A NEW APPROACH FOR UNIVERSAL MONITORING OF MINIMAL RESIDUAL DISEASE IN ACUTE MYELOID LEUKEMIA

RELATED APPLICATION

[0001] This application claims the benefit of U.S. Provisional Application No. 62/577,673, filed on October 26, 2017. The entire teachings of the above application are incorporated herein by reference.

GOVERNMENT SUPPORT

[0002] This invention was made with government support under Grant Nos CA060419 and CA021765 awarded by the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND

[0003] In most patients with acute myeloid leukemia (AML) receiving chemotherapy, leukemic cells initially become undetectable. Nevertheless, leukemia may subsequently relapse due to persisting chemo-resistant cells indistinguishable from normal hematopoietic progenitors by conventional morphologic analysis, i.e., minimal residual disease (MRD). In both childhood and adult AML, MRD is a powerful and independent prognostic factor. Despite compelling evidence supporting its clinical importance, MRD assays in AML have remained largely unchanged over the last decade.

[0004] MRD can be measured by either polymerase chain reaction (PCR) amplification of genetic abnormalities or flow cytometric detection of leukemia-associated cell marker profiles. In about 20% adult and 35% of pediatric AML cases, cells carry gene fusions, such as *RUNX1-RUNX1T1*, *CBFB-MYH11*, or *MLL* fusion transcripts; *NPM1* mutations occur in about 30% of adult and <10% of pediatric cases. Detection of these molecular abnormalities during treatment correlates with relapse. Flow cytometric monitoring of MRD is also prognostically informative and, unlike PCR, is not limited to patients with specific genetic abnormalities. Nevertheless, standard flow cytometric monitoring of MRD has a sensitivity often not exceeding 0.1% (1 leukemic cell in 1,000 normal bone marrow cells), it requires considerable expertise to avoid unreliable results, and is still not applicable to all patients.

The capacity of contemporary flow cytometers to detect 8 or more markers simultaneously can increase the discriminating power of MRD analysis. This potential, however, can be fulfilled only if sufficient leukemia-specific markers are available. Thus, the discovery of new markers differentially expressed in leukemic versus normal myeloid cells should increase applicability, sensitivity, and reliability of MRD monitoring by flow cytometry. In turn, this could widen the implementation of response-guided protocols in AML.

SUMMARY

[0005] Described herein are methods of detecting the quantity of one or more of proteins in a sample from a patient. The proteins quantified can include one or more of CD9, CD32, CD44, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CX3CR1 and Tim-3. The method can further include detecting the quantity of one or more of CD18, CD25, CD47, CD200, CLEC12A and CD300a. As described herein, these proteins can be indicative of acute myeloid leukemia (AML), and are particularly useful for monitoring minimal residual disease (MRD) in AML.

[0006] Described herein are methods of detecting an expression level of a plurality of protein markers in a subject. The methods can include contacting a sample from the subject with a plurality of probes and detecting a complex formed between each probe and corresponding marker. A value is generated corresponding to an expression level of each of the markers. Described herein are methods of diagnosing acute myeloid leukemia, which can further involve diagnosing whether the subject has acute myeloid leukemia based on the generated values corresponding to the expression level of the markers. Also described are methods of treating acute myeloid leukemia, which can further involve administering to the subject diagnosed with acute myeloid leukemia an effective amount of a therapy for treating acute myeloid leukemia.

[0007] Each probe specifically binds to a single marker.

[0008] In some embodiments, the the markers are two or more of CD9, CD18, CD25, CD32, CD44, CD47, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CD200, CD300a, CLEC12A, CX3CR1, and Tim-3. In some embodiments, the markers are two or more of CD9, CD32, CD44, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CX3CR1, and Tim-3. In some embodiments, the markers are CD54, CD18, CD96, CD97, and CD99. In some embodiments, the markers are CD44, CD54, CD18, CD96, CD97 and CD99.

[0009] In some embodiments, the plurality of probes is a first set of probes that specifically bind to: a) CD52; b) CD59, CD96, or CD300a; c) TIM3; d) CD200; and e) CD123. There can be a second set of probes that specifically bind to: a) CD34; b) CD117; c) CD33; and d) CD45.

[0010] In some embodiments, the plurality of probes is a first set of probes that specifically bind to: a) CD9; b) CD93, CD99, or CLEC12A; c) CD44; d) CD32; and e) CD25. There can be a second set of probes that specifically bind to: a) CD34; b) CD117; c) CD33; and d) CD45.

[0011] In some embodiments, the plurality of probes is a first set of probes that specifically bind to: a) CD97; b) CD54, CD68, or CXCR1; c) CD64; d) CD86; and e) CD47. There can be a second set of probes that specifically bind to: a) CD34; b) CD117; c) CD33; and d) CD45.

[0012] In some embodiments, the plurality of probes is a first set of probes that specifically bind to: a) CD54; b) CD18; c) CD96; d) CD97; and e) CD99. There can be a second set of probes that specifically bind to: a) CD34; b) CD117; c) CD33; and d) CD45.

[0013] In some embodiments, the plurality of probes is a first set of probes that specifically bind to: a) CD44; b) CD54; c) CD18; d) CD96; and e) CD97 and CD99. There can be a second set of probes that specifically bind to: a) CD34; b) CD117; c) CD33; and d) CD45.

[0014] Also described herein is a method of detecting an expression level of a plurality of markers in a subject. The method can include contacting a sample from the subject with a first set of one or more probes and with a second set of one or probes, and detecting a complex formed between each probe and corresponding marker. A value is generated corresponding to an expression level of each of the markers.

[0015] In some embodiments, each probe of the first set of one or more probes specifically binds to a single marker. The markers to which the first set of probes binds are selected from the group consisting of CD9, CD18, CD25, CD32, CD44, CD47, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CD200, CD300a, CLEC12A, CX3CR1, and Tim-3. Each probe of the second set of one or more probes specifically binds to a single marker. The markers to which the second set of probes binds are selected from the group consisting of CD45, CD34, CD33, and CD117.

[0016] In some embodiments, each probe of the first set of one or more probes specifically binds to a single marker. The markers to which the first set of probes binds are

selected from the group consisting of CD9, CD18, CD25, CD32, CD44, CD47, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CD200, CD300a, CLEC12A, CX3CR1, and Tim-3. Each probe of the second set of one or more probes specifically binds to a single marker. The markers to which the second set of probes binds are selected from the group consisting of CD34, CD13 and CD33.

[0017] In some embodiment, the first set of probes includes probes that specifically bind to: a) CD52; b) CD59, CD96, or CD300a; c) TIM3; d) CD200; and e) CD123. The second set of probes specifically bind to: a) CD34; b) CD117; c) CD33; and d) CD45.

[0018] In some embodiments, the first set of probes includes probes that specifically bind to: a) CD9; b) CD93, CD99, or CLEC12A; c) CD44; d) CD32; and e) CD25. The second set of probes includes probes that specifically bind to: a) CD34; b) CD117; c) CD33; and d) CD45.

[0019] In some embodiments, the first set of probes includes probes that specifically bind to: a) CD97; b) CD54, CD68, or CXCR1; c) CD64; d) CD86; and e) CD47. The second set of probes includes probes that specifically bind to: a) CD34; b) CD117; c) CD33; and d) CD45.

[0020] In some embodiments, the first set of probes includes probes that specifically bind to: a) CD54; b) CD18; c) CD96; d) CD97; and e) CD99. The second set of probes includes probes that specifically bind to: a) CD34; b) CD117; c) CD33; and d) CD45.

[0021] In some embodiments, the first set of probes includes probes that specifically bind to: a) CD44; b) CD54; c) CD18; d) CD96; and e) CD97 and CD99. The second set of probes specifically bind to: a) CD34; b) CD117; c) CD33; and d) CD45.

[0022] Also described are kits for detecting an expression level of a plurality of markers in a subject. The kits can include a plurality of probes. The plurality of probes can be according to any of the embodiments described herein.

