP9	0.00837	JUP	0.00158
p44S10	0.00158	Metabolism	
Protein Targeting		PP	4.92E-05
TRAM2	0.00384	MAN1C1	0.00016
Intracellular Protein Transport		Miscellaneous	
SEC24C	4.92E-05	FLJ10287	4.92E-05
Miscellaneous		FLJ20152	0.00622
ACTG1	0.00622	LRRN3	1.20E-05
CGI-96	0.00454	LRRN3	0.00027
MGC2963	0.00158	SGPP1	0.00158
STAU	4.92E-05	UBAP2L	2.12E-06
STAU	4.92E-05		

Patient characteristics. The PBMCs from 29 patients with *E. coli* infections, 51 patients with *S. aureus* infections, 25 patients with *S. pneumoniae* infections and 36 patients with influenza A infections. We chose young patients because of fewer concomitant diseases and therapies than in older adults. Patients with underlying immunosuppression, receiving immunomodulatory therapy including corticosteroids, or with significant chronic medical problems were excluded. The median (range) duration of hospitalization at the time of blood draw was 3 days (0 - 9 days) and the median (range) duration of symptoms was 6 days (2 - 22 days). The clinical diagnoses included acute respiratory infections, bacteremia, localized abscesses, bone and joint infections, urinary tract infections and meningitis (Table 1). Patients were treated according to standard hospital protocols and, as such, antimicrobial therapy was promptly initiated in the emergency department.

Step-wise data analysis strategy. To determine whether blood leukocytes isolated from patients with acute infections carry gene expression signatures that allow discrimination between pathogen type, a step-wise analysis was conducted: (1) Statistical group comparison: differentially expressed genes were identified in pair-wise comparisons using non-parametric Mann-Whitney test. Hierarchical clustering ordered the genes according to their expression levels, revealing reciprocal patterns of expression between the two groups. (2) Sample classification: genes capable of discriminating two groups of patients, i.e. classifiers, were identified through comparison of patient groups of comparable age range and treated with similar classes of antimicrobials (training set). These genes were then evaluated within the same set of patients in a leave-one-out cross-validation scheme. (3) Independent validation of classifier genes: the same genes were tested for their ability to classify an independent group of patients (test set). The patients included in the training sets

used to for the identification of the classifier genes were selected very carefully in order to avoid potential confounding factors. After that careful selection, the classifier genes (also described as transcriptional markers) were then evaluated in a new group of patients that was heterogeneous, and therefore more representative of a realistic clinical setting (test set). (4)

- 5 Independent validation across microarray platforms: the results were then further validated in another independent set of patients using a different microarray platform (Illumina BeadChips).

Transcriptional signatures discriminate patients with influenza A infection from those with bacterial infections. To identify genes differentially expressed between samples from
10 patients with either influenza or bacterial infections, 11 patients with influenza A infections and 12 patients with *E. coli* or *S. pneumoniae* infections were selected as a training set on the basis of similar age groups and antibiotic class treatment. There were no significant differences between the influenza A and the bacterial infection training groups in median age [range] (11 months [1 - 20 months] vs. 4 months [2 months - 23 months]; $P=0.22$;) or days
15 of hospitalization prior to sample collection (2 days [1-2 days] vs. 2.5 days [2 - 5 days], $P=0.06$). All 11 patients with influenza A infections were receiving β -lactam antibiotics, as compared with 10 of 12 in the bacterial infection group ($P=0.16$). There were no statistically significant differences in the relative proportions of neutrophils, lymphocytes and monocytes in PBMCs from the two groups (Supplementary Table 1).

- 20 Statistical group comparisons of patients with influenza A and those with bacterial infections yielded 854 differentially expressed genes ($P<0.01$) (Supplementary Table 2), of which 394 were relatively over-expressed in influenza A infections, while 460 were over-expressed in bacterial infections. Patients with influenza A displayed a prominent type I interferon (IFN) signature (Figure 1a), including genes coding for antiviral molecules such as myxovirus
25 resistance genes (MX1, MX2); 2'-5'-oligoadenylate synthetases (OAS1, OAS2); GBP1 (Guanylate Binding Protein 1); and CIG5 (viperin, virus inhibitory protein, endoplasmic reticulum-associated, interferon-inducible). Genes regulating transcription and translation represent up to 25% of the 460 probe sets expressed at higher levels in the bacterial infection group.

- 30 The k-NN algorithm identified 35 genes that discriminated patients with acute influenza infection from acute bacterial infections (Figure 2, Table 2, and Supplementary Table 3).

Leave-one-out cross-validation of this training set correctly classified 21 of the 23 samples (91% accuracy) to either the influenza A or the bacterial infection groups (Figure 1b).

The ability of the identified classifier genes to discriminate influenza A from the bacterial infections was then validated with independent sets of samples (test sets). The first test set of patients included seven new patients with influenza A, and 30 patients with bacterial infections (seven with *S. pneumoniae* and 23 with *E. coli* infections). Patients were included in the test set without regard to age or type of antibiotic treatment (age [range]; influenza A, 4 years [3 weeks - 36 years]; *E. coli*, 2 month [2 weeks - 16 years]). Predictor genes correctly classified 35 of the 37 samples (95% accuracy) (Figure 1c). One sample (INF48) was misclassified and one sample was of indeterminate classification (INF120).

The 35 classifier genes were then evaluated in a second test set, consisting of 7 patients with influenza A infection and 31 patients with *S. aureus* infection, yielding 87% accuracy in discrimination (Figure 1d). Test sets were again selected without regard to age or type of antibiotic treatment (age [range]; influenza A, 4 years [3 weeks - 36 years]; *S. aureus*, 7 years [3 months - 15 years]). Five *S. aureus* samples were misclassified (INF62, INF70, INF89, INF221 and INF242).

About one-third of the patients with bacterial infection displayed elevated expression levels of interferon-related genes. This signature, however, had limited effects on classification outcomes, because samples obtained from patients with bacterial infections lacked the reciprocal expression signature characteristic of influenza infection (under-expressed genes in influenza compared to bacterial infection) and also in part because expression levels of interferon-inducible genes were lower in the context of bacterial infections (Figure 1c). Elevated levels of expression of interferon-inducible genes may be attributed to a response to the documented bacterial infection itself [12], or an undiagnosed or preceding viral infection. Thus, transcriptional signatures of host response to influenza infection and bacterial infection can be identified. These signatures permit the discrimination between these causative agents.

Transcriptional signatures discriminate patients with *E. coli* infections from those with *S. aureus* infections. To identify genes differentially expressed between patients with *E. coli* and *S. aureus* infections, ten patients per group were selected as a training set. There were no significant differences between the *E. coli* and the *S. aureus* infection training groups in median age [range] (2 months [3.5 months - 16 years] vs. 12 months [4 months - 10 years];

P=0.06). Each group included 6 patients treated with β -lactam antibiotics and 4 with other antibiotic classes. Total peripheral leukocyte counts and the relative proportions of the peripheral blood cell types between the two groups were not significantly different (Supplementary Table 1). The median number of days of hospitalization prior to sample collection was 2 days for the *E. coli* group, and 4 days for the *S. aureus* group (P=0.01), a significant difference which may be accounted for by the time interval typically required for definitive microbiological diagnosis.

Statistical group comparisons yielded 211 genes with significantly different expression levels ($p < 0.01$); (Supplementary Table 4 and Figure 3a). Expression levels of a selection of genes were independently confirmed by real time PCR (Figure 3d and 3e). A number of genes over-expressed in *S. aureus* compared to *E. coli* are associated with neutrophil activity, including chemoattractant molecules such as CXCL1 (CXC chemokine ligand 1, GRO-1) and PPIB (cyclophilin B) [13, 14]. Furthermore, the matrix metalloproteinase 9 (MMP9) plays an important role in neutrophil extravasation and migration [15]; PRG1 (secretory granule proteoglycan 1) participates in packaging of granule proteins in human neutrophils [16]; and ALOX5AP activates arachidonate 5-lipoxygenase and prolongs the capacity of neutrophils to synthesize leukotrienes [17]. Finally, neutrophils have recently been identified as the main source of S100A8 and S100A9 (Calgranulin A and B, alias MRP 8 and 14) in a *S. aureus* infection model [18]. These results suggest that neutrophil activity may, in part, explain differences in levels of gene expression between samples obtained from patients with *E. coli* and *S. aureus* infections. Previous studies in patients with Systemic Lupus Erythematosus (SLE) a similar signature was traced down to the presence of low-density immature neutrophils that co-purified with mononuclear cells during density gradient centrifugation [9]. Interestingly, this “granulopoiesis signature”, which corresponds to a faster neutrophil turnover rate, can also be observed in expression profiles derived from whole blood in patients with SLE (unpublished observation).

Thirty classifier genes which discriminate between the training set of patients with *E. coli* and *S. aureus* infections were identified (Figure 4 and Table 3 and Supplementary Table 6). In leave-one-out cross-validation 19 of 20 samples were classified correctly (95% accuracy) (see also Figure 3b). One patient with a *S. aureus* infection (INF 89) was misclassified. The classifier genes were validated with an independent set of patients with *S. aureus* (n=21) and *E. coli* (n=19) infections, which were again selected without regard to age or type of antibiotic treatment (*S. aureus*: 9 years [10 months – 18 years]; *E. coli*: 2 months [2 weeks –

5 months]). The 30 genes correctly classified 34 of the 40 samples (85% accuracy; Figure 3c). Two samples (INF175 and INF206) were misclassified and 4 samples were indeterminate in their classification (INF168, INF220, INF281 and INF315). The greater heterogeneity of clinical disease and severity represented by the patients with *S. aureus* infections may contribute to the lower predictive accuracy for this group, although no specific pattern of misclassification was evident.

Thus, these results demonstrate that blood leukocyte transcriptional signatures distinguish disease etiology in patients with acute infections caused by *S. aureus* or by *E. coli*. Furthermore, notable functional convergence among discriminatory signatures were identified: Interferon-inducible genes were found among genes over-expressed in patient with Influenza A, while genes associated with neutrophils were expressed at higher level in *S. aureus* compared to *E. coli* groups.

Classifier genes discriminating samples from patients with acute influenza A, *E. coli*, *S. aureus* or *S. pneumoniae* infections show minimal overlap. The present inventors have now defined sets of classifier genes that discriminate patients with influenza A versus bacterial infections, and patients with *E. coli* versus *S. aureus* infections. To complete the panel of classifier genes additional pair-wise comparisons and identified sets of genes discriminating patients with *S. pneumoniae* infections were performed. Comparison of *E. coli* (n=11) and *S. pneumoniae* (n=11) infection groups yielded 264 significantly differentially-expressed genes ($P<0.01$), and 45 classifier genes (Figure 4b and 4c and Supplementary Tables 7 and 8); Sample class was assigned correctly for 20 of 22 samples (91% accuracy) in leave-one-out cross-validation of the training set. Comparison of *S. aureus* (n=12) and *S. pneumoniae* (n=11) infection groups yielded 127 differentially expressed genes ($P<0.01$) and 34 classifier genes. Figure 4d and 4e and Supplementary Tables 9 & 10). Sample class was assigned correctly for 19 of 23 samples (83% accuracy) in leave-one-out cross-validation of the training set.

Sets of classifier genes obtained for each pair-wise analysis were systematically compared and found to be almost mutually exclusive (Figure 5a). Furthermore, none of the 102 genes that discriminated one bacterial species from the other was necessary to distinguish influenza A from bacterial infections (Figure 5b). Thus, multiple infectious disease etiologies can be distinguished using independent sets of transcriptional signatures.

Distinct expression patterns in patients with acute respiratory infections caused by different pathogens. Gene expression patterns in a mixed cohort of patients presenting with the same clinical manifestations were examined. Sets of classifier genes identified throughout this study (Figure 5a and 5b) were merged, and used to generate expression patterns for a subset of patients with lower respiratory tract infections (27 samples listed Table 1). Seven samples collected from healthy volunteers were used as a reference (Table 1). Hierarchical clustering of genes and samples identified four prototypical expression signatures: Healthy controls were clearly distinguishable from all the infectious disease groups based on PBMC expression profiles. This finding is in itself remarkable, since none of the training sets used to generate the classifiers included samples from healthy volunteers. A second signature was associated with samples from patients with influenza A infection (including interferon-inducible genes) and was clearly different from a third signature, which characterized infections caused by *S. aureus* and *S. pneumoniae* (including neutrophil-associated genes). Distinctions between these two gram positive bacteria were minimized by the overt dominance of signatures differentiating the three major classes of samples.

Interestingly, four samples belonging to the influenza A group and one from the *S. aureus* group were characterized by a fourth signature, which combined elements of the previous ones (interferon-inducible and neutrophil-associated genes: Figure 5c, indicated by the asterisk). This finding suggests one of at least two possibilities: 1) the mixed signatures arise as the result of co-infections that could not be detected by routine diagnostic methods, or 2) the analysis of PBMC transcriptional signatures can reveal the existence of distinct patient subgroups. A larger patient cohort will be necessary to investigate these possibilities and identify potential clinical implications. Further review of the medical records of the 5 patients with mixed signature, identified 3 patients with influenza (#101, #128 and #132) who had radiological evidence of pneumonia and white blood cell differential counts with 11%, 16% and 28% bands, respectively. The evidence suggests the possibility of co-infections in these 3 cases. These results clearly demonstrate that discriminative blood leukocyte transcriptional patterns can be obtained in patients presenting similar symptoms.

Results can be reproduced in a novel independent set of samples and across microarray platforms. The study design includes a training set for the identification of classifiers (Figure 1b; influenza vs. Bacteria; n=23 samples) and a test set to validate independently these findings (Figure 1c Influenza vs. bacteria n=37 samples; and Figure 1d an additional 31 patients infected with *S. aureus*). These data, obtained from a total of 91 patients, were

generated using Affymetrix U133A and U133B GeneChips. Data validation was taken one step further in order to further confirm these findings, and carried out a similar analysis on additional sets of patients using different microarray platforms. A new cohort of 22 patients was recruited with acute influenza/bacterial infection and analyzed PBMC samples using the most recent version of Affymetrix GeneChips (U133 plus 2.0).

Figures 9a to 9c summarize independent confirmation and validation across microarray platforms. Figure 9a shows the results from a new set of patients with acute influenza (n=10) or bacterial infection (*S. aureus*; n= 6; *S. pneumoniae*: n=6) analyzed using Affymetrix U133 plus 2.0 GeneChips. Classifier genes used to discriminate influenza A from bacterial infections (35 genes, Venn diagram, right; Figure 1 and Supplementary Table 3) were used to cluster this new set of samples. In Figure 9b, a subset of 14 samples from patients with acute respiratory infection included in Figure 9a were clustered using the list of 137 transcripts from Figure 5. Figure 9c shows the results from another independent set of samples (none of which being used in any of the previous analyses) was obtained from a new set of patients with acute influenza (n=8) or bacterial infection (*S. aureus*; n=13; *S. pneumoniae*: n=3) analyzed using Illumina Sentrix Hu6 whole genome BeadChips. Classifier genes used to discriminate influenza A from bacterial infections (35 genes, Venn diagram, right; Figure 1 and Supplementary Table 3) were used to cluster this new set of samples. Transformed expression levels are indicated by color scale, with red representing relative high expression and blue indicating relative low expression compared to the median expression for each gene across all donors.

The present invention was able to distinguish almost perfectly infections caused by *S. aureus* or *S. pneumoniae* from infections caused by influenza (Figure 9a; one influenza sample grouped in the bacterial infection cluster), and to obtain discriminative signature in patients with acute respiratory infection (Figure 9b). Microarray data are notoriously difficult to compare across totally different platforms [19, 24-26], but the present invention was able to, once again, reproduce the initial results when analyzing a new set of 24 samples using Illumina's whole genome Sentrix Hu6 BeadChips (Figure 9c; one sample from the bacterial infection group clustered with influenza samples). In this cohort, only two patient belonging to the *S. aureus* or *S. pneumoniae* group presented with acute respiratory infection.

As such, 148 microarray analyses were conducted, including 141 on samples collected from patients with acute infections. Along with the confirmation obtained by real-time PCR

(Figure 3d) the independent data validation carried out across microarray platforms attest to the robustness of these findings.

Distinct transcriptional signatures differentiate patients with acute infection from those with autoimmune disease. Interferon-inducible genes were found to be over-expressed in patients with acute influenza infection. An interferon signature was also identified previously in blood leukocytes of patients with Systemic Lupus Erythematosus [9]. Next, whether gene expression patterns in blood leukocytes would nevertheless permit differentiation of influenza infection from SLE was determined. Samples obtained from SLE patients were compared to their respective healthy control group. Similarly, patients from the various infectious disease groups were compared to an appropriate cohort of healthy volunteers (11 patients per group: influenza A, *E. coli*, *S. aureus*, *S. pneumoniae*, compared to 9 healthy controls). P-values obtained for each comparison (overall, 5 sets of patients versus their respective control groups) were compiled and collectively analyzed. This approach recapitulates changes observed across multiple studies and a large number of samples, and is particularly well suited when all potentially confounding factors cannot be accounted for (e.g., SLE incidence is much higher in females). Significance patterns were analyzed in order to evaluate the overlap between the gene expression signatures obtained for the influenza and SLE groups (Figure 6). Filtering criteria were applied to select transcripts over- or under-expressed in both groups of patients in comparison to their respective control group (Figure 6, upper panel). It was found that among over-expressed transcripts a cluster including interferon-inducible genes (Figure 6: upper panel - IFN; Supplementary Table 11), that were significantly changed in both influenza and SLE groups, but not in patients with bacterial infections. Conversely, genes that changed significantly versus healthy controls in one group (FLU or SLE, $p < 0.01$), but not the other ($p > 0.5$; Figure 6, middle and lower panels) could also be identified. This approach revealed disease-specific signatures (data not shown). Several clusters uniquely characterizing influenza A patients can be found in Figure 6 and Supplementary Tables 1 to 11). These results further demonstrate that perturbations of blood leukocyte transcriptional profiles are disease-specific.

The comparative analysis of a compendium of host-pathogen microarray datasets (encompassing 32 studies) identified both common host transcriptional responses to infections and as pathogen-specific signatures [27]. Broad similarities exist, with for instance dynamic cascades of cytokines and chemokines involved in the activation and recruitment of immune cells being observed in the context of fungal, bacterial or viral

infections³⁰⁻³⁴. However, two factors contribute to the specificity of transcriptional responses to infections: 1) the diversity of the molecular mechanisms involved in pathogen recognition; and 2) alterations of host responses by pathogens. Upon activation, Toll-like receptor (TLR) family members trigger signaling pathways that share common components while retaining unique characteristics accounting for the specificity of transcriptional responses. Hence, qualitative and quantitative differences in the responses to gram-positive and gram-negative bacteria, respectively recognized by TLR2 and TLR4, have been observed. Furthermore, responses measured in dendritic cells exposed to influenza virus (through TLR3), *E. coli* (through TLR4), and *Candida* (through TLR2/TLR4) were also found to be markedly different. Reprogramming of host cells by pathogens also contributes significantly to the diversification of transcriptional responses to infection. As measured by microarrays mycobacterial products are for instance able to inhibit interferon gamma induced gene regulation in macrophages [28]. Similarly, microarray studies have demonstrated the ability of herpes virus, pseudorabies virus, hepatitis C, varicella-zoster virus or rhinovirus to limit the ability of the host to develop effective anti-viral responses by a variety of mechanisms. Altogether the vast body of experimental data accumulated over the past years suggests that hosts can mount pathogen-specific transcriptional responses to infections.

A number of studies have shown that different transcriptional programs could be triggered upon exposure of immune cells to various pathogens in vitro [19-22]. Here, it was demonstrated that gene expression patterns in blood leukocytes can be used to distinguish acute infections caused by four different pathogens: influenza A virus; the Gram negative bacterium, *E. coli*; and Gram-positive bacteria *S. aureus* and *S. pneumoniae*, which are among the most common infections leading to child hospitalization.

Two parameters might account for differences in gene expression levels observed in blood leukocytes: 1) changes in transcriptional activity (e.g., up-regulation of interferon-inducible genes) and/or 2) an altered cellular composition of blood samples (e.g., neutrophil signature). Changes in expression due to either one or both of these parameters may be mediated directly by pathogen-derived molecules or the action of secondary factors released by the host (e.g., cytokines). Major differences were observed in the cellular composition of blood samples obtained from the different groups of patients. Indeed, it is well established in clinical practice that the routine white blood cell and differential counts can not distinguish between viral and bacterial infections and much less between infections caused by gram

positive and gram negative bacteria. However, the present inventors have found that subtle differences might account for observed transcriptional signatures as exemplified by the neutrophils signature in Systemic Lupus Erythematosus which is due to enhanced efflux of low density neutrophils present in PBMC preparations. The site of disease involvement may also influence expression profiles observed in blood leukocytes and reflects the predilection of certain species of pathogens for different infection sites. *E. coli*, for example, is more likely to cause urinary tract infection, while the most common clinical manifestations of *S. aureus* are skin/soft tissue infections and osteomyelitis. The results obtained in the present study suggest, however, that distinctive expression signatures can be found in the context of a single disease manifestation. Indeed, when analyzing samples from patients with lower respiratory infections a clear separation between infections caused by the different pathogens was observed, confirming the existence of pathogen-associated transcriptional signatures.

The ability to identify etiologic agents responsible for acute infections remains disappointingly low in many clinical situations, and the analysis of blood leukocyte transcriptional profiles has the potential to transform the diagnosis of infectious diseases. In contrast to microbial cultures, serologic assays or even PCR-based tests, leukocyte gene expression results can be obtained quickly and reliably regardless of the site of disease involvement. This information should allow prompt initiation of adequate anti-infective therapy and establishment of the appropriate infection control measures. Furthermore, transcriptional analysis of blood leukocytes provides information about the patient that can be used for disease diagnosis and potentially as markers of disease progression and prognosis. Compared to the inflammatory markers such as white blood cell counts, erythro-sedimentation rate and C-reactive protein, which have traditionally been used as indicators of disease evolution, gene expression arrays provide comprehensive molecular picture that not only reflects the relative cellular composition of the tissue but also gene regulation resulting from ongoing immune reactions and/or pathogen exposure.

These results demonstrate the value of transcriptional signature analysis in blood leukocytes as an adjunctive method of diagnosis of infectious diseases for both single, on the spot analysis, but also for the detection, determination, evaluation, prognosis, diagnosis and prediction of infectious disease outcome, acute, chronic or both. Large multi-center studies will be necessary to collect and independently evaluate large numbers of samples, eventually bringing blood leukocytes gene expression profiling closer to a routine clinical diagnostic application.

Patient Information. Blood samples were obtained from 29 patients with *E. coli* infections (median age: 2 months; range: 2 weeks - 16 years), 31 patients with *S. aureus* infections (7 years; 3 months - 18 years), 13 with *S. pneumoniae* (2 years; 2 months - 16 years), 18 with influenza A infections (1.5 years; 3 weeks - 36 years), and 7 healthy controls (11 months; 3 months – 22 months). Patients were divided into training and test sets according to age and antibiotic treatment (Table 1). All subjects with acute infections and their controls were recruited at Children's Medical Center Dallas (CMC), while the SLE patients and their respective controls were recruited at Texas Scottish Rite Hospital. The study was approved by the Institutional Review Boards and informed consent was obtained for all patients.

Microbiologic diagnosis was established by standard bacterial cultures of relevant tissue specimens or blood, and by direct fluorescent antigen testing and viral cultures. All potentially eligible patients were identified on a daily basis by the investigators from both the microbiology laboratory database and inpatient admissions records. A second step was then undertaken to confirm eligibility on the basis of history, clinical findings, bacterial and viral cultures, and immunofluorescence tests. Patients with suspected (by clinical findings) or documented (by microbiologic tests) polymicrobial infections, history of immunodeficiency, chronic disease or receiving steroids or other immunomodulatory agents, were excluded. Patients were enrolled once a confirmed microbiologic diagnosis was established. Systematic testing for the presence of concomitant viral infection was initiated after the beginning of the study and respiratory viral cultures were performed in 60 of 73 (82%) patients with bacterial infections. Control samples were obtained from healthy individuals scheduled to undergo elective surgical procedures, and from healthy outpatient clinic patients.

Processing of Blood Samples. All blood samples were collected in acid citrate dextrose tubes (BD Vacutainer) at Children's Medical Center or Texas Scottish Rite Hospital, Dallas, TX and immediately delivered at room temperature to the Baylor Institute for Immunology Research, Dallas, TX, for processing. Peripheral blood mononuclear cells (PBMCs) from 3-4 ml of blood were isolated via Ficoll gradient and immediately lysed in RLT reagent (Qiagen, Valencia, CA) with beta-mercaptoethanol (BME) and stored at -80°C (within 4-6 hours from the time of blood draw) in the same laboratory by the same team to standardize the quality and handling of RNA samples.

Microarray assay. Total RNA was isolated using the RNeasy kit (Qiagen, Valencia, CA) according to the manufacturer's instructions and RNA integrity was assessed by using an

Agilent 2100 Bioanalyzer (Agilent, Palo Alto, CA). Double-stranded cDNA was generated from 2-5 micrograms of total RNA, followed by single-round in vitro transcription with biotin-labeled nucleotides, using the Affymetrix RNA transcript labeling kits (Affymetrix Inc, Santa Clara, CA). Biotinylated cRNA targets were purified using the Sample Cleanup
 5 Module (Affymetrix), and subsequently hybridized, according to the manufacturer's standard protocols, to Affymetrix HGU133A GeneChips (which contain 22,283 probe sets). Arrays were scanned using an Affymetrix confocal laser scanner. Expression results of a set of genes were confirmed by real time PCR.

Real-time RT-PCR analysis. Total RNAs were subjected to a second DNase treatment with
 10 the TURBO DNA-free kit (Ambion Inc., Austin, TX). cDNA was synthesized using the Two-Cycle cDNA Synthesis kit (Affymetrix) followed by in vitro transcription (MEGAscript T7 kit , Ambion, Inc., Austin, TX). Two-step RT-PCR was performed using Applied Biosystems TaqMan Assays on Demand probe and primer sets according to the manufacturer's instructions. Reverse
 15 transcription was carried out using the High Capacity cDNA Archive Kit (Applied Biosystems). Real-time PCR was performed on an ABI Prism 7700 Sequence Detection System. Human β -glucuronidase (GUSB) was chosen from a panel of 10 human endogenous controls as the most constitutively expressed in the samples and was therefore used as the reference gene for normalization. Relative mRNA expression was calculated using the comparative cycle time (CT) method according to the manufacturer's
 20 instructions. Results were calculated as the normalized difference in CT for a given patient with infection relative to one healthy donor as baseline whose expression is closest to the mean of all healthy donors ($\Delta\Delta CT$).

Illumina BeadChips: These microarrays consist of 50mer oligonucleotide probes attached to 3 μ m beads, which are lodged into microwells at the surface of a glass slide. Samples were
 25 processed and data acquired by Illumina Inc. (San Diego, CA). Targets were prepared using the Illumina RNA amplification kit (Ambion, Austin, TX). cRNA targets were hybridized to Sentrix Hu6 BeadChips (>46,000 probes), which were scanned on an Illumina BeadStation 500. Illumina's Beadstudio software was used to assess fluorescent hybridization signals.

Raw data obtained for all 148 samples analyzed are deposited with GEO
 30 (www.ncbi.nlm.nih.gov/geo/) (accession number _____).

Microarray data analysis. Microarray Suite, Version 5.0 (MAS 5.0; Affymetrix) software was used to assess fluorescent hybridization signals, to normalize signals, and to evaluate

signal detection calls. Raw signal intensity values for each probe set were analyzed by algorithms in MAS 5.0. A maximum of eight samples were assigned randomly for hybridization and staining each run day in order to minimize technical variability.

Normalization of signal values per chip was achieved using the MAS 5.0 global method of scaling to the target intensity value of 500 per GeneChip. Analysis was restricted to probe sets for which a P (present) call was obtained in at least 75% of GeneChips in at least one patient class evaluated (quality control probes). A gene expression analysis software program, GeneSpring, Version 7.1 (Agilent), was used to perform statistical analysis, hierarchical clustering and classification of samples. Nonparametric univariate tests (Mann-Whitney U or Fishers exact test) were used to rank genes on the basis of their ability to discriminate between pre-defined groups of patients. The ability of the top ranked (i.e., classifier) genes to discriminate the pre-defined class of pathogen was determined by the K-Nearest Neighbors (kNN) method [23].

K-Nearest Neighbors (kNN) method: (1) The algorithm ranks the genes by their predictive strengths, the negative natural log of the p-value as determined by nonparametric tests; and (2) Leave-one-out cross validation was used to estimate the prediction error rate (or accuracy) by the systematic-removal of one donor from the known samples to use as a test sample. This process is repeated until all the donors have been "tested." The discriminating gene lists from both Mann-Whitney U and Fisher's exact test were combined and used for discrimination between sample classes. (3) To assign sample class, the algorithm evaluates class by testing the number of known classes nearest to the sample of unknown class, based on Euclidean distance of normalized expression intensity, and computes a p-value. The class with the lowest p-value is assigned to the unknown sample. A p-value ratio cut-off of 0.5 was used in all discrimination analyses. A class will be assigned to a sample, if the p-value from the predicted class is at least 2 times less than the other class (e.g., p-value of influenza A class/ p-value of bacteria class).

Analysis of significance patterns. Statistical comparisons between each group of patients and its respective healthy control group were performed (Mann-Whitney rank test). Genes significantly changed ($p < 0.01$) were divided into two sets: over-expressed *versus* control and under-expressed *versus* control for the two reference groups (FLU and SLE). Sets of genes were identified by applying selection criteria to these group(s) (e.g. $P < 0.01$ in FLU and $P > 0.5$ in SLE). P-values for these genes were obtained in the context of other diseases

(comparison groups: *S. aureus*, *S. pneumoniae*, *E. coli*). P-values for comparison groups were set to 1 when changes in gene expression were opposite from that of the reference group. P-value data were processed with GeneSpring, Version 7.2 (Agilent), which was used to perform hierarchical clustering and group genes based on significance patterns.

- 5 Transcriptional signatures discriminate patients with influenza A infection from those with bacterial infection. Using a standard gene-level analysis it was found that microarray analysis can be used to differentiate viral infections (influenza A) from bacterial infections (*E. coli* and *S. pneumoniae*) as illustrated in Figure 1C. Figure 1C shows the gene expression signatures discriminate influenza A from bacterial infections. Thirty-five
- 10 classifier genes that best discriminate patients with influenza A virus infection from patients with bacterial infections (*E. coli* or *S. aureus*) with 91% (21/23) accuracy in training set were then independently validated in a test set (n=37). These 35 predictors classified the test set with 95% accuracy (35/37).

- Module-level microarray data analysis. This strategy is based on the initial extraction of 28
- 15 sets of coordinately expressed genes (regrouping nearly 5000 transcripts), or transcriptional modules, from a large microarray gene expression dataset (8 diseases, nearly 250 samples x 44,000 transcripts). These modules were subsequently used as building blocks for analyses that were carried out on a module-by-module basis: functional interpretation through literature analysis first, then group comparison between samples obtained from healthy
 - 20 subjects and patients with acute infections.

- Figure 7 shows gene vectors that may be used for mapping transcriptional changes at the module-levels identifies disease- specific patterns. Group comparisons were carried out between patients and uninfected individuals on a module-by-module basis. The spots represent the percentage of significantly over-expressed (red) or under-expressed (blue)
- 25 genes within a module. This information is displayed on a grid with the coordinates corresponding to one of 28 module IDs (e.g. Module M3.1 is at the intersection of the third row & first column).

- The gene vector and mapping approach permits reducing noise levels and facilitates data interpretation. The group at Dallas has also demonstrated that modular transcriptional data
- 30 were reproducible across microarray platforms.

Identification of diagnostic markers in the blood of patients. Mapping global transcriptional changes at the module-level has helped with the interpretation of patient PBMC

transcriptional profiles. It also revealed disease-specific combinations of modular changes. This is illustrated in Figure 7, comparing changes in module M3.1 (interferon, circled in green - the proportion of differentially over- or under-expressed transcripts indicated by a red and blue spot, respectively) across infections caused by gram positive and negative bacteria. Differences were also found between the two species of gram positive bacteria (Figure 7, orange circles). Most interestingly, marked differences were observed in the modular profiles of influenza and RSV, despite the fact that these viral infections have similar clinical presentations. The complete absence of induction of interferon-inducible transcripts in patients with RSV was a striking difference from influenza infection which was associated with a powerful interferon response in patients (M3.1). Other differences were observed, most strikingly with modules M1.4 and M1.7 (highlighted in purple in Figure 7).

Identification of markers of disease severity: The tools currently available for the diagnosis of infectious diseases rely on the direct detection of the pathogen (e.g. by culture, staining or PCR). In comparison with these methods monitoring gene expression changes of the patient's immune cells offers the possibility of predicting the severity of the disease. Indeed, modular expression levels correlated (averaged values across transcripts) with clinical indicators of disease severity. The modules correlating (positively or negatively) with severity were then consolidated in a single score after carrying out multivariate analysis based on U-statistics (generating "U-scores" – results for *S. aureus* and influenza are shown in Figure 8).

Figure 8 shows the microarray scores for the assessment of disease severity in patients with acute infections. Module-level microarray expression data were combined in a single score through a multivariate analysis based on U-statistics. The microarray scores thus obtained were correlated with a clinical score constituted by relevant indicators of disease severity (e.g. fever, hypotension, acidosis). Markers were identified in a training set and validated in an independent set of patients (test set). Thus a unique microarray-based blood assay produces clinical information that can be used: (1) to determine disease etiology; and (2) to assess disease severity in patients with acute infections. Figures 9a to 9c summarize independent confirmation and validation across microarray platforms.

It will be understood that particular embodiments described herein are shown by way of illustration and not as limitations of the invention. The principal features of this invention

can be employed in various embodiments without departing from the scope of the invention. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, numerous equivalents to the specific procedures described herein. Such equivalents are considered to be within the scope of this invention and are covered by the
5 claims.

All publications and patent applications mentioned in the specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be
10 incorporated by reference.

All of the compositions and/or methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred
15 embodiments, it will be apparent to those of skill in the art that variations may be applied to the compositions and/or methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to
20 those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

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Supplementary Table 1

Supplementary_Table_1

Comparison of clinical parameters between groups of patients included in the training sets
(Mann Whitney test)

Influenza A (n=11) vs Bacteria (n=12)

p-value	Influenza A	Bacteria
Age (years)	0.92 (.33-1.50)	0.33 (.25-.50)
0.20		
WBC/mm ³	7,900 (7,100-10,500)	11,800
(9,050-17,300) 0.02		
Neutrophils (%)	19 (5-34)	30.5 (13.5-57)
0.15		
Lymphocytes (%)	68 (54-91.5)	56.5 (35-74.5)
0.12		
Monocytes (%)	6 (3.5-11)	4 (4-9.5)
0.57		
Days Hospitalization prior to sample	2 (1-2)	2.5 (2-5)
0.06		
C-reactive protein (mg/dL)	1.8 (0.7-7.4)	4.3 (2.1-8.2)
0.24		

E.coli (n=10) vs Saureus (n=10)

p-value	E.coli	S.aureus
Age (years)	0.29 (0.23-4.20)	1.08 (0.50-8.50)
0.06		
WBC/mm ³	10,300 (9,200-17,100)	13,200
(6,500-14,100) 0.10		
Neutrophils (%)	41.6 (21.5-58.85)	43.0 (25.75-55.5)
1.00		
Lymphocytes (%)	46.6 (27.6-64)	41.2 (25.5-55.15)
0.60		
Monocytes (%)	8.0 (4.25-10.5)	6.7 (5.8-10.5)
0.93		
Days Hospitalization prior to sample	2 (2-3.5)	4.5 (3-6.5)
0.01		
C-reactive protein (mg/dL)	5.2 (2.1-7.4)	3.3 (0.9-13.5)
0.48		

E.coli (n=11) vs S.pneumoniae (n=11)

p-value	E.coli	S.pneumo
Age (years)	0.33 (0.25-0.40)	1.33 (0.33-2.00)
0.16		
WBC/mm ³	7,169 (3,328-8,322)	5,725
(2,573-9,252) 0.69		
Neutrophils (%)	27.0 (14-49.3)	53.5 (26-68.3)
0.08		
Lymphocytes (%)	52 (35.8-76.0)	34 (18.75-67.0)
0.06		
Monocytes (%)	10 (7.9-12)	5.5 (3.5-9.35)
0.04		
Days Hospitalization prior to sample	3 (2-3)	5 (3-6)
0.04		
C-reactive protein (mg/dL)	3.7 (0.9-7.5)	5.9 (4.3-10.7)
0.12		

S.aureus (n=12) vs S.pneumoniae (n=11)

S.aureus	S.pneumo
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Supplementary_Table_1

p-value		
Age (years)	0.95 (0.66-1.62)	1.33 (0.33-2.00)
0.95		
WBC/mm ³	12,400 (9,550-17,200)	16,600
(13,800-20,100) 0.08		
Neutrophils (%)	37 (25.5-54)	45 (14.5-63.5)
0.77		
Lymphocytes (%)	46 (28-55.3)	36.5 (27-67)
0.97		
Monocytes (%)	10 (7.1-13)	4.5 (3-10.5)
0.04		
Days Hospitalization prior to sample	4.5 (3.5-5.5)	5 (3-6)
0.80		
C-reactive protein (mg/dL)	3.7 (1.1-6.3)	6.6 (4.4-11.6)
0.16		

Supplementary_Table_2

Supplementary Table 2

Influenza A vs. bacterial infection; class comparison results: Comparison of gene expression levels (normalized values) between patients with acute influenza A infection and patients with acute bacterial infection (E. coli or S. pneumoniae) - $P < 0.01$, Mann-Whitney test = 854. Expression patterns are represented Figure 1a.

Influenza A (n=11)			Affymetrix Bacteria (n=12)			P-value		Fold
Common FLU/Bacteria	GenBank Median	Min	Probe ID Max	uniGeneI Median	Min	Max	Max	
101F6 1.221072562	AF040704 0.8093	0.809	209665_at 1.199	Hs.14944 0.8816	0.733	1.225	0.003	
ABL1 1.227697868	NM_005157 0.9594	0.959	202123_s_at 1.313	Hs.43104 0.8831	0.720	1.025	0.000	
ACLY 1.443518817	NM_001096 0.6475	0.647	201128_s_at 1.527	Hs.38756 0.8543	0.644	1.237	0.005	
ACTN4; 1.707666883 FSGS;	U48734 0.9178	0.917	200601_at 1.562	Hs.27029 0.7186	0.397	1.203	0.000	
ADAR 1.526333555	NM_001111 0.9956	0.995	201786_s_at 1.802	Hs.12341 0.8177	0.563	1.288	0.000	
AGRN 1.442813179	AF016903 0.7047	0.704	212285_s_at 2.031	Hs.27333 0.8397	0.285	1.201	0.000	
AIM2 1.578745244	NM_004833 0.7221	0.722	206513_at 3.471	Hs.28189 0.8150	0.416	1.897	0.006	
AKAP13 1.875901472	AK022014 0.9017	0.901	222024_s_at 1.775	Hs.45921 0.7121	0.498	1.322	0.000	
AKAP13 1.734310879	BF222823 0.7067	0.706	209534_x_at 1.461	Hs.45921 0.6486	0.501	1.022	0.000	
AKT1 1.533889712	NM_005163 0.8681	0.868	207163_s_at 1.657	Hs.52562 0.7523	0.447	1.236	0.003	
ALS2CR3 1.475778110	AV705253 0.8327	0.832	202124_s_at 1.841	Hs.15277 0.7803	0.378	1.194	0.000	
ANGPTL6 1.506777224	AI862559 0.9111	0.911	53720_at 1.890	Hs.17512 0.7408	0.400	1.738	0.003	
APG12L 1.565468786	BE965998 0.7987	0.798	213026_at 1.508	Hs.26448 0.6940	0.467	1.316	0.000	
APOBEC 1.755107168	AF165520 0.9999	0.999	209584_x_at 2.151	Hs.44112 0.7558	0.418	1.000	0.000	
APS 1.593599322	NM_020979 0.7147	0.714	205367_at 1.546	Hs.48944 0.7842	0.569	1.391	0.003	
ARHGAP 1.359872860	AA533284 0.8167	0.816	47069_at 1.816	--- 0.8773	0.628	1.143	0.001	
ARHGDIA 1.594977725	NM_004309 0.7691	0.769	201168_x_at 1.554	Hs.15916 0.7163	0.460	1.144	0.002	
ARIH2	BC000422		201229_s_at	Hs.24155			0.003	

Supplementary Table 2						
1.620178139	0.9696	0.969	1.634	0.7183	0.511	1.555
ARPC5L	NM_030978		220966_x_at	Hs.13249		0.006
1.448620957	0.7400	0.740	1.579	0.8576	0.621	1.249
ASB7	NM_024708		219996_at	Hs.31845		0.001
1.388024965	0.8467	0.846	1.718	0.8460	0.496	1.584
ASH2L	AB020982		209517_s_at	Hs.52153		0.003
1.342958028	0.9561	0.956	1.517	0.8989	0.691	1.545
ATP2A2	M23114		209186_at	Hs.50675		0.000
1.221136532	0.8177	0.817	1.427	0.8752	0.667	1.052
BAG5	AA457021		202984_s_at	Hs.5443		0.000
1.976960440	0.8300	0.830	2.213	0.6868	0.244	1.351
BAT2	NM_004638		208132_x_at	Hs.43609		0.000
1.459923067	0.9336	0.933	1.558	0.8904	0.656	1.240
BAZ1A	AA102574		217985_s_at	Hs.50914		0.000
1.448181093	0.8899	0.889	1.381	0.8317	0.535	1.153
BCMSUNL	AA905286		215629_s_at	Hs.50804		0.004
1.680097673	0.6140	0.614	2.032	0.8611	0.412	1.107
BRD2	S78771		214911_s_at	Hs.75243		0.000
1.834219334	0.9283	0.928	1.508	0.6764	0.466	1.364
BRD2	D42040		208686_s_at	Hs.75243		0.000
1.767305451	0.5556	0.555	1.649	0.7800	0.542	1.274
BRD2	AA902767		208685_x_at	Hs.75243		0.001
1.433881404	0.9120	0.912	1.444	0.7743	0.511	1.381
BST2	NM_004335		201641_at	Hs.11811		0.000
1.952049513	1	1	3.833	0.6265	0.501	1.733
BTN2A1	AL121936		215493_x_at	Hs.15902		0.005
1.265850214	0.6994	0.699	1.884	0.8867	0.562	1.124
C14orf101	NM_017799		219757_s_at	Hs.58491		0.008
1.367000510	0.9588	0.958	1.360	0.8604	0.447	1.564
C1GALT1	NM_020156		219439_at	Hs.23966		0.005
1.262195135	0.8855	0.885	1.353	0.8777	0.411	1.326
C1orf16	NM_014837		201794_s_at	Hs.27077		0.002
1.597630927	0.5872	0.587	1.881	0.8506	0.454	1.162
C1orf29	NM_006820		204439_at	Hs.38972		0.000
11.74888069	0.8232	0.823	3.514	0.1608	0.01	2.288
C20orf6	NM_016649		218859_s_at	Hs.36928		0.000
1.980322789	0.8742	0.874	1.746	0.5907	0.311	1.483
C21orf45	NM_018944		219004_s_at	Hs.19051		0.000
1.376790785	0.8249	0.824	1.558	0.9029	0.544	1.085
C6orf56	NM_014721		204048_s_at	Hs.10247		0.000
1.643578419	1.0434	1.043	1.683	0.7254	0.372	0.999
C6orf56	NM_014721		204049_s_at	Hs.10247		0.000
1.556543549	0.9248	0.924	1.726	0.7520	0.431	1.550
CAGH16	U80737		211352_s_at	Hs.38216		0.000
2.232202481	0.9042	0.904	2.112	0.6928	0.444	1.230

Supplementary_Table_2						
CALR	AI348935	214315_x_at	Hs.51516			0.000
1.666387917	0.7185	0.718	1.536	0.7466	0.425	1.231
CALR	BE251303	212953_x_at	Hs.51516			0.000
1.447465327	0.8482	0.848	1.684	0.7737	0.629	1.155
CAP350	AW299294	213956_at	Hs.41304			0.005
2.181524662	0.7559	0.755	2.123	0.6686	0.406	1.662
CAP350	NM_014810	204373_s_at	Hs.41304			0.000
1.631854810	0.9799	0.979	1.967	0.8413	0.522	1.301
CAP350	AW299294	213957_s_at	Hs.41304			0.005
1.383153896	0.6205	0.620	1.484	0.8666	0.586	1.061
CCL4	NM_002984	204103_at	Hs.75703			0.000
2.965041468	0.6828	0.682	5.469	0.6006	0.056	1.411
CD81	NM_004356	200675_at	Hs.54457			0.002
1.288245881	0.9352	0.935	1.325	0.8718	0.618	1.156
CDC27	AI203880	217879_at	Hs.46329			0.003
1.105257595	0.8403	0.840	1.328	0.9507	0.423	1.047
CDC2L1	AF067524	211289_x_at	Hs.19231			0.001
1.450827376	0.7982	0.798	1.509	0.8880	0.634	1.083
CEB1	NM_016323	219863_at	Hs.26663			0.001
3.328842849	0.8700	0.870	6.816	0.6005	0.199	2.986
CES1	S73751	209616_s_at	Hs.55886			0.001
2.173958413	0.6881	0.688	3.447	0.8201	0.073	1.230
CES2	D50579	209668_x_at	Hs.28297			0.006
1.199316344	0.8209	0.820	1.386	0.9117	0.591	1.097
CFLAR	AF015451	211862_x_at	Hs.39073			0.005
1.477767639	0.7373	0.737	1.524	0.8484	0.433	1.321
CGBP	NM_014593	218058_at	Hs.18093			0.001
1.376988057	0.7532	0.753	1.477	0.8325	0.518	1.293
CGBP	U55777	48580_at	Hs.18093			0.008
1.236104958	0.8977	0.897	1.526	0.9373	0.867	1.131
CGI-49	AL572542	201825_s_at	Hs.49839			0.006
1.332170971	0.8799	0.879	1.658	0.9495	0.856	1.219
CGI-96	AL022316	33307_at	Hs.55353			0.006
1.617129588	0.5098	0.509	1.970	0.8304	0.576	1.628
CHORDC	NM_012124	218566_s_at	Hs.22857			0.003
1.154021522	0.9706	0.970	1.426	0.9539	0.464	1.165
CHS1	U84744	210943_s_at	Hs.53241			0.005
1.898472293	0.8009	0.800	1.466	0.6728	0.243	1.615
CHST12	NM_018641	218927_s_at	Hs.21308			0.000
2.018687801	0.7668	0.766	2.430	0.7803	0.102	1.353
CIAO1	NM_004804	203536_s_at	Hs.12109			0.002
1.154597677	0.8682	0.868	1.459	0.9653	0.710	1.080
cig5	AI337069	213797_at	Hs.17518			0.000
7.944318513	0.5622	0.562	4.457	0.2110	0.149	1.802
CKS2	NM_001827	204170_s_at	Hs.83758			0.000
1.962731036	0.7058	0.705	3.238	0.8507	0.460	1.025

Supplementary_Table_2

CNOT7	NM_013354	218250_s_at	Hs.17055	0.001
1.327993616	0.9413 0.941	1.250 0.8110	0.489	1.186
CNP	BC001362	208912_s_at	Hs.27362	0.005
1.239532401	0.8881 0.888	1.412 0.8398	0.558	1.345
COPEB	BE675435	208960_s_at	Hs.4055	0.005
1.998092311	0.6302 0.630	2.267 0.7968	0.691	2.189
COPEB	AB017493	208961_s_at	Hs.4055	0.000
1.796053082	0.7243 0.724	1.918 0.7264	0.562	1.152
COX8	NM_004074	201119_s_at	Hs.43390	0.000
1.259010725	0.9481 0.948	1.487 0.9049	0.535	1.120
CREB1	NM_004379	204313_s_at	Hs.58475	0.003
1.235431832	0.8633 0.863	2.114 0.9515	0.673	1.201
CSPG6	NM_005445	209257_s_at	Hs.24485	0.005
2.486739454	0.4677 0.467	2.114 0.4815	0.383	1.737
CSPG6	NM_005445	209258_s_at	Hs.24485	0.002
1.375924623	0.8718 0.871	1.696 0.8625	0.216	1.286
CTBP2	AF222711	210835_s_at	Hs.50134	0.006
1.432601343	0.5828 0.582	1.931 0.9036	0.454	1.149
CTSC	NM_001814	201487_at	Hs.12806	0.000
1.556506946	0.9531 0.953	1.514 0.7705	0.595	1.491
CUGBP2	N36839	202156_s_at	Hs.30928	0.001
1.427711687	0.7064 0.706	1.598 0.8872	0.658	1.193
CXorf9	AL023653	204923_at	Hs.61469	0.006
1.234755846	0.8334 0.833	1.475 0.8497	0.487	1.125
DBI	BC006466	211070_x_at	Hs.78888	0.003
1.298257852	0.8043 0.804	1.531 0.9250	0.620	1.128
DC50	NM_031210	221434_s_at	Hs.32452	0.002
1.289760882	0.8579 0.857	1.315 0.8495	0.529	1.177
DCTN1	NM_004082	201082_s_at	Hs.51611	0.000
1.497659582	0.7970 0.797	1.404 0.8284	0.55	1.200
DDB2	NM_000107	203409_at	Hs.44656	0.005
1.805057499	0.5918 0.591	2.038 0.6960	0.441	1.317
DDX24	BG421209	200702_s_at	Hs.51032	0.000
2.623673527	0.7541 0.754	1.692 0.5101	0.259	1.579
DDX26	AL117626	222239_s_at	Hs.43944	0.008
1.432138342	0.7611 0.761	1.671 0.8216	0.514	1.348
DHX29	AL079292	212649_at	---	0.000
1.335398485	0.9258 0.925	1.497 0.8899	0.478	1.320
DKFZp56	AL050028	212005_at	Hs.25296	0.001
1.588525951	0.7601 0.760	1.928 0.7907	0.336	1.406
6C0424				
DKFZP58	AL080220	213199_at	Hs.58487	0.000
1.588165273	0.9141 0.914	1.789 0.8616	0.433	1.183
6P0123				
DKFZP58	AL080220	36552_at	Hs.58487	0.003
1.284115327	0.8130 0.813	1.839 0.9389	0.497	1.167

Supplementary_Table_2

6P0123

DNAPTP	AK002064	222154_s_at	Hs.12032	0.000
4.498070893	0.9999 0.999	2.824 0.3265	0.202 1.444	
DNASE2	AB004574	209831_x_at	Hs.11824	0.003
1.344125788	0.9445 0.944	1.371 0.8439	0.679 1.387	
DNM1L	NM_012062	203105_s_at	Hs.55629	0.000
1.297397127	0.9355 0.935	1.419 0.9052	0.716 1.190	
E2-EPF	NM_014501	202779_s_at	Hs.39639	0.003
1.816943131	0.6517 0.651	2.281 0.6771	0.596 1.407	
E2F3	NM_001949	203693_s_at	Hs.26940	0.002
1.229489831	0.8599 0.859	1.557 0.9797	0.699 1.139	
EBAG9	NM_004215	204278_s_at	Hs.40936	0.003
1.334607110	0.7692 0.769	1.657 0.8820	0.472 1.163	
EEG1	AI630178	213113_s_at	Hs.99962	0.003
1.427187155	0.8559 0.855	1.413 0.9068	0.657 1.299	
EEG1	BC003163	210692_s_at	Hs.99962	0.008
1.335061284	0.6980 0.698	1.573 0.8987	0.528 1.211	
EIF2S1	BC002513	201143_s_at	Hs.15177	0.003
1.262852466	0.8828 0.882	1.771 0.8617	0.624 1.129	
EIF3S10	BE614908	200596_s_at	Hs.52329	0.002
1.356305414	0.9312 0.931	1.636 0.8013	0.448 1.266	
EIF4G1	BE966878	208624_s_at	Hs.43375	0.001
1.483870975	0.7018 0.701	1.375 0.7441	0.553 1.553	
EKI1	NM_018638	219017_at	Hs.58493	0.005
1.486617995	0.5565 0.556	2.017 0.7806	0.394 1.355	
ELAC2	NM_018127	201767_s_at	Hs.43423	0.005
1.415011071	0.5962 0.596	1.894 0.8201	0.082 1.924	
EST1B	AB029012	34868_at	Hs.51683	0.002
1.374385297	0.7096 0.709	1.513 0.8528	0.542 1.132	
FALZ	NM_004459	207186_s_at	Hs.44420	0.000
2.128336159	0.9637 0.963	2.080 0.6319	0.391 1.438	
FLJ10159	NM_018013	218974_at	Hs.44524	0.003
1.708849595	0.6371 0.637	2.219 0.8470	0.396 1.320	
FLJ10290	NM_018047	218134_s_at	Hs.20202	0.002
1.120781391	0.8485 0.848	1.154 0.9274	0.735 1.108	
FLJ10707	BF590997	221806_s_at	Hs.28816	0.003
1.209834939	0.9193 0.919	1.336 0.9246	0.715 1.211	
FLJ10737	AL109978	215792_s_at	Hs.58493	0.000
1.294653872	0.9322 0.932	1.657 0.8812	0.679 1.103	
FLJ10803	BC001743	209446_s_at	---	0.000
1.605220320	0.9421 0.942	2.292 0.8585	0.491 2.182	
FLJ10891	NM_018260	220242_x_at	Hs.41295	0.001
1.378310808	0.8529 0.852	1.736 0.7785	0.447 1.199	
FLJ11011	NM_018299	218521_s_at	Hs.49203	0.006
1.523502587	0.7020 0.702	1.685 0.8776	0.530 2.459	

Supplementary_Table_2						
FLJ12443	NM_024830	201818_at	Hs.36885			
1.276465224	0.8795 0.879	1.830 0.9261	0.537	1.191	0.001	
FLJ12671	NM_030980	208114_s_at	Hs.30190			
1.251285856	0.9331 0.933	1.403 0.8679	0.642	1.221	0.006	
FLJ13409	NM_024617	220933_s_at	Hs.13639			
1.219590272	0.8988 0.898	1.734 0.9644	0.581	1.127	0.001	
FLJ14281	NM_024920	219237_s_at	Hs.51274			
1.383563898	0.7519 0.751	1.905 0.8276	0.438	1.165	0.001	
FLJ20035	NM_017631	218986_s_at	Hs.48114			
4.000839460	0.9790 0.979	2.606 0.3965	0.070	1.717	0.000	
FLJ20073	NM_017654	219691_at	Hs.65641			
2.381804562	0.9506 0.950	3.538 0.6088	0.212	2.332	0.000	
FLJ20113	NM_017670	201246_s_at	Hs.47378			
1.626902311	0.8780 0.878	1.832 0.8969	0.469	1.109	0.000	
FLJ20113	AL523776	201245_s_at	Hs.47378			
1.177062995	0.8671 0.867	1.305 0.9155	0.659	1.249	0.006	
FLJ20241	AI689402	58994_at	Hs.26959			
1.166787667	0.9242 0.924	1.359 0.9043	0.671	1.201	0.000	
FLJ20637	NM_017912	219352_at	Hs.52931			
4.945244927	0.8475 0.847	4.700 0.4401	0.152	2.531	0.000	
FLJ20668	NM_017923	219574_at	Hs.13690			
1.554715263	0.8371 0.837	2.320 0.7674	0.550	1.420	0.000	
FLJ21820	AK021672	222193_at	Hs.18782			
1.300641595	0.7854 0.785	1.385 0.8748	0.395	1.383	0.008	
FLJ22332	NM_024724	219221_at	Hs.51830			
1.972913978	0.7147 0.714	2.891 0.7191	0.450	1.587	0.000	
FLJ22555	NM_024520	219176_at	Hs.15449			
1.414049722	0.7858 0.785	1.606 0.8576	0.519	1.176	0.000	
FLJ22693	NM_022750	218543_s_at	Hs.12646			
1.761766701	0.9012 0.901	2.820 0.8126	0.427	1.691	0.000	
FLJ38348	AV755522	213294_at	Hs.54652			
2.761652399	0.9726 0.972	1.879 0.4938	0.208	1.667	0.001	
FLN29	AB007447	35254_at	Hs.5148			
1.386002789	0.9438 0.943	1.673 0.8911	0.636	1.239	0.001	
FNBPI	AU145053	213940_s_at	Hs.18940			
1.246588671	0.8824 0.882	1.389 0.8543	0.581	1.675	0.005	
FNBPI	Z78308	213729_at	Hs.29873			
1.392703850	0.9535 0.953	1.573 0.7939	0.425	1.324	0.000	
FUSIP1	AF047448	210178_x_at	Hs.3530			
1.493957731	0.8744 0.874	1.526 0.7754	0.553	1.580	0.005	
FYB	AF198052	211794_at	Hs.37050			
1.427016546	0.8037 0.803	1.656 0.7818	0.343	1.432	0.008	
G1P2	NM_005101	205483_s_at	Hs.45848			
4.527162708	0.7919 0.791	4.144 0.3586	0.105	1.901	0.000	
G1P3	NM_022873	204415_at	Hs.52384			
2.102310148	0.7381 0.738	3.211 0.7202	0.368	6.487	0.006	

Supplementary_Table_2

GAK	NM_005255	202281_at	Hs.36960	0.003
1.372848753	0.9410 0.941	1.486 0.8335	0.5525 1.257	
GAPCENA	NM_012197	204028_s_at	Hs.27134	0.006
1.428426972	0.7923 0.792	1.588 0.7435	0.525 1.567	
GBF1	NM_004193	201439_at	Hs.29024	0.003
1.485603884	0.7434 0.743	1.525 0.7488	0.416 1.116	
GBP1	NM_002053	202270_at	Hs.62661	0.000
3.508295920	0.5660 0.566	3.386 0.4733	0.105 5.280	
GBP1	BC002666	202269_x_at	Hs.62661	0.006
2.817269023	0.6616 0.661	3.423 0.4176	0.093 2.178	
GCH1	NM_000161	204224_s_at	Hs.86724	0.003
1.458200584	0.8999 0.899	1.864 0.8168	0.634 1.912	
GLG1	AK025457	214730_s_at	Hs.20171	0.001
1.606020724	0.7915 0.791	1.480 0.7407	0.540 1.234	
GLG1	NM_012201	207966_s_at	Hs.20171	0.003
1.594236722	0.8810 0.881	1.749 0.8251	0.616 1.488	
GLRX2	NM_016066	219933_at	Hs.45828	0.001
1.599558962	0.7560 0.756	1.829 0.8305	0.550 1.403	
GMIP	NM_016573	218913_s_at	Hs.49427	0.001
1.272352818	0.9515 0.951	1.411 0.8876	0.600 1.191	
GMNN	NM_015895	218350_s_at	Hs.23489	0.006
1.651640251	0.7458 0.745	2.723 0.8797	0.473 1.410	
HCAP-G	NM_022346	218662_s_at	Hs.56756	0.003
1.441828180	0.8025 0.802	2.942 0.9376	0.515 1.657	
HELSNF1	U00955	212571_at	Hs.53069	0.003
1.392909099	0.8669 0.866	1.586 0.8858	0.532 1.414	
HLA-E	M31183	217456_x_at	Hs.38100	0.001
1.305635130	0.8562 0.856	1.398 0.8834	0.651 1.214	
HLA-F	NM_018950	204806_x_at	Hs.51997	0.006
1.177554203	0.8642 0.864	1.329 0.9004	0.434 1.040	
HMGAI	NM_002131	206074_s_at	Hs.51880	0.006
1.420603958	0.7456 0.745	1.580 0.7814	0.478 1.405	
HNRPA8	NM_004499	201277_s_at	Hs.24874	0.008
1.367462814	0.8754 0.875	1.881 0.8909	0.699 1.238	
HPS5	NM_007216	204544_at	Hs.43759	0.005
1.224732980	0.8617 0.861	2.313 0.9624	0.451 1.174	
HSPC051	NM_013387	218190_s_at	Hs.28429	0.003
1.555053704	0.6417 0.641	1.499 0.7009	0.472 1.161	
HSPC177	NM_015961	218085_at	Hs.41553	0.005
1.342145503	0.7610 0.761	2.278 0.9155	0.609 1.789	
HSXIAPA	NM_017523	206133_at	Hs.44197	0.000
3.646293491	1 1	2.512 0.5486	0.086 1.707	
HUMGT1	N40555	213708_s_at	Hs.38301	0.003
1.316775991	0.8745 0.874	1.778 0.8660	0.739 1.714	
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Supplementary_Table_2						
ICAM2	NM_000873	204683_at	Hs.43146			
1.671010716	0.6906 0.690	1.923 0.8176	0.559	1.441	0.005	
ID2	AI819238	213931_at	Hs.14834			
1.964582591	0.7482 0.748	1.523 0.6285	0.283	1.253	0.001	
ID2	NM_002166	201565_s_at	Hs.18091			
1.429527546	0.7967 0.796	1.336 0.7938	0.510	1.446	0.005	
IDH2	U52144	210046_s_at	Hs.51314			
1.296429239	0.8234 0.823	3.440 0.8762	0.588	1.487	0.008	
IDH3A	AI826060	202069_s_at	Hs.25061			
1.292148159	0.9302 0.930	1.455 0.8604	0.605	1.267	0.001	
IFI16	BG256677	208965_s_at	Hs.38025			
1.872614959	0.9600 0.960	1.775 0.7223	0.371	1.158	0.000	
IFI16	NM_005531	206332_s_at	Hs.38025			
1.531403014	0.9672 0.967	1.711 0.8730	0.315	2.163	0.005	
IFI27	NM_005532	202411_at	Hs.53263			
53.89107451	1 1	4.510 0.0447	0.01	2.241	0.000	
IFI35	BC001356	209417_s_at	Hs.50842			
2.806714289	0.9187 0.918	3.278 0.4229	0.251	1.675	0.000	
IFI44	NM_006417	214453_s_at	Hs.82316			
6.444369203	0.7232 0.723	2.953 0.2532	0.069	1.845	0.000	
IFI44	BE049439	214059_at	Hs.82316			
3.679544921	0.8637 0.863	8.086 0.6156	0.155	2.931	0.000	
IFIT1	NM_001548	203153_at	Hs.20315			
8.434175471	0.3680 0.368	6.034 0.2783	0.012	2.906	0.000	
IFIT2	BE888744	217502_at	Hs.43760			
1.919250623	0.6438 0.643	3.765 0.6732	0.485	2.137	0.003	
IFIT4	NM_001549	204747_at	Hs.47338			
5.614666748	0.5370 0.537	5.966 0.3098	0.154	2.117	0.000	
IFITM1	AA749101	214022_s_at	Hs.45841			
1.346966518	0.8699 0.869	1.738 0.8904	0.653	1.068	0.000	
IFITM3	BF338947	212203_x_at	Hs.37465			
1.695374621	0.8326 0.832	1.728 0.7448	0.443	1.269	0.001	
IFNAR2	L41944	204786_s_at	Hs.51221			
1.484090119	0.7955 0.795	2.031 0.7992	0.592	1.169	0.000	
IL6	NM_000600	205207_at	Hs.51223			
1.709090874	0.6808 0.680	1.838 0.8929	0.486	1.140	0.005	
ILF3	BG032366	208930_s_at	Hs.46588			
2.212727650	0.6070 0.607	2.133 0.5720	0.269	1.364	0.002	
IPO9	NM_018085	217885_at	Hs.49738			
1.308587275	0.7737 0.773	1.602 0.9704	0.436	1.214	0.001	
IRF2	NM_002199	203275_at	Hs.37409			
1.781725944	0.6555 0.655	2.771 0.8925	0.458	1.765	0.006	
IRF3	NM_001571	202621_at	Hs.75254			
1.358920542	0.6953 0.695	1.579 0.9460	0.566	1.403	0.006	
IRF7	NM_004030	208436_s_at	Hs.16612			
3.620425514	0.5747 0.574	3.854 0.3576	0.295	1.529	0.000	

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ISG20	NM_002201	204698_at	Hs.45926	0.003
1.561357709	0.6510 0.651	3.863 0.8264	0.246 1.480	
ISG20	U88964	33304_at	Hs.45926	0.000
1.519567295	0.7447 0.744	2.867 0.8015	0.392 1.165	
ITCH	AL109923	217094_s_at	Hs.47250	0.000
1.450545001	0.9298 0.929	1.840 0.8008	0.570 1.085	
ITCH	AB056663	209744_x_at	Hs.47250	0.000
1.286927326	0.85 0.85	1.554 0.8717	0.570 1.001	
JJA21	AI924660	213971_s_at	Hs.46273	0.001
1.412727071	0.7238 0.723	1.395 0.8064	0.572 1.039	
KCNAB2	AL520102	203402_at	Hs.44049	0.003
1.200844840	0.8802 0.880	1.699 0.9341	0.782 1.356	
KHSRP	NM_003685	204372_s_at	Hs.91142	0.000
1.328573353	0.9273 0.927	1.779 0.8602	0.522 1.129	
KIAA0082	D43949	212380_at	Hs.52010	0.000
1.732493419	0.8604 0.860	1.786 0.7059	0.358 1.108	
KIAA0121	AI806207	214004_s_at	Hs.37395	0.006
1.321306272	0.963 0.963	2.028 0.9238	0.673 1.422	
KIAA0152	BC000371	200616_s_at	Hs.50707	0.000
2.377021816	0.9975 0.997	2.393 0.5826	0.125 1.186	
KIAA0182	D80004	212057_at	Hs.46164	0.000
1.496475094	0.9667 0.966	1.842 0.8243	0.425 1.600	
KIAA0226	AI798908	212733_at	Hs.47886	0.000
1.309765106	0.9780 0.978	1.512 0.9573	0.395 1.226	
KIAA0467	AB007936	215364_s_at	Hs.30194	0.001
1.406371513	0.8573 0.857	1.854 0.8577	0.546 1.195	
KIAA0553	AB011125	212487_at	Hs.46312	0.000
1.688232854	0.8895 0.889	1.789 0.6926	0.452 1.260	
KIAA0562	AI936976	204074_s_at	Hs.50901	0.008
1.627761477	0.8457 0.845	1.444 0.7119	0.563 1.508	
KIAA0625	NM_015046	201965_s_at	Hs.46031	0.001
1.197224982	0.9610 0.961	1.588 0.9568	0.553 1.300	
KIAA0874	X80821	216563_at	Hs.46458	0.001
1.576501234	0.7763 0.776	1.486 0.7126	0.431 1.401	
KIAA0892	AL110250	212505_s_at	Hs.11275	0.005
1.273713513	0.6785 0.678	1.260 0.8935	0.604 1.193	
KIAA1033	AL137753	212794_s_at	Hs.12144	0.008
1.605729068	0.6022 0.602	1.772 0.7016	0.350 1.376	
KIAA1049	BF000251	213311_s_at	Hs.41534	0.006
1.241482340	0.7252 0.725	1.431 0.8602	0.636 1.108	
KIF3B	NM_004798	203943_at	Hs.36967	0.006
1.262451716	0.9236 0.923	1.475 0.8626	0.434 1.288	
KLIP1	NM_024629	218883_s_at	Hs.48130	0.000
1.698924718	0.9571 0.957	3.092 0.8416	0.570 1.448	
KLRD1	U30610	210606_x_at	Hs.52425	0.003

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1.684713021	0.2831	0.283	5.265	0.8787	0.185	1.220
KLRD1	AB009597	207795_s_at	Hs.52425			0.006
1.464755413	0.3362	0.336	4.496	0.8364	0.138	1.181
KPNA6	NM_012316	212101_at	Hs.47058			0.000
1.517163209	0.7745	0.774	1.594	0.7976	0.491	1.170
LAMP3; DCLAMP; TSC403; DC-LAMP	NM_014398	205569_at	Hs.51844			0.005
3.395995402	0.7192	0.719	7.362	0.4589	0.081	4.229
LARP	BE881529	212193_s_at	Hs.29207			0.000
1.678292792	0.9909	0.990	1.858	0.8412	0.503	1.636
LARP	BC001460	210966_x_at	Hs.29207			0.000
1.395873516	0.8724	0.872	1.703	0.8901	0.518	1.215
LGALS3BP	NM_005567	200923_at	Hs.51453			0.000
2.837264090	0.8143	0.814	3.547	0.6468	0.222	1.807
LGALS9	NM_009587	203236_s_at	Hs.81337			0.000
2.196887361	0.8627	0.862	1.819	0.6618	0.331	1.392
LMO4	BC003600	209205_s_at	Hs.43679			0.000
1.445558906	0.7485	0.748	1.489	0.8624	0.526	1.105
LOC3390	AF229069	221501_x_at	Hs.51339			0.006
1.349664193	0.6025	0.602	1.560	0.8796	0.293	1.079
LOC9037	AI073983	221849_s_at	Hs.44363			0.005
1.496464844	0.4882	0.488	1.566	0.8721	0.373	1.190
LY6E	NM_002346	202145_at	Hs.52190			0.000
4.216806954	0.9492	0.949	3.272	0.3732	0.098	1.228
LYRIC	AI972475	212251_at	Hs.37715			0.000
1.413432074	0.9084	0.908	1.444	0.7597	0.528	1.026
M96	AI566096	203345_s_at	Hs.31016			0.005
1.485535254	0.8358	0.835	1.794	0.7432	0.538	1.265
MAP3K5	D84476	203836_s_at	Hs.18648			0.002
1.395530940	0.6724	0.672	1.769	0.7591	0.599	1.062
MARK2	NM_017490	203942_s_at	Hs.56726			0.000
1.638330074	0.8714	0.871	1.614	0.6914	0.250	1.507
MCM3AP	AJ010089	212269_s_at	Hs.38903			0.008
1.361060628	0.6256	0.625	1.568	0.9319	0.312	1.077
MDA5	NM_022168	219209_at	Hs.16317			0.000
2.786510589	0.8117	0.811	3.331	0.6152	0.097	2.773
MDS010	NM_020231	218587_s_at	Hs.23175			0.003
1.440699744	0.8072	0.807	1.978	0.8196	0.090	1.160
MDS029	NM_018464	218597_s_at	Hs.37010			0.002
1.442752664	0.8334	0.833	1.692	0.9132	0.612	1.380
MGC12197	NM_016625	219507_at	Hs.47806			0.000
1.581189033	0.7861	0.786	1.577	0.8069	0.478	1.066
MGC1953	NM_005167	200885_at	Hs.50265			0.008
1.234137264	0.7389	0.738	2.119	0.9242	0.573	1.111
1;						

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DKFZp43

MGC19570	AL031778	213322_at	Hs.22745	0.001
1.700161363	0.8022 0.802	2.188 0.9197	0.445 1.410	
MGC2477	BC001434	221637_s_at	Hs.9061	0.006
1.788853171	0.5402 0.540	2.026 0.9001	0.662 1.348	
MGC3121	NM_024031	218714_at	Hs.29362	0.008
1.156467321	0.9467 0.946	1.460 0.9602	0.675 1.129	
MGC52022	BG031677	213851_at	Hs.37122	0.001
1.390530474	0.8339 0.833	1.621 0.8420	0.507 1.106	
MGC5347	NM_024063	218933_at	Hs.36965	0.006
1.470732521	0.8220 0.822	1.635 0.8876	0.663 1.259	
MGC955	W37846	62212_at	Hs.14884	0.006
1.164140667	0.9598 0.959	1.243 0.9287	0.796 1.330	
MIC8	NM_005931	206247_at	Hs.21158	0.002
1.301727999	0.7897 0.789	1.708 0.9049	0.499 1.225	
MKI67	BF001806	212020_s_at	Hs.80976	0.003
1.574725775	0.8920 0.892	2.576 0.8101	0.559 1.436	
MLL	NM_005933	212079_s_at	Hs.25885	0.003
1.981355249	0.7668 0.766	1.867 0.6192	0.222 1.810	
MLL	NM_005933	212078_s_at	Hs.25885	0.005
1.801430690	0.8230 0.823	1.651 0.6182	0.414 1.259	
MR1	NM_001531	207565_s_at	Hs.10184	0.002
1.385774022	0.7937 0.793	1.348 0.8088	0.647 1.398	
MR1	AF031469	210224_at	Hs.10184	0.000
1.287289742	0.9516 0.951	1.347 0.8506	0.524 1.177	
MRPL19	NM_014763	203465_at	Hs.44024	0.000
1.894664920	0.7077 0.707	3.228 0.7826	0.431 1.291	
MRPS14	NM_022100	203800_s_at	Hs.24732	0.003
1.311615805	0.6797 0.679	1.801 0.8788	0.648 1.148	
MRPS18	BC005373	208907_s_at	Hs.27441	0.005
1.221289685	0.8622 0.862	1.624 0.9054	0.580 1.320	
MT1F;	M10943	217165_x_at	Hs.51362	0.008
2.358035473	0.5887 0.588	2.216 0.6615	0.309 1.773	
MGC32732				
MTHFD2	NM_006636	201761_at	Hs.46903	0.005
1.234029390	0.9566 0.956	1.416 0.8443	0.529 1.313	
MTOL	AI249752	222014_x_at	Hs.34761	0.008
1.526306124	0.7301 0.730	1.692 0.8335	0.309 1.237	
MX1	NM_002462	202086_at	Hs.51730	0.000
4.249779937	0.8775 0.877	3.665 0.3422	0.122 1.923	
MX2	NM_002463	204994_at	Hs.926	0.000
2.504194560	0.7354 0.735	2.814 0.5707	0.357 1.510	
N4BP1	AB014515	32069_at	Hs.51183	0.001
1.237955266	0.9716 0.971	1.474 0.8720	0.583 1.274	
NBS1	AI796269	202905_x_at	Hs.49220	0.000
1.378745415	0.9421 0.942	1.437 0.8184	0.360 1.084	

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NCOA3	NM_006534	207700_s_at	Hs.38216	0.003
1.884296497	0.8547 0.854	1.518 0.6223	0.507	1.306
NCOA3	AF012108	209060_x_at	Hs.38216	0.006
1.468528660	0.7052 0.705	1.349 0.6906	0.354	1.124
NCOA6	AF128458	208979_at	Hs.36897	0.001
1.204877081	0.9633 0.963	1.219 0.8954	0.686	1.408
NDUFB3	NM_002491	203371_s_at	Hs.10976	0.003
1.276462433	0.7811 0.781	1.279 0.8824	0.712	1.095
NFYC	NM_014223	202215_s_at	Hs.23345	0.000
1.209680026	0.8189 0.818	1.578 0.9250	0.564	1.030
NICE-4	NM_014847	201377_at	Hs.49055	0.008
1.362771891	0.6601 0.660	1.793 0.8169	0.662	1.305
NKG7	NM_005601	213915_at	Hs.10306	0.001
1.756321468	0.5447 0.544	2.659 0.8171	0.254	1.694
NMI	NM_004688	203964_at	Hs.54483	0.000
1.634185735	0.9175 0.917	2.157 0.7879	0.428	1.792
NUP62	NM_016553	202153_s_at	Hs.46713	0.008
1.691149584	0.6575 0.657	2.949 0.8944	0.618	2.044
OAS1	NM_002534	205552_s_at	Hs.52476	0.000
5.333816211	0.7613 0.761	3.266 0.3298	0.168	1.932
OAS2	NM_016817	204972_at	Hs.58478	0.000
3.572108687	0.7703 0.770	1.946 0.3944	0.218	1.856
OAS2	NM_002535	206553_at	Hs.58478	0.005
1.733035353	0.8859 0.885	1.702 0.8187	0.303	1.797
OAS3	NM_006187	218400_at	Hs.52863	0.000
4.653283730	0.7944 0.794	2.541 0.3456	0.143	1.540
OASL	AF063612	210797_s_at	Hs.11863	0.000
3.301330019	0.7460 0.746	2.319 0.4414	0.268	1.312
OASL	NM_003733	205660_at	Hs.11863	0.000
2.853338726	0.6839 0.683	3.749 0.4701	0.323	1.604
OGDH	NM_002541	201282_at	Hs.48818	0.001
1.397596769	0.8710 0.871	1.854 0.7734	0.549	1.410
PS	NM_005742	207668_x_at	Hs.21210	0.003
1.383473485	0.7681 0.768	2.070 0.9336	0.508	1.531
PAFAH1	L13386	200815_s_at	Hs.77318	0.008
1.436244935	0.6820 0.682	1.745 0.8138	0.650	1.124
PAI-	BC003049	209669_s_at	Hs.53041	0.000
1.451343198	0.9398 0.939	1.721 0.8461	0.566	1.210
PALM2	NM_007203	202760_s_at	Hs.25946	0.000
1.968179014	0.6813 0.681	2.008 0.5837	0.170	1.284
PCOLN3	NM_002768	201933_at	Hs.56731	0.000
1.507803612	0.8769 0.876	1.789 0.8619	0.535	1.434
PCQAP	AK000003	222175_s_at	Hs.51742	0.006
1.350640366	0.7532 0.753	1.637 0.8478	0.564	1.338
PFKP	NM_002627	201037_at	Hs.26010	0.008

Supplementary Table 2						
1.510746632	0.8154	0.815	2.187	0.8882	0.443	1.229
PHF11	BF055474		221816_s_at	Hs.36903		0.008
1.449433058	0.9491	0.949	1.731	0.7533	0.460	1.325
PHF3	AW189430		217951_s_at	Hs.34892		0.005
1.647486792	0.7850	0.785	1.763	0.8689	0.647	1.667
PIAS1	NM_016166		217864_s_at	Hs.16245		0.000
1.865433179	0.9526	0.952	1.614	0.7022	0.394	1.199
PLEKHA	BF542055		217677_at	Hs.36912		0.006
1.737208842	0.5974	0.597	1.952	0.7794	0.442	1.466
PLSCR1	AI825926		202446_s_at	Hs.13075		0.001
2.133990131	0.6500	0.650	1.876	0.6854	0.286	1.653
PMS2L5	AA161026		213893_x_at	Hs.39707		0.000
1.517662922	0.9004	0.900	1.508	0.8024	0.525	1.181
PMS2L6	AB017004		214756_x_at	Hs.52057		0.001
1.289493891	0.9477	0.947	1.717	0.9768	0.741	1.388
PMSCL1	AI346350		213226_at	Hs.85137		0.000
1.787794314	0.8376	0.837	3.265	0.8203	0.365	1.243
POM121	AK022555		212178_s_at	Hs.48862		0.005
1.794240142	0.8868	0.886	2.033	0.8984	0.641	1.703
PPARBP	NM_004774		203497_at	Hs.46295		0.007
1.361111039	0.7695	0.769	1.429	0.8103	0.528	1.106
PPAT	AI457120		209433_s_at	Hs.33142		0.001
1.508415866	0.8253	0.825	1.859	0.7823	0.384	1.521
PPIG	NM_004792		208993_s_at	Hs.47054		0.000
1.461953880	0.9098	0.909	1.510	0.8006	0.586	1.326
PPP2R2	NM_002717		202313_at	Hs.14633		0.001
1.422760856	0.8184	0.818	1.485	0.8942	0.704	1.199
PPP2R5	NM_006243		202187_s_at	Hs.49768		0.008
1.235025973	0.8974	0.897	1.206	0.9109	0.691	1.346
PPP2R5	NM_006246		203338_at	Hs.33486		0.002
1.281501706	0.7004	0.700	1.348	0.9209	0.531	1.126
PRDX1	L19184		208680_at	Hs.18090		0.005
1.372537162	0.6434	0.643	1.398	0.8646	0.719	1.210
PRF1	AI445650		214617_at	Hs.2200		0.008
1.694721469	0.2488	0.248	4.337	0.9441	0.168	1.439
PRKR	NM_002759		204211_x_at	Hs.13143		0.000
2.389590299	0.8173	0.817	3.397	0.5536	0.265	1.033
PROSC	NM_007198		214545_s_at	Hs.30479		0.000
1.484747835	0.6521	0.652	1.834	0.8369	0.414	1.027
PRSS15	U02389		209017_s_at	Hs.35026		0.005
1.254617089	0.8453	0.845	1.310	0.9075	0.503	1.090
PSMA6	BC002979		208805_at	Hs.44626		0.000
1.334336473	0.9961	0.996	1.417	0.9028	0.764	1.114
PSMAGE	U82671		215093_at	Hs.57698		0.000
1.128851501	0.8910	0.891	1.272	0.9256	0.616	1.081