[0023] Also described herein are devices for monitoring expression levels of a plurality of markers in a subject. The device can include an input member that receives digital representations of a subject sample. The digital representations can include flow cytometry outputs corresponding to a plurality of markers. The device can also include a processor engine coupled to receive from the input member the digital representations. The processor engine can be responsive to the digital representations and determine parameter values corresponding to an expression level of a marker in the subject sample. The device can also include a graphics memory module communicatively coupled to the processor engine and

transforming the determined parameter values into a graphical representation indicative of expression levels of the plurality of markers in the subject. The device can also include a display monitor coupled to the graphics memory module rendering the graphical representation as generated by the graphics memory module. The processor engine can apply a t-Distributed Stochastic Neighbor Embedding (tSNE) machine learning algorithm to determine the parameter values in a manner enabling generation of the graphical representation.

[0024] Also described herein are processor-based methods for monitoring acute myeloid leukemia. The method can include receiving by a digital processor flow cytometry output representative of a plurality of markers of a subject sample. The method can also include, in the processor, in response to the flow cytometry output, determining parameter values corresponding to an expression level of a marker in the subject sample, and transforming the parameter values into a graphical representation. The method can also include outputting the graphical representation to a graphics memory module. The method can also include rendering on a display monitor the graphical representation by the graphics memory module. Determining parameter values can include applying a t-Distributed Stochastic Neighbor Embedding (tSNE) machine learning algorithm to transform the values corresponding to an expression level of a marker into a graphical representation.

[0025] In any of the embodiments described, one or more of the probes can be an antibody that specifically binds to a single marker. In any of the embodiments described, contacting the sample from the subject with a plurality of probes can include subjecting the sample to flow cytometry. In any of the embodiments described, the value generated can be fluorescence intensity. In any of the embodiments described, the value generated can be mean fluorescence intensity or median fluorescence intensity. In any of the embodiments described, the method can further include contacting the sample with an agent that permeabilizes a cell membrane prior to contacting the sample from the subject with a plurality of probes. In any of the embodiments described, the sample can include one or more of blood cells, bone marrow, and cellular products derived from blood cells or bone marrow cells. In any of the embodiments described, the sample can be a bone marrow sample. In any of the embodiments described, the subject can have been diagnosed previously with acute myeloid leukemia. In any of the embodiments described, the acute myeloid leukemia can be minimal residual disease in acute myeloid leukemia. In any of the

embodiments described, the method can further include contacting the sample with one or more probes that specifically detect one or more genes of Table 2 or Table 3.

BRIEF DESCRIPTION OF THE DRAWINGS

[0026] The foregoing will be apparent from the following more particular description of example embodiments, as illustrated in the accompanying drawings in which like reference characters refer to the same parts throughout the different views. The drawings are not necessarily to scale, emphasis instead being placed upon illustrating embodiments.

[0027] FIG. 1 is a set of graphs showing genes significantly over- and/or under-expressed in AML cells at the protein level as determined by flow cytometry. Plots indicate mean fluorescence intensity (MFI) of each marker in CD34+ cells expressing CD13 and/or CD33 from bone marrow aspirates of healthy donors or patients with ALL (white circles), and in diagnostic AML samples (gray circles). The box on the AML plots indicates the upper and lower normal limits. The number of samples studied is indicated under each plot. By unpaired t-test with Welch's correction, $P < 0.0001$ for CD9, CD44, CD54, CD59, CD64, CD68, CD86, CD96, CD97, CD99, CD123, and CX3CR1; $P < 0.001$ for CD32 and TIM3; $P < 0.01$ for CD52 and CD93.

[0028] FIG. 2 is a set of graphs showing genes whose expression in AML cells by flow cytometry was not statistically different than that of their normal counterparts. Plots indicate mean fluorescence intensity (MFI) of each marker in CD34+ cells expressing CD13 and/or CD33 from bone marrow aspirates of healthy donors or patients with ALL (white circles), and in diagnostic AML samples (gray circles). The box on the AML plots indicates the upper and lower normal limits. The number of samples studied is indicated under each plot. By unpaired t-test with Welch's correction, $P > 0.05$ for all markers, except CD25 ($P = 0.049$) and CD300a ($P = 0.020$). Some AML samples show considerable over- or under-expression.

[0029] FIGs. 3A-C show that the new markers persist at relapse and are expressed on AML cells with stem cell features. FIG. 3A is a chart showing expression of the new markers in paired samples collected at diagnosis ("D") and at relapse ("R"). Bars indicate the number of paired samples studied for each marker; gray bars denote samples with aberrant marker expression at both diagnosis and relapse, white bars samples in which the aberrantly expressed marker was present only at relapse, and black bars samples in which the aberrantly expressed marker at diagnosis was not detectable at relapse. FIG. 3B is a plot showing expression of new markers in AML blasts with the CD34+ CD38 dim/neg immunophenotype

("leukemia stem cells"), in comparison with the more mature CD38 bright cell population. Each symbol is the percent median fluorescence intensity (MFI) of a new marker in the "stem cells" relative to that of the more mature AML cells in the same sample. Horizontal bar correspond to the median value; n = 60). Data for individual markers/samples shown in FIG. 8. FIG. 3C is a set of flow cytometric histograms illustrate expression of selected marker on CD38 dim/neg (upper line) and CD38 bright AML cells (lower line).

[0030] FIGs. 4A-B shows that the new markers allow detection of MRD and remain aberrantly expressed during chemotherapy. FIG. 4A is a graph showing relation between MRD levels measured using the new markers versus those measured with standard markers (see Table 7). Spearman regression analysis of positive MRD results by both methods: $r = 0.9816$, $P < 0.0001$. FIG. 4B is a set of graphs showing median fluorescence intensity (MFI) of the indicated markers measured at diagnosis ("D") and during chemotherapy ("MRD"). Horizontal bars correspond to the median value in each group. Gray areas include MFI of normal CD34+ myeloid progenitors (CD13+ and/or CD33+).

[0031] FIG. 5 is a set of plots showing preferential expression of the new markers in subgroups of AML. Each symbol corresponds to an AML diagnostic sample studied with the indicated marker. Markers significantly over- or underexpressed are in boxes with a thicker frame (all $P < 0.001$ by Fischer's exact test). Additional data shown in FIG. 10.

[0032] FIGs. 6A-C show marker expression in 129 consecutive cases of AML and sensitivity of MRD detection. FIG. 6A is a chart showing percentage of consecutive diagnostic (n = 118) or relapse (n = 11) AML samples with aberrant expression of the indicated markers. FIG. 6B is a chart showing sensitivity of MRD detection afforded by the new markers in comparison to standard MRD assays (see Table 7) in the 129 cases studied. FIG. 6C is a set of graphs showing t-SNE analysis of the cell profile of normal bone marrow (NBM) CD34+ CD33+ CD117+ mononucleated cells from 10 donors (shown in grey) containing various proportions of AML cells (shown in red). The histograms on the right show expression of the individual markers on the leukemia cell cluster (red) compared to the remaining cells (grey).

[0033] FIG. 7 is a set of plots showing expression of new markers at relapse. Plots show percentage of AML cells expressing the indicated marker at diagnosis ("D") and relapse ("R), or at first ("R1") and second relapse ("R2") in 16 patients with AML. Each marker studied is indicated by a symbol.

[0034] FIG. 8 is a set of plots showing expression of new markers in AML blasts with the CD34+ CD38 dim/neg immunophenotype ("S"), in comparison with the more mature CD38 bright cell population ("D). Each symbol is the percent mean fluorescence intensity (MFI) of a new marker in the "stem cells" relative to that of the more mature AML cells in the same sample. Gray areas indicate limits of expression in normal CD34+ CD13 and/or CD33+ cells.

[0035] FIG. 9 is a set of plots showing expression of the new markers on residual AML cells during treatment. Mean fluorescence intensity ("MFI") of the indicated new markers as measured at diagnosis ("0") and in subsequent follow-up samples ("1, 2, etc."). Each symbol represents results obtained in samples from one patient. Gray areas indicate limits of expression in normal CD34+ CD13 and/or CD33+ cells.

[0036] FIG. 10 is a set of plots showing preferential expression of the new markers in subgroups of AML. Each symbol corresponds to an AML diagnostic sample studied with the indicated marker. Markers significantly over- or underexpressed are in boxes with a thicker frame (all $P < 0.001$ by Fischer's exact test). Additional data shown in FIG. 5.

[0037] FIG. 11 shows marker expression in AML cases with <25% CD34+ cells. Markers were tested by flow cytometry in 34 cases of AML with low/absent CD34 and compared to that of CD117+ CD33+ cells from non-leukemic bone marrow samples, including maturing myeloid cells, monoblasts and erythroblasts, and excluding mature monocytes and granulocytes. Plots indicate median fluorescence intensity (MFI) of each marker in normal cells (white circles), and AML cells (gray circles). Boxes on the AML plots indicate upper and lower normal limits. Number of samples studied is shown under each plot. Top row, $P < 0.001$; middle row, $P < 0.05$ but > 0.01; bottom row, $P > 0.05$.

[0038] FIG. 12 shows improved discrimination of AML and normal cells with the new markers. t-SNE analysis of the cell profile of normal bone marrow CD34, CD117, CD45 and CD33 mononucleated cells from 4 donors (shown in blue) mixed with various proportions of AML cells (shown in red). Percentage of AML cells in each mixture is shown.

[0039] FIG. 13 shows MRD visualization in bone marrow mononucleated cells from 2 patients with AML after chemotherapy. In Pt. 1, cells were collected after the first cycle of remission induction chemotherapy. They were labelled with either the best available standard markers (CD38, CD133, CD7, and anti-HLA-Dr) or the new markers CD52 and CD47; both sample aliquots were also labelled with CD34, CD117, CD45 and CD33. tSNE was performed on gated myeloid CD34+ cells. Percent estimated MRD (red contour plots) according to the new markers is shown. In Pt. 2, cell were collected after the second cycle of

remission induction chemotherapy. Cells were labelled with CD34, CD117, CD45 and CD33, in combination with CD7 (the best standard marker in this case) and the new marker CD96. Percent estimated MRD (gray contour plots) according to CD7 plus CD96 is shown; histograms illustrate the individual marker expression in normal (black) versus AML cells (gray).

[0040] FIG. 14 shows marker expression in 129 consecutive cases of AML. Scale map showing the expression of the new markers in the 129 consecutive AML cases. Red cells indicate marker expression, and blue cells lack of expression; blank cells, not tested. A combination of 5 markers (CD54, CD18, CD96, CD97 and CD99) would be sufficient to study 122 of the 129 cases (94.6%).

[0041] FIG. 15 shows leukemia-free survival of children with AML according to MRD at the end of the first course of remission induction chemotherapy. Patients received either chemotherapy alone according the Ma-Spore AML 2006 study (n=26), or chemotherapy plus allogeneic hematopoietic stem cell transplant (2 in the MRD- group, 9 in the MRD+ group); P value by log-rank test.

[0042] FIG. 16 is a schematic illustration of a computer network in which embodiments operate.

[0043] FIG. 17 is a block diagram of one computer node in the computer network of FIG. 16.

DETAILED DESCRIPTION

[0044] A description of example embodiments follows.

[0045] Optimal management of acute myeloid leukemia (AML) requires accurate monitoring of treatment response, but minimal residual disease (MRD) may escape detection. This study contrasts the genome-wide gene expression profiles of AML cells to those of their normal counterparts. The aberrant expression of selected genes was validated by flow cytometry, by analyzing their expression in large sets of normal and leukemic specimens. The findings led to the formulation of new marker panels and analytical algorithms for highly sensitive, clearly evident and universal monitoring of MRD in AML.

[0046] To identify distinctive features of AML cells for MRD monitoring, described herein is a comparison of genome-wide gene expression of leukemic myeloblasts from 157 patients with AML to that of $CD34^+$ myeloblasts from healthy donors. Aberrantly expressed genes, including some previously associated with “leukemia stem-cells”, were studied by

flow cytometry in 191 AML and 63 leukemia-free bone marrow samples. Sixteen (CD9, CD32, CD44, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CX3CR1, and Tim-3) were significantly over- or under-expressed in AML, in agreement with gene array results. Six other markers (CD18, CD25, CD47, CD200, CD300a, and CLEC12A) were expressed at markedly abnormal levels in some AML cases. These 22 markers defined leukemia-associated profiles extending to cells with stem-cell phenotype; markers remained stable during treatment, and at relapse. In 208 samples from 52 patients undergoing chemotherapy, the new markers yielded MRD measurements matching those of standard methods (Spearman $r = 0.9816$, $P < 0.0001$), and also revealed MRD that was otherwise undetectable. Finally, the 22 new markers allowed MRD monitoring in 129 consecutive AML patients; using a machine learning algorithm to reduce the high-dimensional datasets to 2-dimensional data, 1 leukemic cell among more than 100,000 normal cells could be clearly visualized. This new approach to MRD studies should refine treatment of AML, and provide new eligibility and response criteria for studies of novel agents.

Acute Myeloid Leukemia (AML)

[0047] "Diagnosing acute myeloid leukemia (AML)" and/or "detecting minimal residual disease (MRD)" or "diagnosing minimal residual disease (MRD)" is intended to include, for example, diagnosing or detecting the presence of acute myeloid leukemia (AML) by identifying or detecting cells and/or cell products in samples or specimens that are indicative of AML, monitoring the progression of the disease, monitoring and/or detecting the recurrence of AML disease in patients who had been previously treated for AML, and monitoring and/or detecting minimal residual disease. The terms "diagnosing," "detecting," and "identifying" when used with acute myeloid leukemia or minimal residual disease (MRD) are used interchangeably herein to refer to the identifying or detecting cells and/or cell products in specimens that are indicative of disease.

[0048] One method disclosed herein is directed to monitoring remission of leukemia. Remission is defined as the absence of outward signs of cancer, or in the case of AML, the absence of detectable cancer cells in the body after a course of therapy. Remission in AML can be characterized, for example, as a lack of detectable abnormal cells in the blood, and/or cerebrospinal fluid, and less than 5% blast cells in the bone marrow. Embodiments seek to detect cancer cells in instances where there is a relatively minimal amount of disease

(minimal residual disease (MDR)) by phenotypic analysis. Standard detection methods define minimal residual disease as an incidence of less than one leukemic cell in 10,000 normal bone marrow/blood cells. In some embodiments, the methods and compositions described herein can detect minimal residual disease with an incidence of less than one in 100,000 cells.

[0049] Most AML patients achieve at least an initial remission. However, some patients have residual leukemic cells in their marrow. Other patients achieve remission then "relapse" wherein they have a decrease in normal blood cells and a return of leukemia cells in the marrow. Embodiments can detect leukemia and can help evaluate the risk for relapse after initial treatment. In addition to the detection of evidence of minimal residual disease, embodiments can further help to evaluate treatment regimens. For example, the detection and characterization of MRD can be indicative of the efficacy of certain treatment regimes, e.g., stem cell transplant.

[0050] In other embodiments, detection or diagnosing MRD can help determine whether additional treatment may be necessary. One of skill in the art will recognize that in these methods the term "therapy" can include any therapy for treating AML, including but not limited to chemotherapy, radiation therapy, stem cell transplantation, and biological therapy (e.g., tyrosine kinase inhibitor therapy, monoclonal antibody therapy). Depending on the subtype, specific drugs or drug combinations, drug dosages, duration of treatment, and other types of treatment, may be indicated to achieve optimal results.

[0051] In still other embodiments, methods for evaluating the efficacy of a therapy for treating AML in a subject are provided. Embodiments can also be used to test specimens taken from a subject during the course of therapy to monitor the effects of treatment. Such methods typically comprise comparing the level of expression of a plurality of markers in a first specimen procured prior to the initiation of therapy with that from a second sample obtained following administration of at least a portion of the therapy. In some embodiments, a significantly lower and/or an undetectable level of expression of a marker in the second specimen relative to that of the first specimen obtained prior to the initiation of the therapy can be a positive indication of the efficacy of the therapy. In other embodiments, a significantly higher level of expression of a marker in the second sample can be a negative indication of the efficacy of the therapy. A positive indication of the efficacy of the therapy can mean that the therapy is producing beneficial results in the treatment of AML and no minimal residual disease is detected. A negative indication of the efficacy of the therapy can

mean that the therapy is not having beneficial effects with respect to treatment of AML and minimal residual disease is detected.