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PSMB9	NM_002800	204279_at	Hs.38108			0.000
1.810389984	0.8206	0.820	1.727	0.7349	0.406	1.211
PSMC2	NM_002803	201068_s_at	Hs.43736			0.000
1.227517417	0.9624	0.962	1.630	0.9262	0.664	1.395
PSMD11	AF001212	208777_s_at	Hs.44337			0.000
1.763067678	0.8828	0.882	1.646	0.8024	0.613	1.085
PSMD3	NM_002809	201388_at	Hs.12970			0.003
1.317177462	0.6913	0.691	1.528	0.8346	0.415	1.237
PSME2	NM_002818	201762_s_at	Hs.43408			0.001
1.496939804	0.8894	0.889	1.779	0.7205	0.356	1.361
PTX1	NM_016570	218135_at	Hs.33945			0.000
2.043363751	0.9352	0.935	2.191	0.7220	0.411	1.346
PURA	NM_005859	204021_s_at	Hs.44312			0.000
2.268108441	0.8810	0.881	1.870	0.6350	0.321	1.250
PWP1	BE796924	201606_s_at	Hs.50665			0.002
1.288841454	0.9002	0.900	1.474	0.8653	0.471	1.335
RAB14	AF112206	211503_s_at	Hs.37156			0.006
1.460030521	0.8628	0.862	1.337	0.7811	0.504	1.319
RAB7L1	BC002585	218700_s_at	Hs.11532			0.008
1.261632611	0.4985	0.498	1.854	0.9085	0.370	1.230
RBBP2	NM_005056	202040_s_at	Hs.76272			0.008
1.299252967	0.7226	0.722	1.463	0.8841	0.682	1.191
RBX1	NM_014248	218117_at	Hs.47494			0.005
1.292116185	0.9201	0.920	1.722	0.8684	0.719	1.330
REC8L1	NM_005132	218599_at	Hs.41925			0.005
1.293441072	0.7053	0.705	3.065	0.8689	0.561	1.114
RGS3	NM_021106	203823_at	Hs.49487			0.006
1.304503006	0.7166	0.716	2.149	0.9590	0.370	1.281
RNF5	BC004155	209111_at	Hs.53434			0.006
1.344955257	0.7451	0.745	1.506	0.8136	0.518	1.283
RNF8	AK022075	203160_s_at	Hs.48527			0.005
1.516135550	0.8494	0.849	1.855	0.9366	0.594	1.227
RNPC7	BE466128	212027_at	Hs.53110			0.005
1.762588462	0.8469	0.846	1.843	0.6734	0.348	1.375
RPS6KB	NM_003952	203777_s_at	Hs.53434			0.002
1.175378956	0.8792	0.879	1.252	0.9101	0.617	1.137
RRAGC	NM_022157	218088_s_at	Hs.53246			0.000
1.349911957	0.8974	0.897	1.266	0.8120	0.662	1.124
RRBP1	NM_004587	201206_s_at	Hs.47221			0.005
1.871135464	0.6553	0.655	2.270	0.7133	0.307	1.630
SART3	NM_014706	209127_s_at	Hs.58484			0.005
1.509099288	0.7606	0.760	2.201	0.7792	0.450	1.565
SCAMP1	BF058944	212417_at	Hs.48258			0.001
1.842081244	0.4085	0.408	2.084	0.6277	0.081	1.320
SDF2L1	NM_022044	218681_s_at	Hs.30311			0.006
1.436086194	0.7416	0.741	2.400	0.8408	0.543	1.392

Supplementary_Table_2

SERPING1	NM_000062	200986_at	Hs.38459	0.000
2.621299255	0.8265 0.826	5.027 0.5167	0.186 3.884	
SFRS2IP	AI984932	213850_s_at	Hs.21036	0.000
1.694163351	0.8117 0.811	1.497 0.7339	0.498 1.163	
SFRS4	NM_005626	201696_at	Hs.46997	0.003
1.207470488	0.8007 0.800	1.548 0.9573	0.590 1.158	
SHFM1	NM_006304	202276_at	Hs.48920	0.005
1.350886104	0.6315 0.631	2.612 0.8810	0.595 1.260	
SIGLEC7	AJ130713	216537_s_at	Hs.27447	0.001
1.362662764	0.7825 0.782	1.393 0.8497	0.525 1.341	
SLC20A1	NM_005415	201920_at	Hs.18794	0.001
1.300698106	0.7084 0.708	1.632 0.8446	0.630 1.390	
SLC25A1	AF070548	209003_at	Hs.18487	0.003
1.501456960	0.8779 0.877	1.250 0.7592	0.678 1.360	
SLC25A1	NM_003562	207088_s_at	Hs.18487	0.000
1.319290074	0.8396 0.839	1.457 0.8371	0.595 1.330	
SLC26A2	AI025519	205097_at	Hs.30273	0.005
1.290183453	0.8908 0.890	2.171 0.8822	0.571 1.578	
SMARCA4	AI684141	212520_s_at	Hs.32752	0.001
1.330106328	0.9376 0.937	1.562 0.8707	0.470 1.531	
SMARCD1	AI869240	209518_at	Hs.79335	0.001
1.334732551	0.9189 0.918	1.366 0.8805	0.416 1.601	
SMG1	U32581	210057_at	Hs.46017	0.000
2.003686611	0.8163 0.816	2.005 0.7662	0.360 1.782	
SN	NM_023068	219519_s_at	Hs.31869	0.000
84.59401594	0.3382 0.338	5.209 0.0306	0.012 2.542	
SN	N53555	44673_at	Hs.31869	0.000
8.022413457	0.5767 0.576	4.232 0.2502	0.150 1.876	
SNRPB	J04564	208821_at	Hs.83753	0.003
1.160778005	0.9234 0.923	1.289 0.9373	0.669 1.386	
SNTB2	NM_006750	205315_s_at	Hs.46111	0.000
1.445333240	0.7467 0.746	1.794 0.7832	0.586 1.266	
SNW1	AV689564	215424_s_at	Hs.44549	0.006
1.138086599	0.8846 0.884	1.234 0.9190	0.703 1.035	
SON	AA664291	201085_s_at	Hs.51726	0.000
2.429084686	0.8227 0.822	1.533 0.4700	0.288 1.609	
SP100	NM_003113	202864_s_at	Hs.36905	0.001
1.346797495	0.8094 0.809	2.045 0.8055	0.445 1.232	
SP110	NM_004509	208012_x_at	Hs.14515	0.001
1.479754341	0.9105 0.910	2.544 0.7603	0.464 1.397	
SP110	AF280094	209761_s_at	Hs.14515	0.005
1.416799744	0.8254 0.825	2.714 0.8642	0.472 1.129	
SP110	AF280094	209762_x_at	Hs.14515	0.000
1.388298324	0.9713 0.971	1.786 0.8464	0.599 1.276	
SP110	NM_004510	208392_x_at	Hs.14515	0.003

Supplementary_Table_2						
1.348087972	0.7028	0.702	1.844	0.9218	0.492	1.294
SOLE	AF098865	209218_at	Hs.71465			0.000
1.292607193	0.8795	0.879	2.842	0.8404	0.623	1.072
SRRM2	AI655799	208610_s_at	Hs.43334			0.000
2.051059247	0.8408	0.840	1.742	0.5829	0.508	1.507
SSA2	M25077	210438_x_at	Hs.28817			0.006
1.545348232	0.8780	0.878	1.407	0.7822	0.455	1.376
SSA2	AK024044	212852_s_at	Hs.28817			0.008
1.147671384	0.9116	0.911	1.239	0.8857	0.673	1.242
SSB	BG532929	201138_s_at	Hs.54630			0.000
1.331452490	0.8675	0.867	1.381	0.8519	0.483	1.123
STAT1	BC002704	209969_s_at	Hs.47094			0.006
2.620952510	0.7237	0.723	2.595	0.4762	0.121	1.991
STAT1;	M97935	AFFX-	---			0.005
2.174824730	0.5569	0.556	2.070	0.5022	0.226	1.358
ISGF-3;		HUMISGF3				
STAT91		A/M97935_				
STK4	Z25430	211085_s_at	Hs.47283			0.005
1.559945194	0.6976	0.697	1.472	0.6852	0.308	1.982
SYK	NM_003177	207540_s_at	Hs.37172			0.006
1.404408870	0.6022	0.602	1.840	0.8446	0.387	1.185
SYNCRIP	AI472757	209024_s_at	Hs.48587			0.003
1.893783050	0.8716	0.871	1.567	0.6294	0.355	1.391
TAP1	NM_000593	202307_s_at	Hs.35201			0.000
2.242344426	0.7643	0.764	2.645	0.5397	0.304	1.725
TBDN100	NM_025085	219158_s_at	Hs.55598			0.000
2.219147634	0.9140	0.914	1.573	0.5821	0.400	1.413
TBK1	NM_013254	218520_at	Hs.50587			0.000
1.330688147	0.8930	0.893	1.399	0.8309	0.357	1.132
TCF4	AK021980	212382_at	Hs.20028			0.001
2.063659549	0.8009	0.800	1.890	0.6741	0.458	1.487
TCF4	NM_003199	203753_at	Hs.20028			0.000
1.321085083	0.8560	0.856	1.751	0.8741	0.466	1.283
TCF7L2	AI703074	212762_s_at	Hs.50108			0.008
1.439467183	0.9078	0.907	3.521	0.8119	0.404	1.945
TCN2	NM_000355	204043_at	Hs.41794			0.000
2.023444194	0.7469	0.746	2.497	0.7258	0.382	1.329
TDG	BF674842	203742_s_at	Hs.58480			0.006
1.331002772	0.8974	0.897	1.641	0.8247	0.570	1.467
TFEB	AL035588	221866_at	Hs.48536			0.000
1.446756893	0.9789	0.978	1.802	0.8155	0.556	1.174
TFEB	AI524138	50221_at	Hs.48536			0.005
1.446272685	0.6669	0.666	1.498	0.8702	0.582	1.297
THOC2	BG403671	222122_s_at	Hs.14999			0.002
1.325711538	0.8276	0.827	1.580	0.9057	0.325	1.136
TJMM17B	NM_005834	203342_at	Hs.30570			0.000

Supplementary_Table_2						
1.476233246	0.9418	0.941	1.884	0.8944	0.496	1.163
TLN1	NM_006289		203254_s_at	Hs.37500		0.001
1.990988347	0.7301	0.730	1.788	0.6009	0.232	1.300
TNFSF10	AW474434		214329_x_at	Hs.47827		0.006
2.729134990	0.5197	0.519	2.838	0.4858	0.192	3.114
TNFSF10	U57059		202687_s_at	Hs.47827		0.008
2.128234411	0.6453	0.645	2.822	0.6509	0.339	2.821
TOMM34	NM_006809		201870_at	Hs.51706		0.001
1.172584650	0.9081	0.908	1.450	0.9341	0.795	1.192
TOP1	J03250		208901_s_at	Hs.47273		0.001
1.299188550	0.8617	0.861	1.663	0.9189	0.660	1.102
TPR	BF110993		201730_s_at	Hs.27964		0.008
1.567682001	0.9718	0.971	1.971	0.7510	0.367	1.363
TRAM2	AI986461		202368_s_at	Hs.52018		0.000
1.482885955	0.9161	0.916	1.618	0.8354	0.486	1.153
TREX1	NM_016381		205875_s_at	Hs.34481		0.000
1.733512986	0.8289	0.828	4.086	0.7896	0.491	1.550
TRIF	AF070530		213191_at	Hs.29344		0.008
1.395998778	0.7192	0.719	1.652	0.8684	0.550	1.309
TRIM14	BE962483		203147_s_at	Hs.55590		0.000
2.070929536	1	1	2.555	0.7011	0.385	1.622
TRIM14	AF220130		210846_x_at	Hs.55590		0.000
1.419646773	0.9652	0.965	1.832	0.8875	0.471	1.243
TRIM22	AA083478		213293_s_at	Hs.50177		0.003
1.547014594	0.9224	0.922	1.636	0.8361	0.416	1.680
TRIM26	NM_003449		202702_at	Hs.48504		0.001
1.276293214	0.8406	0.840	1.536	0.9041	0.689	1.061
TRIM38	NM_006355		203610_s_at	Hs.58485		0.003
1.544125548	0.7052	0.705	2.142	0.8090	0.625	1.152
TTC3	D84294		208663_s_at	Hs.36821		0.002
1.808545705	0.8674	0.867	2.236	0.6574	0.352	1.640
TUBG1	NM_001070		201714_at	Hs.27966		0.008
1.768885451	0.8008	0.800	2.683	0.8937	0.5	1.419
U2AF2	NM_007279		218381_s_at	Hs.52800		0.005
1.207442871	0.9099	0.909	1.537	0.9425	0.499	1.085
UBE2L6	NM_004223		201649_at	Hs.42577		0.000
1.535743795	0.9124	0.912	1.882	0.7374	0.337	1.581
UBXD2	D87684		212007_at	Hs.35080		0.000
1.826678836	0.6468	0.646	1.634	0.6174	0.444	1.116
USP1	AW499935		202412_s_at	Hs.35086		0.000
1.700265265	0.9725	0.972	1.987	0.6515	0.493	1.061
USP10	BC000263		209137_s_at	Hs.13677		0.001
1.410353191	0.9468	0.946	1.751	0.7362	0.454	1.295
USP11	BC000350		208723_at	Hs.17150		0.008
1.266221506	0.7135	0.713	1.374	0.8636	0.494	1.114

Supplementary_Table_2						
USP18	NM_017414	219211_at	Hs.38260			0.000
6.059939868	0.9410 0.941	3.813 0.2299	0.056	1.532		
WAS	NM_000377	205400_at	Hs.2157			0.005
2.132735918	0.4523 0.452	2.041 0.6669	0.356	1.627		
WSB1	AL110243	210561_s_at	Hs.44601			0.002
1.531482824	0.8556 0.855	1.796 0.7574	0.634	1.310		
XTP2	AW238632	214052_x_at	Hs.49461			0.003
1.301684624	0.5919 0.591	1.640 0.8718	0.412	1.441		
YWHAE	U43430	210996_s_at	Hs.51385			0.003
1.368030641	0.8011 0.801	1.470 0.7969	0.385	1.147		
YY1	NM_003403	201901_s_at	Hs.38892			0.001
1.545302492	0.9306 0.930	1.407 0.7695	0.497	1.405		
ZBP1	NM_030776	208087_s_at	Hs.30212			0.000
3.066386888	1 1	2.406 0.5520	0.063	1.175		
ZNF161	NM_007146	202173_s_at	Hs.46356			0.008
1.507853335	0.7859 0.785	1.524 0.8056	0.506	1.654		
ZNF264	NM_003417	205917_at	Hs.51563			0.000
1.400548398	0.9548 0.954	2.333 0.9210	0.659	1.364		
39.34233190	M10098	AFFX- HUMRGE/M 10098_5_at	11.44 0.1525 ---	0.018	10.66	0.001
30.14490715	M10098	AFFX-r2- Hs18SrRNA-	9.703 0.1454 ---	0.032	6.805	0.005
20.70241296	M10098	AFFX- HUMRGE/M 10098_3_at	6.115 0.1658 ---	0.075	13.70	0.003
17.18716286	M10098	AFFX-r2- Hs18SrRNA- 3_s_at	9.365 0.2453 ---	0.046	16.83	0.005
9.119613327	M10098	AFFX- HUMRGE/M 10098_M_at	6.619 0.2537 ---	0.023	6.429	0.008
2.321329537	AU145711	215617_at	---	0.219	1.078	0.000
1.981982119	W86781	222366_at	Hs.29373			0.008
	0.5826 0.582	2.755 0.6095	0.317	1.647		
1.515042613	AL121994	216565_x_at	Hs.58518			0.002
	0.7722 0.772	2.096 0.7803	0.494	1.459		
1.193248542	AK026926	216640_s_at	Hs.21210			0.008
	0.7803 0.780	1.805 0.8579	0.702	1.097		
C20orf11	NM_017896	218448_at	Hs.35301			0.001
0.944787795	0.6793 0.679	1.008 1.0181	0.891	1.192		
GMFG	NM_004877	204220_at	Hs.5210			0.003
0.933422785	0.8643 0.864	1.066 1.0569	0.941	1.516		

Supplementary_Table_2

DOCK2	D86964	213160_at	Hs.32552	0.003
0.925637339	0.7683 0.768	1.048 1.0271	0.962 1.222	
0.918757760	AL023553	212528_at	Hs.57045	0.007
	0.9065 0.906	1.081 1.0750	0.950 1.419	
HSPC023	NM_014047	217926_at	Hs.23161	0.006
0.905868464	0.6018 0.601	1.122 1.0260	0.817 1.417	
DJ473B4	NM_019556	218853_s_at	Hs.37850	0.005
0.894420862	0.7635 0.763	1.065 1.0610	0.863 1.395	
IDE	NM_004969	203328_x_at	Hs.50054	0.003
0.886430683	0.7800 0.780	1.117 1.0882	0.897 1.455	
DSTN	NM_006870	201022_s_at	Hs.30419	0.008
0.884791830	0.6930 0.693	1.031 1.0845	0.892 1.204	
PLSCR3	AI783924	56197_at	Hs.43315	0.002
0.883795488	0.7935 0.793	1.204 1.0565	0.957 1.271	
CTNNA1	AI826881	200764_s_at	Hs.44598	0.005
0.883551822	0.5423 0.542	1.246 1.0335	0.886 1.500	
EEF1A1	BE964125	213583_x_at	Hs.53147	0.006
0.879485408	0.7877 0.787	1.264 1.0557	0.855 1.311	
0.878842252	N80935	49111_at	Hs.56892	0.005
	0.5888 0.588	1.417 1.0454	0.884 1.590	
ANXA7	J04543	209860_s_at	Hs.38643	0.005
0.877347039	0.7239 0.723	1.168 1.0426	0.959 1.383	
DDX3X	R60068	212514_x_at	Hs.38077	0.006
0.872129513	0.2650 0.265	1.101 1.0489	0.863 1.623	
ASL	NM_000048	204608_at	Hs.44204	0.008
0.864586154	0.6428 0.642	1.069 1.0371	0.813 1.425	
NPL4	NM_017921	217796_s_at	Hs.46433	0.001
0.863446770	0.8275 0.827	1.061 1.0876	0.886 1.296	
PSMA1	M64992	210759_s_at	Hs.10279	0.008
0.863294437	0.7644 0.764	1.277 1.0995	0.683 1.393	
GDI2	D13988	200008_s_at	Hs.29905	0.008
0.862453985	0.5827 0.582	1.138 1.0939	0.851 1.490	
GHITM	AF131820	209249_s_at	Hs.35265	0.006
0.862287759	0.8332 0.833	1.156 1.0766	0.939 1.379	
PMPCA	BF570122	212088_at	Hs.49547	0.006
0.861693109	0.6680 0.668	1.208 1.0882	0.754 1.323	
MUC3B	AF007194	217117_x_at	Hs.55476	0.003
0.860967026	0.6575 0.657	1.038 1.1076	0.830 1.535	
SYBL1	NM_005638	202829_s_at	Hs.24167	0.003
0.860948289	0.7146 0.714	1.384 1.0831	0.848 1.551	
BCAS3	NM_017679	220488_s_at	Hs.46370	0.008
0.859535433	0.6361 0.636	1.062 1.0770	0.894 1.574	
SFR55	AW084582	212266_s_at	Hs.16697	0.008
0.853682127	0.6572 0.657	1.061 1.0760	0.794 1.379	
SRP72	NM_006947	208801_at	Hs.23782	0.003

Supplementary_Table_2						
0.852728262	0.7378	0.737	1.019	1.1265	0.890	1.275
PTEN	U96180		204053_x_at	Hs.50046		0.006
0.851130892	0.5670	0.567	1.097	1.0321	0.718	1.458
ZXDA	BF509566		215263_at	Hs.55009		0.008
0.849564181	0.5974	0.597	1.243	1.1135	0.589	1.364
DIS155E	AA167775		202646_s_at	Hs.69855		0.001
0.848736962	0.7277	0.727	1.201	1.1013	0.894	1.373
PHKB	BG149218		202738_s_at	Hs.78060		0.002
0.848448690	0.7466	0.746	1.152	1.1111	0.900	1.429
p47	AL109658		217830_s_at	Hs.12865		0.002
0.845326046	0.6913	0.691	1.057	1.0377	0.886	1.309
RPS10	NM_001014		200817_x_at	Hs.53910		0.005
0.844613970	0.6977	0.697	1.384	1.0767	0.821	1.279
DDX5	NM_004396		200033_at	Hs.27980		0.001
0.842253194	0.7677	0.767	1.096	1.0744	0.780	1.344
DKFZP43	AL117499		212131_at	Hs.40736		0.008
0.841809090	0.7219	0.721	1.048	1.1384	0.629	1.461
4D1335						
RPL22	NM_000983		220960_x_at	Hs.51532		0.005
0.841743733	0.7746	0.774	1.106	1.0536	0.804	1.281
SLC25A5	NM_001152		200657_at	Hs.52276		0.003
0.841432324	0.7026	0.702	1.335	1.0845	0.904	1.364
COL11A2	U32169		216993_s_at	Hs.39017		0.000
0.838520228	0.7294	0.729	1.038	1.0829	0.882	1.557
AKR7A2	NM_003689		202139_at	Hs.51280		0.008
0.838172877	0.7789	0.778	1.122	1.0849	0.828	1.576
NAP1L1	AI985751		213864_s_at	Hs.52459		0.005
0.836727532	0.7268	0.726	1.030	1.0759	0.646	1.405
CS	BC000105		208660_at	Hs.43060		0.001
0.834069132	0.6390	0.639	1.006	1.0628	0.755	1.373
NAP1L1	AI888672		208752_x_at	Hs.52459		0.000
0.833846225	0.7675	0.767	1.233	1.0655	0.881	1.282
COX7A2L	NM_004718		201256_at	Hs.33963		0.000
0.833195118	0.8145	0.814	1.254	1.1217	0.944	1.439
VEGFB	NM_003377		203683_s_at	Hs.78781		0.000
0.832975640	0.7387	0.738	1.183	1.1361	0.914	1.720
HNRPA1	AL568186		213356_x_at	Hs.55609		0.005
0.832124538	0.7976	0.797	1.160	1.0750	0.892	1.483
RPL32	NM_000994		200674_s_at	Hs.26517		0.008
0.831209019	0.7210	0.721	1.300	1.0305	0.809	1.532
DAZAP2	NM_014764		200794_x_at	Hs.36976		0.006
0.830710342	0.7243	0.724	1.171	1.0569	0.924	1.627
	AF119846		210501_x_at	Hs.31435		0.001
0.830400082	0.7839	0.783	1.152	1.0482	0.858	1.266
RPS25	AA888388		200091_s_at	Hs.51267		0.003
0.829661196	0.6743	0.674	1.283	1.0766	0.771	1.564

Supplementary_Table_2

RPL28	NM_000991	200003_s_at	Hs.35637	0.006			
0.828253715	0.8117	0.811	1.364	1.1174	0.989	1.261	
RPLP0	NM_001002	201033_x_at	Hs.54628	0.003			
0.827566190	0.7415	0.741	1.397	1.0933	0.990	1.401	
RPS20	BF184532	214003_x_at	Hs.8102	0.000			
0.822806436	0.7941	0.794	1.222	1.1003	0.976	1.290	
RPLP1	NM_001003	200763_s_at	Hs.35650	0.006			
0.821368059	0.7631	0.763	1.296	1.0479	0.892	1.377	
SYT1	NM_005639	203999_at	---	0.001			
0.821221381	0.4853	0.485	1.212	1.1288	0.852	1.863	
	Z82202	217347_at	---	0.002			
0.819304971	0.7239	0.723	1.309	1.1043	0.877	1.623	
PABPC1	AI734929	215157_x_at	Hs.38780	0.000			
0.818327633	0.8084	0.808	1.040	1.1184	0.896	1.409	
RPLP0	BC003655	208856_x_at	Hs.54628	0.003			
0.818206200	0.7314	0.731	1.377	1.0436	0.909	1.385	
SMARCA2	AV725365	206542_s_at	Hs.29899	0.001			
0.818093907	0.6530	0.653	1.187	1.1428	0.457	1.918	
DKFZP56	AK025446	212018_s_at	Hs.40184	0.000			
0.817524423	0.5336	0.533	1.000	1.0325	0.692	1.535	
4M182							
SUI1	BF246436	211956_s_at	Hs.15058	0.001			
0.817484430	0.6370	0.637	1.046	1.1037	0.901	1.555	
RPL12	AA281332	214271_x_at	Hs.40805	0.008			
0.816597856	0.7435	0.743	1.195	1.1415	0.901	1.295	
NONO	NM_007363	200057_s_at	Hs.53328	0.000			
0.816397335	0.7667	0.766	1.090	1.0753	0.878	1.327	
RPL8	NM_000973	200936_at	Hs.17855	0.005			
0.815996416	0.7502	0.750	1.039	1.1308	0.621	1.442	
ZYG	NM_006336	202448_s_at	Hs.14795	0.003			
0.815864023	0.5283	0.528	1.029	1.1648	0.757	1.742	
PSCDBP	L06633	209606_at	Hs.270	0.006			
0.815676814	0.7534	0.753	1.081	1.1254	0.511	2.093	
EEF2	NM_001961	204102_s_at	Hs.51507	0.008			
0.815519895	0.7319	0.731	1.037	1.1172	0.673	1.653	
RPS19	BE259729	213414_s_at	Hs.43842	0.008			
0.814925221	0.7394	0.739	1.225	1.0437	0.782	1.234	
RAB2	NM_002865	208732_at	Hs.36901	0.001			
0.812873930	0.4620	0.462	1.089	1.0494	0.776	1.450	
HMGN3	AF274949	209377_s_at	Hs.77558	0.006			
0.811562465	0.5088	0.508	1.087	1.0862	0.839	1.354	
MGC3035	AL040896	221983_at	Hs.51670	0.001			
0.811300805	0.6245	0.624	1.215	1.0756	0.821	1.787	
RPS6	BE741754	200081_s_at	Hs.40807	0.000			
0.811269552	0.7315	0.731	1.007	1.1269	0.801	1.362	

Supplementary_Table_2						
MAP3K4	NM_006724	204089_x_at	Hs.39042			0.007
0.810196039	0.5675	0.567	1.167	1.0928	0.826	1.508
eIF3k	AW083133	212716_s_at	Hs.31435			0.001
0.808503314	0.7416	0.741	1.129	1.1249	0.856	1.287
DAP3	U18321	208822_s_at	Hs.51674			0.003
0.807675707	0.5055	0.505	1.067	1.0684	0.705	1.640
HLA-DRA	M60333	210982_s_at	Hs.52004			0.006
0.807632850	0.7203	0.720	1.090	1.1368	0.522	1.429
RPS6	BC000524	209134_s_at	Hs.40807			0.003
0.807000092	0.7867	0.786	1.206	1.0979	0.894	1.436
E46L	AW241832	208832_at	Hs.47512			0.006
0.806742229	0.7774	0.777	1.183	1.1361	0.869	1.328
SLC25A3	NM_002635	200030_s_at	Hs.29040			0.003
0.806648592	0.8170	0.817	1.299	1.1848	0.921	1.554
RPS4X	NM_001007	200933_x_at	Hs.44662			0.000
0.805962506	0.7233	0.723	1.171	1.0388	0.825	1.217
RPS27	NM_001030	200741_s_at	Hs.54629			0.008
0.804914637	0.7663	0.766	1.232	1.0576	0.915	1.205
RPL27	NM_000988	200025_s_at	Hs.51419			0.000
0.804774181	0.6773	0.677	1.133	1.0730	0.894	1.358
RRAGB	NM_016656	205540_s_at	Hs.50282			0.006
0.804380662	0.5772	0.577	1.446	1.1493	0.892	1.619
RPL17	NM_000985	200038_s_at	Hs.48509			0.000
0.803920499	0.7931	0.793	1.022	1.0919	0.866	1.321
XRCC5	J04977	208643_s_at	Hs.38873			0.002
0.803909387	0.7479	0.747	1.319	1.0572	0.870	1.315
OSBPL8	AB040884	212585_at	Hs.43084			0.008
0.803285409	0.6402	0.640	1.129	1.1660	0.872	1.439
DKFZP43	NM_015610	202031_s_at	Hs.12236			0.001
0.802971323	0.7056	0.705	1.436	1.1073	0.899	1.214
41154						
NACA	BF976260	208635_x_at	Hs.50573			0.000
0.802529913	0.8172	0.817	1.005	1.1712	0.901	1.294
KPNA1	NM_002264	202059_s_at	Hs.57066			0.008
0.802049503	0.6039	0.603	1.372	1.1480	0.736	1.580
RPL7	NM_000971	200717_x_at	Hs.42125			0.000
0.802039223	0.7550	0.755	1.240	1.1008	0.904	1.389
RPS7	AI805587	200082_s_at	Hs.54628			0.003
0.801287721	0.8691	0.869	1.137	1.1725	0.896	1.347
RPS11	NM_001015	200031_s_at	Hs.43352			0.003
0.801202272	0.7275	0.727	1.116	1.0152	0.818	1.158
RPS19	NM_001022	202649_x_at	Hs.43842			0.005
0.801200636	0.7490	0.749	1.239	1.1650	0.918	1.372
Clorf6	AK023354	222252_x_at	Hs.28373			0.001
0.800977274	0.6073	0.607	1.021	1.1030	0.761	1.505
CDKN1B	BC001971	209112_at	Hs.23899			0.003

Supplementary Table 2						
0.800246472	0.4742	0.474	1.100	1.1529	0.680	1.558
CTSK	NM_000396	202450_s_at	Hs.52359			0.000
0.799659690	0.7626	0.762	1.060	1.1305	0.856	1.779
RPS27A	NM_002954	200017_at	Hs.54629			0.000
0.798920488	0.7645	0.764	1.042	1.1164	0.943	1.518
SLC25A6	AI961224	212826_s_at	Hs.35092			0.001
0.798342904	0.6507	0.650	1.056	1.1165	0.856	1.684
NEDF	NM_016079	217837_s_at	Hs.25501			0.000
0.797144536	0.6298	0.629	1.042	1.0894	0.816	1.379
CRF	NM_006688	205575_at	Hs.13401			0.008
0.797058866	0.6636	0.663	1.156	1.1571	0.733	1.601
RPL27A	NM_000990	203034_s_at	Hs.56797			0.005
0.796990710	0.7714	0.771	1.217	1.0444	0.904	1.260
15-Sep	NM_004261	200902_at	Hs.36272			0.006
0.796729525	0.7174	0.717	1.358	1.1388	0.763	1.779
FLJ10726	NM_018195	218314_s_at	Hs.19506			0.008
0.796000451	0.6465	0.646	1.064	1.1253	0.769	1.414
LOC5175	NM_016520	218116_at	Hs.27842			0.008
0.794597967	0.6688	0.668	1.212	1.1088	0.909	1.760
NAP1L1	AW148801	212967_x_at	Hs.52459			0.008
0.794346367	0.7468	0.746	1.244	1.1263	0.803	1.308
KIF2	BE872563	203086_at	Hs.55835			0.000
0.794182299	0.4253	0.425	1.090	1.1307	0.862	1.704
MTCPL	BC002600	210212_x_at	Hs.6917			0.000
0.793787129	0.7450	0.745	1.039	1.0804	0.890	1.426
SET	NM_003011	200631_s_at	Hs.43668			0.008
0.793441093	0.8321	0.832	1.205	1.1768	0.816	1.467
LENG7	BE786672	213614_x_at	Hs.43955			0.000
0.793344354	0.8001	0.800	1.230	1.0908	0.886	1.310
LOC5597	NM_018845	219125_s_at	Hs.29215			0.000
0.793050187	0.5677	0.567	1.327	1.1150	0.912	1.278
PSARL	NM_018622	218271_s_at	Hs.47846			0.002
0.792935623	0.8121	0.812	1.184	1.1922	0.835	1.481
EIF3S6	BC000734	208697_s_at	Hs.40559			0.000
0.790405851	0.7624	0.762	1.072	1.1532	0.780	1.309
FUT2	BC001899	210608_s_at	Hs.44316			0.001
0.790047379	0.5609	0.560	1.096	1.0516	0.869	1.456
RPS23	NM_001025	200926_at	Hs.56733			0.008
0.789713873	0.7769	0.776	1.317	1.1233	0.969	1.258
MTX1	AI693193	213448_at	Hs.51198			0.003
0.789256263	0.4082	0.408	1.111	1.1656	0.864	1.530
TINP1	NM_014886	201922_at	Hs.48252			0.006
0.788903214	0.7797	0.779	1.295	1.0845	0.837	1.413
RPS15A	NM_001019	200781_s_at	Hs.37050			0.005
0.788187216	0.7430	0.743	1.212	1.0563	0.888	1.285

Supplementary_Table_2						
PTDSS1	NM_014754		201433_s_at	Hs.29257		0.006
0.787956798	0.6628	0.662	1.082	1.1389	0.679	1.522
DKFZP58	N67741		213861_s_at	Hs.52835		0.008
0.787745039	0.5754	0.575	1.250	1.1441	0.745	1.662
6D0919						
EEF2	AI004246		200094_s_at	Hs.51507		0.005
0.787638699	0.6287	0.628	1.033	1.1302	0.653	1.657
RPL3	BG339228		212039_x_at	Hs.11959		0.003
0.787383181	0.7207	0.720	1.139	1.0678	0.750	1.265
RPL22	D17652		208768_x_at	Hs.51532		0.000
0.787022857	0.6688	0.668	1.166	1.1042	0.833	1.256
CASP2	BC002427		209811_at	Hs.36898		0.008
0.786581306	0.4477	0.447	1.137	1.1552	0.657	1.426
RPL12	NM_000976		200809_x_at	Hs.40805		0.001
0.786224378	0.7501	0.750	1.327	1.1876	0.925	1.393
ACTG1	BC001920		221607_x_at	Hs.51458		0.002
0.786008409	0.7080	0.708	1.167	1.1235	0.922	1.541
C21orf97	NM_021941		218019_s_at	Hs.28449		0.000
0.785454553	0.6600	0.660	1.123	1.1113	0.890	1.573
ARFRP1	AL121845		215984_s_at	Hs.38927		0.005
0.784782227	0.2542	0.254	1.501	1.1032	0.883	1.630
RPL34	NM_000995		200026_at	Hs.51219		0.008
0.783968047	0.6821	0.682	1.204	1.0625	0.849	1.291
CD44	AF098641		210916_s_at	Hs.50232		0.003
0.782278069	0.6638	0.663	1.272	1.1383	0.747	2.188
RPS9	NM_001013		217747_s_at	Hs.54628		0.000
0.782107781	0.7573	0.757	1.054	1.2115	0.963	1.358
RPL3	NM_000967		201217_x_at	Hs.11959		0.000
0.781589834	0.7050	0.705	1.174	1.0801	0.938	1.233
NDUFA10	NM_004544		217860_at	Hs.27767		0.000
0.780526419	0.6517	0.651	1.074	1.0972	0.666	1.315
COX4I1	AA854966		200086_s_at	Hs.43341		0.000
0.780465268	0.6651	0.665	1.031	1.1584	0.891	1.351
RPL11	NM_000975		200010_at	Hs.38866		0.002
0.780458082	0.7102	0.710	1.156	1.1120	0.827	1.492
PTD015	BC002752		221600_s_at	Hs.50335		0.005
0.779026248	0.7341	0.734	1.057	1.2328	0.761	1.685
RTN3	NM_006054		219549_s_at	Hs.47376		0.008
0.778784021	0.5817	0.581	1.248	1.1660	0.925	2.764
	AL356115		216823_at	Hs.35657		0.005
0.778645858	0.6191	0.619	1.409	1.1939	0.783	1.716
RFPL3	NM_006604		207936_x_at	Hs.55845		0.000
0.778094132	0.7190	0.719	1.234	1.2101	0.946	1.762
SPINT2	AF027205		210715_s_at	Hs.31439		0.003
0.777714331	0.5847	0.584	1.185	1.1582	0.897	1.560
ATP5E	NM_006886		217801_at	Hs.17753		0.003

Supplementary_Table_2						
0.777676697	0.6538	0.653	1.098	1.0586	0.824	1.217
RPS14	AF116710		208645_s_at	Hs.38112		0.008
0.777661245	0.7676	0.767	1.191	1.1934	0.879	1.790
ZNF154	U20648		216677_at	Hs.43971		0.000
0.776901016	0.4379	0.437	1.156	1.1081	0.907	1.894
EIF2C4	NM_017629		219190_s_at	Hs.47149		0.006
0.776232575	0.6862	0.686	1.618	1.1800	0.850	2.024
RPS3A	AI925635		212391_x_at	Hs.35657		0.000
0.776154356	0.7597	0.759	1.048	1.0774	0.929	1.309
RPS13	NM_001017		200018_at	Hs.44658		0.000
0.775523396	0.7936	0.793	1.141	1.1300	0.903	1.310
LRRN4	AI654857		90610_at	Hs.12574		0.002
0.775340553	0.7124	0.712	1.171	1.1370	0.855	1.453
RPS20	NM_001023		200949_x_at	Hs.8102		0.000
0.775000097	0.7370	0.737	1.067	1.1240	0.971	1.332
PABPCP	U64661		215823_x_at	Hs.38780		0.000
0.774092034	0.7581	0.758	1.034	1.2003	0.912	1.465
3; PABP3						
RPS10	BC004334		211542_x_at	Hs.53910		0.008
0.773689736	0.7144	0.714	1.235	1.0800	0.803	1.268
RPL24	AI560573		214143_x_at	Hs.48387		0.002
0.773327710	0.6064	0.606	1.377	1.0896	0.806	1.493
RPL9	NM_000661		200032_s_at	Hs.51308		0.000
0.772510790	0.7343	0.734	1.132	1.1112	0.947	1.390
APEX1	M80261		210027_s_at	Hs.73722		0.000
0.772121730	0.7824	0.782	1.041	1.1697	0.866	1.561
CCNG1	BC000196		208796_s_at	Hs.79101		0.000
0.772080934	0.7008	0.700	1.133	1.1551	0.902	1.471
RPL7A	NM_000972		217740_x_at	Hs.49983		0.003
0.771267883	0.7231	0.723	1.182	1.0979	0.792	1.501
SLC12A6	NM_005135		220740_s_at	Hs.51093		0.001
0.771244126	0.6364	0.636	1.281	1.0907	0.763	1.687
RPL7	BG389744		212042_x_at	Hs.42125		0.000
0.771107826	0.6660	0.666	1.159	1.0481	0.760	1.312
	AL050348		216559_x_at	Hs.55609		0.000
0.770011797	0.6872	0.687	1.110	1.1429	0.896	1.769
COX4I1	NM_001861		202698_x_at	Hs.43341		0.000
0.769995202	0.7321	0.732	1.002	1.1620	0.785	1.497
SSR1	AI016620		200890_s_at	Hs.11403		0.008
0.769937767	0.5209	0.520	1.351	1.1085	0.908	1.788
RPS6	NM_001010		201254_x_at	Hs.40807		0.000
0.769280036	0.6815	0.681	1.038	1.0832	0.783	1.213
RPS4X	AW132023		213347_x_at	Hs.44662		0.003
0.766546646	0.6998	0.699	1.235	1.0766	0.800	1.256
ACYP2	NM_001108		206833_s_at	Hs.51617		0.002
0.766326673	0.5607	0.560	1.077	1.1244	0.897	1.510

Supplementary_Table_2

TIAL1	BF432532	202405_at	Hs.50120	0.008
0.766085941	0.5236 0.523	1.235 1.1455	0.839 1.790	
CHRN83	NM_000749	207859_s_at	Hs.96094	0.008
0.765723302	0.5584 0.558	1.252 1.1799	0.808 2.069	
FECH	AU152635	203115_at	Hs.46522	0.000
0.765384594	0.1460 0.146	1.108 1.0937	0.721 3.446	
UXS1	NM_025076	219675_s_at	Hs.46956	0.002
0.765323886	0.6361 0.636	1.139 1.0803	0.877 1.374	
FLJ43654	AI346043	202681_at	Hs.77500	0.001
0.765311816	0.8270 0.827	1.112 1.2810	0.921 1.594	
	BE963164	211927_x_at	Hs.14483	0.000
0.765278674	0.7517 0.751	1 1.0600	0.876 1.576	
DDX6	NM_004397	204909_at	Hs.40846	0.005
0.764439947	0.4822 0.482	1.171 1.1377	0.688 1.913	
SYPL	AI768845	201259_s_at	Hs.80919	0.006
0.763275320	0.5515 0.551	1.245 1.1361	0.797 1.965	
SLC12A9	NM_020246	220371_s_at	Hs.52108	0.003
0.762440737	0.7291 0.729	1.106 1.1297	0.871 1.461	
PFDN5	AB055804	210908_s_at	Hs.28885	0.000
0.761106033	0.6727 0.672	1 1.1544	0.994 1.259	
NACA	NM_005594	200735_x_at	Hs.50573	0.000
0.761021760	0.8522 0.852	1 1.1967	0.925 1.345	
SRP72	AF069765	208803_s_at	Hs.23782	0.001
0.760985315	0.5682 0.568	1.111 1.0767	0.756 1.588	
STK19	L26260	36019_at	Hs.48510	0.003
0.760779951	0.7807 0.780	1.028 1.0866	0.770 1.612	
IGL	AF047245	216366_x_at	Hs.58476	0.008
0.759460862	0.5545 0.554	1.244 1.0657	0.810 1.776	
RPS16	NM_001020	201258_at	Hs.39760	0.005
0.759234220	0.7476 0.747	1.252 1.1804	0.857 1.340	
RPL30	L05095	200062_s_at	Hs.40029	0.002
0.758735618	0.7383 0.738	1.155 1.0970	0.912 1.276	
ATP5L	AL050277	210453_x_at	Hs.48636	0.005
0.758591132	0.7279 0.727	1.163 1.0719	0.910 1.199	
MGC12335	AL022724	215100_at	Hs.12640	0.003
0.758085142	0.6120 0.612	1.050 1.2307	0.876 1.865	
CASP9	AB015653	210775_x_at	Hs.32950	0.005
0.757935784	0.7082 0.708	1.084 1.1215	0.726 1.902	
RPS2	AA630314	212433_x_at	Hs.49856	0.000
0.757842411	0.8041 0.804	1.114 1.1894	0.919 1.424	
PIGL	NM_004278	205873_at	Hs.56975	0.005
0.757131271	0.6275 0.627	1.324 1.1074	0.893 1.481	
KIAA1041	AK027075	217310_s_at	Hs.26023	0.005
0.757038597	0.7301 0.730	1.239 1.0873	0.758 1.581	
UBA52	AF348700	221700_s_at	Hs.5308	0.000

Supplementary Table 2						
0.756924441	0.6977	0.697	1.096	1.0581	0.806	1.324
GDF9	NM_005260	221314_at	Hs.25022			0.005
0.756818176	0.7721	0.772	1.083	1.1937	0.709	1.463
SLC2A1	NM_006516	201250_s_at	Hs.47372			0.003
0.756748085	0.6061	0.606	1.311	1.1182	0.946	2.586
PGRMC2	NM_006320	201701_s_at	Hs.50791			0.003
0.756618231	0.4906	0.490	1.060	1.1774	0.440	2.280
RPL14	AA838274	213588_x_at	Hs.44652			0.005
0.756282661	0.7286	0.728	1.274	1.1446	0.821	1.380
RPL19	NM_000981	200029_at	Hs.38106			0.000
0.756133881	0.7057	0.705	1.152	1.1082	0.885	1.262
	AL121916	216342_x_at	---			0.003
0.756016195	0.6123	0.612	1.341	1.1275	0.802	1.502
LOC2829	AI695595	222307_at	---			0.003
0.755865570	0.5985	0.598	1.259	1.1477	0.782	1.646
MYL5	L03785	205144_at	Hs.56761			0.001
0.754633859	0.6990	0.699	1.184	1.2201	0.911	1.568
PFNS	NM_002624	207132_x_at	Hs.28885			0.000
0.754003470	0.6073	0.607	1.028	1.0781	0.948	1.280
RPL34	BF216701	200092_s_at	Hs.80545			0.000
0.753860392	0.7946	0.794	1.089	1.1028	0.944	1.268
PRPF31	BF342707	202407_s_at	Hs.51559			0.008
0.753573686	0.6225	0.622	1.201	1.2746	0.649	1.493
ATP5L	NM_006476	207573_x_at	Hs.48636			0.000
0.753375331	0.7688	0.7688	1.056	1.1038	0.833	1.193
CLDN10	NM_006984	205328_at	Hs.53437			0.008
0.753368537	0.6772	0.677	1.247	1.2055	0.843	1.678
DNAH9	AF257737	210345_s_at	Hs.56725			0.000
0.753227016	0.5612	0.561	1.039	1.1285	0.905	1.824
CCRN4L	NM_012118	220671_at	Hs.54809			0.002
0.752764798	0.6475	0.647	1.021	1.1694	0.644	1.699
	AV704017	222376_at	Hs.15833			0.006
0.752316277	0.7329	0.732	1.177	1.1290	0.755	1.663
NNT	NM_012343	202784_s_at	Hs.48204			0.005
0.752197811	0.5790	0.579	1.389	1.1305	0.862	1.543
RPL22	BG152979	221775_x_at	Hs.51532			0.000
0.751748304	0.7262	0.726	1.206	1.1711	0.929	1.242
HLA-DMA	X76775	217478_s_at	Hs.35127			0.008
0.751603068	0.7111	0.711	1.100	1.0897	0.653	1.455
PWP1	BE796924	201607_at	Hs.50665			0.003
0.751320578	0.7254	0.725	1.241	1.2237	0.805	1.512
	Z98200	215963_x_at	Hs.11959			0.005
0.750927750	0.7757	0.775	1.029	1.1769	0.793	1.470
ITGAE	NM_002208	205055_at	Hs.51386			0.003
0.750817882	0.5891	0.589	1.193	1.1841	0.796	1.655

Supplementary_Table_2						
ARPC4	AF019888		211672_s_at	Hs.32334		0.000
0.749976910	0.3500	0.350	1.043	1.0340	0.778	1.797
DAZAP2	N34846		214334_x_at	Hs.36976		0.000
0.749835974	0.7053	0.705	1.022	1.1849	0.875	1.613
TDRKH	NM_006862		221053_s_at	Hs.58485		0.002
0.749635367	0.3622	0.362	1.153	1.1754	0.561	1.649
PNN	Y09703		212036_s_at	Hs.40996		0.005
0.749611627	0.6437	0.643	1.265	1.1239	0.778	1.472
MCP	AL570661		208783_s_at	Hs.51040		0.006
0.749552182	0.6739	0.673	1.305	1.2360	0.878	1.654
BTF3	X74070		211939_x_at	Hs.52979		0.000
0.748561046	0.6823	0.682	1.061	1.1470	0.894	1.324
RPL13A	BF979419		211942_x_at	Hs.54635		0.000
0.748089298	0.6584	0.658	1.195	1.0890	0.903	1.315
RPL31	NM_000993		200963_x_at	Hs.46947		0.002
0.748032359	0.6932	0.693	1.132	1.0791	0.804	1.277
GCAT;	Z97630		36475_at	Hs.54609		0.000
0.747004083	0.5844	0.584	1.144	1.1530	0.906	1.585
KBL;						
RPL6	NM_000970		200034_s_at	Hs.54628		0.000
0.746640685	0.7884	0.788	1.029	1.1973	0.942	1.465
UBE28	NM_003337		202335_s_at	Hs.38598		0.008
0.746619653	0.4617	0.461	1.673	1.1618	0.676	2.333
SFRS5	NM_006925		203380_x_at	Hs.16697		0.000
0.746457620	0.7921	0.792	1.131	1.2216	0.922	1.504
	AL356115		200099_s_at	Hs.35657		0.000
0.745904512	0.7305	0.730	1.011	1.1499	0.881	1.439
ATP5L	AF070655		208746_x_at	Hs.48636		0.002
0.745724095	0.7086	0.708	1.135	1.1059	0.942	1.243
TPCN1	NM_017901		217914_at	Hs.52476		0.002
0.744810503	0.7550	0.755	1.162	1.1755	0.806	1.580
USP12	AI820101		213327_s_at	Hs.42400		0.000
0.744543691	0.4182	0.418	1.075	1.0769	0.888	1.703
	AK026168		211973_at	Hs.18888		0.001
0.742548548	0.5299	0.529	1.346	1.1178	0.856	1.691
CLN5	AV700514		214252_s_at	Hs.30213		0.005
0.740445362	0.6164	0.616	1.269	1.2716	0.845	1.883
RPL29	BF683426		213969_x_at	Hs.42512		0.000
0.740235585	0.7563	0.756	1.186	1.1433	0.933	1.357
TOMM40	NM_006114		202264_s_at	Hs.31054		0.006
0.739441714	0.7630	0.763	1.331	1.1953	0.805	1.862
RPS16	AI200589		213890_x_at	Hs.39760		0.000
0.737857302	0.7598	0.759	1.143	1.1249	0.888	1.241
SRP46	AI343248		213152_s_at	Hs.58901		0.006
0.737571942	0.6693	0.669	1.121	1.2756	0.596	1.641
GPAA1	NM_003801		201618_x_at	Hs.4742		0.003

Supplementary_Table_2						
0.736212627	0.5338	0.533	1.131	1.0958	0.782	1.298
RABGEF	NM_014504		218310_at	Hs.53005		0.000
0.736165588	0.6451	0.645	1.097	1.1227	0.723	2.206
C14orf2	NM_004894		202279_at	Hs.10905		0.000
0.735964731	0.7011	0.701	1.110	1.1367	0.796	1.591
RPL3	BC006483		211073_x_at	Hs.11959		0.000
0.735924959	0.6690	0.669	1.014	1.0473	0.777	1.204
CASP2	U13022		34449_at	Hs.36898		0.002
0.735539594	0.6083	0.608	1.163	1.1917	0.745	1.853
RPL18A	NM_000980		200869_at	Hs.33776		0.000
0.734934807	0.6594	0.659	1.067	1.1141	0.778	1.266
RPL17	BG168283		212270_x_at	Hs.48509		0.000
0.734466543	0.6840	0.684	1.052	1.1415	0.897	1.285
FLJ21941	NM_025040		220721_at	Hs.29233		0.001
0.733474276	0.5970	0.597	1.150	1.2829	0.679	1.679
ZNF237	NM_014242		206744_s_at	Hs.53098		0.009
0.732240440	0.5630	0.563	1.401	1.2302	0.872	2.324
KRTHB6	X99142		215189_at	Hs.27865		0.002
0.732162524	0.5997	0.599	1.226	1.1903	0.823	1.656
KPNB3	NM_002271		211955_at	Hs.51305		0.003
0.731032551	0.5372	0.537	1.335	1.0686	0.836	1.493
RPL13	AA961748		212933_x_at	Hs.41081		0.000
0.730957236	0.6067	0.606	1	1.0625	0.904	1.230
RPS3A	NM_001006		201257_x_at	Hs.35657		0.000
0.729980616	0.7541	0.754	1.091	1.1274	0.934	1.454
GNB2L1	NM_006098		200651_at	Hs.5662		0.000
0.729647152	0.7727	0.772	1.068	1.1776	0.906	1.604
EEF1G	NM_001404		200689_x_at	Hs.14483		0.000
0.729193537	0.6543	0.654	1.024	1.1977	0.768	1.310
TPT1	AL565449		211943_x_at	Hs.37459		0.000
0.728528777	0.7159	0.715	1.087	1.0684	0.881	1.198
PABPC3	NM_030979		208113_x_at	Hs.45828		0.000
0.728142757	0.5719	0.571	1.167	1.1612	0.762	1.574
BTNL3	AK025267		217207_s_at	Hs.22594		0.000
0.727189100	0.6602	0.660	1.079	1.1860	0.899	1.454
RAB11B	AL575337		217793_at	Hs.43388		0.003
0.726937947	0.4598	0.459	1.166	1.1799	0.544	1.920
RPL35A	BE968801		213687_s_at	Hs.52963		0.000
0.726098067	0.7548	0.754	1.088	1.2247	0.874	1.412
IRA1	NM_030921		221428_s_at	Hs.43897		0.005
0.725406331	0.2842	0.284	1.265	1.1898	0.422	1.889
AKR7A2	AW074911		214259_s_at	Hs.51280		0.006
0.724108768	0.6808	0.680	1.298	1.0916	0.894	1.569
DDT	NM_001355		202929_s_at	Hs.43390		0.000
0.722513706	0.6962	0.696	1.077	1.1614	0.888	1.693

Supplementary_Table_2						
NR3C1	U01351		211671_s_at	Hs.12292		0.001
0.722397435	0.6059	0.605	1.064	1.1129	0.720	1.359
NAP1L1	NM_004537		204528_s_at	Hs.52459		0.003
0.722026425	0.6177	0.617	1.230	1.1802	0.712	1.469
DIS155E	NM_007158		219939_s_at	Hs.69855		0.002
0.721440223	0.7166	0.716	1.120	1.2631	0.771	1.625
NEDD4	D42055		213012_at	Hs.1565		0.003
0.720472474	0.4044	0.404	1.111	1.1607	0.641	1.834
RPL36A	NM_021029		201406_at	Hs.43248		0.000
0.719184269	0.6499	0.649	1.134	1.1075	0.830	1.307
GNA12	NM_007353		221737_at	Hs.48734		0.001
0.719042379	0.5944	0.594	1.298	1.1140	0.878	1.572
FLJ11127	AF052146		214947_at	Hs.15508		0.004
0.718465604	0.5516	0.551	1.155	1.1193	0.768	1.916
PTPRO; PTPU2; GLEPP1; PTP-U2	U20489		211600_at	---		0.000
0.718274030	0.6235	0.623	1.011	1.1577	0.839	1.651
RPL18	NM_000979		200022_at	Hs.51551		0.000
0.717866449	0.6057	0.605	1.124	1.1325	0.845	1.340
	AF103295		216371_at	---		0.000
0.717432388	0.4683	0.468	1.184	1.1799	0.932	1.876
HSA9761	W87688		213598_at	Hs.53322		0.002
0.717339432	0.6331	0.633	1.335	1.2387	0.874	1.447
OR2C1	NM_012368		221460_at	Hs.25857		0.008
0.717143752	0.5732	0.573	1.154	1.1126	0.679	1.997
RPS7	AI970731		213941_x_at	Hs.54628		0.000
0.716655322	0.7054	0.705	1.081	1.1528	0.957	1.581
RPS5	NM_001009		200024_at	Hs.37810		0.000
0.716456708	0.7256	0.725	1.081	1.1780	0.870	1.410
PPP1C8	AI186712		201408_at	Hs.46801		0.003
0.715827366	0.5194	0.519	1.131	1.2241	0.772	2.203
KIAA0485	AB007954		214294_at	---		0.008
0.715231744	0.6118	0.611	1.082	1.2928	0.746	2.360
PAK2	AF092132		208877_at	Hs.51853		0.000
0.715208913	0.7480	0.748	1.083	1.2542	0.874	1.570
LGTN	NM_006893		218253_s_at	Hs.49758		0.000
0.714576388	0.5870	0.587	1.040	1.1657	0.835	1.515
EEF1G	AF119850		211345_x_at	Hs.14483		0.000
0.714573425	0.6759	0.675	1	1.1832	0.857	1.393
	AL136306		216806_at	---		0.002
0.714507221	0.3578	0.357	1.208	1.2005	0.734	1.647
RPL15	NM_002948		221475_s_at	Hs.38121		0.000
0.714171663	0.7628	0.762	1.107	1.2464	0.906	1.375
FLJ13195	NM_022906		218994_s_at	Hs.21339		0.006
0.713888865	0.2497	0.249	1.084	1.2040	0.714	1.668

Supplementary_table_2

EIF3S7	NM_003753	200005_at	Hs.55682	0.000
0.713862972	0.7303 0.730	1 1.2088	0.975 1.564	
IGSF3	AB007935	202421_at	Hs.17105	0.003
0.712822634	0.6604 0.660	1.275 1.2556	0.856 2.455	
JAK3	NM_000215	207187_at	Hs.51524	0.000
0.712818945	0.5721 0.572	1.244 1.1337	0.983 1.398	
ZNF277	NM_021994	218645_at	Hs.48972	0.000
0.712724472	0.5086 0.508	1.082 1.2279	0.843 1.649	
F7	NM_000131	207300_s_at	Hs.36989	0.000
0.712711855	0.5646 0.564	1.295 1.2407	0.930 1.852	
EIF3S3	NM_003756	201592_at	Hs.49259	0.000
0.711305117	0.7452 0.745	1.027 1.2227	0.813 1.445	
HNRPA0	BE966599	201054_at	Hs.96996	0.003
0.709943213	0.6074 0.607	1.211 1.1516	0.681 1.865	
RPS21	NM_001024	200834_s_at	Hs.19096	0.000
0.709351464	0.6732 0.673	1.072 1.0779	0.894 1.305	
RPL22	BE250348	221726_at	Hs.51532	0.000
0.709341720	0.6558 0.655	1.034 1.1793	0.877 1.586	
GLUD1	NM_005271	200947_s_at	Hs.50040	0.000
0.706017162	0.5767 0.576	1.069 1.1479	0.765 1.547	
RPL15	AF279903	221476_s_at	Hs.38121	0.000
0.705602673	0.7952 0.795	1.051 1.2754	0.855 1.528	
FLJ22843	NM_025184	220591_s_at	Hs.52195	0.000
0.705209872	0.6408 0.640	1.274 1.1688	0.926 1.563	
WFDC2	NM_006103	203892_at	Hs.2719	0.000
0.705162746	0.4945 0.494	1.132 1.2310	0.762 1.803	
PIP5K1B	U78581	217477_at	Hs.53437	0.008
0.704786354	0.4680 0.468	1.306 1.2000	0.737 1.482	
SLC25A6	AA916851	212085_at	Hs.35092	0.000
0.703909347	0.4309 0.430	1.013 1.1725	0.940 1.570	
MGC10940	BC004331	209513_s_at	Hs.59486	0.000
0.703876380	0.5063 0.506	1.090 1.1814	0.881 1.518	
TOMM20	BG165094	212773_s_at	Hs.53319	0.000
0.703506404	0.4607 0.460	1.009 1.1547	0.654 1.498	
KIAA0882	AB020689	212960_at	Hs.48081	0.003
0.703316378	0.6772 0.677	1.087 1.2414	0.614 2.101	
RPL13	AW574664	212191_x_at	Hs.41081	0.000
0.702596354	0.7099 0.709	1.139 1.1821	0.888 1.401	
PRKAR1	M18468	200604_s_at	Hs.28034	0.008
0.702416493	0.5032 0.503	1.204 1.1195	0.762 1.605	
DDX3X	AF061337	201211_s_at	Hs.38077	0.000
0.701102175	0.1945 0.194	1.095 1.1247	0.780 2.022	
HADHA	BG472176	208630_at	Hs.51603	0.000
0.700856415	0.6562 0.656	0.999 1.2743	0.767 1.597	
NUDT4	AF191654	212181_s_at	Hs.50632	0.001

Supplementary_Table_2						
0.700498357	0.6700	0.670	1.266	1.1716	0.772	1.529
EIF3S5	NM_003754	200023_s_at	Hs.51602			0.000
0.699730497	0.6729	0.672	0.902	1.1155	1	1.308
ATP5L	AA917672	208745_at	Hs.48636			0.000
0.698209158	0.6521	0.652	1.270	1.0772	0.891	1.728
RPL5	NM_000969	200937_s_at	Hs.53235			0.000
0.697806812	0.7089	0.708	1.075	1.3261	0.899	1.537
TOMM7	NM_019059	201812_s_at	Hs.38092			0.003
0.696981558	0.6999	0.699	1.093	1.2566	0.762	1.642
YF13H12	NM_014297	204034_at	Hs.7486			0.000
0.696382290	0.5738	0.573	1.162	1.1711	0.846	1.358
CYBB	NM_000397	203923_s_at	Hs.29235			0.003
0.695868632	0.2607	0.260	1.123	1.2192	0.432	2.085
SERPINE2	AL541302	212190_at	Hs.38449			0.008
0.695446994	0.6885	0.688	1.348	1.2623	0.780	1.807
WIG1	NM_022470	219628_at	Hs.38629			0.003
0.695047532	0.5529	0.552	1.128	1.2350	0.702	1.647
PABPC4	NM_003819	201064_s_at	Hs.16990			0.000
0.694979970	0.6919	0.691	1.032	1.2558	0.991	1.677
ELK1	M25269	210376_x_at	Hs.18112			0.006
0.694545404	0.5507	0.550	1.103	1.1072	0.658	1.345
API5	AF229254	201686_x_at	Hs.43577			0.005
0.693961120	0.6690	0.669	1.415	1.2182	0.694	1.480
PITPNC1	NM_012417	219155_at	Hs.23129			0.005
0.693267781	0.6115	0.611	1.305	1.2369	0.871	1.671
MMP14	Z48481	160020_at	Hs.2399			0.003
0.691461736	0.3971	0.397	1.064	1.1773	0.525	1.862
BRP44L	NM_016098	218024_at	Hs.17275			0.001
0.690524849	0.6267	0.626	1.108	1.1319	0.805	1.496
GSPT1	NM_002094	201912_s_at	Hs.52878			0.006
0.689846320	0.6621	0.662	1.162	1.1740	0.643	1.982
MGC4276	BG387555	209273_s_at	Hs.44929			0.003
0.688844761	0.4562	0.456	1.150	1.1275	0.768	1.647
ICAM3	NM_002162	204949_at	Hs.35321			0.000
0.688736001	0.6525	0.652	1.173	1.1715	0.902	1.406
ST13	NM_003932	207040_s_at	Hs.54630			0.000
0.686889969	0.6529	0.652	1.045	1.2244	0.815	1.572
RPL10	NM_006013	200725_x_at	Hs.40192			0.000
0.686854456	0.6116	0.611	1.193	1.1136	0.864	1.603
KCNN4	NM_002250	204401_at	Hs.10082			0.001
0.686216989	0.8099	0.809	1.440	1.3429	0.865	3.161
BTF3	NM_001207	208517_x_at	Hs.52979			0.000
0.686141690	0.6286	0.628	1.068	1.1260	0.873	1.318
FLJ39616	NM_016534	219817_at	Hs.33312			0.002
0.685505232	0.4761	0.476	1.327	1.1830	0.619	1.862

Supplementary_Table_2						
RPL4	BC005817	211710_x_at	Hs.43289			0.000
0.685042351	0.6234	0.623	1.121	1.1578	0.901	1.439
STX16	AF008936	221499_s_at	Hs.30791			0.002
0.684658833	0.6360	0.636	1.377	1.2111	0.851	1.547
RPL13	BC004954	208929_x_at	Hs.41081			0.000
0.684409396	0.6787	0.678	1.078	1.0668	0.839	1.218
PRKCA	AI471375	213093_at	Hs.53170			0.003
0.684250960	0.5823	0.582	1.034	1.1713	0.563	1.429
dj507r15.	Z98950	217256_x_at	---			0.000
0.683924592	0.5745	0.574	1	1.2431	0.591	1.699
MAL	NM_002371	204777_s_at	Hs.80395			0.006
0.683336620	0.4553	0.455	1.091	1.2118	0.404	1.655
DKFZP56	NM_005016	204031_s_at	Hs.54627			0.000
0.682158631	0.6997	0.699	0.957	1.2290	0.999	1.809
4J157						
C15orf15	NM_016304	217915_s_at	Hs.27477			0.000
0.680541747	0.5183	0.518	1.083	1.1814	0.769	1.584
RPL17	BE733979	212537_x_at	Hs.48509			0.000
0.679542698	0.7337	0.733	1.012	1.1809	0.924	1.259
RPL13A	BC000514	200715_x_at	Hs.54635			0.000
0.679354374	0.7716	0.771	1.169	1.2296	0.896	1.367
RPL4	AI953886	200089_s_at	Hs.43289			0.000
0.678963698	0.6927	0.692	1	1.1846	0.978	1.395
C6orf149	NM_020408	218561_s_at	Hs.38775			0.000
0.677471580	0.5614	0.561	1.118	1.2498	0.853	1.911
C11orf2	NM_013265	217969_at	Hs.27751			0.000
0.677094605	0.7386	0.738	1.087	1.3082	0.888	1.706
ALPPL2;	X07247	216377_x_at	Hs.33350			0.000
0.677030946	0.4523	0.452	1.120	1.1632	0.912	1.966
ALPG;						
ATP6AP2	AF248966	201443_s_at	Hs.49596			0.003
0.676573743	0.6291	0.629	1.328	1.1139	0.794	1.396
	AC004692	217313_at	---			0.000
0.676364493	0.5932	0.593	1.085	1.2966	0.925	1.692
CHP	NM_007236	207993_s_at	Hs.40623			0.005
0.675888317	0.2727	0.272	1.528	1.0651	0.753	3.818
ZNF91	NM_003430	206059_at	Hs.53163			0.001
0.672220203	0.6293	0.629	1.115	1.1951	0.787	1.829
	BF541557	213753_x_at	Hs.53431			0.000
0.670926071	0.6074	0.607	1	1.3468	0.902	2.043
NUTF2	NM_005796	202397_at	Hs.35663			0.002
0.667882236	0.5878	0.587	1.265	1.1829	0.844	1.690
MAP3K1	AW025150	213264_at	---			0.003
0.667822617	0.4048	0.404	1.211	1.2266	0.780	1.666
SDBCAG	AF091085	216032_s_at	Hs.47255			0.000
0.667433273	0.7161	0.716	1.000	1.2639	0.827	1.418

Supplementary_Table_2						
NAP1L1	AL162068	208754_s_at	Hs.52459			0.000
0.667350854	0.7125 0.712	1.112 1.2804	0.866	1.612		
CCNG2	NM_004354	202770_s_at	Hs.13291			0.005
0.666068737	0.2182 0.218	1.536 1.1300	0.634	1.751		
UBBP1	X04801	217144_at	Hs.35619			0.001
0.665803327	0.5007 0.500	1.292 1.2142	0.897	1.832		
RAB2	NM_002865	208733_at	Hs.36901			0.000
0.664775064	0.4334 0.433	1.575 1.1326	0.724	1.914		
RPS20	AF113008	216247_at	Hs.57468			0.000
0.664576810	0.4869 0.486	1.180 1.0838	0.938	1.681		
UBL3	NM_007106	201535_at	Hs.14557			0.000
0.664508765	0.5743 0.574	1.144 1.2096	0.822	1.459		
CSNK2B	M30448	211623_s_at	Hs.29900			0.000
0.662488026	0.6221 0.622	1.308 1.3505	0.964	2.104		
ZFR	BC000376	201856_s_at	Hs.43523			0.000
0.662472032	0.6635 0.663	1.378 1.2040	0.859	1.976		
	AL118502	216505_x_at	Hs.53910			0.000
0.661861285	0.6481 0.648	1.014 1.2232	0.806	1.695		
FLJ10252	NM_018040	219078_at	Hs.42075			0.001
0.660946719	0.7288 0.728	1.093 1.2075	0.817	1.574		
	AW973834	222326_at	Hs.19807			0.006
0.660602376	0.3727 0.372	1.358 1.1510	0.745	4.366		
	AL121871	222229_x_at	Hs.50619			0.000
0.659842004	0.6554 0.655	1.069 1.1679	0.792	1.688		
RPL5	BF214492	213080_x_at	Hs.53235			0.000
0.657254548	0.6314 0.631	1.277 1.2861	0.943	1.475		
DJ971N1	AL544094	201581_at	Hs.16935			0.003
0.656158018	0.5563 0.556	1.098 1.1599	0.667	1.780		
GALNT12	NM_024642	218885_s_at	Hs.47099			0.005
0.653438696	0.3894 0.389	1.222 1.2134	0.489	1.697		
BCAT2	NM_001190	203576_at	Hs.51267			0.008
0.653193222	0.6437 0.643	1.389 1.2998	0.526	1.555		
C14orf45	AF130089	221590_s_at	Hs.29397			0.000
0.652578149	0.5570 0.557	1.133 1.2505	0.957	1.976		
RPLP0	AA555113	214167_s_at	Hs.44822			0.000
0.652025430	0.7263 0.726	1.005 1.2586	0.987	1.523		
AP1S2; DC22; SIGMA1B ;	AF251295	203299_s_at	Hs.12159			0.000
0.651445587	0.5717 0.571	1.280 1.1572	0.821	2.332		
EPM2A	NM_005670	205231_s_at	Hs.48669			0.005
0.650689865	0.6218 0.621	1.146 1.1729	0.579	1.444		
SC5DL	D85181	211423_s_at	Hs.28774			0.008
0.650024344	0.3690 0.369	1.710 1.4105	0.667	3.840		
FKSG2	NM_021631	208588_at	Hs.30201			0.001
0.648569773	0.4783 0.478	1.142 1.1589	0.613	2.037		

Supplementary_Table_2

0.648184121	BG491393	222280_at	Hs.24801	0.000		
0.6049	0.604	1.005	1.1852	0.592	1.414	
SLC19A2	AF153330	209681_at	Hs.30246	0.003		
0.647993057	0.1771	0.177	1.191	1.1444	0.692	2.179
RNP24	NM_006815	204427_s_at	Hs.75914	0.003		
0.645596976	0.3508	0.350	1.186	1.1393	0.553	1.852
SBN01	NM_018183	218737_at	Hs.7012	0.000		
0.644544125	0.6339	0.633	1.204	1.2518	0.753	1.664
FXR1	NM_005087	201637_s_at	Hs.47840	0.000		
0.643845585	0.5897	0.589	1.058	1.2817	0.775	1.508
HRMT1L1	AL570294	221564_at	Hs.15416	0.008		
0.642897399	0.4187	0.418	1.490	1.2437	0.607	1.739
0.642875060	AL353580	216387_x_at	---	0.000		
0.1470	0.147	1.135	1.2399	0.780	1.936	
CD44	M24915	204490_s_at	Hs.50232	0.000		
0.642246974	0.5079	0.507	1.118	1.2974	0.871	1.964
RPL3	L22453	211666_x_at	Hs.11959	0.000		
0.640213587	0.6907	0.690	1.047	1.1992	0.817	1.487
EPB41	NM_004437	207793_s_at	Hs.17543	0.005		
0.637887959	0.2708	0.270	1.427	1.2326	0.605	1.728
CD44	BE903880	212063_at	Hs.50232	0.000		
0.637039888	0.5725	0.572	1	1.2215	0.998	1.487
FLJ22559	NM_024928	219100_at	Hs.13449	0.000		
0.636745229	0.5045	0.504	1.311	1.1392	0.784	1.723
RPL22	AW071997	214042_s_at	Hs.51532	0.000		
0.635856822	0.7319	0.731	1	1.3234	0.974	1.583
RPL10L	AI001784	217559_at	Hs.30833	0.000		
0.634623742	0.1988	0.198	1.122	1.1546	0.901	2.785
IL13RA1	U81380	210904_s_at	Hs.49664	0.003		
0.634451251	0.3703	0.370	2.313	1.2787	0.710	3.678
DHRS8	NM_016245	217989_at	Hs.28298	0.000		
0.633785091	0.5328	0.532	1.211	1.1174	0.783	1.816
CKAP2	NM_018204	218252_at	Hs.44402	0.008		
0.630733340	0.7223	0.722	1.401	1.3631	0.465	2.622
KPNB3	NM_002271	211954_s_at	Hs.51305	0.008		
0.630457225	0.6691	0.669	1.330	1.1769	0.676	1.291
RPL31	BC001663	221593_s_at	Hs.46947	0.000		
0.629547665	0.5337	0.533	1	1.1938	0.773	2.086
FLJ13263	NM_025125	218174_s_at	Hs.16998	0.003		
0.628444398	0.4677	0.467	1.089	1.3957	0.776	2.078
SORL1	NM_003105	203509_at	Hs.36859	0.000		
0.628254050	0.6191	0.619	1.027	1.2368	0.958	1.650
SLC11A2	NM_000617	203124_s_at	Hs.50554	0.003		
0.628162017	0.5116	0.511	1.725	1.0603	0.619	1.468
CSDA	AL556190	201160_s_at	Hs.22188	0.005		

Supplementary_Table_2						
0.627950383	0.5254	0.525	1.536	1.3492	0.823	2.026
BNIP3L	AL132665	221478_at	Hs.13122			0.001
0.627481612	0.5319	0.531	1.284	1.2200	0.766	2.628
	AK021960	214744_s_at	Hs.51254			0.002
0.627304126	0.6666	0.666	1.107	1.3943	0.757	2.131
FLJ12969	NM_022838	219335_at	Hs.52272			0.003
0.626809067	0.7040	0.704	1.051	1.3214	0.537	2.564
KIAA0759	AB018302	36865_at	Hs.49744			0.001
0.625592434	0.5687	0.568	1.140	1.1709	0.633	1.611
RPL29	AW582267	216177_at	Hs.53153			0.008
0.624837655	0.6147	0.614	1.313	1.1742	0.623	2.531
	Z95126	215780_s_at	Hs.43668			0.000
0.622678406	0.6750	0.675	1.679	1.2663	0.883	1.691
BPGM	NM_001724	203502_at	Hs.19836			0.002
0.621079014	0.5237	0.523	1.368	1.3653	0.735	4.149
	AL096829	216570_x_at	Hs.29409			0.000
0.614523356	0.6061	0.606	1.074	1.2414	0.912	1.635
PP	NM_021129	217848_s_at	Hs.43740			0.000
0.613888903	0.2809	0.280	1.250	1.2826	0.681	1.944
EIF4B	NM_018507	219599_at	Hs.58556			0.000
0.613804279	0.5746	0.574	0.999	1.2489	0.871	1.743
RPL4	NM_000968	201154_x_at	Hs.43289			0.000
0.613557434	0.6396	0.639	1.110	1.2610	0.939	1.408
UXT	NM_004182	218495_at	Hs.17279			0.000
0.613128383	0.6624	0.662	1.102	1.2326	0.925	1.745
SMU-1	NM_018225	218393_s_at	Hs.17402			0.000
0.612700448	0.4026	0.402	1.227	1.2927	0.406	2.177
QARS	NM_005051	217846_at	Hs.79322			0.000
0.611184728	0.6383	0.638	1	1.3618	0.958	1.694
B4GALT1	U10473	216627_s_at	Hs.27201			0.000
0.611042924	0.3911	0.391	1.242	1.3919	0.673	4.882
RPL18	AV738806	222297_x_at	---			0.000
0.610971025	0.3004	0.300	1.270	1.5064	0.760	2.609
APBA2	AW571582	209870_s_at	Hs.52571			0.008
0.606536822	0.5819	0.581	1.437	1.0855	0.806	1.544
	AL035687	217142_at	---			0.005
0.605517542	0.4440	0.444	1.148	1.4327	0.403	2.104
SORL1	AV728268	212560_at	---			0.000
0.603747377	0.4751	0.475	1.055	1.3000	0.745	1.654
EEF1B2	NM_001959	200705_s_at	Hs.42160			0.000
0.603747075	0.6612	0.661	1.002	1.2456	0.894	1.445
FHL1	AF063002	210299_s_at	Hs.43536			0.005
0.602731445	0.2798	0.279	1.741	1.2952	0.673	2.870
CD44	BC004372	209835_x_at	Hs.50232			0.000
0.602180694	0.4668	0.466	1.082	1.2182	0.870	1.957

Supplementary_Table_2							
CD44	NM_000610		204489_s_at	Hs.50232			
0.601992640	0.5708	0.570	0.999	1.1673	0.848	1.537	0.000
TRIM10	AF220122		210579_s_at	Hs.27429			
0.601336289	0.1907	0.190	1.141	1.1319	0.887	1.674	0.000
	AL021937		217406_at	---			
0.601279313	0.5989	0.598	1.389	1.4396	0.813	2.570	0.000
PRDX2;	L19185		39729_at	Hs.43212			
0.599562848	0.4708	0.470	1.260	1.1418	0.742	1.969	0.002
PRP;							
TSA;							
NKEFB;							
PRXII;							
TDPX1;							
MGC4104							
RPL10A	NM_007104		200036_s_at	Hs.54626			
0.598684152	0.5971	0.597	1.042	1.2067	0.908	1.329	0.000
	AK001448		215625_at	Hs.45828			
0.598322453	0.3565	0.356	1.186	1.0993	0.381	1.952	0.006
MHC2TA	NM_000246		205101_at	Hs.58478			
0.596893616	0.5465	0.546	1.121	1.2920	0.364	1.855	0.002
EIF4B	BF247371		211938_at	Hs.55628			
0.596505836	0.6489	0.648	1.102	1.3755	0.932	1.905	0.000
CD44	AJ251595		212014_x_at	Hs.50232			
0.595152437	0.4554	0.455	1.309	1.3020	0.819	1.978	0.000
RPS14	AF116710		208646_at	Hs.38112			
0.593039116	0.6743	0.674	1.611	1.4934	0.859	2.705	0.001
PCTP	NM_021213		218676_s_at	Hs.28521			
0.591831969	0.5473	0.547	1.846	1.2449	0.786	3.897	0.005
DPP4	NM_001935		203717_at	Hs.36891			
0.588222735	0.5697	0.569	1.088	1.1476	0.685	1.793	0.001
NQO1	NM_000903		201468_s_at	Hs.40651			
0.586974048	0.5596	0.559	1.130	1.5442	0.655	2.336	0.003
RPS10P2	AL118510		217336_at	Hs.58523			
0.584822433	0.5495	0.549	1.298	1.3223	0.618	1.882	0.000
;							
DREV1	NM_016025		217868_s_at	Hs.27958			
0.581033931	0.5459	0.545	1.479	1.3305	0.940	2.122	0.001
HBS1L	AK024258		209314_s_at	Hs.37853			
0.580083800	0.3443	0.344	1.222	1.2255	0.423	1.867	0.003
	AA768909		217544_at	Hs.49841			
0.576219509	0.5268	0.526	1.265	1.4107	0.707	2.043	0.001
	AL049693		216348_at	Hs.43342			
0.573223678	0.4580	0.458	1.136	1.1632	0.870	1.734	0.000
MXI1	NM_005962		202364_at	Hs.50102			
0.571483550	0.5881	0.588	1.912	1.3644	0.773	2.760	0.000
ITGA6	AV733308		215177_s_at	Hs.13339			
0.570823431	0.4225	0.422	1.550	1.3586	0.536	2.337	0.005
NELL2	NM_006159		203413_at	Hs.50532			
0.565003229	0.3263	0.326	1.171	1.1520	0.615	2.243	0.000

Supplementary_Table_2

HDGFRP	AL133102	216693_x_at	Hs.51395	0.000
0.557504126	0.5341 0.534	1.452 1.1639	0.985 1.925	
GYPE	NM_002101	202947_s_at	Hs.59138	0.000
0.555327918	0.5422 0.542	1.033 1.2840	0.780 2.036	
	AU145411	222164_at	Hs.26488	0.003
0.554554958	0.4663 0.466	1.222 1.1224	0.502 1.599	
BTG2	BG339064	201235_s_at	Hs.51916	0.000
0.545554502	0.3031 0.303	1.008 1.2473	0.806 1.703	
	AL031589	217092_x_at	Hs.58524	0.000
0.545542874	0.5661 0.566	1.041 1.2355	0.803 1.959	
HDGFRP	AB029156	209526_s_at	Hs.51395	0.000
0.543819642	0.4482 0.448	1.990 1.4323	0.798 2.314	
TIX1	AB007855	217367_s_at	Hs.38013	0.002
0.539577891	0.5316 0.531	1.186 1.2957	0.598 1.726	
EIF4B	NM_001417	211937_at	Hs.55628	0.000
0.537469163	0.5938 0.593	1.286 1.4671	0.737 2.146	
	Z97353	217266_at	Hs.38121	0.008
0.533005318	0.5605 0.560	1.642 1.4152	0.688 2.635	
LTA4H	J02959	208771_s_at	Hs.52464	0.000
0.530165714	0.3611 0.361	1.297 1.1033	0.647 2.079	
PCSK5	AU152579	213652_at	Hs.36854	0.006
0.529630467	0.3693 0.369	1.267 1.2474	0.599 2.506	
EIF3S6IP	NM_016091	217719_at	Hs.44685	0.000
0.526174776	0.5359 0.535	0.999 1.4493	0.941 1.750	
	AA203487	217503_at	---	0.000
0.513518936	0.4646 0.464	1.151 1.4884	0.575 2.506	
NR4A2	S77154	216248_s_at	Hs.16525	0.006
0.510175825	0.0520 0.052	1.493 1.2972	0.299 2.997	
FXD2	NM_021603	207434_s_at	Hs.41313	0.001
0.503524667	0.3556 0.355	1.462 1.3584	0.662 1.844	
KRT1	NM_006121	205900_at	Hs.80828	0.002
0.502713147	0.5420 0.542	2.472 1.6206	0.742 8.466	
TGIF	NM_003244	203313_s_at	Hs.37355	0.008
0.502306536	0.4048 0.404	1.359 1.1949	0.410 2.331	
	AL137162	217019_at	---	0.000
0.494924535	0.3035 0.303	1 1.3361	0.365 2.980	
	AL024509	217340_at	Hs.54110	0.000
0.492607279	0.3989 0.398	1.174 1.4828	0.367 2.035	
ba209A2.1	AL121934	217379_at	---	0.000
0.489800774	0.4507 0.450	1.194 1.3896	0.737 2.055	
RPS9	BE348997	214317_x_at	Hs.54628	0.000
0.482084663	0.6381 0.638	1.477 1.6137	0.746 2.499	
HDGFRP	NM_016073	209524_at	Hs.51395	0.000
0.479537563	0.0682 0.068	1.606 1.3058	0.763 1.964	
PDE4B	AU144792	215671_at	----	0.002