Samples from Subjects

[0052] In embodiments, the method comprises obtaining a "specimen" from a subject. The term "specimen" is intended to include blood cells, bone marrow cells, and cellular products that are derived from blood and bone marrow cells. Cellular products can include, but are not limited to, expressed proteins, expressed RNA, and DNA. In embodiments, a specimen can include cells derived from a variety of sources including, but not limited to, single cells, a collection of cells, tissue, cell culture, bone marrow, blood, or other bodily fluids. A tissue or cell source may include a tissue biopsy sample, a cell sorted population, cell culture, or a single cell. Sources for the specimen include cells from peripheral blood or bone marrow, such as blast cells from peripheral blood or bone marrow. The term "specimen" can be used interchangeably with the term "sample" or "patient sample."

[0053] A specimen may be processed in another embodiment to release or otherwise make available a nucleic acid or a protein for detection as described herein. Such processing may include, in one embodiment, steps of nucleic acid manipulation, e.g., preparing a cDNA by reverse transcription of RNA from the specimen. Thus, the nucleic acid to be amplified in one embodiment by the methods described herein may be DNA or RNA. Isolation of protein, RNA, and DNA from the aforementioned sources is known to those of skill in the art, and is discussed herein.

[0054] In one embodiment, the method comprises obtaining a peripheral blood sample from a subject and analyzing the expression level of specific markers in leukocytes from the blood sample taken from the subject. To do blood tests, blood samples are generally taken from a vein in the subject's arm.

[0055] In another embodiment, the method comprises obtaining a bone marrow sample from a subject and analyzing the expression level of specific markers combinations in leukocytes from the blood sample taken from the subject. Specimens of marrow cells are obtained by bone marrow aspiration and biopsy.

[0056] The obtaining of a specimen uses methods well known in the art, as is the means to analyze leukocyte populations. For example, leukocyte populations can be prepared from whole blood by differential centrifugation, or for example, by density gradient centrifugation. The method can be conducted on leukocytes in blood samples which have not undergone any

leukocyte enrichment, on whole blood samples, or where red blood cells have been lysed. In other embodiments the method can be conducted on enriched and purified subpopulations of cells, using methods well known in the art.

Analyzing Samples

[0057] In embodiments, the method comprises "contacting" the specimen with a plurality of probes. In one embodiment, the term "contacting" is in reference to probes that are antibodies and generally referring to methods of "cell staining." In an embodiment, an antibody is added to a specimen and the antibody recognizes and binds to a specific protein for example, on the surface of cells in the specimen. A complex is thereby formed between the probe and the expressed protein. The complex can be detected and visualized by various techniques, as will be discussed herein. Combinations of antibody probes can be collectively added to a specimen and thereby "stain" the cell for later analysis by visualization with a flow cytometer or microscope, for example. One of skill in the art could determine whether a cell expressed a specific protein based on the level of antibody that bound to the cell using standard methods.

[0058] In embodiments, the term "contacting" in reference to probes that are nucleic acids, refers to methods of detecting expression of an mRNA of interest in a specimen. A detectable complex can be formed when a nucleic acid probe specific to an expressed gene of interest hybridizes and binds an mRNA/cDNA expressed by cells in a specimen. One of skill in the art could determine whether a cell expressed a specific mRNA based on the level of detectable PCR product, for example, using standard methods.

Detecting Expression of Markers for Minimal Residual Disease

[0059] As used herein a "marker" can be any gene or protein whose level of expression in a tissue or cell is used comparatively to evaluate the level of expression to that of a normal or healthy cell or tissue. In particular embodiments, antibodies are used to detect marker expression at the protein level. In other aspects, marker expression is detected at the nucleic acid level.

[0060] Markers may be referred to herein interchangeably as "markers," "immunophenotypic markers," "leukemia-associated phenotypic markers," "phenotypic markers," or "cell markers." "Leukemia-associated markers" can refer to particular combinations of markers used to diagnosis a particular leukemia, for example, an expression

profile of different combinations of markers may be particular to a patient with AML. In particular embodiments, markers can refer to "antigenic markers," "antigens," or "cell surface antigens," referring to proteins that are expressed on the cell surface. Combinations of markers are selective for AML, and specifically minimal residual disease.

[0061] The various markers employed in the methods and compositions disclosed herein, can have a modulated level of expression when compared to an appropriate control. Alternatively, a given marker need not show a modulated level of expression, but rather must only be expressed in the given sample. Specific expression profiles of the given marker combinations that are predictive of the various states disclosed herein are discussed in further detail elsewhere herein.

[0062] As used herein, a "modulated level" of a marker can comprise any statistically significant increase (overexpression) or decrease (underexpression) of the given marker when compared to an appropriate control. The modulated level can be assayed by monitoring either the concentration of and/or activity of the marker polypeptide and/or the level of the mRNA encoding the marker polypeptide. In general, a modulated level of marker can include either an increase or a decrease of at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or higher relative to an appropriate control.

[0063] By "overexpressed" it is intended that the marker of interest is overexpressed in AML cells but is not overexpressed in conditions classified as nonmalignant, benign, and/or any conditions that are not considered to be indicative of clinical disease. In general, an overexpressed marker can include any statistically significant increase in expression when compared to an appropriate control, including for example, an increase of at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or higher relative to an appropriate control.

[0064] By "underexpressed" it is intended that the marker of interest is underexpressed in AML cells but is not underexpressed in conditions classified as nonmalignant, benign, and/or any conditions that are not considered to be indicative of clinical disease. Thus, detection of various combinations of markers permit the differentiation of specimens indicative of an increased likelihood of minimal residual disease associated with AML as compared to those of normal control specimens that are indicative of nonmalignant and benign proliferation.

[0065] The level of expression of a particular marker that is sufficient to constitute "overexpression" will vary depending on the specific marker used. In particular embodiments, a "threshold level" of expression over a normal control is established for a

particular marker, wherein expression levels above this value are deemed overexpression. Overexpression of a particular marker can refer to an increase in the percentage of a population detected as expressing a particular marker or marker combination. Overexpression can also refer to the level of expression on a population of cells as detected by an increase in the mean fluorescence intensity (MFI), though median fluorescence intensity can also be detected. For example, in one embodiment, "overexpression" may be determined if the marker MFI for the specimen is at least three-fold above the normal control, wherein a three-fold increase in MFI is the "threshold level." In other embodiments, an overexpressed marker can include any statistically significant decrease in expression when compared to an appropriate control, including for example, an increase of at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or higher relative to an appropriate control or at least a 1 fold, 2 fold, 3 fold, 4 fold, 5 fold, 6 fold, 10 fold or higher expression level relative to an appropriate control.

[0066] The level of expression of a particular marker that is sufficient to constitute "underexpression" will vary depending on the specific marker used. In particular embodiments, a "threshold level" of expression is established for a particular marker, wherein expression levels below this value are deemed underexpression. Underexpression of a particular marker can refer to a decrease in the percentage of a population detected as expressing a particular marker or marker combination. Underexpression can also refer to the level of expression on a population of cells as detected by a decrease in the mean fluorescence intensity (MFI), though median fluorescence intensity can also be detected. For example, in one embodiment, "underexpression" may be determined for that particular marker if the marker MFI for the specimen is less than the normal control by at least half, wherein a 50% reduction MFI is the "threshold level". In other embodiments, an underexpressed marker can include any statistically significant decrease in expression when compared to an appropriate control, including for example, a decrease of at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or lower relative to an appropriate control or at least a 1 fold, 2 fold, 3 fold, 4 fold, 5 fold, 6 fold, 10 fold or lower expression level relative to an appropriate control.

[0067] The methods described herein comprise diagnosing minimal residual disease in a sample taken from a subject by detecting the expression of a plurality of markers that are modulated in AML.

[0068] The methods described herein can comprise MRD detection by flow cytometry with preferred combinations of probes to specific markers. MRD detection can be combined with at least 4 different probes, and can include in some embodiments at least 5, 6, 7, 8, 9, 10, 11, and 12 different probes. When incorporated with at least 6-probes, the new marker combinations afford the detection of one leukemic cell amongst 10^5 bone marrow cells.

Probes to Detect Markers of Minimal Residual Disease (MRD)

[0069] The term "probe" refers to any molecule that is capable of specifically binding to an intended target molecule, for example, a nucleotide transcript or a protein encoded by a marker gene. RNA/DNA probes can be synthesized by one of skill in the art, or derived from appropriate biological preparations. Likewise, antibody probes to specific targets can be generated by one of skill in the art, or derived from appropriate sources. Probes may be specifically designed to be labeled. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic molecules.