Supplementary_Table_2						
0.470904165	0.4961	0.496	1.179	1.4431	0.635	3.099
PDE4B	NM_002600	203708_at	Hs.19807			0.006
0.443686685	0.3450	0.345	1.808	1.7086	0.688	3.409
	NM_013307	221419_s_at	---			0.000
0.439419965	0.3874	0.387	1.399	1.0741	0.685	2.739
CD1C	NM_001765	205987_at	Hs.1311			0.000
0.435832178	0.4803	0.480	2.677	1.5098	0.936	3.669
SSR3	NM_007107	217790_s_at	Hs.51834			0.000
0.414536219	0.3345	0.334	1.043	1.4447	0.666	3.125
EBI2	NM_004951	205419_at	Hs.784			0.008
0.413407799	0.3935	0.393	2.073	1.4648	0.630	2.191
EIF5A	BC000751	201122_x_at	Hs.53431			0.000
0.406608765	0.4233	0.423	1.101	1.5107	0.807	2.014
CTNNA1	NM_001904	201533_at	Hs.47601			0.003
0.353737379	0.5444	0.544	3.258	2.2209	0.576	3.578
NEBL	NM_006393	203962_s_at	Hs.5025			0.000
0.349760114	0.2838	0.283	1.397	2.0998	0.672	5.668
EIF2S3	NM_001415	205321_at	Hs.53968			0.000
0.327711964	0.1622	0.162	1.620	2.0617	0.331	3.078
EIF5A	NM_001970	201123_s_at	Hs.53431			0.000
0.298178956	0.1129	0.112	1.095	1.3335	0.832	2.118
SFRS6	NM_006275	206108_s_at	Hs.6891			0.001
0.270111142	0.3541	0.354	2.168	2.1185	0.617	6.861

Supplementary_Table_3

Supplementary Table 3

Influenza A vs. bacterial infection; classifier genes: List of 35 classifier genes discriminating samples obtained from patients with Influenza A and Bacterial infections (data shown Figure 1b and Figure 2). P-values = Class comparison results - Mann Whitney test

Common	Influenza A (n=11)		Affymetrix Bacteria (n=12)		uniGeneX Max	P-value	Fold FLU/Bacteri
	Median	GenBank Min Max	Probe ID Median	Min			
APOBEC		AF165520	209584_x_at		Hs.44112	0.000	
1.755107386	1010.3	1010.3	2174.1	763.6	423	1010.8	
BST2		NM_004335	201641_at		Hs.11811	0.000	
1.952049497	1031.9	1031.9	3956.2	646.5	517.7	1788.7	
C1orf29		NM_006820	204439_at		Hs.38972	0.000	
11.74888063	2685.9	2685.9	1146	524.85	6.7	7465.3	
CD44		BE903880	212063_at		Hs.50232	0.000	
0.637039865	3683.3	3683.3	6432.6	7857.7	6423.1	9569	
cig5		AI337069	213797_at		Hs.17518	0.000	
7.944318696	588.4	588.4	4664.9	220.9	156.9	1886.4	
d3507115.		Z98950	217256_x_at		---	0.000	
0.683924517	2015.8	2015.8	3508.4	4361.3	2076.6	5963.2	
DNAPTP		AK002064	222154_s_at		Hs.12032	0.000	
4.498070987	793.8	793.8	2242.2	259.2	161.1	1146.6	
EEF1G		AF119850	211345_x_at		Hs.14483	0.000	
0.714573417	11629.	1162	1720	20358.	1474	2397	
EEF1G		BE963164	211927_x_at		Hs.14483	0.000	
0.765278690	14455.	1445	1922	20384.	1685	3032	
EIF3S5		NM_003754	200023_s_at		Hs.51602	0.000	
0.699730451	5124.7	5124.7	6876.4	8495.7	7615.8	9962.6	
EIF3S7		NM_003753	200005_at		Hs.55682	0.000	
0.713863000	2593	2593	3550.5	4292	3462.4	5554.6	
EIF4B		NM_018507	219599_at		Hs.58556	0.000	
0.613804289	255.3	255.3	444.3	554.9	387.1	774.6	
FLJ20035		NM_017631	218986_s_at		Hs.48114	0.000	
4.000839489	1470.5	1470.5	3914.4	595.6	105.9	2579.2	
FLJ38348		AV755522	213294_at		Hs.54652	0.001	
2.761652261	1856.9	1856.9	3587.8	942.95	398.9	3183.3	
GLP2		NM_005101	205483_s_at		Hs.45848	0.000	
4.527163072	4704.3	4704.3	2462	2130.6	623.8	1129	
HADHA		BG472176	208630_at		Hs.51603	0.000	
0.700856413	514.1	514.1	783.4	998.35	601.4	1251.8	
HSXIAPA		NM_017523	206133_at		Hs.44197	0.000	
3.646293684	1163.1	1163.1	2921.9	638.1	100.7	1986	
IFI27		NM_005532	202411_at		Hs.53263	0.000	
53.89107315	3466.9	3466.9	1563	155.15	24.4	7771.3	

Supplementary_Table_3

IFI35	BC001356	209417_s_at	Hs.50842	0.000		
2.806714391	1760.1	1760.1	6281.2	810.2	482.4	3209.1
IFI44	BE049439	214059_at	Hs.82316	0.000		
3.679544530	172.5	172.5	1614.9	122.95	31.1	585.5
IFI44	NM_006417	214453_s_at	Hs.82316	0.000		
6.444369247	2110.1	2110.1	8615.7	738.8	203.4	5384.8
KIAA0152	BC000371	200616_s_at	Hs.50707	0.000		
2.377021982	412.8	412.8	990.3	241.1	52.1	490.8
LY6E	NM_002346	202145_at	Hs.52190	0.000		
4.216806982	3292.7	3292.7	1135	1294.7	341.1	4259.7
MX1	NM_002462	202086_at	Hs.51730	0.000		
4.249779813	3639.3	3639.3	1519	1419.2	506.9	7975.1
OAS1	NM_002534	205552_s_at	Hs.52476	0.000		
5.333815865	797.4	797.4	3421.2	345.4	176.5	2023.9
PCBP2	NM_005016	204031_s_at	Hs.54627	0.000		
0.682158626	5667.3	5667.3	7756.9	9953.5	8098.9	1465
PFDN5	AB055804	210908_s_at	Hs.28885	0.000		
0.761106022	4867.8	4867.8	7235.2	8352.4	7197.8	9109.8
PHACTR	NM_014721	204048_s_at	Hs.10247	0.000		
1.643578304	612.6	612.6	988.1	425.9	218.5	587.1
QARS	NM_005051	217846_at	Hs.79322	0.000		
0.611184716	2193.5	2193.5	3436.2	4679.6	3295.1	5823.3
RPL31	BC001663	221593_s_at	Hs.46947	0.000		
0.629547641	464.5	464.5	870.3	1039	673.3	1815.8
RPL4	AI953886	200089_s_at	Hs.43289	0.000		
0.678963705	6857.7	6857.7	9898.9	11726.	9684.8	1381
SON	AA664291	201085_s_at	Hs.51726	0.000		
2.429084537	999	999	1861.8	570.75	349.9	1954.4
TRIM14	BE962483	203147_s_at	Hs.55590	0.000		
2.070929512	806.3	806.3	2060.9	565.35	311.2	1308
USP18	NM_017414	219211_at	Hs.38260	0.000		
6.059939301	539.3	539.3	2185.7	131.8	32.6	878.2
ZBP1	NM_030776	208087_s_at	Hs.30212	0.000		
3.066387141	129.6	129.6	311.9	71.55	8.2	152.3

Supplementary_Table_4

Supplementary Table 4

S. aureus vs E. coli; class comparison results: Comparison of gene expression levels (normalized values) between patients with acute S. aureus infection and patients with acute E. coli infection - $P < 0.01$, Mann-Whitney test = 211 genes. Expression patterns are represented Figure 3a.

Common	S.aureus (n=10)		Affymetrix E.coli (n=10)		uniGeneI Max	P-value	Fold Sa/Ec
	Median	GenBank Min Max	Probe ID Median Min				
ACTG1		AU145192	212363_x_at	Hs.51458	0.006		
1.222744556	0.9922	0.992	1.208 0.8631	0.744	1.229		
ADD3		BE545756	201034_at	Hs.50101	0.004		
0.751690817	0.7304	0.730	1.420 1.2184	0.951	1.503		
ADH5		M30471	208848_at	Hs.78989	0.004		
0.662028139	0.6212	0.621	1.163 1.3377	0.771	2.087		
ADK		NM_001123	204120_s_at	Hs.58473	0.002		
0.638837784	0.2502	0.250	1.216 1.3554	0.788	1.865		
AF1Q		BC006471	211071_s_at	Hs.75823	0.001		
0.742133014	0.5429	0.542	1.303 1.1014	0.950	1.346		
AKAP10		NM_007202	205045_at	Hs.46245	0.002		
0.666580357	0.5184	0.518	1.269 1.1878	0.849	1.720		
AKAP11		NM_016248	203156_at	Hs.10510	0.008		
0.692090188	0.5388	0.538	1.594 1.3032	0.757	1.655		
AKAP7;		AL137063	205771_s_at	Hs.48648	0.006		
0.621783650	0.6582	0.658	1.520 1.4399	0.833	2.532		
AKAP18							
ALOX5AP		NM_001629	204174_at	Hs.50765	0.004		
1.504791375	0.9014	0.901	3.401 0.8613	0.576	2.699		
APIGBP		AI472320	64418_at	---	0.006		
0.547929992	0.4862	0.486	1.420 1.4172	0.735	1.732		
ARD1		NM_003491	203025_at	Hs.43329	0.004		
1.155341897	0.8278	0.827	1.211 0.9326	0.761	1.034		
ARH		AL545035	221790_s_at	Hs.18978	0.001		
0.574903624	0.4071	0.407	1.116 1.2329	0.782	2.459		
ATRX		U09820	208860_s_at	Hs.53352	0.004		
0.792985806	0.6624	0.662	1.160 1.1722	0.927	1.865		
BNIP3		NM_004052	201849_at	Hs.14487	0.006		
0.683344043	0.6042	0.604	1.237 1.1022	0.796	1.537		
BRDG1		NM_012108	220059_at	Hs.43557	0.008		
0.696298912	0.5096	0.509	1.953 1.2662	0.786	3.458		
C1orf37		AL133052	212165_at	Hs.49744	0.008		
1.180587263	0.9115	0.911	1.263 0.9618	0.799	1.118		
C20orf24		NM_018840	217835_x_at	Hs.18406	0.002		
1.265006834	0.8766	0.876	1.478 0.8462	0.594	1.095		
C5orf13		NM_004772	201310_s_at	Hs.48306	0.008		

Supplementary Table 4						
0.558933801	0.4739	0.473	1.245	1.3263	0.566	1.506
C6orf149	NM_020408		218561_s_at	Hs.38775		0.004
0.653202457	0.5000	0.500	1.160	1.2366	0.857	1.920
C6orf32	NM_015864		206707_x_at	Hs.55945		0.008
0.699477230	0.4957	0.495	1.387	1.1104	0.964	2.049
C6orf32	AB002384		209829_at	Hs.55945		0.004
0.591125834	0.3665	0.366	1.429	1.3755	0.867	2.641
C6orf74	NM_016063		203260_at	Hs.32826		0.004
0.684187458	0.4712	0.471	1.174	1.2509	0.719	2.049
CASP8A	AB037736		222201_s_at	Hs.55821		0.006
0.370886329	0.5997	0.599	1.963	2.0325	0.744	3.285
CAST	BG111635		212580_at	Hs.43618		0.004
0.744673004	0.5509	0.550	1.645	1.1192	0.758	1.859
CDC16	NM_003903		202717_s_at	Hs.37412		0.006
0.731992153	0.5352	0.535	1.405	1.1101	0.765	1.311
CDK5R1	AL567411		204995_at	Hs.50001		0.003
0.563524559	0.5018	0.501	1.094	1.2851	0.465	1.492
CEP1	NM_007018		205642_at	Hs.24634		0.002
0.766232681	0.5892	0.589	1.106	1.2454	0.876	1.568
CGI-96	AL022316		33307_at	Hs.55353		0.004
1.372652810	0.7828	0.782	2.176	0.9073	0.654	1.147
CHAC	AB023203		214785_at	Hs.45979		0.001
0.690969754	0.2551	0.255	1.174	1.1795	0.910	1.454
CLN3	AF015593		209275_s_at	Hs.44674		0.003
1.458379825	0.8800	0.880	1.629	0.8761	0.531	1.267
CNOT3	NM_014516		203239_s_at	Hs.34357		0.004
0.681573922	0.3590	0.359	1.344	1.2240	0.810	2.092
COX8	NM_004074		201119_s_at	Hs.43390		0.008
1.245403823	0.9198	0.919	1.504	0.9140	0.799	1.183
CPSF1	U37012		33132_at	Hs.49320		0.008
0.770775302	0.5001	0.500	1.276	1.1803	0.815	1.943
CREB1	NM_004379		204312_x_at	Hs.58475		0.003
0.761551967	0.4627	0.462	1.293	1.2246	0.868	1.435
CXCL1	NM_001511		204470_at	Hs.789		0.001
2.761107697	0.9056	0.905	3.966	0.5726	0.255	4.504
CYB5	M22976		215726_s_at	Hs.46541		0.003
0.707177321	0.4730	0.473	1.052	1.2010	0.877	1.618
CYLD	AA555096		213295_at	Hs.43299		0.006
0.634982175	0.5123	0.512	1.353	1.1738	0.759	1.747
DC13	NM_020188		218447_at	Hs.38825		0.006
1.168473362	0.9437	0.943	1.969	0.9245	0.752	1.323
DCLRE1	NM_022487		219678_x_at	Hs.52415		0.003
0.839486595	0.7201	0.720	1.717	1.0946	0.925	1.520
DHX8	NM_004941		203334_at	Hs.46310		0.001
1.166253119	0.9605	0.960	1.574	0.9038	0.547	1.182

Supplementary_Table_4						
DKFZP56	NM_014042		204218_at	Hs.38044	0.002	
1.283913702	0.5369	0.536	1.640	0.8353	0.717	1.036
4M082						
DKFZp68	NM_019045		219297_at	Hs.98510	0.008	
0.822637821	0.4460	0.446	1.152	1.1021	0.845	1.365
6L20145						
DPH2L1;	NM_001383		202632_at	Hs.51385	0.008	
1.377157687	0.7447	0.744	1.776	0.8929	0.661	1.265
OVCA1						
DZIP3	BG502305		213186_at	Hs.40921	0.008	
0.772616880	0.5242	0.524	1.388	1.1730	0.804	1.759
E46L	AW241832		208832_at	Hs.47512	0.000	
0.646124791	0.6369	0.636	1.198	1.2397	0.893	1.414
EDAR	NM_022336		220048_at	Hs.17197	0.008	
0.680431057	0.3681	0.368	1.710	1.2335	0.816	2.004
EPM2A	NM_005670		205231_s_at	Hs.48669	0.000	
0.677419350	0.3347	0.334	1.070	1.2194	0.848	1.482
EXTL2	AF000416		209537_at	Hs.35763	0.004	
0.757221606	0.4610	0.461	1.264	1.2611	0.865	2.400
FLJ10287	NM_019083		219130_at	Hs.44037	0.000	
0.589930880	0.5660	0.566	1.362	1.3356	0.991	1.689
FLJ10842	NM_018238		218568_at	Hs.56165	0.008	
0.730530701	0.4050	0.405	1.188	1.0955	0.710	1.762
FLJ11806	N64802		213063_at	Hs.32584	0.003	
0.693181801	0.5172	0.517	1.079	1.1322	0.574	1.739
FLJ14007	NM_024699		218919_at	Hs.39039	0.006	
0.696844061	0.5179	0.517	1.546	1.1342	0.863	1.358
FLJ20152	NM_019000		218532_s_at	Hs.48170	0.006	
0.463507856	0.3693	0.369	1.733	1.6676	0.689	4.163
FLJ20249	NM_015590		220596_at	Hs.19383	0.003	
0.543394558	0.3871	0.387	1.252	1.2031	0.844	1.441
FLJ20265	NM_017733		218652_s_at	Hs.7099	0.002	
0.738608863	0.5366	0.536	1.171	1.2285	0.898	1.670
FLJ20373	NM_017792		218181_s_at	Hs.43155	0.000	
0.661528939	0.6422	0.642	1.253	1.1943	0.952	1.708
FLJ20531	NM_017865		220661_s_at	Hs.37770	0.000	
0.635812275	0.7271	0.727	1.265	1.4396	0.930	1.786
FLJ20604	NM_017897		219133_at	Hs.55781	0.006	
0.840216558	0.8337	0.833	1.110	1.0673	0.864	1.781
FLJ21908	NM_024604		218842_at	Hs.43785	0.003	
0.715629949	0.4885	0.488	1.114	1.1217	0.818	1.927
FLJ23017	NM_022840		219698_s_at	Hs.12688	0.003	
0.748086494	0.6363	0.636	1.176	1.2257	0.937	1.584
FLJ23235	NM_024943		220169_at	Hs.37414	0.004	
0.708754168	0.0795	0.079	1.118	1.2889	0.609	1.878
FLOT1	AF085357		208749_x_at	Hs.17998	0.006	
1.440791308	0.8501	0.850	1.810	0.8946	0.744	1.250

Supplementary_Table_4

GAPD	BF689355	213453_x_at	Hs.54457	0.000		
1.366829763	0.6297	0.629	1.495	0.8602	0.586	1.030
GAPD	AK026525	217398_x_at	Hs.47972	0.002		
1.290628040	0.7277	0.727	1.322	0.8815	0.618	1.067
GAPD	BE561479	212581_x_at	Hs.54457	0.008		
1.147080850	0.7235	0.723	1.254	0.9323	0.761	1.055
GCHFR	NM_005258	204867_at	Hs.53079	0.008		
1.252011660	0.8114	0.811	1.973	0.8639	0.531	1.321
GCLC	BF676980	202922_at	Hs.27126	0.006		
0.757486100	0.6057	0.605	1.141	1.1012	0.785	1.492
GPRK5	NM_005308	204396_s_at	Hs.52462	0.001		
0.663916678	0.4259	0.425	1.033	1.2258	0.704	2.147
GTF2F1	NM_002096	202356_s_at	Hs.68257	0.004		
1.169204353	0.7728	0.772	1.296	0.9377	0.690	1.241
HCG8; HCGVIII; HCGVIII-1	X92110	215985_at	Hs.30203	0.004		
0.716146528	0.3469	0.346	1.315	1.2993	0.932	2.014
HLA-DMB	NM_002118	203932_at	Hs.1162	0.008		
0.623293678	0.4685	0.468	1.315	1.3197	0.539	2.316
HMG20A	NM_018200	218152_at	Hs.69594	0.008		
0.687383616	0.5783	0.578	1.231	1.2692	0.741	2.171
hnRNP3	BE867771	211929_at	Hs.51653	0.008		
0.784464947	0.3421	0.342	1.518	1.1339	0.907	1.762
HNRPDL	AI762552	212454_x_at	Hs.52710	0.003		
0.785202321	0.5032	0.503	1.208	1.1008	0.920	1.535
HNRPR	BC001449	208766_s_at	Hs.58484	0.008		
0.832182012	0.8032	0.803	1.023	1.0743	0.786	1.315
HRMT1L1	AL570294	221564_at	Hs.15416	0.006		
0.671230976	0.5995	0.599	1.267	1.2462	0.762	1.884
HTGN29	NM_020199	203024_s_at	Hs.35517	0.006		
0.776345582	0.7036	0.703	1.460	1.0793	0.977	1.749
IF2	NM_015904	201025_at	Hs.15868	0.001		
0.770361036	0.6782	0.678	1.228	1.1449	0.970	1.333
IGF2R	BG031974	201392_s_at	Hs.48706	0.004		
1.466406289	0.8744	0.874	2.038	0.8064	0.549	1.310
INPP4B	NM_003866	205376_at	Hs.48083	0.008		
0.562083332	0.3917	0.391	1.197	1.2827	0.570	1.782
IPP	NM_005897	219843_at	Hs.15718	0.008		
0.729607214	0.6311	0.631	1.214	1.2936	0.705	2.367
IRAK1	NM_001569	201587_s_at	Hs.52281	0.002		
1.292410713	0.8815	0.881	1.776	0.8805	0.770	1.111
ITGA6	NM_000210	201656_at	Hs.13339	0.002		
0.590289317	0.4370	0.437	1.324	1.4770	0.851	2.154
ITPR1	NM_002222	203710_at	Hs.56729	0.006		
0.666482122	0.7318	0.731	1.256	1.3107	0.566	1.969

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JAG1	U77914	216268_s_at	Hs.22401	0.001		
2.871402540	0.7627	0.762	4.849	0.6159	0.468	3.306
JAG1	U73936	209099_x_at	Hs.22401	0.006		
2.207514073	0.7956	0.795	5.215	0.6940	0.454	3.599
JTB	BC004239	210927_x_at	Hs.6396	0.001		
1.140656892	0.7360	0.736	1.433	0.9476	0.655	1.021
JUP	NM_021991	201015_s_at	Hs.51417	0.001		
0.402138936	0.2992	0.299	1.498	1.8871	0.623	3.665
KAB	NM_014812	207719_x_at	Hs.53363	0.006		
0.746203770	0.5765	0.576	1.203	1.1072	0.879	1.361
KIAA0372	NM_014639	203049_s_at	Hs.48286	0.002		
0.685472514	0.4938	0.493	1.172	1.1878	0.762	2.337
KIAA0922	AL136932	209760_at	Hs.20557	0.003		
0.806343581	0.4594	0.459	1.089	1.0406	0.902	1.583
DKFZp58						
KIAA1007	NM_016284	200861_at	Hs.46092	0.006		
0.834049763	0.5207	0.520	1.051	1.0513	0.862	1.218
KIAA1040	AI760249	212754_s_at	Hs.38937	0.004		
0.675492515	0.5434	0.543	1.181	1.2776	0.813	1.654
KIAA1078	AW593213	212765_at	Hs.23585	0.002		
0.573622380	0.6005	0.600	2.178	1.3331	0.821	1.710
KPNA1	BC002374	202058_s_at	Hs.57066	0.006		
0.773509050	0.6944	0.694	1.076	1.0757	0.822	1.263
LGALS3	BC001120	208949_s_at	Hs.53108	0.000		
1.632151582	0.8467	0.846	1.371	0.6918	0.442	1.109
LGTN	NM_006893	218253_s_at	Hs.49758	0.006		
0.861813594	0.6510	0.651	1.108	1.0690	0.920	1.495
LOC2210	AU150943	212771_at	Hs.66762	0.001		
0.688427274	0.4551	0.455	1.126	1.1736	0.865	1.593
LPHN1	AI525402	47560_at	Hs.56530	0.006		
0.660447227	0.3345	0.334	1.431	1.0958	0.903	1.659
LPIN2	U55968	202459_s_at	Hs.13234	0.001		
0.665846917	0.4247	0.424	1.282	1.2447	0.844	1.713
LRPPRC	AF052133	211971_s_at	Hs.36808	0.006		
0.790227714	0.8339	0.833	1.244	1.2012	0.920	1.637
LRRN3	AI221950	209840_s_at	Hs.3781	0.000		
0.416931634	0.2996	0.299	1.120	1.5577	0.856	2.289
LRRN3	AL442092	209841_s_at	Hs.3781	0.000		
0.326572435	0.3944	0.394	1.443	1.7511	0.777	3.454
LYZ	AV711904	213975_s_at	Hs.52457	0.003		
1.179622245	0.9646	0.964	2.178	0.9425	0.594	1.234
MADH2	AW151617	203075_at	Hs.12253	0.001		
0.809716893	0.7698	0.769	1.151	1.1735	0.915	1.446
MADH2	NM_005901	203077_s_at	Hs.12253	0.000		
0.764126781	0.5781	0.578	1.200	1.1258	0.963	1.562

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MADH4	NM_005359	202527_s_at	Hs.75862	0.008
0.738124739	0.4629 0.462	1.224 1.2050	0.840	2.018
MAN1C1	NM_020379	218918_at	Hs.19704	0.000
0.562790433	0.4101 0.410	1.681 1.5222	0.980	2.516
MAP3K7	NM_003188	206854_s_at	Hs.48596	0.008
0.807441564	0.7833 0.783	1.163 1.0955	0.963	1.194
MBNL1	NM_021038	201153_s_at	Hs.47800	0.008
0.769779051	0.6599 0.659	1.269 1.1974	0.947	1.520
MEN1	NM_000244	202645_s_at	Hs.42334	0.008
0.757909418	0.5659 0.565	1.126 1.1579	0.799	1.498
MGC2963	NM_031298	221255_s_at	Hs.30011	0.001
1.383034266	0.9529 0.952	1.401 0.7722	0.629	1.157
MGC3067	NM_024295	219402_s_at	Hs.24157	0.003
1.502613343	0.6226 0.622	1.587 0.7380	0.518	1.108
MMP9	NM_004994	203936_s_at	Hs.29741	0.008
1.765131944	0.7773 0.777	14.17 0.8507	0.482	1.533
MRPL19; RLX1; RPML15; MRP-L15; KIAA010 4; MGC2067 5; RPML15	AC005034	216305_s_at	Hs.30380	0.001
0.658335968	0.4963 0.496	1.439 1.2902	0.848	2.172
MRTF-B	NM_014048	218259_at	Hs.49143	0.008
0.583547909	0.5873 0.587	1.724 1.2777	0.929	1.768
MST4	NM_016542	218499_at	Hs.44424	0.004
0.775816505	0.6912 0.691	1.291 1.1692	0.890	1.621
MTMR4	AB014547	212277_at	Hs.51437	0.008
0.789043141	0.6667 0.666	1.125 1.1203	0.800	1.494
MTSS1	NM_014751	203037_s_at	Hs.33699	0.003
0.782176623	0.5050 0.505	1.352 1.1716	0.839	1.507
NAT1	NM_000662	214440_at	Hs.15595	0.008
1.297275468	0.9206 0.920	1.840 0.8401	0.607	1.364
NCDN	AB011179	209556_at	Hs.12187	0.002
0.819887406	0.6131 0.613	1.101 1.1040	0.817	1.496
NCOA1	U19179	209106_at	Hs.41229	0.008
0.757497592	0.5653 0.565	1.560 1.0914	0.850	1.346
NEDD4	D42055	213012_at	Hs.1565	0.008
0.653348950	0.4408 0.440	1.381 1.2982	0.827	1.837
NFATC3	NM_004555	207416_s_at	Hs.34171	0.008
0.774557154	0.6502 0.650	1.159 1.0823	0.893	1.833
NFX1	AW291398	202584_at	Hs.41307	0.004
0.804744952	0.7975 0.797	1.147 1.1686	0.927	1.269
NICE-4	BC003170	209947_at	Hs.49055	0.000
0.669119780	0.4265 0.426	1.051 1.1294	0.948	1.517

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NP220	AI357871	213775_x_at	Hs.43440	0.008		
0.753437791	0.5952	0.595	1.811	1.1411	0.896	1.940
NP220;	AF273049	211257_x_at	Hs.43440	0.004		
0.731470891	0.6697	0.669	1.384	1.1545	0.707	1.641
MGC26130						
NUP210	NM_024923	220035_at	Hs.47552	0.008		
0.760437483	0.5181	0.518	2.181	1.1489	0.840	1.748
NUP50	AF267865	218294_s_at	Hs.47510	0.003		
0.871060218	0.5774	0.577	1.150	1.1087	0.968	1.515
OGG1	NM_016821	205760_s_at	Hs.38027	0.003		
0.728366258	0.5744	0.574	1.164	1.1197	0.771	2.448
ORC5L	AF081459	211212_s_at	Hs.43294	0.008		
0.729103702	0.4321	0.432	1.182	1.1322	0.842	1.610
P38IP	NM_017569	220408_x_at	Hs.43581	0.003		
0.744199171	0.6972	0.697	1.040	1.1600	0.719	1.507
P38IP	AW003334	221774_x_at	Hs.43581	0.002		
0.740311976	0.6537	0.653	1.225	1.1894	0.915	1.526
p44S10	NM_014814	202753_at	Hs.15253	0.001		
1.358370967	0.9937	0.993	1.589	0.9010	0.766	1.252
PAFAH1	L13386	200815_s_at	Hs.77318	0.006		
1.359305177	0.8905	0.890	1.637	0.8645	0.607	1.154
PAK2	AF092132	208878_s_at	Hs.51853	0.002		
0.828762927	0.5933	0.593	1.100	1.1186	0.900	1.837
PAK2	AF092132	208877_at	Hs.51853	0.006		
0.608889782	0.4529	0.452	1.318	1.3018	0.783	1.487
PDXK	NM_003681	202671_s_at	Hs.28449	0.004		
1.642937642	0.6980	0.698	2.172	0.7482	0.539	1.267
PEFKM	U24183	210976_s_at	Hs.75160	0.003		
0.792110959	0.6405	0.640	1.164	1.0902	0.697	1.327
PKIA	NM_006823	204612_at	Hs.43370	0.008		
0.618371205	0.5712	0.571	1.425	1.1671	0.745	2.298
POT1	BC002923	204353_s_at	Hs.31968	0.004		
0.678810420	0.6975	0.697	1.214	1.2730	0.900	1.960
PP	NM_021129	217848_s_at	Hs.43740	0.000		
0.651410775	0.6256	0.625	1.162	1.1674	0.993	1.417
PP1B	NM_000942	200967_at	Hs.43493	0.000		
1.588310833	0.8543	0.854	1.613	0.8658	0.645	1.006
PPP2R5	NM_006243	202187_s_at	Hs.49768	0.001		
1.255404237	0.7868	0.786	1.587	0.9004	0.735	1.099
PRG1	J03223	201858_s_at	Hs.1908	0.008		
1.453335795	0.5918	0.591	1.282	0.7631	0.576	1.492
PSMA7	NM_002792	201114_x_at	Hs.23395	0.001		
1.196144820	0.8030	0.803	1.324	0.9421	0.662	1.024
PTD002	NM_016144	218439_s_at	Hs.48313	0.004		
0.722579852	0.5648	0.564	1.189	1.1118	0.682	1.562

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PTK2	AL037339	208820_at	Hs.39548	0.004	
0.653100801	0.4090	0.409	1.258	1.2115	0.780
1.510					
PTP4A2	U48297	208616_s_at	Hs.47047	0.006	
1.167428898	0.9121	0.912	1.112	0.9126	0.806
1.047					
PTPRO	NM_002848	208121_s_at	Hs.16087	0.001	
0.617181585	0.5442	0.544	1.291	1.4052	0.853
2.581					
PUM1	BG474429	201165_s_at	Hs.28170	0.008	
0.842515900	0.4751	0.475	1.035	1.1229	0.860
1.285					
QRS11	NM_018292	218949_s_at	Hs.40691	0.008	
0.712186794	0.6481	0.648	1.342	1.2259	0.586
2.752					
RAE1	NM_003610	201558_at	Hs.37169	0.006	
1.250013509	0.9691	0.969	1.999	0.9031	0.587
1.394					
RASA1	M23612	210621_s_at	Hs.55350	0.000	
0.722320584	0.5231	0.523	1.084	1.1609	0.988
1.756					
RERE	AB036737	200940_s_at	Hs.46304	0.003	
0.710878505	0.6192	0.619	1.105	1.0674	0.790
1.374					
RG52	NM_002923	202388_at	Hs.78944	0.000	
1.330501928	0.7307	0.730	1.495	0.9108	0.503
1.013					
RICS	NM_014715	203431_s_at	Hs.44037	0.008	
0.617449642	0.1266	0.126	1.503	1.1301	0.778
2.148					
RIF1	NM_018372	220235_s_at	Hs.25245	0.004	
0.695798332	0.5826	0.582	1.039	1.2036	0.460
2.195					
RPA1	BG398414	201528_at	Hs.46192	0.003	
0.783483478	0.5959	0.595	1.113	1.1688	0.637
1.594					
RPN2	BC003560	208689_s_at	Hs.37089	0.003	
1.343797525	0.8287	0.828	1.425	0.8470	0.714
1.123					
RPN2	AL514285	213491_x_at	Hs.37089	0.003	
1.298556001	0.9743	0.974	1.711	0.9051	0.693
1.368					
RPS6KA	AF074393	204633_s_at	Hs.51022	0.001	
0.837424188	0.5268	0.526	1.1095	1.0953	0.962
1.568					
S100A10	NM_002966	200872_at	Hs.14387	0.006	
1.578571294	0.8310	0.831	2.235	0.7278	0.635
1.178					
S100A8	NM_002964	202917_s_at	Hs.41607	0.006	
1.291983905	0.9829	0.982	1.679	0.8681	0.775
1.420					
S100A9	NM_002965	203535_at	Hs.11240	0.003	
1.514143549	0.9278	0.927	1.767	0.8185	0.669
1.311					
SEC24C	NM_004922	202361_at	Hs.81964	0.000	
1.263002215	0.9809	0.980	1.823	0.8536	0.756
1.066					
SEPHS1	BC000941	208939_at	Hs.12402	0.004	
0.829006477	0.4547	0.454	1.083	1.0918	0.724
1.348					
SGPP1	NM_030791	221268_s_at	Hs.24678	0.001	
0.566027410	0.2950	0.295	1.568	1.3150	0.910
1.691					
SH3GL1	NM_003025	201851_at	Hs.97616	0.006	
1.378040511	0.7852	0.785	1.890	0.7853	0.573
1.492					
SH3GLB1	AF263293	209091_s_at	Hs.13630	0.002	
1.245390746	0.7334	0.733	1.616	0.9050	0.664
1.032					

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SHCBP1	NM_024745	219493_at	Hs.12325	0.008
1.674507355	0.7128 0.712	1.970 0.7515	0.318	1.249
SIRT7	NM_016538	218797_s_at	Hs.52864	0.004
1.224838710	0.9225 0.922	1.518 0.9055	0.712	1.252
SLC1A4	BF340083	209610_s_at	Hs.32387	0.004
1.534340248	0.6016 0.601	2.088 0.7813	0.164	1.170
SLC30A1	AI972416	212907_at	Hs.51946	0.004
1.439147917	0.8616 0.861	2.300 0.7334	0.492	1.140
SLC35B1	NM_005827	202433_at	Hs.15407	0.003
1.445839197	0.7296 0.729	1.598 0.8553	0.676	1.088
SMARCA1	NM_003069	203874_s_at	Hs.15229	0.008
0.643718918	0.2961 0.296	1.174 1.1399	0.778	1.412
SMARCA2	AV725365	206542_s_at	Hs.29899	0.003
0.742443363	0.6029 0.602	1.403 1.0864	0.925	1.787
SNAPC3	NM_003084	204001_at	Hs.54629	0.004
0.703416862	0.4530 0.453	1.138 1.2187	0.715	1.530
SNX4	AA524345	212652_s_at	Hs.50724	0.000
0.795600481	0.3873 0.387	1.002 1.1674	0.939	1.641
SRP19	NM_003135	205335_s_at	Hs.48309	0.003
1.176941306	0.9865 0.986	1.451 0.9200	0.565	1.122
ST13	U17714	208666_s_at	Hs.54630	0.002
0.665880093	0.4843 0.484	1.070 1.2060	0.766	1.566
STAU	AJ132258	213037_x_at	Hs.37018	0.000
1.216418212	0.9160 0.916	1.290 0.9011	0.795	1.056
STAU	NM_004602	207320_x_at	Hs.37018	0.000
1.141324390	0.9910 0.991	1.180 0.9669	0.894	1.113
TCEAL1	NM_004780	204045_at	Hs.95243	0.001
0.667446619	0.4722 0.472	1.191 1.1313	0.799	1.436
TFB1M	NM_016020	219169_s_at	Hs.27990	0.006
0.717309856	0.5639 0.563	1.625 1.2431	0.779	1.531
TIA1	NM_022037	201447_at	Hs.51607	0.008
0.700954169	0.4288 0.428	1.218 1.2377	0.853	1.829
TIA1	NM_022037	201449_at	Hs.51607	0.001
0.608020276	0.3338 0.333	1.186 1.1700	0.736	1.535
TIAM1	U90902	213135_at	Hs.51722	0.001
0.665558367	0.6181 0.618	1.151 1.0732	0.712	1.178
TIMM23	NM_006327	218118_s_at	Hs.52430	0.001
1.609044934	0.8725 0.872	1.940 0.8401	0.464	1.871
TNIP2	AA522816	48531_at	Hs.36855	0.008
1.157769790	0.8366 0.836	1.633 0.9414	0.620	1.111
TOMM70	BC003633	201512_s_at	Hs.22725	0.001
0.686464985	0.7229 0.722	1.077 1.1421	0.729	1.364
TRA@	AW966434	215524_x_at	Hs.36938	0.001
0.586254177	0.4205 0.420	1.140 1.1853	0.748	1.850
TRAM2	AI986461	202368_s_at	Hs.52018	0.003

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1.582788120	0.3773	0.377	1.735	0.8934	0.753	1.029
TRIAD3	BC000787		218425_at		Hs.48745	0.001
0.860240506	0.4613	0.461	1.040	1.1107	0.892	1.622
TRIM	AJ240085		217147_s_at		Hs.13870	0.003
0.538209465	0.3728	0.372	1.571	1.3915	0.550	2.815
UBE2V2	U62136		209096_at		Hs.49169	0.001
0.745681612	0.5169	0.516	1.217	1.1132	0.937	1.377
UCHL5	NM_016017		220083_x_at		Hs.14546	0.004
0.857565670	0.4428	0.442	1.102	1.0688	0.816	1.601
ULK2	NM_014683		204063_s_at		Hs.16876	0.003
0.775725622	0.6862	0.686	1.172	1.1217	0.854	1.312
ULK2	BG526973		204062_s_at		Hs.16876	0.003
0.664152110	0.5917	0.591	1.377	1.3184	0.895	1.773
UST	NM_005715		205139_s_at		Hs.30925	0.006
0.648763518	0.5592	0.559	1.2	1.1710	0.733	1.797
VRK2	NM_006296		205126_at		Hs.46862	0.006
0.702970320	0.6067	0.606	1.078	1.2130	0.794	2.443
WHSC1L	NM_017778		218173_s_at		Hs.32099	0.006
0.807500612	0.7358	0.735	1.074	1.1264	0.721	1.492
X123	AA524029		213900_at		Hs.11800	0.004
0.748087918	0.5311	0.531	1.149	1.2161	0.679	1.835
YWHAE	AA502643		213655_at		Hs.51385	0.003
1.594024325	0.5620	0.562	2.663	0.7889	0.247	1.094
ZNF137	NM_003438		207394_at		Hs.37364	0.001
0.585919997	0.4850	0.485	1.097	1.2590	0.633	1.863
ZNF313	NM_018683		200868_s_at		Hs.14494	0.006
1.284783916	0.8854	0.885	1.503	0.8876	0.719	1.144
	N95443		213405_at		Hs.52904	0.006
0.803410601	0.6647	0.664	1.316	1.1190	0.841	1.494
	BC000519		201613_s_at		Hs.34324	0.002
0.792186274	0.6665	0.666	1.286	1.1516	0.945	1.584
	AL031589		217092_x_at		Hs.58524	0.003
0.766507602	0.6778	0.677	1.128	1.1723	0.783	1.663
	AA355179		204552_at		Hs.58672	0.004
0.766456745	0.5300	0.530	1.226	1.1512	0.912	1.421

Supplementary_Table_5

Supplementary Table 5:

Spearman correlation between microarray and taqman gene expression results

Affymetrix Probe ID	unigeneID	Common Name	r	p
204174_at	Hs.507658	ALOX5AP	0.8018	<.0001
204470_at	Hs.789	CXCL1	0.8182	<.0001
209774_x_at	Hs.75765	CXCL2	0.9506	<.0001
208891_at	Hs.298654	DUSP6	0.8314	<.0001
208893_s_at	Hs.298654	DUSP6	0.8888	<.0001
208892_s_at	Hs.298654	DUSP6	0.8275	<.0001
207674_at	Hs.193122	FCAR	0.8982	<.0001
211307_s_at	Hs.193122	FCAR	0.8804	<.0001
211816_x_at	Hs.193122	FCAR	0.8775	<.0001
39402_at	Hs.126256	IL1B	0.9851	<.0001
205067_at	Hs.126256	IL1B	0.9401	<.0001
207859_x_at	Hs.624	IL8	0.9516	<.0001
211506_s_at	Hs.624	IL8	0.9459	<.0001
201859_at	Hs.1908	PRG1	0.6509	0.0008
201858_s_at	Hs.1908	PRG1	0.678	0.0004
202388_at	Hs.78944	RGS2	0.8073	<.0001
204614_at	Hs.514913	SERPINE2	0.9279	<.0001

Supplementary_Table_6

Supplementary Table 6

S. aureus vs E. coli infection; classifier genes: List of 30 classifier genes discriminating samples obtained from patients with S. aureus and E. coli infections (data shown Figure 3b and Figure 4). P-values = Class comparison results - Mann Whitney test

Common	S.aureus (n=10)		Affymetrix E.coli (n=10)		uniGeneX Max	P-value	Fold Sa/EC
	Median	GenBank Min Max	Probe ID Median	Min			
ACTG1 1.222744622		AU145192 21700 2170	212363_x_at 2641 18876.		Hs.51458 1627	0.006 2688	
CGI-96 1.372652864		AL022316 179.2 179.2	33307_at 498.1 207.7		Hs.55353 149.9	0.004 262.7	
CXCL1 2.761107533		NM_001511 122.8 122.8	204470_at 537.9 77.65		Hs.789 34.7	0.001 610.8	
GAPD 1.366829676		BF689355 10844. 1084	213453_x_at 2575 14815.		Hs.54457 1009	0.000 1773	
JAG1 2.871402327		U77914 101.1 101.1	216268_s_at 642.8 81.65		Hs.22401 62.1	0.001 438.3	
MGC2963 1.383034223		NM_031298 591.3 591.3	221255_s_at 869.4 479.2		Hs.30011 390.3	0.001 718.4	
MMP9 1.765132002		NM_004994 283.8 283.8	203936_s_at 5174.6 310.6		Hs.29741 176.3	0.008 559.7	
p44S10 1.358370872		NM_014814 2668.6 2668.6	202753_at 4267.5 2419.7		Hs.15253 2057.9	0.001 3362.8	
PPIB 1.588310844		NM_000942 3111.6 3111.6	200967_at 5875.4 3153.3		Hs.43493 2352.2	0.000 3664.5	
PSMA7 1.196144741		NM_002792 2268.3 2268.3	201114_x_at 3741.3 2661.3		Hs.23395 1871.6	0.001 2893.1	
RGS2 1.330501814		NM_002923 5869.9 5869.9	202388_at 1201 7316.4		Hs.78944 4046.4	0.000 8141.9	
SEC24C 1.263002169		NM_004922 873.8 873.8	202361_at 1624.5 760.45		Hs.81964 673.8	0.000 950	
STAU 1.216418304		AJ132258 1923.7 1923.7	213037_x_at 2709.3 1892.4		Hs.37018 1670.4	0.000 2217.5	
STAU 1.141324436		NM_004602 2135 2135	207320_x_at 2543.8 2083.1		Hs.37018 1927	0.000 2399.4	
TRAM2 1.582788122		AI986461 125.9 125.9	202368_s_at 579.1 298.05		Hs.52018 251.5	0.003 343.5	
AF1Q 0.742133002		BC006471 318 318	211071_s_at 763.4 645.1		Hs.75823 556.6	0.001 788.5	
EIF5B 0.770361041		NM_015904 141.1 141.1	201025_at 255.6 238.2		Hs.15868 201.9	0.001 277.4	
FLJ10287 0.589930924		NM_019083 159.5 159.5	219130_at 383.9 376.4		Hs.44037 279.5	0.000 476.1	

Supplementary_Table_6

FLJ20152 0.463507885	NM_019000 162.2 162.2	218532_s_at 761.4 732.35	Hs.48170 302.8	0.006 1828.3
JUP 0.402138951	NM_021991 98.6 98.6	201015_s_at 493.8 621.8	Hs.51417 205.4	0.001 1207.7
LRRN3 0.416931637	AI221950 121 121	209840_s_at 452.5 629	Hs.3781 345.7	0.000 924.5
LRRN3 0.326572423	AL442092 164.9 164.9	209841_s_at 603.7 732.15	Hs.3781 325	0.000 1444.3
MAN1C1 0.562790434	NM_020379 237.7 237.7	218918_at 974.6 882.3	Hs.19704 568.1	0.000 1458.5
MAP4K4 0.661528912	NM_017792 259.9 259.9	218181_s_at 507.1 483.35	Hs.43155 385.6	0.000 691.5
PP 0.651410812	NM_021129 1957.4 1957.4	217848_s_at 3635.9 3652.1	Hs.43740 3109.3	0.000 4435.8
RASA1 0.722320600	M23612 267.2 267.2	210621_s_at 554 592.95	Hs.55350 504.7	0.000 897
SGPP1 0.566027397	NM_030791 81.9 81.9	221268_s_at 435.3 365	Hs.24678 252.6	0.001 469.6
SMAD2 0.764126770	NM_005901 190.4 190.4	203077_s_at 395.4 370.75	Hs.12253 317.2	0.000 514.4
SNX4 0.795600463	AA524345 157.6 157.6	212652_s_at 408.1 475.05	Hs.50724 382.2	0.000 668
UBAP2L 0.669119783	BC003170 195 195	209947_at 480.5 516.35	Hs.49055 433.8	0.000 693.9

Supplementary_Table_7

Supplementary Table 7

E. coli vs S. pneumoniae; class comparison results: Comparison of gene expression levels (normalized values) between patients with acute E.coli infection and patients with acute S.pneumoniae infection - $P < 0.01$, Mann-Whitney test = 264 genes. Expression patterns are represented supplementary Figure 2a.

E.coli (n=11)			Affymetrix S.pneumoniae (n=11)			P-value	Fold Sp/Ec
Common Median	GenBank Min Max	Probe ID Median Min Max	uniGeneI Max				
FLJ13220 0.585152836	NM_021927 0.8622 0.862	218884_s_at 1.260 0.6836	Hs.54641 0.416	0.000 1.014			
VRK2 0.626862759	NM_006296 0.9088 0.908	205126_at 2.321 0.8468	Hs.46862 0.614	0.000 1.037			
STAT1; 0.408639387 ISGF-3; STAT91	M97935 0.8030 0.803	AFFX- 4.703 0.6575 HUMISGF3 A/M97935_	--- 0.264	0.000 1.814			
AF1Q 0.679697147	BC006471 0.9636 0.963	211071_s_at 1.392 0.7770	Hs.75823 0.410	0.000 1.122			
TCN1 3.332568055	NM_001062 0.5507 0.550	205513_at 2.354 2.6585	Hs.2012 0.812	0.000 15.51			
C20orf24 1.208514866	NM_018840 0.6610 0.661	217835_x_at 1.043 1.0802	Hs.18406 0.770	0.000 1.900			
STAT1; 0.269299213 ISGF-3; STAT91 FLJ10055 1.848766959	M97935 0.8803 0.880 NM_017983 0.3985 0.398	AFFX- 3.278 0.5088 HUMISGF3 A/M97935_ 203827_at 1.687 1.2624	--- 0.412 Hs.46396 0.997	0.000 1.981 0.000 2.983			
PADI4 2.868701486	NM_012387 0.4392 0.439	220001_at 1.056 1.9703	Hs.52296 0.623	0.000 11.67			
STAT1; 0.553456684 ISGF-3; STAT91	M97935 0.7807 0.780	AFFX- 2.855 0.7437 HUMISGF3 A/M97935_3	--- 0.205	0.000 1.276			
IL1R2 4.117744880	NM_004633 0.0674 0.067	205403_at 5.947 2.5375	Hs.25333 0.791	0.000 74.27			
HIP1 1.439311439	NM_005338 0.5376 0.537	205425_at 1.083 1.2472	Hs.32926 0.699	0.000 3.146			
STAT1; 0.228370987 ISGF-3; STAT91	M97935 0.7187 0.718	AFFX- 6.417 0.4536 HUMISGF3 A/M97935_5	--- 0.327	0.000 1.804			
PPIA 0.594936698	AI191118 0.7185 0.718	217602_at 2.215 0.8318	Hs.35633 0.267	0.000 1.461			
LTF 13.61686839	NM_002343 0.0212 0.021	202018_s_at 5.314 7.3436	Hs.52951 0.085	0.000 21.09			
JTB	AF151056	210434_x_at	Hs.6396	0.000			

Supplementary_Table_7						
1.156680121	0.8269	0.826	1.126	1.0898	0.954	1.623
C20orf3	BC000353		206656_s_at	Hs.47233		0.000
1.688941958	0.4829	0.482	1.109	1.3996	0.858	2.249
FLJ20195	AI949010		57739_at	Hs.55879		0.000
0.811719192	0.9075	0.907	1.486	0.9125	0.619	1.075
NKTR	NM_005385		202380_s_at	Hs.52950		0.000
0.692722067	0.8382	0.838	1.803	0.8171	0.575	1.198
MRPL9	AB049636		211594_s_at	Hs.28893		0.000
0.711010299	0.6218	0.621	1.719	0.8430	0.285	1.182
SORL1	NM_003105		203509_at	Hs.36859		0.000
1.492742437	0.7319	0.731	1.071	1.2601	0.844	2.335
MMP9	NM_004994		203936_s_at	Hs.29741		0.000
7.040609526	0.4151	0.415	1.413	4.7257	0.651	30.83
GBP2	NM_004120		202748_at	Hs.38656		0.000
0.629205921	0.9002	0.900	2.078	0.7232	0.600	1.096
KIAA0971	AK021557		216996_s_at	Hs.84429		0.000
0.800946971	0.9223	0.922	1.244	0.8764	0.349	1.154
TPD52L2	NM_003288		201379_s_at	Hs.47329		0.001
1.341076315	0.7210	0.721	1.405	1.1322	0.888	2.344
ENPP2	L35594		209392_at	Hs.19097		0.001
0.451076326	0.6557	0.655	2.741	0.7180	0.188	1.214
C20orf13	NM_017714		219443_at	Hs.36993		0.001
0.705134024	0.8199	0.819	1.330	0.7602	0.215	1.229
EPM2A	NM_005670		205231_s_at	Hs.48669		0.001
0.674982682	0.7709	0.770	1.346	0.7733	0.539	1.126
CXCL10	NM_001565		204533_at	Hs.41392		0.001
0.5 0.7937	0.793	12.71	0.6947	0.153	1.874	
CHI3L1	M80927		209396_s_at	Hs.38220		0.001
9.620332716	0.0440	0.044	3.781	5.8327	0.444	21.10
CAMP	U19970		210244_at	Hs.51120		0.001
5.115320430	0.0580	0.058	5.440	3.0238	0.244	19.65
KIAA1240	AB033066		213387_at	Hs.46786		0.001
0.583915142	0.7060	0.706	1.473	0.6744	0.459	1.102
CYP4F3	NM_000896		206515_at	Hs.10624		0.001
6.163912225	0.1607	0.160	1.455	3.8677	0.341	16.85
ALOX5AP	NM_001629		204174_at	Hs.50765		0.001
2.005505616	0.4782	0.478	1.301	1.5337	0.832	4.338
SCA1	NM_000332		203232_s_at	Hs.43496		0.001
1.374257289	0.5458	0.545	1.063	1.1821	0.697	1.780
PSMB9	NM_002800		204279_at	Hs.38108		0.001
0.642477028	0.8523	0.852	1.797	0.7734	0.414	1.187
PAQR3	AW173157		213372_at	Hs.55865		0.001
0.690946243	0.7067	0.706	1.565	0.7188	0.565	1.286
C14orf112	AW088547		217645_at	Hs.13710		0.001
0.661017009	0.9842	0.984	1.405	0.7293	0.476	1.436

Supplementary_Table_7						
SP110	AF280094	209761_s_at	Hs.14515	0.001		
0.740863936	0.8938 0.893	1.435 0.8630	0.553	1.263		
TADA3L	AK024982	215273_s_at	Hs.38639	0.001		
1.279031921	0.5675 0.567	1.178 1.1084	0.905	1.754		
RECQL	BC001052	210568_s_at	Hs.23506	0.001		
0.731759672	0.9177 0.917	1.698 0.8808	0.434	1.349		
NFKB1	M55643	209239_at	Hs.43192	0.001		
0.905001534	0.9306 0.930	1.519 0.9667	0.587	1.101		
Cab45	AL571362	221972_s_at	Hs.42806	0.001		
1.182206125	0.8298 0.829	1.013 1.0963	0.848	1.601		
IGHG3	M87789	211430_s_at	Hs.51063	0.001		
3.560838865	0.1421 0.142	1.699 1.9837	0.401	3.524		
FLOT2	BC003683	211299_s_at	Hs.51403	0.001		
1.370593003	0.6688 0.668	1.095 1.1591	0.615	2.763		
SP329	NM_030793	221257_x_at	Hs.48377	0.001		
0.733659140	0.9335 0.933	1.567 0.8401	0.545	1.320		
STAT1	BC002704	209969_s_at	Hs.47094	0.001		
0.234259074	0.7242 0.724	4.095 0.3855	0.245	2.987		
WBSCR5	AF257135	221581_s_at	Hs.56607	0.001		
1.430966263	0.4187 0.418	1.298 1.2910	0.958	1.601		
UBE2L6	NM_004223	201649_at	Hs.42577	0.001		
0.620412413	0.9056 0.905	2.062 0.6948	0.439	1.288		
STAT1	NM_007315	200887_s_at	Hs.47094	0.001		
0.407492121	0.6394 0.639	2.535 0.7017	0.278	2.076		
SNRPA1	AJ130972	216977_x_at	Hs.52876	0.001		
0.693260117	0.8287 0.828	2.832 0.8615	0.680	1.367		
ISGF3G	NM_006084	203882_at	Hs.1706	0.001		
0.745313326	0.7808 0.780	1.446 0.7689	0.405	1.317		
LCN2;	NM_005564	212531_at	Hs.20423	0.001		
12.19503979	0.0858 0.085	3.191 7.7279	0.230	29.96		
NaGLT1;	AK000168	216379_x_at	Hs.37510	0.001		
7.342736666	0.3249 0.324	3.889 3.6958	0.620	16.62		
KIAA1919						
;						
IREB2	AI204981	214666_x_at	Hs.43603	0.001		
0.790932015	0.8510 0.851	2.020 0.8937	0.684	1.116		
CEACAM8	M33326	206676_at	Hs.41	0.001		
13.89591590	0.1913 0.191	8.666 10.575	0.233	42.46		
HLA-DPB1	NM_002121	201137_s_at	Hs.48513	0.001		
0.717712006	0.7199 0.719	1.961 0.7974	0.169	1.096		
PSME2	NM_002818	201762_s_at	Hs.43408	0.001		
0.593987093	0.8446 0.844	2.002 0.8265	0.438	2.087		
NBS1	AI796269	202905_x_at	Hs.49220	0.001		
0.730784900	0.9524 0.952	1.705 0.8456	0.461	1.303		
MMP25	NM_022718	207890_s_at	Hs.58495	0.001		
2.389139994	0.3081 0.308	2.264 1.375	0.556	3.757		

Supplementary_Table_7						
MGC5560	NM_019054	220547_s_at	Hs.50041	0.001		
0.778983622	0.7538	0.753	1.531	0.8506	0.411	1.384
GAS7	NM_005890	202192_s_at	Hs.46221	0.001		
1.595017521	0.5143	0.514	1.694	1.3907	0.856	2.475
DKC1	U59151	201478_s_at	Hs.4747	0.001		
0.635417974	0.4348	0.434	1.543	0.7516	0.519	1.266
LRP10	NM_014045	201412_at	Hs.52523	0.001		
1.190721676	0.4869	0.486	1.131	1.1317	0.922	1.787
CTNND1	NM_001331	208407_s_at	Hs.16601	0.001		
0.652348417	0.8522	0.852	1.872	0.8252	0.403	1.406
PLP2	NM_002668	201136_at	Hs.77422	0.001		
1.637361551	0.5612	0.561	1.619	1.4128	0.932	3.605
SLC4A7	AF053755	210286_s_at	Hs.25007	0.002		
0.606102701	0.6397	0.639	1.422	0.7515	0.053	1.153
POT1	NM_015450	204354_at	Hs.31968	0.002		
0.801688924	0.3164	0.316	1.613	0.9038	0.309	1.017
NDUFS8	NM_002496	203190_at	Hs.90443	0.002		
0.825187561	0.9750	0.975	1.423	0.8972	0.811	2.000
RFX5	AW027312	202963_at	Hs.16689	0.002		
0.724574034	0.5476	0.547	1.752	0.8450	0.317	1.262
SH3GL1	NM_003025	201851_at	Hs.97616	0.002		
1.425984829	0.4221	0.422	1.314	1.2376	0.876	1.807
GALNS	NM_000512	206335_at	Hs.27138	0.002		
1.429892678	0.5842	0.584	1.409	1.1691	0.884	2.113
MYHFD1	NM_005956	202309_at	Hs.43597	0.002		
0.772362402	0.6926	0.692	1.797	0.8802	0.403	1.034
DKFZP56	AA928506	213750_at	Hs.40184	0.002		
0.711000398	0.6881	0.688	1.485	0.8430	0.624	1.231
4M182						
KIAA0776	AW298092	212634_at	Hs.14936	0.002		
0.571876934	0.8606	0.860	1.817	0.8150	0.609	1.811
JTB	BC004239	210927_x_at	Hs.6396	0.002		
1.185937527	0.8003	0.800	1.146	1.0837	0.907	1.689
ASL	NM_000048	204608_at	Hs.44204	0.002		
1.270077244	0.6731	0.673	1.167	1.1713	0.938	1.755
UPF3B	NM_023010	218757_s_at	Hs.10383	0.002		
0.737649342	0.7129	0.712	1.473	0.7939	0.477	1.035
CIAO1	NM_004804	203536_s_at	Hs.12109	0.002		
0.843655392	0.7810	0.781	1.486	0.8935	0.709	1.124
MS4A3	L35848	210254_at	Hs.99960	0.002		
6.490612874	0.3161	0.316	5.299	3.2397	0.412	17.91
TRA@	AE000659	215797_at	Hs.36938	0.002		
0.712736129	0.7925	0.792	1.855	0.8546	0.341	1.443
CAV2	BF197655	203323_at	Hs.21233	0.002		
1.526555332	0.3390	0.339	1.176	1.1444	0.695	1.627
MRPL19;	AC005034	216305_s_at	Hs.30380	0.002		

Supplementary_Table_7						
0.596170088	0.7360	0.736	1.898	0.7549	0.229	1.525
RLX1; RPML15; MRP-L15; KIAA010 4; MGC2067 5; RPML15						
FLJ10747	NM_018202	218562_s_at	Hs.58492	0.002		
0.686831116	0.7406	0.740	1.666	0.9522	0.379	1.323
BPI	NM_001725	205557_at	Hs.52901	0.002		
13.78160153	0.0980	0.098	4.701	7.8246	0.241	21.86
OPA1	AA209332	214306_at	Hs.47870	0.002		
0.701097853	0.7931	0.793	1.499	0.8063	0.367	1.185
SIP1	AB037701	210779_x_at	Hs.53386	0.002		
0.735451512	0.8825	0.882	1.360	0.8009	0.591	1.264
CAMK4	L24959	210349_at	Hs.43880	0.002		
0.641472412	0.7042	0.704	2.322	0.6999	0.261	1.139
SLC4A7	AF047033	209884_s_at	Hs.25007	0.002		
0.629080103	0.8970	0.897	2.531	0.8268	0.216	1.471
CYLD	AJ250014	221905_at	Hs.43299	0.002		
0.688145335	0.7433	0.743	1.510	0.7804	0.374	1.355
HSXIAPA	NM_017523	206133_at	Hs.44197	0.002		
0.721865909	0.7816	0.781	3.531	0.7954	0.161	1.562
HBPI	NM_012257	207361_at	Hs.16203	0.002		
0.612650613	0.8951	0.895	1.772	0.8492	0.139	1.402
CD24	AA761181	209771_x_at	Hs.37510	0.002		
8.086289993	0.1855	0.185	3.858	3.7302	0.657	14.11
CD9	NM_001769	201005_at	Hs.11428	0.003		
1.663689752	0.4619	0.461	2.207	1.1218	0.708	2.448
S100P	NM_005980	204351_at	Hs.2962	0.003		
4.405612829	0.1404	0.140	1.664	1.6248	0.144	9.342
CD24	M58664	208651_x_at	Hs.37510	0.003		
2.173256198	0.2231	0.223	1.208	1.8056	0.448	6.569
IGF2R	NM_000876	201393_s_at	Hs.48706	0.003		
1.649461602	0.5310	0.531	1.839	1.3436	0.809	3.420
PAICS	NM_006452	201014_s_at	Hs.51877	0.003		
0.688476037	0.8318	0.831	2.106	0.7662	0.442	1.223
ADH5	M30471	208848_at	Hs.78989	0.003		
0.552114569	0.6100	0.610	1.789	0.7137	0.295	1.330
ANXA3	M63310	209369_at	Hs.48004	0.003		
6.227773395	0.5392	0.539	3.116	4.7899	0.542	27.29
ITGAM	NM_000632	205786_s_at	Hs.17263	0.003		
1.838080018	0.5901	0.590	1.439	1.4355	0.802	3.769
ODX18	BC003360	208896_at	Hs.36349	0.003		
0.506280478	0.4743	0.474	2.301	0.7533	0.486	1.255
HK3	NM_002115	205936_s_at	Hs.41169	0.003		

Supplementary Table 7						
2.499039960	0.2326	0.232	1.561	1.6822	0.573	3.902
SNX3	BE962615		213545_x_at	Hs.12102		0.003
1.252339130	0.8230	0.823	1.334	1.1595	0.893	1.604
ICAM3	NM_002162		204949_at	Hs.35321		0.003
1.344486724	0.5209	0.520	1.333	1.1226	0.840	1.693
FLJ20534	NM_017867		218646_at	Hs.40675		0.003
0.675277755	0.7509	0.750	1.699	0.8972	0.440	1.318
USP9X	AA824386		201099_at	Hs.77578		0.003
0.805125593	0.9183	0.918	1.265	0.8674	0.491	1.112
PDXK	NM_003681		202671_s_at	Hs.28449		0.004
1.442612478	0.5353	0.535	1.258	1.1716	0.849	2.863
GART	BE966876		212378_at	Hs.47364		0.004
0.610637833	0.6311	0.631	2.440	0.6831	0.311	1.280
P2RX1	U45448		210401_at	Hs.41735		0.004
1.457038614	0.3220	0.322	1.907	1.1761	0.571	2.638
CD24	BG327863		208650_s_at	Hs.37510		0.004
4.241007291	0.2452	0.245	1.696	2.1006	0.424	12.07
	BE965029		212473_s_at	Hs.50192		0.004
1.680127322	0.4941	0.494	2.461	1.2438	0.639	2.631
UTRN	NM_007124		213023_at	Hs.13313		0.004
0.620031782	0.9181	0.918	2.031	0.7813	0.479	1.563
FLOT1	AF085357		208749_x_at	Hs.17998		0.004
1.583174578	0.6096	0.609	1.214	1.3011	0.746	2.701
FLJ20152	AI816291		218510_x_at	Hs.48170		0.004
0.596575296	0.7474	0.747	2.420	0.7922	0.250	1.185
DHRS7	AF126782		210788_s_at	Hs.59719		0.004
1.413363202	0.6254	0.625	1.243	1.1343	0.752	2.312
RHOBTB	N21138		202975_s_at	Hs.44503		0.004
0.612944164	0.5600	0.560	2.214	0.8087	0.488	1.430
UTRN	NM_007124		213022_s_at	---		0.004
0.637700518	0.6576	0.657	1.613	0.7081	0.288	1.409
DGAT1	NM_012079		203669_s_at	Hs.52195		0.004
1.237943169	0.6418	0.641	1.182	1.1428	0.914	1.338
BBS4	AI813772		212744_at	Hs.20868		0.004
0.658084489	0.8979	0.897	1.482	0.7785	0.598	1.251
SNX3	AB047360		210648_x_at	Hs.12102		0.004
1.305185812	0.7340	0.734	1.341	1.2231	0.834	1.948
CYP1B1	NM_000104		202437_s_at	Hs.15465		0.004
3.050317387	0.2926	0.292	3.475	1.8827	0.728	4.806
LARS2	D21851		34764_at	Hs.52697		0.004
0.680172835	0.4576	0.457	2.066	0.7871	0.527	1.387
CDC23	NM_004661		202892_at	Hs.15354		0.004
0.776484776	0.7155	0.715	1.370	0.8688	0.489	1.049
CCND3	NM_001760		201700_at	Hs.53430		0.004
1.359935810	0.6377	0.637	1.358	1.1409	0.785	1.346

Supplementary Table 7						
STOM	AI537887		201060_x_at	Hs.25390		0.004
1.926503529	0.5375	0.537	1.359	1.4760	0.676	4.316
CKAP4	NM_006825		200999_s_at	Hs.74368		0.004
1.713783138	0.2333	0.233	1.634	1.2307	0.715	2.351
CTSL	NM_001912		202087_s_at	Hs.41812		0.004
0.690987245	0.7318	0.731	2.529	0.8154	0.567	1.609
CAT	NM_001752		201432_at	Hs.50230		0.004
1.260454698	0.5712	0.571	1.244	1.1126	0.842	1.692
DIA1	NM_000398		201885_s_at	Hs.51766		0.004
1.650452347	0.6183	0.618	1.395	1.2825	0.532	2.121
	AA527515		65585_at	Hs.55660		0.005
0.706313377	0.6474	0.647	1.647	0.8602	0.109	1.229
POLA	NM_016937		204835_at	Hs.56731		0.006
0.664905263	0.8311	0.831	1.650	0.8213	0.329	1.303
SPTBN1	NM_003128		200672_x_at	Hs.50317		0.006
0.759458373	0.9018	0.901	2.447	0.9154	0.464	1.372
WSB2	NM_018639		201760_s_at	Hs.50698		0.006
1.456547357	0.7294	0.729	1.401	1.2048	0.889	2.213
FLJ10298	NM_018050		220945_x_at	Hs.5999		0.006
2.029197148	0.4022	0.402	1.133	1.5359	0.148	5.465
HLX1	M60721		214438_at	Hs.74870		0.006
2.872691895	0.3409	0.340	1.229	1.3330	0.477	2.787
MAP3K7I	AL031133		215452_x_at	----		0.006
0.844720447	0.9097	0.909	1.287	0.9062	0.811	1.182
P2; TAB2; FLJ21885						
MGC3121	AA161130		45687_at	Hs.29362		0.006
1.337346706	0.6510	0.651	1.203	1.1432	0.804	1.521
STX16	AF008936		221499_s_at	Hs.30791		0.006
0.751823313	0.7616	0.761	1.301	0.8205	0.620	1.085
RRM1	AI692974		201476_s_at	Hs.55839		0.006
0.729028530	0.7791	0.779	1.576	0.8207	0.418	1.530
CYP1B1	NM_000104		202436_s_at	Hs.15465		0.006
2.668988140	0.1734	0.173	1.780	1.1279	0.404	2.728
NAB1	AF045451		209272_at	Hs.10747		0.006
0.721504961	0.8434	0.843	1.741	0.8211	0.467	1.246
NDUF54	BC005270		209303_at	Hs.52822		0.006
0.825968658	0.9157	0.915	1.309	0.8708	0.767	1.193
CYB5	M22865		209366_x_at	Hs.46541		0.006
0.811132322	0.9084	0.908	1.441	0.8526	0.441	1.216
HAL	NM_002108		206643_at	Hs.19078		0.006
1.652447628	0.3005	0.300	1.340	1.4734	0.645	2.821
CYB5	M22976		215726_s_at	Hs.46541		0.006
0.651249313	0.8724	0.872	1.944	0.8817	0.349	1.356
SIRT7	NM_016538		218797_s_at	Hs.52864		0.006
1.156640948	0.7368	0.736	1.111	1.0823	0.877	1.399

Supplementary_Table_7

DKFZP56 1.305194742 4M082	NM_014042 0.7083	0.708	204218_at 1.230	1.0969	Hs.38044 0.868	0.006 1.974
DDB2 0.619729789	NM_000107 0.5986	0.598	203409_at 1.652	0.7726	Hs.44656 0.528	0.006 1.396
DDX10 0.758686891	NM_004398 0.9161	0.916	204977_at 1.449	0.8855	Hs.50379 0.325	0.006 1.310
RGS19 1.354836775	NM_005873 0.4798	0.479	204336_s_at 1.671	1.1389	Hs.42233 0.841	0.006 1.595
RAB2L 1.250032012	AL050259 0.5387	0.538	209110_s_at 1.197	1.0508	Hs.50962 0.949	0.006 1.9712
S100A8 0.317057733	AW238654 0.5962	0.596	214370_at 4.875	0.5078	Hs.41607 0.183	0.006 2.328
TIAM1 0.787662472	U90902 0.6116	0.611	213135_at 1.513	0.8208	Hs.51722 0.451	0.006 1.262
MLLT3 0.801628201	NM_004529 0.7525	0.752	204918_s_at 1.409	0.9475	Hs.49358 0.443	0.006 1.102
CSTB 1.238771293	NM_000100 0.7516	0.751	201201_at 1.358	1.0909	Hs.695 0.905	0.006 2.029
FLJ20259 0.743751175	BC000978 0.9279	0.927	209174_s_at 1.737	0.8400	Hs.29738 0.462	0.006 1.271
LOC3405 0.738562050	BE221922 0.8724	0.872	213282_at 1.755	0.9022	Hs.51218 0.418	0.006 1.364
DATF1 0.700236713	AL035669 0.7872	0.787	213213_at 1.612	0.8287	Hs.51717 0.383	0.006 1.168
CRISP3 8.202749464	NM_006061 0.0473	0.047	207802_at 5.173	3.1366	Hs.40446 0.027	0.006 33.33
ada 0.528063079	X02189 0.7553	0.755	216705_s_at 2.820	0.7044	Hs.25547 0.320	0.006 1.491
DECR1 0.789610390	NM_001359 0.6535	0.653	202447_at 1.535	0.9211	Hs.49221 0.660	0.006 1.095
EIF2B2 0.757180980	NM_014239 0.7738	0.773	202461_at 1.247	0.8409	Hs.40913 0.603	0.006 1.163
DPP4 0.574930856	NM_001935 0.7884	0.788	203717_at 1.595	0.7460	Hs.36891 0.346	0.006 1.752
PDCD4 0.611704544	N92498 0.6403	0.640	212593_s_at 1.762	0.8785	Hs.23254 0.480	0.006 1.599
CD24 4.370169959	X69397 0.0728	0.072	209772_s_at 1.849	2.4829	Hs.37510 0.367	0.006 11.38
CSF3R 2.413783904	NM_000760 0.2337	0.233	203591_s_at 1.870	1.2911	Hs.52451 0.605	0.006 3.060
MTSG1 0.570097828	AL096842 0.5688	0.568	212096_s_at 1.580	0.7727	Hs.7946 0.195	0.006 1.341
ELA2 7.690576364	NM_001972 0.2119	0.211	206871_at 5.721	4.9743	Hs.99863 0.271	0.006 28.65

Supplementary_Table_7					
CSNK2A	NM_001895	206075_s_at	Hs.44648	0.006	
0.841384972	0.9174	0.917	1.157	0.8881	0.442
					1.133
S100A10	NM_002966	200872_at	Hs.14387	0.006	
1.326704639	0.7033	0.703	1.272	1.1544	0.716
					2.056
TRIM44	NM_017583	217760_at	Hs.19210	0.006	
0.696257272	0.6319	0.631	1.478	0.8129	0.621
					1.112
FLJ10824	AV728658	214946_x_at	Hs.36528	0.006	
0.885871282	0.9090	0.909	1.699	0.9606	0.750
					1.242
PF20	NM_024532	219109_at	Hs.47131	0.006	
0.714194720	0.7807	0.780	1.617	0.8133	0.189
					1.294
TAF10	NM_006284	200055_at	Hs.58480	0.007	
1.190336449	0.5431	0.543	1.068	1.0709	0.641
					1.750
PPP4R1	NM_005134	201594_s_at	Hs.46459	0.007	
1.386571184	0.7686	0.768	1.153	1.2685	0.809
					2.028
WARS	NM_004184	200629_at	Hs.49759	0.007	
0.494521539	0.9360	0.936	5.280	0.8391	0.639
					3.343
HT021	NM_020685	219288_at	Hs.47166	0.007	
0.611778899	0.7713	0.771	2.152	0.8111	0.412
					1.505
MAN2A2	NM_006122	202032_s_at	Hs.11645	0.007	
1.236951764	0.4459	0.445	1.193	1.0414	0.882
					2.356
LUC7A	NM_006107	203804_s_at	Hs.13029	0.007	
0.735863792	0.8630	0.863	1.562	0.8107	0.277
					1.650
FLJ22662	NM_024829	218454_at	Hs.13193	0.007	
2.530612928	0.3225	0.322	1.268	1.6019	0.578
					4.668
IDS	AL117536	212221_x_at	Hs.46096	0.007	
1.208524870	0.6244	0.624	1.065	1.1698	0.706
					1.656
GBP1	BC002666	202269_x_at	Hs.62661	0.007	
0.357109258	0.4926	0.492	4.047	0.4407	0.129
					2.031
NELL2	NM_006159	203413_at	Hs.50532	0.007	
0.734774387	0.8426	0.842	1.890	0.8319	0.275
					1.660
STOM; BND7; EPB7;	M81635	201061_s_at	Hs.25390	0.007	
1.975731106	0.5007	0.500	1.680	1.7056	0.595
					4.013
ALDOA	AK026577	214687_x_at	Hs.51349	0.007	
1.349513658	0.5912	0.591	1.341	1.2226	0.858
					2.152
RAB33A	NM_004794	206039_at	Hs.56294	0.007	
0.552767660	0.6586	0.658	2.788	0.7439	0.503
					1.541
MGC2744	AI093187	222064_s_at	Hs.31740	0.007	
0.795982428	0.8050	0.805	1.515	0.9344	0.742
					1.142
GYG	AF087942	211275_s_at	Hs.47789	0.007	
1.857572214	0.5787	0.578	1.377	1.5346	0.827
					3.568
APOL3	NM_014349	221087_s_at	Hs.47473	0.007	
0.715280291	0.6648	0.664	1.566	0.8643	0.454
					1.151
PSMC1	NM_002802	204219_s_at	Hs.35665	0.007	
0.889511931	0.8622	0.862	1.226	0.9568	0.795
					1.052

Supplementary_Table_7						
ENPP2	D45421		210839_s_at	Hs.19097	0.007	
0.694499922	0.6321	0.632	1.908	0.8122	0.328	1.133
UBL1	U83117		208762_at	Hs.81424	0.007	
0.677988235	0.7412	0.741	1.949	0.9440	0.409	1.325
RAB13	NM_002870		202252_at	Hs.15153	0.007	
2.973469095	0.4387	0.438	1.345	1.8454	0.579	4.508
CD24	L33930		266_s_at	Hs.37510	0.007	
4.921580312	0.2106	0.210	2.791	3.2487	0.558	15.76
ILF3; MMP4; MPP4; NF90; NFAR; TCP80; DRBP76; NFAR-1; MPHOS H4; NF- AT-90	AF147209		208931_s_at	Hs.46588	0.007	
0.616917277	0.8452	0.845	1.883	0.8365	0.532	1.708
KIAA0540	AB011112		212443_at	Hs.43704	0.007	
1.773258763	0.3732	0.373	1.142	1.2372	0.463	1.568
	AC004692		217313_at	---	0.007	
0.821679091	0.5709	0.570	1.361	0.9116	0.609	1.090
HRB	AI742626		213926_s_at	Hs.35296	0.007	
2.031983031	0.3700	0.370	1.695	1.6874	0.723	5.138
APLP2	BC000373		208702_x_at	Hs.37024	0.007	
1.489974111	0.4953	0.495	1.338	1.1532	0.605	3.178
RAB5C	AF141304		201156_s_at	Hs.56732	0.007	
1.550859558	0.5899	0.589	1.182	1.3045	0.709	1.973
IGF2R	BG031974		201392_s_at	Hs.48706	0.007	
1.364715562	0.5238	0.523	1.249	1.1877	0.787	3.018
ADA	NM_000022		204639_at	Hs.25547	0.007	
0.536177477	0.4903	0.490	2.440	0.6753	0.214	1.103
HPR	NM_020995		208470_s_at	Hs.51215	0.007	
8.670290062	0.0553	0.055	5.313	7.1948	0.206	58.57
EIF2B1	NM_001414		201632_at	Hs.78592	0.007	
0.781983065	0.7823	0.782	1.286	0.8540	0.719	1.108
PGD	NM_002631		201118_at	Hs.46407	0.007	
2.082260785	0.4418	0.441	1.453	1.4489	0.619	4.430
FGR	NM_005248		208438_s_at	Hs.1422	0.007	
1.438049892	0.5446	0.544	1.190	1.1426	0.560	2.290
APLP2	NM_001642		208248_x_at	Hs.37024	0.007	
1.456139011	0.4724	0.472	1.421	1.1522	0.778	2.270
USP25	NM_013396		220419_s_at	Hs.47337	0.007	
0.748573900	0.6780	0.678	1.435	0.9189	0.542	1.111
TPK1	NM_022445		221218_s_at	Hs.49045	0.007	
0.728688965	0.8530	0.853	1.565	0.8447	0.560	1.366
TFB1M	NM_016020		219169_s_at	Hs.27990	0.007	

Supplementary Table 7						
0.678876669	0.8722	0.872	1.515	0.8015	0.562	1.443
FH	AA669797		214170_x_at	Hs.49823		0.007
0.867676204	0.7444	0.744	1.686	0.9325	0.573	1.068
EIF4EBP	AB044548		221539_at	Hs.41164		0.009
1.333333426	0.6434	0.643	1.372	1.2395	0.918	2.360
FH	NM_000143		203033_x_at	Hs.49823		0.009
0.834490988	0.8440	0.844	1.773	0.8801	0.533	1.188
CSPG2	J02814		221731_x_at	Hs.44368		0.009
2.334738818	0.3393	0.339	1.667	1.5972	0.635	2.978
ACP1	NM_004300		201630_s_at	Hs.55829		0.009
0.811353340	0.8263	0.826	1.768	0.9234	0.582	1.228
F8A	NM_012151		203274_at	Hs.53354		0.009
1.389720915	0.4608	0.460	1.242	1.1559	0.797	1.367
RAB27A	AF125393		210951_x_at	Hs.49351		0.009
1.470225269	0.6887	0.688	1.369	1.2409	0.805	3.516
KIAA0669	NM_014779		204094_s_at	Hs.52526		0.009
0.699439019	0.7816	0.781	1.317	0.7505	0.532	1.377
LOC5125	AF151074		210075_at	Hs.44511		0.009
2.244291343	0.4136	0.413	2.906	1.5740	0.620	2.164
MAP1LC	BE893893		208785_s_at	Hs.35606		0.009
1.155432644	0.5979	0.597	1.611	1.0418	0.960	3.438
RNF8	AK022075		203160_s_at	Hs.48527		0.009
0.728941294	0.8175	0.817	1.841	0.8394	0.582	1.610
FLJ20254	NM_017727		217899_at	Hs.53393		0.009
1.285900829	0.6378	0.637	1.478	1.1868	0.919	1.341
GNAZ	NM_002073		204993_at	Hs.58476		0.009
1.705004600	0.4977	0.497	2.296	1.1212	0.868	2.211
MAGED2	AI924630		213627_at	Hs.52266		0.009
0.803476037	0.5562	0.556	1.841	0.8771	0.628	1.114
KARS	AF285758		200079_s_at	Hs.3100		0.009
0.871007859	0.9663	0.966	1.333	0.9640	0.690	1.267
LAP3	NM_015907		217933_s_at	Hs.47926		0.009
0.707175211	0.6753	0.675	3.236	0.8897	0.525	2.002
HCLS1	NM_005335		202957_at	Hs.14601		0.009
1.149030568	0.7829	0.782	1.222	1.0754	0.926	1.524
HTATSF1	NM_014500		202602_s_at	Hs.20447		0.009
0.645378981	0.5425	0.542	1.450	0.7449	0.499	1.126
NOTCH1	NM_017617		218902_at	Hs.49547		0.009
1.254313966	0.7058	0.705	1.134	1.0565	0.804	1.172
CITED2	NM_006079		207980_s_at	Hs.82071		0.009
1.433604273	0.3537	0.353	2.346	1.3122	0.823	3.667
FLJ20220	NM_017718		219279_at	Hs.46578		0.009
0.534751957	0.6590	0.659	2.660	0.8866	0.273	1.612
GYG	NM_004130		201554_x_at	Hs.47789		0.009
1.634702679	0.6204	0.620	1.481	1.3916	0.797	4.513