[0070] By "specifically binds," it is generally meant that an antibody binds to an epitope via its antigen binding domain, and that the binding entails some complementarity between the antigen binding domain and the epitope. An epitope is a site on an antigen or marker where the antibody binds via its variable region. The epitope is therefore a part of the antigen or marker, but the epitope is only a portion of the marker recognized by the antibody. According to this definition, an antibody is said to "specifically bind" to an epitope or have "antigen specificity" when it binds to that epitope, via its antigen binding domain more readily than it would bind to a random, unrelated epitope. As used herein, therefore, "specifically binds" is used interchangeably with recognition of a defined epitope on an antigen or marker, or any epitope contained in the antigen or marker. For example, the term "specifically binds" when used in conjunction with a particular antibody is used to indicate that there is recognition of a certain epitope of the antigen and the interaction between the antibody and epitope is a non-random interaction indicative of the presence or "expression" of the certain epitope. The term "specifically binds" when used in conjunction with a particular marker is used to indicate that there is recognition of a certain antigen or marker and the interaction between the antibody and antigen or marker is a non-random interaction indicative of the presence or "expression" of the certain antigen or marker.

[0071] Embodiments include methods and kits comprising probes to detect markers and combinations of markers in Table 5 comprising genes overexpressed or underexpressed in AML.

Generating Expression Profiles

[0072] As used herein, an "expression profile" comprises one or more values corresponding to a measurement of the relative abundance of a gene expression product (e.g, a marker). Such values may include measurements of RNA levels or protein abundance. Thus, an expression profile can comprise values representing the measurement of the transcriptional state or the translational state of the gene. As is known to those of skill in the art, the transcriptional state and translational state are related.

[0073] In embodiments, an "expression profile" of a specimen can include the identities and relative abundance, or "expression level," of the RNA species, especially mRNAs present in populations of cells in the specimen. Preferably, a sufficient fraction or mRNA is used generate an expression profile using combinations of markers predictive of minimal residual disease. An expression profile can be conveniently determined by measuring transcript abundance by any of several existing gene expression technologies.

[0074] In embodiments, an "expression profile" of a specimen can include the identities and relative abundance, or "expression level", of the constituent protein species expressed in populations of cells in the specimen. Expression profiles of embodiments comprise one or more values representing the expression level of a gene having differential expression in minimal residual disease as compared to a normal control specimen. Each expression profile can contain a sufficient number of values such that the profile can be used to distinguish samples containing a minimal number of leukemic cells or minimal residual disease as compared to specimens taken from normal controls. In some embodiments, an expression profile can comprise four values. In other embodiments, an expression profile can comprise more than four values corresponding to differentially expressed genes, for example at least 5, 6, 7, 8, 9, 10, 11, or 12 values.

[0075] In other embodiments, an expression profile can comprise values corresponding to mRNA expression levels as detected by nucleic acid probes. In exemplary embodiments, it may be advantageous to use a greater number of probes and therefore analyze the expression of a greater number of genes simultaneously. Therefore, in other embodiments, 10, 20, 30,

40, 50, 60, 70, 80, 90, 100, 120, 130, 140, 150, 160, 170, 180, 190, 200, or >200 probes are reasonable. Embodiments can include, but are not limited to, the detection of mRNA expression with probe sets shown in Table 5 comprising genes overexpressed or underexpressed in AML.

"Normal Controls"

[0076] In one embodiment, a "normal control" used in the methods and kits are taken from a subject, or pool of subjects diagnosed and validated as "normal." As discussed elsewhere herein, the corresponding predictive markers which are assayed in these samples can include, but are not limited to, CD9, CD32, CD44, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CX3CR1, Tim-3, CD18, CD25, CD47, CD200, CLEC12A, and CD300a or combinations thereof. In embodiments, specimens from normal controls correspond to blood or bone marrow specimens classified as nonmalignant, benign, and/or other conditions that are not considered to be indicative of clinical disease.

RNA Expression Profiling

[0077] The values in the expression profiles are measurements representing the absolute or the relative expression level of differentially expressed genes. The expression levels of marker genes may be determined by any method known in the art for assessing the expression level of an RNA molecule in a specimen. For example, expression levels of RNA may be monitored using a 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 U.S. Pat. Nos. 5,770,722, 5,874,219, 5,744,305, 5,677,195 and 5,445,934, which are expressly incorporated herein by reference. Gene expression detection may also comprise nucleic acid probes in solution. Expression levels of RNA may also be monitored using the reverse transcriptase polymerase chain reaction (e.g., TaqMan®).

[0078] In one embodiment, microarrays are used to measure the values to be included in the expression profiles. Microarrays are particularly well suited for this purpose because of the reproducibility between different experiments. DNA microarrays provide one method for the simultaneous measurement of the expression levels of large numbers of genes. Each array consists of a reproducible pattern of capture probes attached to a solid support. Labeled RNA or DNA is hybridized to complementary probes on the array and then detected by laser

scanning. Hybridization intensities for each probe on the array are determined and converted to a quantitative value representing relative gene expression levels. High-density oligonucleotide arrays are particularly useful for determining the gene expression profile for a large number of RNA's in a sample.

[0079] In one approach, total mRNA isolated from cells taken from the subject is converted to labeled cDNA and then hybridized to an oligonucleotide array. Each specimen is hybridized to a separate array. Relative transcript levels are calculated by reference to appropriate controls present on the array and in the sample.

[0080] Embodiments can include, but are not limited to, the detection of mRNA expression with probes specific for genes described herein.

[0081] In embodiments an expression profile is generated by the detection of nucleic acid corresponding to the expression of mRNA from a specimen.

Protein Expression Profile and Antibody Detection

[0082] In other embodiments, the values in the expression profile are obtained by measuring the abundance of the protein products of the differentially-expressed genes. The abundance of these protein products can be determined, for example, using antibodies specific for the protein products of the differentially-expressed genes. The term “antibody” as used herein refers to an immunoglobulin molecule or immunologically active portion thereof, e.g., an antigen-binding portion. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab′)2 fragments, which can be generated by treating the antibody with an enzyme such as pepsin.

[0083] The terms “antibody” and “antibodies” broadly encompass naturally occurring forms of antibodies and recombinant antibodies such as single-chain antibodies, chimeric and humanized antibodies and multi-specific antibodies as well as fragments and derivatives of all of the foregoing, which fragments and derivatives have at least an antigenic binding site (e.g., Fab′, F(ab)2, Fv, single chain antibodies, diabodies). Antibody derivatives may comprise a protein or chemical moiety conjugated to the antibody.

[0084] In embodiments, the antibody can be a polyclonal, monoclonal, or recombinant, e.g., a chimeric or humanized, fully human, non-human (e.g., murine, or single chain antibody). The term “monoclonal antibody” as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, e.g., the individual antibodies

comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

[0085] The term "polyclonal antibody" as used herein refers to an antibody obtained from a population of heterogeneous antibodies derived from a multiple B cell response to an antigen which will recognize a variety of epitopes on the antigen. Polyclonal antibodies can be prepared by immunizing a suitable subject (e.g., rabbit, goat, mouse, or other mammal) with a marker protein immunogen. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized biomarker protein. At an appropriate time after immunization, e.g., when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, C. (1975) Nature 256:495-497, the human B cell hybridoma technique (Kozbor, et al. (1983) Immunol. Today 4:72), the EBV-hybridoma technique (Cole, et al. (1985) in Monoclonal Antibodies and Cancer Therapy, ed. Reisfeld and Sell (Alan R. Liss, Inc., New York, N.Y.), pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally Coligan, et al. eds. (1994) Current Protocols in Immunology (John Wiley & Sons, Inc., New York, N.Y.); Galfre et al. (1977) Nature 266:550-52; Kenneth (1980) in Monoclonal Antibodies: A New Dimension In Biological Analyses (Plenum Publishing Corp., NY); and Lerner (1981) Yale J. Biol. Med., 54:387 402).

[0086] As an alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with a marker protein to thereby isolate immunoglobulin library members that bind the marker protein.

[0087] Antigen-binding fragments and variants of the monoclonal antibodies disclosed herein are contemplated. Such variants, for example, will retain the desired binding properties of the parent antibody. Methods for making antibody fragments and variants are generally available in the art. For example, amino acid sequence variants of a monoclonal antibody described herein can be prepared by mutations in the cloned DNA sequence encoding the antibody of interest. Methods for mutagenesis and nucleotide sequence alterations are well known in the art.

[0088] Preferably, variants of an antibody to a reference marker will have amino acid sequences that have at least 70% or 75% sequence identity, preferably at least 80% or 85%

sequence identity, more preferably at least 90%, 91%, 92%, 93%, 94% or 95% sequence identity to the amino acid sequence for the reference antibody molecule, or to a shorter portion of the reference antibody molecule. More preferably, the molecules share at least 96%, 97%, 98% or 99% sequence identity.

[0089] In embodiments, an antibody can be used to detect the marker or protein product of a differentially expressed gene in order to evaluate the abundance and pattern of expression of the protein. These antibodies can also be used diagnostically to monitor protein expression levels over time as part of a clinical monitoring procedure, e.g., determine the efficacy of a given therapy and reoccurrence of disease.

Optical Detection Methods

[0090] Detection of antibodies can be facilitated by coupling (e.g., physically linking) the antibody to a detectable substance (e.g., antibody labeling). Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials (fluorophores, flurochromes), luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of fluorophores/flurochromes, include phycoerythrin (PE), fluorescein isothiocyanate (FITC), peridinin-chlorophyll (PerCP), allophycocyanin (APC), R-phycoerythrin conjugated with cyanine dye (PE-Cy7), allophycocyanin-cyanine tandem (APC-H7), coumarin dye (Horizon v450), sulphonyl chloride (Texas Red), cyanine (CY3, CY5, Cy7), FAM, JOE, TAMRA, TET, VIC, rhodamine; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include 125I, 131I, 35S or 3H. The skilled artisan will understand that additional moieties may be suitable.

[0091] A detectable moiety generally refers in one embodiment to a composition or moiety that is detectable by spectroscopic, photochemical, biochemical, immunochemical, electromagnetic, radiochemical or chemical means such as fluorescence, chemifluorescence, or chemiluminescence, or any other appropriate means. The terms “fluorophore” and “fluorochrome” are defined as a chemical group, or component of a molecule that causes a molecule to be fluorescent. It is a functional group in a molecule which will absorb energy of a specific wavelength and re-emit energy at a different (but equally specific) wavelength. A

fluorophore/fluorchrome can refer to various fluorescent substances, including dyes, used in fluorescence microscopy or flow cytometry to stain specimens. The terms fluorophore" and "fluorochrome" are herein used interchangeably.

[0092] Fluorochromes may be conjugated to antibodies, proteins, polypeptides, peptides, or nucleotide probes which specifically bind to antigens, proteins, polypeptides, peptides, polysaccharides, DNA, or RNA sequences. Thus, binding of an antibody, protein, polypeptide, peptide, or nucleotide probe to an antigen, protein, polypeptide, peptide, polysaccharide, DNA, or RNA may be detected by measuring a signal generated from a fluorochrome by flow cytometry, or any suitable optical imaging technique. Detection of a signal may indicate binding, whereas lack of detection of a signal may indicate lack of binding.

[0093] Methods and compositions for detectably labeling nucleic acid probes, such as oligonucleotides, DNA-RNA hybrids, etc. are well known in the art.

[0094] The compositions further comprise monoclonal antibodies and variants and fragments thereof that specifically bind to marker proteins of interest, thereby forming a detectable complex. The monoclonal antibodies may be labeled with a detectable substance to facilitate marker protein detection in the sample. Such antibodies find use in practicing the methods described herein. Monoclonal antibodies having the binding characteristics of the antibodies disclosed herein are also contemplated. Compositions further comprise antigen-binding variants and fragments of the monoclonal antibodies.

[0095] In embodiments, a probe is an antibody, including but not limited to a whole antibody molecule, a F(ab′)2, Fab′, Fv, Fd′, or Fd fragment. In yet other embodiments, an antibody can be conjugated with a detectable moiety, wherein the detectable moiety can be, for example, a fluorophore, a chromophore, a radionuclide, or an enzyme. In embodiments, a fluorophore can for example, can be, but is not limited to, phycoerythrin (PE), fluorescein isothiocyanate (FITC), peridinin-chlorophyll (PerCP), allophycocyanin (APC), R-phycoerythrin conjugated with cyanine dye (PE-Cy7), allophycocyanin-cyanine tandem (APC-H7), and coumarin dye (Horizon v450). Detection of complexes formed between an antibody probe and marker can be achieved by an optical detection technique, including, but not limited to flow cytometry and microscopy.

[0096] "Cell staining" when used in reference to an antibody means that the antibody recognizes an marker and binds to marker in the specimen forming a complex, thereby "labeling" or otherwise "staining" the cell expressing the marker to make it visible and/or

detectable by microscopy or flow cytometry. Combinations of antibodies can be collectively added a specimen and thereby "stain the cell" for later analysis by visualization with a flow cytometer or microscope, for example. One of skill in the art could determine whether a cell expressed a specific protein based on the level of antibody that bound to the cell using standard methods.

[0097] The methods described herein can also be used in immunofluorescence histochemistry. This technique involves the use of antibodies labeled with various fluorophores to detect substances within a specimen. In exemplary embodiments a pathologist can derive a great deal of morphological information of diagnostic value by examining a specimen from a subject by microscope. Immunohistochemistry is particularly relevant to, for example, the early diagnosis of cancer or pre-acute states such as minimal residual disease in AML. Combinations of fluorophores or other detectable labels can be used by the methods described herein, thereby greatly increasing the number of distinguishable signals in multicolor protocols.

[0098] In another embodiment, the method employs flow cytometry. In another embodiment, in a peripheral blood sample or blood sample, lymphocyte, monocyte and granulocyte populations can be defined on the basis of forward and side scatter. Forward and side scatter are used in one embodiment to exclude debris and dead cells.

[0099] Flow cytometry is an optical technique that analyzes particles or cells in a fluid mixture based on their optical characteristics, via the use of a flow cytometer (See, for example, Shapiro, "Practical Flow Cytometry," Third Ed. (Alan R. Liss, Inc., 1995); and Melamed et al. "Flow Cytometry and Sorting," Second Ed. (Wiley-Liss 1990)). Flow cytometers hydrodynamically focus a fluid suspension of particles/cells into a thin stream so that they flow down the stream in substantially single file and pass through an examination zone. A focused light beam, such as a laser beam illuminates the particles as they flow through the examination zone. Optical detectors within the flow cytometer measure certain characteristics of the light as it interacts with the particles/cells. Commonly used flow cytometers such as the Becton-Dickinson Immunocytometry Systems "FACSCAN" (San Jose, Calif.) can measure forward light scatter (generally correlated with the refractive index and size of the particle/cell being illuminated), side light scatter (generally correlated with the cell granularity), and particle fluorescence at one or more wavelengths. Data acquisition and analysis can be done using FASCALIBER® LSRII flow cytometers (Becton Dickinson), and CELLQUEST Pro™, BD FACSDIVA™ software (both from Becton Dickinson), FLOWJO

software (Tree Star, Ashland, Oreg.) and/or KALUZA™ software (Beckman Coulter, Miami, Fla.).

Cell Sorting and Selection of Subpopulations of Cells in a Specimen

[00100] Multiparameter flow cytometric cell analysis can be used as part of the methods described herein. The simultaneous analysis of multiple predictive parameters using flow cytometry is known to those of skill in the art. In one embodiment, the population of cells to be analyzed is contacted with a panel of antibodies directed against distinct cell surface markers, under conditions effective to allow antibody probe binding. The antibodies employed can be monoclonal antibodies, and can, in another embodiment, be labeled in a manner to allow their subsequent detection.

[00101] In embodiments, fluorochromes can be excited by at least two different lasers to give off light of at least four different wavelengths, with the potential, for simultaneous analysis of at least four different markers. An additional two parameters include two light scattering parameters; direct and orthogonal, or side-scattering capability which can be analyzed concurrently with antibody detection, thereby allowing for cell analysis on the basis of at least 6 parameters. In embodiments, at least five, six, seven, eight, nine, ten, eleven, or twelve different antibody probes, can be used simultaneously, thereby allowing for cell analysis on the basis of at least seven, eight, nine, ten, eleven, twelve, thirteen, or fourteen different parameters.