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SNX4	AA524345	212652_s_at	Hs.50724	0.009
0.761967751	0.6451 0.645	1.372 0.8508	0.406	1.240
MEOX1	NM_004527	205619_s_at	Hs.438	0.009
0.625714274	0.4692 0.469	1.666 0.7203	0.246	1.288
76P	BF592982	213266_at	Hs.58488	0.009
0.715510006	0.7316 0.731	1.451 0.8193	0.625	1.278
PTX3	NM_002852	206157_at	Hs.56732	0.009
2.202499872	0.3684 0.368	1.288 1.8287	0.416	9.001
SEC61A1	NM_013336	217716_s_at	Hs.51823	0.009
1.115061795	0.6295 0.629	1.032 1.0860	0.888	1.370
PRTN3	NM_002777	207341_at	Hs.928	0.009
5.377071935	0.2366 0.236	1.735 2.7015	0.189	6.676
KIAA1128	AF241785	209379_s_at	Hs.46198	0.009
0.613898674	0.5202 0.520	1.810 0.8508	0.311	1.228
NCALD	AF251061	211685_s_at	Hs.49242	0.009
0.794177938	0.8572 0.857	1.627 0.8454	0.388	1.746
HM74	NM_006018	205220_at	Hs.45842	0.009
1.919619426	0.3839 0.383	1.394 1.7660	0.636	6.226
ZNF198	NM_003453	202778_s_at	Hs.50743	0.009
0.844955666	0.9459 0.945	1.319 0.8734	0.485	1.122
MCM4	AI859865	222036_s_at	Hs.46018	0.009
0.615843529	0.3121 0.312	3.062 0.8065	0.398	1.278
IGLJ3	X57812	214677_x_at	Hs.44958	0.009
1.499225877	0.1515 0.151	1.270 1.0774	0.381	2.038
CSTF2T	BF732638	212905_at	Hs.53849	0.009
0.755870902	0.8816 0.881	2.009 0.9013	0.476	1.552
KDEL2	NM_006854	200700_s_at	Hs.52021	0.009
1.288744430	0.6607 0.660	1.195 1.1734	0.858	1.992
P4HB	J02783	200654_at	Hs.46433	0.009
1.376473986	0.5167 0.516	1.123 1.0759	0.368	1.718
DYRK2	Y09216	202970_at	Hs.17313	0.009
0.635816604	0.4171 0.417	1.899 0.8249	0.243	1.428
TM6SF1	NM_023003	219892_at	Hs.51309	0.009
1.637378632	0.3727 0.372	1.344 1.4959	0.651	2.754
TEGT	AF033095	200803_s_at	Hs.35052	0.009
1.382133917	0.6337 0.633	1.305 1.0808	0.849	1.538
BLVRB	NM_000713	202201_at	Hs.51578	0.009
2.115779614	0.4077 0.407	1.544 1.3896	0.446	2.779
TBC1D4	AI650848	203386_at	Hs.21089	0.009
0.534456742	0.8503 0.850	1.761 0.6956	0.438	1.553
SH3GLB1	AF263293	209091_s_at	Hs.13630	0.009
1.194201325	0.6642 0.664	1.194 1.1549	0.831	2.729
TACSTD2	J04152	202286_s_at	Hs.23582	0.009
2.524475471	0.1956 0.195	2.228 2.3548	0.853	8.742
; M1S1; EGP-1; GA733;				

Supplementary_Table_7

TROP2;

NFYB	AI804118	218128_at	Hs.84928	0.009
0.461107631	0.4480 0.448	2.152 0.7155	0.502	1.353
ATP2B1	M95541	209281_s_at	Hs.50627	0.009
0.663661751	0.7090 0.709	1.905 0.8558	0.523	1.362
IGLJ3	D84140	217235_x_at	Hs.44958	0.009
1.724728265	0.4814 0.481	1.511 1.3641	0.666	5.765
FLJ10233	NM_018034	219193_at	Hs.21369	0.009
0.764595764	0.8327 0.832	1.401 0.9477	0.682	1.186
TARBP1	NM_005646	202813_at	Hs.49811	0.009
0.646206761	0.5940 0.594	2.910 0.8004	0.259	1.222
CD163	NM_004244	203645_s_at	Hs.50464	0.009
1.337935717	0.2594 0.259	2.075 1.0194	0.509	3.020
ZNF202	N91520	204327_s_at	Hs.11255	0.009
0.819284094	0.7726 0.772	1.278 0.8924	0.346	1.169
ALDOA	NM_000034	200966_x_at	Hs.51349	0.009
1.278058117	0.5797 0.579	1.213 1.1881	0.823	2.091
GPRK6	AF040752	211543_s_at	Hs.23511	0.009
1.248754729	0.6819 0.681	1.406 1.1845	0.870	1.720

Supplementary_Table_8

Supplementary Table 8

E. coli vs. *S. pneumoniae* infection; classifier genes: List of 45 classifier genes discriminating samples obtained from patients with *E. coli* vs. *S. pneumoniae* infections (data shown supplementary Figure 2b).

<i>E. coli</i> (n=12)		<i>S. pneumoniae</i> (n=11)		Affymetrix	uniGeneI	Fold Sp/Ec
Common Median	Min	GenBank Max	Median	Probe ID Min Max		
LTF 13.61686900	30.9	NM_002343 30.9	7710.6	202018_s_at 10655. 3060	Hs.52951 123.6	
LCN2; NGAL 12.19504095	61.2	NM_005564 61.2	2275	212531_at 5508.5 2135	Hs.20423 164.4	
CRISP3 8.202749140	3.6	NM_006061 3.6	393.7	207802_at 238.7 2537	Hs.40446 2.1	
NaGLT1; 7.342736989 KIAA1919;	368.4	AK000168 368.4	4410.4	216379_x_at 4190.5 1884	Hs.37510 703.8	
MMP9 7.040609137	170.6	NM_004994 170.6	581	203936_s_at 1941.8 1266	Hs.29741 267.5	
CYP4F3 6.163911845	18.6	NM_000896 18.6	168.4	206515_at 447.5 1950.3	Hs.10624 39.5	
PRTN3 5.377071823	34.1	NM_002777 34.1	250.1	207341_at 389.3 962.1	Hs.928 27.3	
IL1R2 4.117744610	6.6	NM_004633 6.6	582	205403_at 248.3 7268.1	Hs.25333 77.4	
IGHG3 3.560838842	1119.3	M87789 1119.3	1338	211430_s_at 15621. 2775	Hs.51063 3161.5	
TCN1 3.332568055	210.5	NM_001062 210.5	899.9	205513_at 1016.1 5928.9	Hs.2012 310.7	
CYP1B1 3.050317316	104.6	NM_000104 104.6	1242.1	202437_s_at 672.9 1717.7	Hs.15465 260.5	
PADI4 2.868701410	222.1	NM_012387 222.1	534	220001_at 996.3 5905.8	Hs.52296 315.4	
CD24 2.173256452	97.8	M58664 97.8	529.9	208651_x_at 791.5 2879.6	Hs.37510 196.7	
ALOX5AP 2.005505724	1715.1	NM_001629 1715.1	4668	204174_at 5500.3 1555	Hs.50765 2984.3	
FLJ10055 1.848767123	106.5	NM_017983 106.5	450.9	203827_at 337.4 797.3	Hs.46396 266.5	
GNAZ 1.705004812	157.3	NM_002073 157.3	725.8	204993_at 354.3 698.7	Hs.58476 274.4	
PLP2 1.637361458	1819.2	NM_002668 1819.2	5249.8	201136_at 4579.7 1168	Hs.77422 3023	
P2RX1 1.457038741	208	U45448 208	1231.8	210401_at 759.7 1704.5	Hs.41735 369	

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SCAL		NM_000332	203232_s_at	Hs.43496
1.374257425	224.3	224.3 437.2	485.8 731.8	286.8
IDS		AL117536	212221_x_at	Hs.46096
1.208524797	814.3	814.3 1389.9	1525.4 2160.5	921.8
C20orf24		NM_018840	217835_x_at	Hs.18406
1.208514868	3496.8	3496.8 5518.7	5714.1 1005	4078.1
Cab45		AL571362	221972_s_at	Hs.42806
1.182206101	419.4	419.4 512.1	554.1 809.4	429
MAP1LC3B		BE893893	208785_s_at	Hs.35606
1.155432689	1067.4	1067.4 2877.1	1859.9 6138.2	1713.9
NDUFS8		NM_002496	203190_at	Hs.90443
0.825187566	836.7	836.7 1221.1	769.9 1716.5	696.1
POT1		NM_015450	204354_at	Hs.31968
0.801688992	96.4	96.4 491.6	275.3 310	94.2
CDC23		NM_004661	202892_at	Hs.15354
0.776484848	263.8	263.8 505.3	320.3 386.9	180.4
MTHFD1		NM_005956	202309_at	Hs.43597
0.772362385	424	424 1100.4	538.8 633	247
SIP1		AB037701	210779_x_at	Hs.53386
0.735451505	242.3	242.3 373.4	219.9 347.2	162.5
SP329		NM_030793	221257_x_at	Hs.48377
0.733659132	533.8	533.8 896.3	480.4 754.8	311.9
RECQL		BC001052	210568_s_at	Hs.23506
0.731759656	248.7	248.7 460.4	238.7 365.7	117.8
AF1Q		BC006471	211071_s_at	Hs.75823
0.679697156	545.5	545.5 788.5	439.9 635.3	232.6
C14orf112		AW088547	217645_at	Hs.13710
0.661016949	284.2	284.2 405.8	210.6 414.7	137.6
SLC4A7		AF047033	209884_s_at	Hs.25007
0.629080118	230	230 649.1	212 377.4	55.6
VRK2		NM_006296	205126_at	Hs.46862
0.626862706	338.6	338.6 864.7	315.5 386.6	229
UBE2L6		NM_004223	201649_at	Hs.42577
0.620412419	2404	2404 5475.1	1844.3 3418.9	1167
SIAT9		NM_003896	203217_s_at	Hs.41511
0.609501435	831.9	831.9 1442.9	700.5 1401.9	288.9
KIAA0776		AW298092	212634_at	Hs.14936
0.571876961	192.4	192.4 406.3	182.2 404.9	136.2
STAT1; ISGF-3; STAT91		M97935	AFFX- 1429.8 2454.6 HUMISGF3 A/M97935_3	--- 395.9
DDX18		BC003360	208896_at	Hs.36349
0.506280440	248.7	248.7 1206.8	395 658.3	255.3
CXCL10		NM_001565	204533_at	Hs.41392
0.5 184.5	184.5	2956.3 161.5	435.8 35.6	

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STAT1; ISGF-3; 0.408639408 432.1 STAT91	M97935 432.1 2530.5	AFFX- 353.8 976.3 HUMISGF3 A/M97935_	--- 142.3
STAT1 0.407492154 2271.8	NM_007315 2271.8 9009.2	200887_s_at 2493.2 7378.6	Hs.47094 990.6
STAT1; ISGF-3; 0.269299206 680.8 STAT91	M97935 680.8 2535.6	AFFX- 393.5 1532.6 HUMISGF3 A/M97935_	--- 318.6
STAT1 0.234259076 670.3	BC002704 670.3 3790.6	209969_s_at 356.8 2764.5	Hs.47094 227.6
STAT1; ISGF-3; 0.228371005 185.7 STAT91	M97935 185.7 1658	AFFX- 117.2 466.1 HUMISGF3 A/M97935_5	--- 84.5

Supplementary_Table_9

Supplementary Table 9

S. aureus vs S. pneumoniae; class comparison results: Comparison of gene expression levels (normalized values) between patients with acute S. aureus infection and patients with acute S. pneumoniae infection - $P < 0.01$, Mann-Whitney test = 127 genes. Expression patterns are represented supplementary Figure 2c.

Common	S.aureus (n=12)		Affymetrix S.pneumoniae (n=11)		P-value	Fold Sa/Sp
	Median	GenBank Min Max	Probe ID Median	Min Max		
RAC2		NM_002872	207419_s_at	Hs.51760	0.000	
0.717685828	0.5928	0.592	1.045	1.0951	0.898	1.368
BBP		AA012917	213882_at	Hs.27687	0.000	
0.620776434	0.3738	0.373	1.189	1.2531	0.855	2.397
ZNF313		NM_018683	200868_s_at	Hs.14494	0.000	
1.348934482	0.8243	0.824	1.503	0.8067	0.709	1.112
PHKB		BG149218	202738_s_at	Hs.78060	0.000	
0.734751000	0.6641	0.664	1.225	1.1253	0.906	1.357
		AA827892	65588_at	Hs.40087	0.000	
1.804566280	0.6593	0.659	1.810	0.7916	0.409	1.387
FLJ11193		AI421192	203738_at	Hs.51924	0.000	
0.713430280	0.6330	0.633	1.071	1.1302	0.797	1.276
ARFIP1		AF124489	214483_s_at	Hs.41608	0.000	
0.552772458	0.2810	0.281	1.591	1.3486	0.830	1.728
G10		NM_003910	205690_s_at	Hs.38023	0.000	
1.266197644	0.9050	0.905	1.517	0.8376	0.571	1.236
PTK9		NM_002822	201745_at	Hs.18907	0.000	
1.490769736	0.5978	0.597	1.532	0.7103	0.444	1.052
KIAA0152		NM_014730	200617_at	Hs.50707	0.000	
0.723861353	0.6403	0.640	1.433	1.2771	0.876	1.599
RNF10		AL578551	208632_at	Hs.44279	0.000	
1.558682397	0.6498	0.649	1.610	0.7825	0.381	1.256
		AI820796	217704_x_at	Hs.58526	0.000	
2.775903750	0.3088	0.308	6.566	0.6693	0.331	1.518
NDUF88		NM_005004	201227_s_at	Hs.52321	0.000	
1.212083339	0.9459	0.945	1.449	0.9573	0.759	1.150
FLJ10246		NM_018038	220458_at	Hs.27427	0.000	
1.497470481	0.7804	0.780	2.064	0.8162	0.255	1.508
SELPLG		U02297	209880_s_at	Hs.12734	0.000	
0.645218331	0.5432	0.543	1.531	1.2571	0.866	1.830
UBL1		BC006462	211069_s_at	Hs.81424	0.000	
1.142822790	0.8281	0.828	1.514	0.9554	0.788	1.102
HSP70-4		NM_016299	219212_at	Hs.53416	0.000	
1.378369411	0.8634	0.863	2.184	0.8715	0.721	1.265
TACSTD2		J04152	202286_s_at	Hs.23582	0.000	

Supplementary Table 9					
0.264451663	0.1305	0.130	2.355	1.8584	0.656
; M1S1; EGP-1; GA733; TROP2;					
TSG101	NM_006292	201758_at	Hs.52351	0.000	
1.288887969	0.8992	0.899	1.581	0.8480	0.551
CD24	M58664	208651_x_at	Hs.37510	0.000	
0.299664931	0.2860	0.286	3.683	1.8685	0.799
SLC16A3	AL513917	202855_s_at	Hs.50076	0.001	
0.505622551	0.1398	0.139	1.303	1.4740	0.628
OAZ1	AF090094	215947_s_at	Hs.51607	0.001	
1.157909126	0.9440	0.944	1.236	0.9233	0.591
COX4I1	AW337510	213758_at	Hs.43341	0.001	
1.568988182	0.5259	0.525	1.977	0.8209	0.163
SAT	NM_002970	203455_s_at	Hs.28491	0.001	
1.254655659	0.9007	0.900	1.585	0.8996	0.545
LOC5696	NM_020213	219639_x_at	Hs.27024	0.001	
1.385941038	0.7739	0.773	1.304	0.7602	0.608
ARPC5L	NM_030978	220966_x_at	Hs.13249	0.001	
1.540636752	0.5455	0.545	2.621	0.8533	0.415
TFRC	BC001188	208691_at	Hs.52961	0.001	
1.368817821	0.4868	0.486	1.567	0.8967	0.313
CASP10	NM_001230	205467_at	Hs.5353	0.001	
0.632830305	0.3830	0.383	1.251	1.2164	0.574
C13orf12	NM_015932	217769_s_at	Hs.26874	0.001	
1.282585252	0.8160	0.816	1.407	0.8627	0.711
TNFSF5	NM_000074	207892_at	Hs.652	0.001	
0.658233682	0.4129	0.412	1.481	1.1688	0.803
BRD3	NM_007371	203825_at	Hs.52247	0.001	
0.702571387	0.6148	0.614	1.160	1.2808	0.839
CDV-1	W05463	64432_at	Hs.33312	0.001	
1.693497485	0.6782	0.678	1.641	0.7307	0.355
OPTN	NM_021980	202074_s_at	Hs.33270	0.001	
1.414750172	0.7583	0.758	2.043	0.8347	0.407
	AW003091	64488_at	Hs.55755	0.001	
1.991291264	0.6328	0.632	2.322	0.6496	0.383
DUSP12	NM_007240	218576_s_at	Hs.41621	0.001	
1.313153042	0.5463	0.546	1.561	0.8403	0.576
NDUFA4	NM_002489	217773_s_at	Hs.50098	0.001	
1.227295710	0.8365	0.836	1.536	0.9170	0.504
HPCAL1	NM_002149	205462_s_at	Hs.46769	0.002	
0.848803983	0.7966	0.796	1.253	1.1261	0.886
PSMC1	NM_002802	204219_s_at	Hs.35665	0.002	
1.185110732	0.7623	0.762	1.414	0.9358	0.775
EI24	NM_004879	208289_s_at	Hs.34391	0.002	
1.377670180	0.8320	0.832	1.891	0.8267	0.558

Supplementary_Table_9

ILF3; 1.718759022 MMP4; MPP4; NF90; NFAR; TCP80; DRBP76; NFAR-1; MPHOSP H4; NF- AT-90	AF147209 0.8311 0.831	208931_s_at 2.196 0.8068	Hs.46588 0.498	0.002 1.597
DNAJB6 1.757659962	AF080569 0.7390 0.739	208810_at 1.975 0.7628	Hs.49074 0.603	0.002 1.320
UBE2B 1.303480183	AA877765 0.7789 0.778	202334_s_at 1.415 0.8500	Hs.38598 0.653	0.002 1.044
HT021 1.521610959	NM_020685 0.7675 0.767	219288_at 2.386 0.8303	Hs.47166 0.500	0.003 1.305
SCO2 1.680530335	NM_005138 0.5960 0.596	205241_at 2.032 0.6611	Hs.56740 0.253	0.003 1.367
RAE1 1.407645517	U85943 0.7612 0.761	211318_s_at 1.969 0.8468	Hs.37169 0.806	0.003 1.187
COQ7 0.752204667	AF032900 0.7670 0.767	209746_s_at 1.135 1.1837	Hs.15711 0.869	0.003 1.537
SCML1 2.039952630	NM_006746 0.5272 0.527	218793_s_at 2.143 0.5593	Hs.10965 0.266	0.003 1.217
HTCD37 0.633834716	AF123539 0.4996 0.499	209586_s_at 1.337 1.2548	Hs.78524 0.818	0.003 1.994
PIGH 1.277751119	BC004100 0.8886 0.888	209625_at 1.788 0.8954	Hs.55349 0.583	0.003 1.274
TEGT 0.872522222	AF033095 0.6243 0.624	200803_s_at 1.273 1.0716	Hs.35052 0.944	0.003 1.375
BZW1 1.268257351	NM_014670 0.7446 0.744	200777_s_at 1.660 0.9010	Hs.35598 0.718	0.003 1.217
CTSL 2.059118995	NM_001912 0.7624 0.762	202087_s_at 9.677 0.7296	Hs.41812 0.564	0.003 3.727
HNRPH3 1.385463530	NM_021644 0.8446 0.844	207127_s_at 1.661 0.8304	Hs.49989 0.686	0.003 1.239
0.680758808	N31716 0.4843 0.484	44669_at 2.535 1.1339	Hs.35646 0.790	0.003 2.103
CDC42 1.316996164	BC003682 0.9274 0.927	208728_s_at 1.551 0.8431	Hs.46763 0.755	0.003 1.186
CAMSAP1 1.310983917	BE222901 0.8741 0.874	212711_at 2.350 0.8833	Hs.52249 0.691	0.003 1.279
CAPN1 0.746049388	NM_005186 0.6262 0.626	200752_s_at 1.160 1.2838	Hs.50284 0.796	0.003 1.673
KIAA0561 0.798856700	AB011133 0.5198 0.519	213045_at 1.339 1.0570	Hs.46618 0.938	0.003 1.596

Supplementary_Table_9					
SRP14	NM_003134	200007_at	Hs.53373	0.003	
1.146689209	0.8449 0.844	1.380 0.9096	0.821	1.037	
SNRPB2	NM_003092	202505_at	Hs.28037	0.003	
1.437143543	0.9387 0.938	1.445 0.8051	0.523	1.442	
PFTK1	NM_012395	204604_at	Hs.43074	0.005	
0.743678151	0.6197 0.619	1.277 1.1198	0.790	1.671	
CD24	AA761181	209771_x_at	Hs.37510	0.005	
0.179926488	0.1376 0.137	2.114 2.2850	0.402	8.645	
NEK4	NM_003157	204634_at	Hs.12955	0.005	
0.657591415	0.3706 0.370	1.533 1.2369	0.880	2.344	
YWHAQ	NM_006826	200693_at	Hs.74405	0.005	
1.112755855	0.7992 0.799	1.381 0.9329	0.654	1.049	
CUL2	U83410	203078_at	Hs.82919	0.005	
1.272192498	0.9027 0.902	1.866 0.9378	0.438	1.555	
PTCRA	AL035587	215492_x_at	Hs.16900	0.005	
0.646230768	0.3540 0.354	1.485 1.0667	0.810	1.587	
SELPLG	AI741056	209879_at	Hs.12734	0.005	
0.672958633	0.6484 0.648	1.135 1.3346	0.711	1.473	
RNGTT	AB012142	204207_s_at	Hs.56737	0.005	
0.657388750	0.6346 0.634	1.570 1.3190	0.794	1.779	
CD24	BG327863	208650_s_at	Hs.37510	0.005	
0.254824013	0.1876 0.187	2.315 1.7554	0.354	10.08	
CLN2	AA602532	214196_s_at	Hs.52345	0.005	
0.743658178	0.4671 0.467	1.324 1.2567	0.746	1.723	
NFKBIE	NM_004556	203927_at	Hs.45827	0.005	
1.309025249	0.6554 0.655	1.649 0.8982	0.523	1.452	
NDUFS3	NM_004551	201740_at	Hs.50252	0.005	
1.274563602	0.7560 0.756	1.275 0.8884	0.647	1.154	
CIR	U03644	209571_at	Hs.47067	0.005	
1.494380146	0.8681 0.868	1.794 0.8493	0.720	1.512	
1.432121544	0.6516 0.651	AFFX-r2-Ec- bioB-M_at	0.590	0.005	1.140
TFG	NM_006070	217839_at	Hs.51812	0.005	
1.306543645	0.8184 0.818	1.718 0.9375	0.649	1.210	
HLA-E	NM_005516	200905_x_at	Hs.38100	0.005	
1.221512347	0.8804 0.880	1.350 0.9155	0.796	1.124	
DC13	NM_020188	218447_at	Hs.38825	0.005	
1.255239586	0.8018 0.801	2.165 0.9202	0.824	1.082	
DGAT1	NM_012079	203669_s_at	Hs.52195	0.005	
0.686043772	0.4928 0.492	1.233 1.1858	0.866	1.399	
HSPC111	BE314601	214011_s_at	Hs.52947	0.005	
1.338436959	0.8627 0.862	1.526 0.8677	0.720	1.328	
NBS1	NM_002485	202907_s_at	Hs.49220	0.006	
0.771921418	0.6960 0.696	1.296 1.1475	0.900	1.490	
HMOX2	D21243	218120_s_at	Hs.28427	0.006	

Supplementary_Table_9						
0.794486399	0.4656	0.465	1.170	1.0723	0.600	1.405
PTMA	BF686442		200772_x_at	Hs.45992		0.006
1.327177668	0.7909	0.790	1.798	0.8269	0.639	1.227
TAX1BP1	NM_006024		200976_s_at	Hs.34576		0.006
1.170640900	0.8714	0.871	1.136	0.9081	0.709	1.094
MAGED2	AI924630		213627_at	Hs.52266		0.006
1.363322954	0.5358	0.535	1.729	0.8126	0.494	1.061
DHPS	NM_001930		202802_at	Hs.79064		0.006
0.674582947	0.4991	0.499	1.222	1.2175	0.730	1.391
ADCK2	N32831		221893_s_at	Hs.53414		0.006
0.745828270	0.4786	0.478	1.410	1.1559	0.837	1.327
CD24	X69397		209772_s_at	Hs.37510		0.006
0.227929556	0.0328	0.032	1.962	1.4398	0.272	8.433
HRB	AI742626		213926_s_at	Hs.35296		0.006
0.719798742	0.4362	0.436	1.614	1.1088	0.76	2.872
PKIG	NM_007066		202732_at	Hs.47283		0.006
0.816549807	0.5020	0.502	1.554	1.1236	0.886	1.362
SPG4	NM_014946		207724_s_at	Hs.46809		0.006
0.707821648	0.5565	0.556	1.351	1.1065	0.725	1.791
ELAVL1	BC003376		201726_at	Hs.18449		0.006
0.799492788	0.5587	0.558	1.099	1.1503	0.844	1.288
UBE2D3	BF448062		200667_at	Hs.51877		0.006
1.193949407	0.9556	0.955	1.539	0.9111	0.703	1.416
RAB1A	BC000905		208724_s_at	Hs.31064		0.006
1.262293724	0.8671	0.867	1.554	0.8952	0.680	1.442
LOC5714	BE963444		203897_at	Hs.18548		0.006
1.151406183	0.7816	0.781	1.571	0.8973	0.690	1.016
SF3A3	NM_006802		203818_s_at	Hs.77897		0.006
1.165141220	0.8267	0.826	1.209	0.9294	0.634	1.167
GALNT11	NM_022087		219013_at	Hs.32997		0.006
1.298751708	0.8155	0.815	1.456	0.8645	0.555	1.220
KIAA0830	AL573201		212573_at	Hs.16711		0.006
0.669748287	0.4986	0.498	1.191	1.1730	0.660	1.476
HNRPH3	AF132363		210110_x_at	Hs.49989		0.006
1.235797506	0.7689	0.768	1.692	0.8922	0.522	1.156
RNASEH	NM_002936		218497_s_at	Hs.50276		0.006
1.337310379	0.6681	0.668	1.360	0.9061	0.592	1.120
NaGLT1;	AK000168		216379_x_at	Hs.37510		0.006
0.167724625	0.1393	0.139	2.103	2.3023	0.386	10.35
KIAA1919						
;						
H41	AK025647		212010_s_at	Hs.51826		0.008
1.153728642	0.8799	0.879	1.636	0.8976	0.649	1.080
UBE2L3	NM_003347		200684_s_at	Hs.10810		0.008
0.643954118	0.3440	0.344	1.083	1.2063	0.636	1.911
CAPN3	BC003169		210944_s_at	Hs.14326		0.008

Supplementary_Table_9						
0.716856318	0.6173	0.617	1.724	1.2840	0.912	3.230
SS18L2	NM_016305	218283_at	Hs.53445	0.008		
1.328869550	0.8374	0.837	1.467	0.8535	0.698	1.341
CGI-43	AL550875	201973_s_at	Hs.53000	0.008		
1.278083879	0.6575	0.657	1.335	0.8383	0.757	1.011
SORL1	NM_003105	203509_at	Hs.36859	0.008		
0.745325964	0.6481	0.648	1.441	1.0977	0.845	1.726
EZH2	NM_004456	203358_s_at	Hs.44408	0.008		
1.208437825	0.7453	0.745	1.645	0.9645	0.632	1.344
SPIB	NM_003121	205861_at	Hs.43790	0.008		
0.557915698	0.3303	0.330	2.945	1.4633	0.640	2.958
	AF333388	211456_x_at	Hs.56824	0.008		
1.729616126	0.7342	0.734	8.285	0.8204	0.436	3.680
COP9	BC003090	202141_s_at	Hs.53171	0.008		
1.246724013	0.8336	0.833	1.677	0.9205	0.694	1.175
SFRS3	AF107405	208673_s_at	Hs.40514	0.008		
1.482913738	0.6981	0.698	1.838	0.7601	0.657	1.235
KIAA0703	AW291664	214798_at	Hs.6168	0.008		
0.673913031	0.4104	0.410	1.367	1.1459	0.799	3.338
SNRPA1	AJ130972	216977_x_at	Hs.52876	0.008		
1.573209699	0.6628	0.662	2.592	0.8347	0.658	1.441
YWHAQ	AA854017	213699_s_at	Hs.74405	0.008		
1.204444709	0.9057	0.905	1.591	0.9342	0.635	1.211
NDUFC2	NM_004549	218101_s_at	Hs.40786	0.008		
1.236698544	0.8268	0.826	1.490	0.8694	0.762	1.115
TLE3	AI567426	212770_at	Hs.28736	0.008		
1.948565918	0.4403	0.440	2.343	0.6835	0.387	1.556
LRRCS	NM_018103	218684_at	Hs.48208	0.008		
0.746100906	0.6427	0.642	1.343	1.2209	0.484	1.639
		AFFX-r2-EC-	---	0.008		
1.462380818	0.7123	0.712	1.377	0.7284	0.415	1.275
		bioB-3_at				
SLC16A3	NM_004207	202856_s_at	Hs.50076	0.008		
0.378219595	0.1891	0.189	1.605	1.6712	0.553	4.737
TNRC11	NM_005120	203506_s_at	Hs.40922	0.008		
0.796044080	0.5132	0.513	1.166	1.0738	0.602	2.093
PPP1R7	BF718769	213465_s_at	Hs.36587	0.008		
1.297112972	0.8368	0.836	1.719	0.9079	0.698	1.173
UBE2L3	NM_003347	200682_s_at	Hs.10810	0.008		
1.115371617	0.8886	0.888	1.353	0.9852	0.822	1.100
WBSCR5	AF257135	221581_s_at	Hs.56607	0.008		
0.787657875	0.4388	0.438	1.699	1.1390	0.968	1.746
MUS81	NM_025128	218463_s_at	Hs.28879	0.008		
0.760786788	0.6298	0.629	1.218	1.1871	0.688	1.517
	BC000265	209435_s_at	Hs.51679	0.008		
0.796080748	0.6725	0.672	1.417	1.1354	0.707	1.535

Supplementary_Table_9

DAPK3	BF686824	203890_s_at	Hs.23330	0.008		
0.711591542	0.2812	0.281	1.471	1.1448	0.755	1.908
OSBPL10	NM_017784	219073_s_at	Hs.15012	0.008		
0.681796189	0.4689	0.468	1.671	1.2139	0.528	3.953

Supplementary_Table_10

Supplementary Table 10

S. aureus vs. *S. pneumoniae* infection; classifier genes: List of 30 classifier genes discriminating samples obtained from patients with *E. coli* vs. *S. pneumoniae* infections (data shown supplementary Figure 2d).

<i>S. aureus</i> (n=12)			<i>S. pneumoniae</i> (n=11)		Affymetrix		uniGene	Fold Sa/Sp
Common Median	Min	Max	GenBank Median	Probe ID	Min	Max		
2.775903614	38.3	38.3	AI820796 814.2	217704_x_at 83	41.1		Hs.58526 188.3	
1.804566100	348.4	348.4	AA827892 956.9	65588_at 418.3	216.6		Hs.40087 733.4	
RNF10 1.558682472	917.7	917.7	AL578551 2274.3	208632_at 1105.1	539.3		Hs.44279 1774.6	
ARPC5L 1.540636724	1158.6	1158.6	NM_030978 5567.7	220966_x_at 1812.4	882.4		Hs.13249 2852.8	
FLJ10246 1.497470489	113.4	113.4	NM_018038 299.9	220458_at 118.6	37.1		Hs.27427 219.2	
PTK9 1.490769876	401.2	401.2	NM_002822 1028.5	201745_at 476.7	298.6		Hs.18907 706.1	
SNRPB2 1.437143604	2228.6	2228.6	NM_003092 3431.9	202505_at 1911.5	1242.3		Hs.28037 3424.4	
SAT 1.366609691	10895.	1089	M55580 1757	210592_s_at 10179.	8058.5		Hs.28491 1816	
ZNF313 1.348934411	1112.4	1112.4	NM_018683 2029.3	200868_s_at 1088.6	957.3		Hs.14494 1501.7	
DUSP12 1.313153042	317.3	317.3	NM_007240 906.8	218576_s_at 488.1	335.1		Hs.41621 589.9	
G10 1.266197610	1067.2	1067.2	NM_003910 1789.2	205690_s_at 987.8	674.2		Hs.38023 1457.9	
CSNK1G3 1.221717695	413.7	413.7	NM_004384 740.3	220768_s_at 385.4	313.6		Hs.12920 678.4	
MATR3 1.212459260	6290.1	6290.1	AA129420 8206.8	214363_s_at 5768.4	4796.9		Hs.26893 8432.5	
PSMC1 1.185110748	1945.4	1945.4	NM_002802 3609.7	204219_s_at 2388.3	1977.8		Hs.35665 2617.1	
UBL1 1.142822689	1796.9	1796.9	BC006462 3286.2	211069_s_at 2073.2	1710.6		Hs.81424 2391.6	
NOTCH2 0.834305814	1423.3	1423.3	AA291203 2999.6	202443_x_at 2416.5	1880.8		Hs.58478 3049.6	
KIAA1354 0.815270139	324.9	324.9	AA460694 728.2	213233_s_at 618.2	395.3		Hs.52202 911.8	
KIAA0561 0.798856687	369.9	369.9	AB011133 953.3	213045_at 752.2	667.6		Hs.46618 1136.3	

Supplementary_Table_10

WBSCR5			AF257135	221581_s_at	Hs.56607
0.787657872	790	790	3060.3	2050.7 1743.1	3144.2
LRRCS			NM_018103	218684_at	Hs.48208
0.746100862	664.9	664.9	1390.3	1263.1 500.8	1696.5
PHKB			BG149218	202738_s_at	Hs.78060
0.734750979	527.3	527.3	973	893.5 719.7	1078
KIAA0152			NM_014730	200617_at	Hs.50707
0.723861401	331.4	331.4	742	660.9 453.7	827.6
RAC2			NM_002872	207419_s_at	Hs.51760
0.717685839	1937.8	1937.8	3418.4	3579.7 2935.4	4473.3
KPNB1			AA861608	213573_at	Hs.53279
0.669506208	148.6	148.6	515.2	346.3 179.9	471.4
GNAZ			NM_002073	204993_at	Hs.58476
0.666243296	154.5	154.5	607.4	354.3 274.4	611.9
CASP10			NM_001230	205467_at	Hs.5353
0.632830296	110.6	110.6	361.4	351.2 165.9	434.3
TK2			BE895437	204276_at	Hs.51261
117.3	382.8	382.8	194.8	156 312.1	
ARFIP1			AF124489	214483_s_at	Hs.41608
144.55	308.5	308.5	261.5	161.1 335.1	
SLC16A3			AL513917	202855_s_at	Hs.50076
368.7	644.6	644.6	729.2	310.8 1888.6	
TACSTD2; M1S1;			J04152	202286_s_at	Hs.23582
48.95	234.6	234.6	185.1	65.4 627.6	
EGP-1; GA733;					
TROP2; GA733-1					

Supplementary_Table_11

Supplementary Table 11:

List of genes common or specific to FLU (Influenza A) and/or SLE (Lupus) groups
(Data shown Figure 6)

PROBE ID	DESCRIPTION	
OVER-EXPRESSED: P<0.01 SLE & FLU - IFN		
	uniGeneID	
219519_s_at	Hs.31869	sialoadhesin
217933_s_at	Hs.479264	leucine aminopeptidase 3
205569_at	Hs.518448	"synonyms: LAMP, DCLAMP, TSC403, DC-LAMP; go_component: lysosomal membrane [goid 0005765] [evidence TAS] [pmid 9721848]; go_process: oncogenesis [goid 0007048] [evidence TAS] [pmid 9721848]; go_process: cell proliferation [goid 0008283] [evidence TAS] [pmid 9721848]; Homo sapiens lysosomal-associated membrane protein 3 (LAMP3), mRNA."
222036_s_at cerevisiae)	Hs.460184	MCM4 minichromosome maintenance deficient 4 (S.
217165_x_at metallothionein-If gene (hMT-If).	Hs.513626	human metallothionein-If; Human
212185_x_at	Hs.418241	metallothionein 2A
205660_at	Hs.118633	2'-5'-oligoadenylate synthetase-like
204747_at repeats 4	Hs.47338	interferon-induced protein with tetratricopeptide
214453_s_at	Hs.82316	interferon-induced protein 44
213294_at	Hs.546523	hypothetical protein FLJ38348
204972_at	Hs.584785	"2'-5'-oligoadenylate synthetase 2, 69/71kDa"
205483_s_at IFI-15K)"	Hs.458485	"interferon, alpha-inducible protein (clone
219607_s_at 4"	Hs.325960	"membrane-spanning 4-domains, subfamily A, member
212262_at	Hs.510324	"quaking homolog, KH domain RNA binding (mouse)"
219211_at	Hs.38260	ubiquitin specific protease 18
202086_at interferon-inducible protein p78 (mouse)"	Hs.517307	"myxovirus (influenza virus) resistance 1,
204439_at	Hs.389724	chromosome 1 open reading frame 29
218400_at	Hs.528634	"2'-5'-oligoadenylate synthetase 3, 100kDa"
212099_at	Hs.502876	"ras homolog gene family, member B"

Supplementary_Table_11

218115_at cerevisiae)	Hs.26516	ASF1 anti-silencing function 1 homolog B (S.
219863_at	Hs.26663	cyclin-E binding protein 1
204415_at IFI-6-16)"	Hs.523847	"interferon, alpha-inducible protein (clone
205552_s_at	Hs.524760	"2',5'-oligoadenylate synthetase 1, 40/46kDa"
203595_s_at repeats 5	Hs.252839	interferon-induced protein with tetratricopeptide
203236_s_at (galectin 9)"	Hs.81337	"lectin, galactoside-binding, soluble, 9
204170_s_at	Hs.83758	CDC28 protein kinase regulatory subunit 2
222154_s_at	Hs.120323	DNA polymerase-transactivated protein 6
220947_s_at	Hs.513498	DKFZP434P1750 protein
203153_at repeats 1	Hs.20315	interferon-induced protein with tetratricopeptide
202145_at	Hs.521903	"lymphocyte antigen 6 complex, locus E"
207668_x_at	Hs.212102	protein disulfide isomerase-related protein
44673_at	Hs.31869	sialoadhesin
202107_s_at mitotin (S. cerevisiae)"	Hs.477481	"MCM2 minichromosome maintenance deficient 2,
204211_x_at stranded RNA dependent"	Hs.131431	"protein kinase, interferon-inducible double
208912_s_at	Hs.273621	"2',3'-cyclic nucleotide 3' phosphodiesterase"
203342_at homolog B (yeast)	Hs.30570	translocase of inner mitochondrial membrane 17
202863_at	Hs.369056	nuclear antigen Sp100
204994_at	Hs.926	myxovirus (influenza virus) resistance 2 (mouse)
201890_at	Hs.226390	ribonucleotide reductase M2 polypeptide
203744_at	Hs.19114	high-mobility group box 3
218520_at	Hs.505874	TANK-binding kinase 1

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206491_s_at	Hs.126938	"N-ethylmaleimide-sensitive factor attachment protein, alpha"
208676_s_at	Hs.524498	"proliferation-associated 2G4, 38kDa"
204805_s_at	Hs.75307	"H1 histone family, member X"
212203_x_at	Hs.374650	interferon induced transmembrane protein 3 (1-80)
200766_at	Hs.546248	cathepsin D (lysosomal aspartyl protease)
200808_s_at	Hs.490415	zyxin
202589_at	Hs.369762	thymidylate synthetase
204858_s_at	Hs.546251	endothelial cell growth factor 1
(platelet-derived)		
38710_at	Hs.473788	ubiquitin-specific protease otubain 1
214315_x_at	Hs.515162	calreticulin
201119_s_at	Hs.433901	cytochrome c oxidase subunit VIII
203254_s_at	Hs.375001	talin 1
37965_at	Hs.475074	"parvin, beta"
200948_at	Hs.524214	myeloid leukemia factor 2
200649_at	Hs.515524	nucleobindin 1
OVER-EXPRESSED: P<0.01 SLE; P>0.5 FLU - CI		
218935_at	Hs.368808	EH-domain containing 3
200931_s_at	Hs.500101	vinculin
211634_x_at	Hs.538461	"Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), isolate B-CLL G026"
216401_x_at	Hs.429466	"Homo sapiens partial IGKV gene for immunoglobulin kappa chain variable region, clone 38."
	///	
	Hs.449621	
	///	
	Hs.516184	"Homo sapiens partial IGKV gene for immunoglobulin kappa chain variable region, clone 38."
	///	
	Hs.551722	

Supplementary_Table_11

216576_x_at	Hs.552522	"Homo sapiens clone H10 anti-HLA-A2/A28 immunoglobulin light chain variable region mRNA, partial cds"
201412_at 10	Hs.525232	low density lipoprotein receptor-related protein
200634_at	Hs.494691	profilin 1
213241_at	Hs.584845	plexin C1
220496_at	Hs.409794	C-type lectin-like receptor-2
202030_at kinase	Hs.513520	branched chain alpha-ketoacid dehydrogenase
205936_s_at	Hs.411695	hexokinase 3 (white cell)
217853_at	Hs.520814	tensin-like SH2 domain-containing 1
209765_at (meltrin beta)	Hs.483944	a disintegrin and metalloproteinase domain 19
201186_at associated protein 1	Hs.533136	low density lipoprotein receptor-related protein
204613_at (phosphatidylinositol-specific)"	Hs.413111	"phospholipase C, gamma 2
220964_s_at	Hs.300816	"RAB1B, member RAS oncogene family"
211644_x_at mRNA, partial cds"	Hs.449621	"Homo sapiens immunoglobulin kappa light chain
201301_s_at	Hs.422986	annexin A4
201403_s_at	Hs.191734	microsomal glutathione S-transferase 3
201903_at	Hs.119251	ubiquinol-cytochrome c reductase core protein I
218482_at	Hs.492555	DC6 protein
215379_x_at	Hs.449585	immunoglobulin lambda joining 3
200055_at protein (TBP)-associated factor, 30kDa"	Hs.584805	"TAF10 RNA polymerase II, TATA box binding
202325_s_at complex, subunit F6"	Hs.246310	"ATP synthase, H ⁺ transporting, mitochondrial F0
35820_at	Hs.483873	
213113_s_at gene 1	Hs.99962	likely ortholog of mouse embryonic epithelial

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201302_at	Hs.422986	annexin A4
218026_at	Hs.16059	HSPC009 protein
207157_s_at gamma 5"	Hs.513557	"guanine nucleotide binding protein (G protein),
203155_at	Hs.516278	"SET domain, bifurcated 1"
208829_at	Hs.370937	TAP binding protein (tapasin)
203880_at	Hs.534383	popeye domain containing 2
205469_s_at	Hs.521181	interferon regulatory factor 5
201234_at	Hs.5158	integrin-linked kinase
216323_x_at alpha-tubulin isotype H2-alpha	Hs.503749	"alpha-tubulin isotype H2-alpha; Human gene, last exon."
213011_s_at IMAGE:3570991 3' mRNA sequence."	Hs.524219	"7n79g04.x1 NCI_CGAP_Ov18 Homo sapiens CDNA clone similar to SW:TPIS_HUMAN P00938 TRIOSEPHOSPHATE ISOMERASE ;,
211430_s_at	Hs.510635	
201264_at	Hs.10326	"coatamer protein complex, subunit epsilon"
200737_at	Hs.78771	phosphoglycerate kinase 1
203028_s_at	Hs.513803	"cytochrome b-245, alpha polypeptide"
207571_x_at	Hs.10649	chromosome 1 open reading frame 38
203617_x_at	Hs.181128	"ELK1, member of ETS oncogene family"
202343_x_at	Hs.1342	cytochrome c oxidase subunit Vb
217995_at	Hs.511251	sulfide quinone reductase-like (yeast)
202110_at	Hs.522699	cytochrome c oxidase subunit VIIB
201483_s_at	Hs.439481	suppressor of Ty 4 homolog 1 (S. cerevisiae)
209628_at	Hs.25010	nuclear transport factor 2-like export factor 2
211047_x_at subunit"	Hs.119591	"adaptor-related protein complex 2, sigma 1

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217827_s_at	Hs.242458	acid cluster protein 33
209397_at	Hs.233119	"malic enzyme 2, NAD(+)-dependent, mitochondrial"
202675_at sulfur (Ip)"	Hs.465924	"succinate dehydrogenase complex, subunit 8, iron
219079_at	Hs.5741	NADPH cytochrome B5 oxidoreductase
203781_at	Hs.515879	mitochondrial ribosomal protein L33
202592_at 5-like 1 (yeast)	Hs.94672	GCM5 general control of amino-acid synthesis
OVER-EXPRESSED: P<0.01 FLU; P>0.5 SLE - C2		
208087_s_at	Hs.302123	Z-DNA binding protein 1
219996_at	Hs.31845	ankyrin repeat and SOCS box-containing 7
203653_s_at	Hs.532795	coilin
217765_at	Hs.515876	nuclear receptor binding protein
210443_x_at	Hs.67896	opioid growth factor receptor
212505_s_at	Hs.112751	KIAA0892 protein
53720_at	Hs.175120	angiopoietin-like 6
213893_x_at similarity to protein pir:JC2399 (H.sapiens) JC2399 PMS4 homolog mismatch repair protein - human	Hs.397073	Homo sapiens transcribed sequence with strong
200675_at antibody 1)	Hs.54457	CD81 antigen (target of antiproliferative
215364_s_at	Hs.301943	KIAA0467 protein
212251_at	Hs.377155	LYRIC/3D3
210846_x_at	Hs.555909	tripartite motif-containing 14
203147_s_at	Hs.555909	tripartite motif-containing 14
201680_x_at	Hs.111801	arsenate resistance protein ARS2

Supplementary_Table_11		
219112_at	---	PDZ domain containing guanine nucleotide exchange factor (GEF) 2
218143_s_at	Hs.458917	secretory carrier membrane protein 2
202123_s_at	Hs.431048	v-abl Abelson murine leukemia viral oncogene homolog 1
212101_at	Hs.470588	karyopherin alpha 6 (importin alpha 7)
212601_at	Hs.277624	KIAA0399 protein
32209_at	Hs.25723	Mouse Mammary Tumor Virus Receptor homolog 1
218429_s_at	Hs.175120	hypothetical protein FLJ11286
213763_at	Hs.397465	homeodomain interacting protein kinase 2
202073_at	Hs.332706	optineurin
219673_at	Hs.279008	chromosome 6 open reading frame 61
219006_at	Hs.512144	chromosome 6 open reading frame 66
208784_s_at	Hs.412468	kelch domain containing 3
202841_x_at	Hs.67896	opioid growth factor receptor
209518_at	Hs.79335	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1"
202269_x_at	Hs.62661	"guanylate binding protein 1, interferon-inducible, 67kDa"
207824_s_at	Hs.23650	MYC-associated zinc finger protein (purine-binding transcription factor)
211300_s_at	Hs.408312	tumor protein p53 (Li-Fraumeni syndrome)
221851_at	Hs.443636	hypothetical protein BC002926
204804_at	Hs.532357	"Sjogren syndrome antigen A1 (52kDa, ribonucleoprotein autoantigen SS-A/Ro)"
212569_at	Hs.8118	KIAA0650 protein
201246_s_at	Hs.473788	ubiquitin-specific protease otubain 1
211136_s_at	Hs.444441	cleft lip and palate associated transmembrane

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protein 1		
201282_at (lipoamide)	Hs.488181	oxoglutarate (alpha-ketoglutarate) dehydrogenase
209137_s_at	Hs.136778	ubiquitin specific protease 10
219613_s_at regulation 2 homolog)	Hs.423756 (S. cerevisiae)	sirtuin (silent mating type information)
210378_s_at	Hs.530314	Sjogren's syndrome nuclear autoantigen 1
205400_at (eczema-thrombocytopenia)	Hs.2157	wiskott-Aldrich syndrome
221882_s_at domains)	Hs.288940	transmembrane protein 8 (five membrane-spanning
201864_at	Hs.74576	GDP dissociation inhibitor 1
37462_i_at complete cds."	Hs.115232	"Human spliceosomal protein (SAP 62) gene,
632_at	Hs.466828	glycogen synthase kinase 3 alpha
201895_at 1	Hs.446641	v-raf murine sarcoma 3611 viral oncogene homolog
218010_x_at	Hs.79625	chromosome 20 open reading frame 149
209760_at DKFZp586H1322	Hs.205572 (from clone DKFZp586H1322); complete cds."	"KIAA0922, elongation; Homo sapiens mRNA; cDNA
205207_at	Hs.512234	"interleukin 6 (interferon, beta 2)"
201377_at	Hs.490551	NICE-4 protein
205682_x_at	Hs.534468	apolipoprotein M
203728_at	Hs.485139	BCL2-antagonist/killer 1
211572_s_at transporters), member 2"	Hs.516866	"solute carrier family 23 (nucleobase
212218_s_at	Hs.83190	F-box only protein 9
55081_at	Hs.517610	molecule interacting with Rab13
45572_s_at ARF binding protein 1"	Hs.499158	"golgi associated, gamma adaptin ear containing,
217497_at (platelet-derived)	Hs.546251	endothelial cell growth factor 1

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77508_r_at	Hs.555978	Fos-related antigen
213931_at	Hs.148340	Homo sapiens transcribed sequence with strong similarity to protein pir:A40227 (H.sapiens) A40227 transcription repressor Id-2 - human
1598_g_at	Hs.369201	growth arrest-specific 6
213523_at	Hs.244723	cyclin E1
209744_x_at	Hs.472509	itchy homolog E3 ubiquitin protein ligase (mouse)
219040_at	Hs.7258	hypothetical protein FLJ22021
218655_s_at	Hs.406223	hypothetical protein FLJ20291
211947_s_at	Hs.494614	HBxAg transactivated protein 2
212069_s_at	Hs.495349	hypothetical protein MGC10526
220748_s_at	Hs.94392	LDL induced EC protein
202725_at A, 220kDa"	Hs.270017	"polymerase (RNA) II (DNA directed) polypeptide
214847_s_at IMAGE:4369100 5', mRNA sequence."	Hs.520046	"602281582F1 NIH_MGC_86 Homo sapiens cDNA clone
208842_s_at	Hs.431317	"golgi reassembly stacking protein 2, 55kDa"
203388_at	Hs.435811	"arrestin, beta 2"
41386_i_at	---	KIAA0346 protein
205909_at subunit)"	Hs.162777	"polymerase (DNA directed), epsilon 2 (p59
203052_at	Hs.408903	complement component 2
212558_at protein 1-like 1	Hs.436944	ganglioside-induced differentiation-associated
33768_at	Hs.584752	dystrophia myotonica-containing WD repeat motif
217419_x_at	Hs.273330	agrin
202221_s_at	Hs.517517	E1A binding protein p300
222139_at	Hs.147710	KIAA1466 protein

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213504_at	Hs.15591	COP9 constitutive photomorphogenic homolog
subunit 6 (Arabidopsis)		
206332_s_at	Hs.380250	"interferon, gamma-inducible protein 16"
204001_at	Hs.546299	"small nuclear RNA activating complex,
polypeptide 3, 50kDa"		
202270_at	Hs.62661	"guanylate binding protein 1,
interferon-inducible, 67kDa"		
AFFX-HUMISGF3A/ --- complete cds."		"Homo sapiens transcription factor ISGF-3 mRNA,
M97935_5_at		
203593_at	Hs.485518	CD2-associated protein
209100_at	Hs.315177	interferon-related developmental regulator 2
208968_s_at	Hs.4900	hypothetical protein LOC57019
212285_s_at	Hs.273330	agrin
201378_s_at	Hs.490551	NICE-4 protein
204813_at	Hs.125503	mitogen-activated protein kinase 10
209011_at	Hs.130031	triple functional domain (PTPRF interacting)
201128_s_at	Hs.387567	ATP citrate lyase
UNDER-EXPRESSED: P<0.01 SLE; P>0.5 FLU - C3		
222330_at	Hs.445711	Homo sapiens transcribed sequences
205372_at	Hs.14968	pleiomorphic adenoma gene 1
221311_x_at	Hs.112909	hypothetical protein d112208.2
209139_s_at	Hs.405537	"protein kinase, interferon-inducible double
stranded RNA dependent activator"		
207755_at	---	
205559_s_at	Hs.368542	proprotein convertase subtilisin/kexin type 5

214972_at	Hs.500842	Supplementary_Table_11 meningioma expressed antigen 5 (hyaluronidase)
76897_s_at	Hs.522351	KIAA0674 protein
209504_s_at (evectins) member 1"	Hs.445489	"pleckstrin homology domain containing, family B
210690_at member 4"	Hs.268510	"killer cell lectin-like receptor subfamily C,
212966_at	Hs.517434	hypermethylated in cancer 2
207596_at (OATPX), mRNA."	----	"synonym: PR02176; Homo sapiens OATPX protein
209574_s_at	Hs.149363	chromosome 18 open reading frame 1
203203_s_at	Hs.584861	HIV-1 rev binding protein 2
202268_s_at 1, 59kDa"	Hs.460978	"amyloid beta precursor protein binding protein
213958_at	Hs.502710	CD6 antigen
202969_at regulated kinase 2	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation
214252_s_at 3', mRNA sequence."	Hs.30213	"AV700514 GKC Homo sapiens cDNA clone GKCDQC04
216823_at	Hs.356572	
213743_at	Hs.292754	cyclin T2
208026_at	Hs.247816	"histone 1, H4f"
215204_at MAMMA1000264."	---	"Homo sapiens cDNA FLJ14090 fis, clone
205799_s_at neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1"	Hs.112916	"solute carrier family 3 (cystine, dibasic and
217353_at chromosome 6p24.1-25.3, complete sequence."	Hs.556099	"Human DNA sequence from clone RP1-256G22 on
204432_at	Hs.43627	SRY (sex determining region Y)-box 12
214848_at S26 (LOC375677), mRNA"	Hs.492407	"Homo sapiens similar to 40S ribosomal protein
215718_s_at IMAGE:2471854 3' similar to TR:Q92576 Q92576 MYELOBLAST KIAA0244 ;, mRNA sequence."	Hs.348921	"wg20e12.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone
212105_s_at	Hs.191518	DEAH (Asp-Glu-Ala-His) box polypeptide 9

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205934_at	Hs.153322	phospholipase C-like 1
209913_x_at	---	KIAA0415 gene product
216261_at antigen CD61)"	Hs.218040	"integrin, beta 3 (platelet glycoprotein IIIa,
222370_x_at similarity to protein ref:NP_060312.1 (H.sapiens) [Homo sapiens]	Hs.369054	Homo sapiens transcribed sequence with weak hypothetical protein FLJ20489
212297_at cells	Hs.529609	ATPase family homolog up-regulated in senescence
218277_s_at	Hs.29403	DEAH (Asp-Glu-Ala-His) box polypeptide 40
215383_x_at	Hs.242458	acid cluster protein 33
204793_at protein	Hs.522730	G protein-coupled receptor-associated sorting
202266_at	Hs.403010	TRAF and TNF receptor associated protein
213135_at	Hs.517228	T-cell lymphoma invasion and metastasis 1
202524_s_at proteoglycan (testican) 2"	Hs.523009	"sparc/osteonectin, cwcv and kazal-like domains
203526_s_at	Hs.158932	adenomatosis polyposis coli
203375_s_at	Hs.432424	tripeptidyl peptidase II
214716_at	Hs.146551	BMP2 inducible kinase
220460_at member 1C1"	Hs.47261	"solute carrier organic anion transporter family,
214855_s_at	Hs.113150	GTPase activating RANGAP domain-like 2
214688_at homolog, Drosophila)"	Hs.444213	"transducin-like enhancer of split 4 (E(sp1)
207845_s_at	Hs.480876	anaphase-promoting complex subunit 10
202183_s_at	Hs.119324	kinesin family member 22
221919_at	---	heterogeneous nuclear ribonucleoprotein A1
217142_at chromosome 6p11.1-12.3, complete sequence."	---	"Human DNA sequence from clone RP1-14209 on
200607_s_at	Hs.81848	RAD21 homolog (S. pombe)

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217713_x_at	Hs.369471	Homo sapiens transcribed sequence with weak similarity to protein ref:NP_060312.1 (H.sapiens) hypothetical protein FLJ20489 [Homo sapiens]
209481_at	Hs.476052	"Homo sapiens HSNFRK (HSNFRK) mRNA, complete cds."
202165_at	Hs.567321	"protein phosphatase 1, regulatory (inhibitor) subunit 2"
202747_s_at	Hs.17109	integral membrane protein 2A
212413_at	Hs.496666	septin 6
221905_at	Hs.432993	cylindromatosis (turban tumor syndrome)
203874_s_at	Hs.152292	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1"
215366_at	Hs.487648	KIAA0713 (Homo sapiens); Homo sapiens mRNA; cDNA DKFZp761E0611 (from clone DKFZp761E0611).
214081_at	Hs.125036	plexin domain containing 1
203387_s_at	Hs.210891	"TBC1 domain family, member 4"
210424_s_at	Hs.182982	golgin-67
209726_at	Hs.428446	carbonic anhydrase XI
213370_s_at	Hs.343679	Scm-like with four mbt domains 1
221207_s_at	Hs.491172	neurobeachin
212107_s_at	Hs.191518	DEAH (Asp-Glu-Ala-His) box polypeptide 9
211681_s_at	Hs.480311	LIM protein (similar to rat protein kinase C-binding enigma)
221508_at	---	STE20-like kinase
208410_x_at	Hs.46329	"amelogenin (amelogenesis imperfecta 1, x-linked)"
209997_x_at	Hs.491148	pericentriolar material 1
205218_at	Hs.472227	"polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa"
216220_s_at	Hs.77867	adenosine A1 receptor

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220115_s_at	Hs.92489	"cadherin 10, type 2 (T2-cadherin)"
204992_s_at	Hs.91747	profilin 2
211721_s_at	Hs.184846	hypothetical protein BC005868
56919_at	Hs.109778	"golgi reassembly stacking protein 1, 65kDa"
202970_at regulated kinase 2	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation
78383_at cds"	Hs.535961	"Homo sapiens, clone IMAGE:4152599, mRNA, partial
201139_s_at	Hs.546301	Sjogren syndrome antigen 8 (autoantigen La)
203188_at beta-1,3-N-acetylglucosaminyltransferase 6"	Hs.8526	"UDP-GlcNAc:betaGal
217659_at similarity to protein ref:NP_060312.1 (H.sapiens) [Homo sapiens]	Hs.203099	Homo sapiens transcribed sequence with weak hypothetical protein FLJ20489
207216_at member 8"	Hs.494901	"tumor necrosis factor (ligand) superfamily,
211828_s_at	Hs.34024	Traf2 and NCK interacting kinase
210034_s_at	Hs.449095	ribosomal protein L5
207283_at	Hs.567545	"spectrin, beta, non-erythrocytic 1"
209953_s_at cerevisiae)	Hs.160958	CDC37 cell division cycle 37 homolog (S.
215009_s_at	Hs.370024	yeast Sec31p homolog
219535_at	Hs.109437	hormonally upregulated Neu-associated kinase
221537_at	Hs.585335	hypothetical protein DKFZp564A176
217394_at	Hs.508883	
214823_at pseudogene, mRNA sequence"	Hs.8198	"Homo sapiens C2H2 zinc finger protein
215262_at	Hs.142570	Homo sapiens clone 24629 mRNA sequence
206546_at	Hs.202676	synaptonemal complex protein 2
219495_s_at	Hs.130683	zinc finger protein 180 (HHZ168)

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204699_s_at	Hs.194754	hypothetical protein MGC29875
203202_at	Hs.584861	HIV-1 rev binding protein 2
206744_s_at	Hs.530988	zinc finger protein 237
202407_s_at (yeast)	Hs.515598	PRP31 pre-mRNA processing factor 31 homolog
33148_at	Hs.435231	zinc finger RNA binding protein
201070_x_at	Hs.567433	"splicing factor 3b, subunit 1, 155kDa"
210268_at	Hs.413074	"nuclear transcription factor, X-box binding 1"
200751_s_at	Hs.508848	heterogeneous nuclear ribonucleoprotein C (C1/C2)
205245_at (C.elegans)	Hs.112933	par-6 partitioning defective 6 homolog alpha
201182_s_at	Hs.162233	chromodomain helicase DNA binding protein 4
205511_at subunit 2, 47kDa"	Hs.511316	"GA binding protein transcription factor, beta
221757_at	Hs.26670	
217610_at KIDNE2014489."	---	"Homo sapiens cDNA FLJ38765 fis, clone
202979_s_at	Hs.535319	HCF-binding transcription factor Zhangfei
222099_s_at	Hs.407368	DKFZP434D1335 protein
216288_at THYR01001262 3', mRNA sequence."	Hs.201300	"AU159276 THYR01 Homo sapiens cDNA clone
207735_at	Hs.272800	ring finger protein 125
208120_x_at	---	
211085_s_at	Hs.472838	serine/threonine kinase 4
220796_x_at	Hs.134074	"solute carrier family 35, member E1"
208994_s_at	Hs.470544	peptidyl-prolyl isomerase G (cyclophilin G)
206648_at	Hs.567496	HSPC059 protein

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206636_at	Hs.98445	RAS p21 protein activator 2
220368_s_at	Hs.533887	KIAA2010
206792_x_at	Hs.437211	"phosphodiesterase 4C, CAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)"
216242_x_at	Hs.571355	Homo sapiens mRNA; cDNA DKFZp686J18198 (from clone DKFZp686J18198)
214066_x_at	Hs.78518	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)
221558_s_at	Hs.555947	Lymphoid enhancer-binding factor 1
219864_s_at	Hs.468261	"synonym: MCIP3; putative; Down syndrome candidate region 1-like 2; go_function: RNA binding [goid 0003723] [evidence TAS] [pmid 10756093]; go_process: embryogenesis and morphogenesis [goid 0007345] [evidence TAS] [pmid 10756093]; go_process: calcium-mediated signaling [goid 0019722] [evidence IEA]; Homo sapiens Down syndrome critical region gene 1-like 2 (DSCR1L2), mRNA."
200914_x_at	Hs.509414	"naa40c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258639 3' similar to TR:Q13999 Q13999 CGI PROTEIN ;, mRNA sequence."
210892_s_at	Hs.520459	"general transcription factor II, i"
220048_at	Hs.171971	"ectodysplasin 1, anhidrotic receptor"
209746_s_at	Hs.157113	"coenzyme Q7 homolog, ubiquinone (yeast)"
214197_s_at	Hs.516278	"SET domain, bifurcated 1"
205510_s_at	Hs.511316	"GA binding protein transcription factor, beta subunit 2, 47kDa"
209023_s_at	Hs.496710	stromal antigen 2
212744_at	Hs.208681	Bardet-Biedl syndrome 4
221826_at	Hs.157078	similar to RIKEN cDNA 2610307I21
208903_at	Hs.557301	FLJ46061 protein
202137_s_at	Hs.292265	adenovirus 5 E1A binding protein
218259_at	Hs.49143	myocardin-related transcription factor B
218425_at	Hs.487458	TRIAD3 protein
210568_s_at	Hs.235069	RecQ protein-like (DNA helicase Q1-like)

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210607_at	Hs.428	fms-related tyrosine kinase 3 ligand
218532_s_at	Hs.481704	hypothetical protein FLJ20152
206976_s_at	Hs.36927	heat shock 105kDa/110kDa protein 1
218754_at	Hs.59425	hypothetical protein FLJ23323
205250_s_at	Hs.150444	KIAA0373 gene product
206337_at	Hs.370036	chemokine (C-C motif) receptor 7
214251_s_at	Hs.558362	nuclear mitotic apparatus protein 1
202479_s_at	Hs.467751	tribbles homolog 2
201115_at subunit 50kDa"	Hs.306791	"polymerase (DNA directed), delta 2, regulatory
202971_s_at regulated kinase 2	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation
211464_x_at	Hs.3280	"caspase 6, apoptosis-related cysteine protease"
219156_at	Hs.443661	synaptojanin 2 binding protein
201837_s_at	Hs.6232	SPTF-associated factor 65 gamma
201977_s_at	Hs.210532	KIAA0141 gene product
203580_s_at transporter, y+ system), member 6"	Hs.559983	"solute carrier family 7 (cationic amino acid
201836_s_at	Hs.6232	SPTF-associated factor 65 gamma
221899_at	Hs.507680	hypothetical protein from BCRA2 region
202182_at 5-like 2 (yeast)	Hs.463045	GCN5 general control of amino-acid synthesis
217729_s_at	Hs.515053	amino-terminal enhancer of split
211795_s_at	Hs.370503	FYN binding protein (FYB-120/130)
217547_x_at	Hs.264345	TRAF6-inhibitory zinc finger protein
218510_x_at	Hs.481704	hypothetical protein FLJ20152

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41329_at	Hs.435560	ezrin-binding partner PACE-1
213803_at	Hs.532793	karyopherin (importin) beta 1
218428_s_at	Hs.443077	REV1-like (yeast)
212454_x_at	Hs.527105	heterogeneous nuclear ribonucleoprotein D-like
218430_s_at	Hs.282855	hypothetical protein FLJ12994
203579_s_at	Hs.559983	"solute carrier family 7 (cationic amino acid transporter, y+ system), member 6"
203804_s_at	Hs.130293	cisplatin resistance-associated overexpressed protein
212709_at	Hs.372099	nucleoporin 160kDa
221221_s_at	Hs.434434	kelch-like 3 (Drosophila)
209927_s_at	Hs.371788	DKFZP547E1010 protein
201424_s_at	Hs.339735	cullin 4A
209884_s_at	Hs.250072	"solute carrier family 4, sodium bicarbonate cotransporter, member 7"
218764_at	Hs.333907	"synonyms: PKCL, PKC-L, PRKCL, MGC5363; go_function: protein kinase C activity [goid 0004697] [evidence E] [pmid 1986216]; go_process: protein amino acid phosphorylation [goid 0006468] [evidence E] [pmid 1986216]; go_process: signal transduction [goid 0007165] [evidence P] [pmid 1986216]; Homo sapiens protein kinase C, eta (PRKCH), mRNA."
218124_at	Hs.440401	hypothetical protein FLJ20296
204651_at	Hs.298069	nuclear respiratory factor 1
204773_at	Hs.558346	"interleukin 11 receptor, alpha"
213278_at	Hs.528673	myotubularin related protein 9
205661_s_at	Hs.118666	FAD-synthetase
UNDER-EXPRESSED: P<0.01 FLU; P>0.5 SLE - C4		
206100_at	Hs.567251	0.00918 carboxypeptidase M

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201506_at	Hs.369397	0.000506	"transforming growth factor, beta-induced, 68kDa"
37384_at	Hs.112728	0.00687	protein phosphatase 1F (PP2C domain containing)
207573_x_at	Hs.486360	3.03E-05	"ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit g"
210241_s_at	Hs.274329	0.00178	TP53 activated protein 1
212829_at	Hs.57079	0.00921	"Homo sapiens cDNA FLJ13267 fis, clone OVARC1000964."
204227_s_at	Hs.512619	0.00921	"thymidine kinase 2, mitochondrial"
208370_s_at	Hs.282326	0.00918	Down syndrome critical region gene 1
209513_s_at	Hs.59486	3.03E-05	hypothetical protein MGC10940
204906_at	Hs.147119	0.00257	"ribosomal protein S6 kinase, 90kDa, polypeptide 2"
218557_at	Hs.439152	0.00257	Nit protein 2
202929_s_at	Hs.433902	0.00257	D-dopachrome tautomerase
209318_x_at	Hs.444975	0.00687	pleiomorphic adenoma gene-like 1
203621_at	Hs.518424	0.0012	"NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa"
212526_at	Hs.440414	0.00685	"spastic paraplegia 20, spartin (Troyer syndrome)"
218502_s_at	Hs.253594	0.00178	trichorhinophalangeal syndrome I
221472_at	Hs.272168	0.00921	tumor differentially expressed 1
200760_s_at	Hs.518060	0.00079	cytoskeleton related vitamin A responsive protein
200761_s_at	Hs.518060	0.000313	cytoskeleton related vitamin A responsive protein
201413_at	Hs.406861	0.000313	hydroxysteroid (17-beta) dehydrogenase 4
208877_at	Hs.518530	0.0012	p21 (CDKN1A)-activated kinase 2
204559_s_at	Hs.512610	0.00363	"LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)"
208643_s_at	Hs.388739	0.00257	"X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku

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autoantigen, 80kDa)"			
209934_s_at 2C, member 1"	Hs.584884	0.00687	"ATPase, Ca++ transporting, type
217790_s_at (translocon-associated protein gamma)"	Hs.518346	0.00504	"signal sequence receptor, gamma
218450_at	Hs.294133	0.00687	heme binding protein 1
212010_s_at	Hs.518265	0.00504	hypothetical protein H41
217982_s_at	Hs.374503	0.00178	mortality factor 4 like 1
210774_s_at	Hs.522932	0.0012	nuclear receptor coactivator 4
208746_x_at mitochondrial F0 complex, subunit g"	Hs.486360	1.47E-05	"ATP synthase, H+ transporting,
202279_at 2	Hs.109052	0.000107	chromosome 14 open reading frame
200833_s_at family"	Hs.369920	0.00363	"RAP1B, member of RAS oncogene
200080_s_at	Hs.533624	0.00257	"H3 histone, family 3A"
204319_s_at 10	Hs.501200	0.00687	regulator of G-protein signalling
211671_s_at	Hs.122926	0.000187	
217989_at family) member 8	Hs.282984	0.000313	dehydrogenase/reductase (SDR
210453_x_at mitochondrial F0 complex, subunit g"	Hs.486360	0.000506	"ATP synthase, H+ transporting,
200008_s_at	Hs.299055	0.00921	GDP dissociation inhibitor 2
202416_at C, member 7"	Hs.500156	0.00178	"DnaJ (Hsp40) homolog, subfamily
201398_s_at protein 1	Hs.491988	0.000187	translocation associated membrane
210759_s_at subunit, alpha type, 1"	Hs.102798	0.00687	"proteasome (prosome, macropain)
208742_s_at 18kDa"	Hs.524899	0.00921	"sin3-associated polypeptide,
218228_s_at ankyrin-related ADP-ribose polymerase 2"	Hs.329327	0.00687	"tankyrase, TRF1-interacting
200969_at reticulum protein 1	Hs.518326	0.00921	stress-associated endoplasmic

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208405_s_at	Hs.520313	0.00921	"CD164 antigen, sialomucin"
217983_s_at	Hs.529989	0.00921	ribonuclease T2
204690_at	Hs.431109	0.00687	syntaxin 8
203265_s_at kinase 4	Hs.514681	0.00921	mitogen-activated protein kinase
200981_x_at	Hs.125898	0.00687	GNAS complex locus
201581_at	Hs.169358	0.000187	hypothetical protein DJ971N18.2
208755_x_at	Hs.533624	3.03E-05	"H3 histone, family 3A"
221607_x_at	Hs.514581	3.03E-05	"actin, gamma 1"
213828_x_at	Hs.533624	0.000107	"H3 histone, family 3A"
214097_at	Hs.190968	0.00079	ribosomal protein S21
211997_x_at	Hs.180877	0.00921	"H3 histone, family 3B (H3.3B)"
215313_x_at complex, class I, A"	Hs.584763	0.00363	"major histocompatibility
209480_at complex, class II, DQ beta 1"	Hs.409934	0.00858	"major histocompatibility
208623_s_at	Hs.487027	0.00921	villin 2 (ezrin)
212886_at	Hs.132994	0.00363	DKFZP434C171 protein
211654_x_at complex, class II, DQ beta 1"	Hs.409934	0.00079	"major histocompatibility
213513_x_at complex, subunit 2, 34kDa"	Hs.529303	0.00687	"actin related protein 2/3
208756_at initiation factor 3, subunit 2 beta, 36kDa"	Hs.530096	0.00257	"eukaryotic translation
217779_s_at coactivator 2	Hs.512636	0.00504	proline-rich nuclear receptor
221791_s_at	Hs.356440	0.000107	hypothetical protein HSPC016

Claims

1. A method of identifying a human subject suspected of having an infectious disease comprising determining the expression level of a biomarker comprising one or more of the following genes: DNAPTP6; IFI27; IFI35; IFI44; OAS1; BST2; GIP2; LY6E; MX1; SON; TRIM14; APOBEC3C; Clorf29; FLJ20035; FLJ38348; HSXIAPAF1; KIAA0152; PHACTR2; and USP18.
2. The method of claim 1, wherein the step of determining expression levels is performed by measuring amounts of mRNA, protein and combinations thereof.
3. The method of claim 1, wherein the step of determining expression levels is performed using hybridization of nucleic acids on a solid support, an oligonucleotide array, sequencing and combinations thereof.
4. The method of claim 1, wherein the step of determining expression levels is performed using cDNA which is made using mRNA collected from the human cells as a template.
5. The method of claim 1, wherein the biomarker comprises mRNA level and is quantitated by a method selected from the group consisting of polymerase chain reaction, real time polymerase chain reaction, reverse transcriptase polymerase chain reaction, hybridization, probe hybridization, and gene expression array.
6. The method of claim 1, wherein the step of determining the level of expression is accomplished using at least one technique selected from the group consisting of polymerase chain reaction, heteroduplex analysis, single strand conformational polymorphism analysis, ligase chain reaction, comparative genome hybridization, Southern blotting, Northern blotting, Western blotting, enzyme-linked immunosorbent assay, fluorescent resonance energy-transfer and sequencing.
7. The method of claim 1, wherein the sample comprises a peripheral blood mononuclear cell.
8. A method of identifying a human subject suspected of having an infectious disease comprising determining the expression level of a biomarker comprising one or more of the following genes: EEF1G; EIF3S5; EIF3S7; EIF4B; QARS; RPL31; RPL4; PFDN5; CD44; HADHA; PCBP2; and dJ507I15.1.
9. The method of claim 1, wherein the step of determining expression levels is performed by measuring amounts of mRNA, protein and combinations thereof.
10. The method of claim 1, wherein the step of determining expression levels is performed using hybridization of nucleic acids on a solid support, an oligonucleotide array, sequencing and combinations thereof.
11. The method of claim 1, wherein the step of determining expression levels is performed using cDNA which is made using mRNA collected from the human cells as a template.

12. The method of claim 1, wherein the biomarker comprises mRNA level and is quantitated by a method selected from the group consisting of polymerase chain reaction, real time polymerase chain reaction, reverse transcriptase polymerase chain reaction, hybridization, probe hybridization, and gene expression array.
13. The method of claim 1, wherein the step of determining the level of expression is accomplished using at least one technique selected from the group consisting of polymerase chain reaction, heteroduplex analysis, single stand conformational polymorphism analysis, ligase chain reaction, comparative genome hybridization, Southern blotting, Northern blotting, Western blotting, enzyme-linked immunosorbent assay, fluorescent resonance energy-transfer and sequencing.
14. The method of claim 1, wherein the sample comprises a peripheral blood mononuclear cell.
15. A method of identifying a human subject suspected of having a infectious disease comprising differentiating between an infection with *S. aureus* infection and an *E. coli* infection by determining the expression level of a biomarker comprising one or more of the following genes: CXCL1; JAG1; RGS2; GAPD; PPIB; PSMA7; MMP9; p44S10; TRAM2; SEC24C; ACTG1; CGI-96; MGC2963; and STAU.
16. The method of claim 15, wherein the step of determining expression levels is used to detect *E. coli* infection as compared with *S. aureus* by determining the expression level of a biomarker comprising one or more of the following genes: RASA1; SNX4; AF1Q; SMAD2; JUP; PP; MAN1C1; FLJ10287; FLJ20152; LRRN3; SGPP1; and UBAP2L.
17. The method of claim 1, wherein the step of determining expression levels is performed by measuring amounts of mRNA, protein and combinations thereof.
18. The method of claim 1, wherein the step of determining expression levels is performed using hybridization of nucleic acids on a solid support, an oligonucleotide array, sequencing and combinations thereof.
19. The method of claim 1, wherein the step of determining expression levels is performed using cDNA which is made using mRNA collected from the human cells as a template.
20. The method of claim 1, wherein the biomarker comprises mRNA level and is quantitated by a method selected from the group consisting of polymerase chain reaction, real time polymerase chain reaction, reverse transcriptase polymerase chain reaction, hybridization, probe hybridization, and gene expression array.
21. The method of claim 1, wherein the step of determining the level of expression is accomplished using at least one technique selected from the group consisting of polymerase chain reaction, heteroduplex analysis, single stand conformational polymorphism analysis, ligase chain reaction, comparative genome hybridization, Southern blotting, Northern blotting, Western blotting, enzyme-linked immunosorbent assay, fluorescent resonance energy-transfer and sequencing.

22. The method of claim 1, wherein the sample comprises a peripheral blood mononuclear cell.

23. A method of identifying a human subject suspected of having an infectious disease by determining the expression level of a biomarker having one or more of the following genes to differentiate between a bacterial versus a viral infection: EEF1G; EIF3S5; EIF3S7; EIF4B; QARS; RPL31; RPL4; PFDN5; CD44; HADHA; PCBP2; and dJ507115.1.

24. A computer implemented method for determining the phenotype of a sample comprising: obtaining one or more probe intensities from a sample; diagnosing an infectious disease based upon the probe intensities; calculating linear correlation coefficient between the probe intensities and reference probe intensities; and accepting the tentative phenotype as the genotype of the sample if the linear correlation coefficient is greater than a threshold value.

25. A computer readable medium comprising computer-executable instructions for performing the method for determining the transcriptome of a sample comprising: obtaining a plurality of sample probe intensities; diagnosing an infectious disease based upon the sample probe intensities for six or more genes selected those genes listed in Table 2, Table 3, Supplementary Tables 1 to 11 and combinations thereof; and calculating a linear correlation coefficient between the sample probe intensities and reference probe intensities; and accepting the tentative genotype as the genotype of the sample if the linear correlation coefficient is greater than a threshold value.

26. The system of claim 25, wherein the biomarkers are selected from 5, 6, 7, 8, 9, 10, 11, 12 or more genes.

27. The system of claim 25, wherein the biomarkers are selected from one or more genes listed in Supplementary Tables 1 to 11, and combinations thereof.

28. A computer-based method for creating a datasets that correlates to the presence of an infectious disease in an individual, the method comprising computer-implemented steps of: obtaining a plurality of gene probe intensities from the individual; determining the probe intensities for six or more genes selected those genes listed in Table 2, Table 3, Supplementary Tables 1 to 11 and combinations thereof; and calculating a linear correlation coefficient between the sample probe intensities and a reference probe intensity for each of the six or more genes, wherein the correlations are averaged across the six or more genes to calculate a transcriptome expression vector that correlates with the presence or absence of the infectious disease.