[00102] Multiparameter cell sorting can be used in an embodiment to isolate cells based on a specific expression profile. For example, in one embodiment cell sorting analysis can be achieved using fluorescence-activated flow cytometry, by methods well described in the art. In one embodiment cells can be sorted based on the co-expression of markers CD19 and CD10, wherein in combination with the expression of CD19 and CD10 the expression of other markers can be interrogated. In another embodiment, mRNA expression profiles can be generated from a purified population of CD19+ and CD10+ cells isolated from a subject specimen for the purpose of diagnosing minimal residual disease.

[00103] In yet other embodiments, enrichment of specific subpopulations of cells can be achieved by other methods as well. For example, a wide variety of magnetic bead separation and isolation procedures can be used to selectively negatively and positively enrich samples for specific subpopulations of cells. For example, in some embodiments a mixture of magnetic beads coupled to lineage specific antibodies can be used to deplete, T cells, NK

cells, monocytes, platelets, dendritic cells, granulocytes and erythrocytes, thereby negatively isolating B cells. The skilled artisan will understand that combinations of different antibodies can be used alone or in combination, and in multiple successive rounds of isolation, to positively and/or negatively select for subpopulations of cells.

[00104] One of skill in the art will recognize that optimization of reagents and conditions, for example, antibody titer and parameters for detection of antigen-antibody binding, is needed to maximize the signal to noise ratio for a particular antibody. Antibody concentrations that maximize specific binding to the markers and minimize non-specific binding (or "background") will be determined. In particular embodiments, appropriate antibody titers are determined by initially testing various antibody dilutions on patient serum samples. The design of assays to optimize antibody titer and detection conditions is standard and well within the routine capabilities of those of ordinary skill in the art. Some antibodies require additional optimization to reduce background and/or to increase specificity and sensitivity.

[00105] The skilled artisan will recognize that optimization of multiparameter assays designed to detect a plurality of antibody probes simultaneously will be necessary. In embodiments, maximization of signal to noise ratio, as well an optimization of fluorochrome combinations will be necessary for each of the antibody probes combinations. Conjugated-antibody concentrations that maximize specific binding to the markers and minimize non-specific binding (or "background") will be determined with other such conjugated antibody probes as is known in the art. The design of assays to optimize and compensate the signals detected for the various conjugated antibodies is standard and well within the routine capabilities of those of ordinary skill in the art. Some antibodies require additional optimization to reduce background and/or to increase specificity and sensitivity.

Antibody and Nucleic Acid Probes to Target Genes

[00106] The antibodies used to practice the methods described herein are selected to have high specificity for the marker proteins of interest. Methods for making antibodies and for selecting appropriate antibodies are known in the art. In some embodiments, commercial antibodies directed to specific marker proteins may be used to practice the methods described herein. The antibodies may be selected on the basis of desirable staining of cytological, rather than histological, samples. That is, in particular embodiments the antibodies are selected with the desired combination in mind and for binding specificity.

[00107] The markers and combinations of markers include genes or proteins that are selectively expressed, overexpressed or underexpressed in leukemia, and specifically in AML, as defined herein above, and may be combined with known markers as well as those presently unknown in the art. In particular embodiments, markers are intracellular proteins, secreted proteins or proteins that are predicted to encode membranous proteins with transmembrane segments and extracellular domains. In some embodiments, probes can detect markers that are polypeptides expressed at the surface of the cell. In other embodiments, probes can detect markers that are polypeptides expressed intracellularly. In still other embodiments, probes detect markers that are polynucleotides. In still other embodiments, kits and methods can comprise probes that can detect markers that include polypeptides and polynucleotide.

Intracellular Protein Targets

[00108] In some embodiments, the expression of intracellular proteins, for example, BCL2 and HSPB1, are detected using flow cytometry by first permeablizing the cell surface membrane to allow access of antibody through the membrane. In one embodiment a permeabilization reagent, such as those containing various surfactants (e.g., saponin, Triton X-100, Tween-20, N-acyl sarcosine, etc) or organic solvents (e.g., alcohols, acetone) or other similar solution, is used. A permeabilization reagent is optimally used in a sufficient amount enabling penetration of antibodies to the intercellular space, while substantially preserving the cellular membrane. Ideally, the permeabilizing agent creates apertures in the cell membrane without affecting the gross morphology of the cell such that flow cytometric light scattering characteristics of the cell are not affected. Such methods of permeabilizing cells are well known in the art.

[00109] In embodiments, the cell may be fixed prior to or during permeabilization to maintain the integrity of the cell. Methods of fixation are also well known in the art. In some embodiments, fixation and permeabilization can be combined. An example of a fixation/permeabilizing agent is INTRAPREP™ (Beckman Coulter, Inc.) which comprises 5.5% v/v formaldehyde as a fixation reagent and a phosphate buffered saline (PBS)-saponin-based permeabilization reagent.

RNA Expression Profiling

[00110] In other embodiments, the expression of a marker of interest is detected at the nucleic acid level. Nucleic acid-based techniques for assessing expression are well known in the art and include, for example, determining the level of marker mRNA in a specimen taken from a patient. Many expression detection methods use isolated RNA. Generally, blood, serum, or tissue samples can readily be processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski (1989, U.S. Pat. No. 4,843,155).

[00111] Isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction analyses and probe arrays. One method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to an mRNA or genomic DNA encoding a marker. Hybridization of an mRNA with the probe indicates that the marker in question is being expressed.

[00112] In one embodiment, the mRNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative embodiment, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the probe(s), for example, in an Affymetrix gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in detecting the level of mRNA encoded by the markers.

[00113] An alternative method for determining the level of marker mRNA in a sample involves the process of nucleic acid amplification, e.g., by RT-PCR (the experimental embodiment set forth in Mullis, 1987, U.S. Pat. No. 4,683,202), ligase chain reaction (Barany (1991) Proc. Natl. Acad. Sci. USA 88:189-193), self sustained sequence replication (Guatelli et al. (1990) Proc. Natl. Acad. Sci. USA 87:1874-1878), transcriptional amplification system (Kwoh et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), Q-Beta Replicase (Lizardi et al. (1988) Bio/Technology 6:1197), rolling circle replication (Lizardi et al. U.S. Pat. No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules

are present in very low numbers. In particular aspects, marker expression is assessed by quantitative fluorogenic RT-PCR (e.g., the TaqMan® System). Such methods typically utilize pairs of oligonucleotide primers that are specific for the marker of interest. Methods for designing oligonucleotide primers specific for a known sequence are well known in the art.

[00114] Marker expression levels of RNA may be monitored using a 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 U.S. Pat. Nos. 5,770,722, 5,874,219, 5,744,305, 5,677,195 and 5,445,934, which are incorporated herein by reference. The detection of marker expression may also comprise using nucleic acid probes in solution.

[00115] In one embodiment, microarrays are used to detect marker expression. Microarrays are particularly well suited for this purpose because of the reproducibility between different experiments. DNA microarrays provide one method for the simultaneous measurement of the expression levels of large numbers of genes. Each array consists of a reproducible pattern of capture probes attached to a solid support. Labeled RNA or DNA is hybridized to complementary probes on the array and then detected by laser scanning. Hybridization intensities for each probe on the array are determined and converted to a quantitative value representing relative gene expression levels. See, U.S. Pat. Nos. 6,040,138, 5,800,992 and 6,020,135, 6,033,860, and 6,344,316, which are incorporated herein by reference. High-density oligonucleotide arrays are particularly useful for determining the gene expression profile for a large number of RNA's in a sample.

[00116] Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, e.g., U.S. Pat. No. 5,384,261, incorporated herein by reference in its entirety for all purposes. Although a planar array surface is preferred, the array may be fabricated on a surface of virtually any shape or even a multiplicity of surfaces. Arrays may be peptides or nucleic acids on beads, gels, polymeric surfaces, fibers such as fiber optics, glass or any other appropriate substrate, see U.S. Pat. Nos. 5,770,358, 5,789,162, 5,708,153, 6,040,193 and 5,800,992, each of which is hereby incorporated in its entirety for all purposes. 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. Nos. 5,856,174 and 5,922,591.

[00117] In one approach, total mRNA isolated from a specimen is converted to labeled cRNA and then hybridized to an oligonucleotide array. Each specimen is hybridized to a

separate array. Relative transcript levels may be calculated by reference to appropriate controls present on the array and in the sample. In one embodiment, RNA can be isolated from a subpopulation of cells with a characteristic expression profile.

[00118] In embodiments, an expression profile can comprise values corresponding to gene expression detected by mRNA expression levels where the expression of many genes can be analyzed simultaneously and interpreted in one sample.

Kits for Detection of Minimal Residual Disease

[00119] Kits for practicing the screening and diagnostic methods are further provided. The kits may also include methods for use in diagnosing minimal residual disease in AML, detecting or diagnosing AML, monitoring disease status in a patient for the recurrence of AML, or monitoring the efficacy of a treatment for AML. These methods are described elsewhere herein.

[00120] As used herein, "kit" refers to a set of reagents for the purpose of performing the method embodiments, more particularly, the detection of minimal residual disease in patient specimens. The term "kit" is intended to mean any manufacture (e.g., a package or a container) comprising at least one reagent, e.g., an antibody, a nucleic acid probe, etc. for specifically detecting the expression of a marker. The kit may be promoted, distributed, or sold as a unit for performing the methods described herein. Additionally, the kits may contain a package insert describing the kit and methods for its use.

[00121] In embodiments, expression of markers can be assessed at the protein level or nucleic acid level, or both in combination. In some embodiments, expression of protein expression is detected using specific antibody probes. Expression of identified markers can also be detected by nucleic acid based techniques, including, for example, hybridization and RT-PCR. Expression can be evaluated in a variety of specimens taken from the body including, but not limited to, blood cells or bone marrow cells, and cellular products extracted from blood and bone marrow cells, including, but not limited to protein and RNA extracted from blood and bone marrow cells.

Computer Implementation

[00122] FIG. 16 illustrates a computer network or similar digital processing environment in which the present subject matter may be implemented.

[00123] Client computer(s)/devices 50 and server computer(s) 60 provide processing, storage, and input/output devices executing application programs and the like. Client computer(s)/devices 50 can also be linked through communications network 70 to other computing devices, including other client devices/processes 50 and server computer(s) 60. Communications network 70 can be part of a remote access network, a global network (e.g., the Internet), cloud computing servers or service, a worldwide collection of computers, Local area or Wide area networks, and gateways that currently use respective protocols (TCP/IP, Bluetooth, etc.) to communicate with one another. Other electronic device/computer network architectures are suitable.

[00124] FIG. 17 is a diagram of the internal structure of a computer (e.g., client processor/device 50 or server computers 60) in the computer system of FIG. 16. Each computer 50, 60 contains system bus 79, where a bus is a set of hardware lines used for data transfer among the components of a computer or processing system. Bus 79 is essentially a shared conduit that connects different elements of a computer system (e.g., processor, disk storage, memory, input/output ports, network ports, etc.) that enables the transfer of information between the elements. Attached to system bus 79 is I/O device interface 82 for connecting various input and output devices (e.g., keyboard, mouse, displays, printers, speakers, etc.) to the computer 50, 60. Network interface 86 allows the computer to connect to various other devices attached to a network (e.g., network 70 of FIG. 16). Memory 90 provides volatile storage for computer software instructions 92 and data 94 used to implement an embodiment of the present subject matter (e.g., input module, processor engine, and graphics memory code detailed above). Disk storage 95 provides non-volatile storage for computer software instructions 92 and data 94 used to implement an embodiment of the present subject matter. Central processor unit 84 is also attached to system bus 79 and provides for the execution of computer instructions.

[00125] In one embodiment, the processor routines 92 and data 94 are a computer program product (generally referenced 92), including a computer readable medium (e.g., a removable storage medium such as one or more DVD-ROM’s, CD-ROM’s, diskettes, tapes, etc.) that provides at least a portion of the software instructions for the system. Computer program product 92 can be installed by any suitable software installation procedure, as is well known in the art. In another embodiment, at least a portion of the software instructions may also be downloaded over a cable, communication and/or wireless connection. In other embodiments, the programs are a computer program propagated signal product 107 embodied on a

propagated signal on a propagation medium (e.g., a radio wave, an infrared wave, a laser wave, a sound wave, or an electrical wave propagated over a global network such as the Internet, or other network(s)). Such carrier medium or signals provide at least a portion of the software instructions for the routines/program 92.

[00126] In alternate embodiments, the propagated signal is an analog carrier wave or digital signal carried on the propagated medium. For example, the propagated signal may be a digitized signal propagated over a global network (e.g., the Internet), a telecommunications network, or other network. In one embodiment, the propagated signal is a signal that is transmitted over the propagation medium over a period of time, such as the instructions for a software application sent in packets over a network over a period of milliseconds, seconds, minutes, or longer. In another embodiment, the computer readable medium of computer program product 92 is a propagation medium that the computer system 50 may receive and read, such as by receiving the propagation medium and identifying a propagated signal embodied in the propagation medium, as described above for computer program propagated signal product.

[00127] Generally speaking, the term "carrier medium" or transient carrier encompasses the foregoing transient signals, propagated signals, propagated medium, storage medium and the like.

[00128] In other embodiments, the program product 92 may be implemented as a so called Software as a Service (SaaS), or other installation or communication supporting end-users.

EXEMPLIFICATION

Materials and Methods

Patients and cells

[00129] Bone marrow samples were collected at diagnosis from 370 patients with de novo or secondary AML, aged <1 to 63 years; patients with acute promyelocytic leukemia were not included in this study. Of the 370 samples, 157 from pediatric AML were used for genome-wide gene expression studies, and 213 from pediatric and adult AML for the studies by flow cytometry. Bone marrow (n = 190) and peripheral blood (n = 18) obtained from 52 patients with AML during therapy, and bone marrow samples collected from 27 patients at relapse were also studied. The diagnosis of AML was established according to morphology, cytochemistry and cell marker profile. Bone marrow samples from 30 healthy donors (7 included in the gene expression studies), and from 40 patients with acute leukemia during

therapy were studied to determine marker expression in non-AML myeloid progenitors. These studies were approved by the St Jude Children's Research Hospital institutional review board and by the National University Hospital of Singapore Domain Specific Ethics Board, with informed consent obtained from donors, patients, their parents or their guardians, and assent from the patients, as appropriate.

[00130] Leukemic and normal mononucleated cells were obtained by centrifugation on a density gradient (AccuPrep, Nycomed, Oslo, Norway) and washed three times in phosphate-buffered saline (PBS). All samples used in the gene expression studies were cryopreserved. To obtain normal myeloid progenitor cells for gene expression analysis, CD19+ B-cells were removed from cryopreserved bone marrow mononucleated cells of 7 healthy donors using a MACS separation system (Miltenyi Biotec, Auburn, CA). The remaining cells were labeled with anti-CD34 conjugated to phycoerythrin (PE; BD Biosciences, San Jose, CA), anti-CD13 (from Dako, Carpinteria, CA) and anti-CD33 (BD Biosciences), both conjugated to fluorescein isothyocyanate (FITC). We then sorted CD34+ cells expressing CD13 and/or CD33 using a MoFlo fluorescence-activated cell sorter (Cytomation, Beckman Coulter, Brea, CA).

Gene expression arrays studies

[00131] Gene expression array studies were performed as previously described (32). Briefly, after isolating total RNA from 157 AML samples and 7 normal myeloid progenitor cell samples using Trizol reagent (Invitrogen, Carlsbad, CA), we generated cDNA and prepared biotin-labeled cRNA hybridization solutions (Affymetrix; Santa Clara, CA). Three of the 7 normal myeloid progenitor cell preparation yielded low RNA and were pooled into one. The solutions were hybridized to HG-U133A oligonucleotide microarrays (Affymetrix), which were stained with phycoerythrin-conjugated streptavidin. The arrays were read with a laser confocal scanner (Agilent, Palo Alto, CA), with signal values computed using Affymetrix GeneChip Operating Software.

Flow cytometric analysis and MRD studies

[00132] The antibodies used to determine marker expression by flow cytometry are listed in Table 1. These antibodies were used in combination with anti-CD34 peridinin chlorophyll protein (PerCP), CD117 conjugated to allophycocyanin (APC), CD45 conjugated to APC-H7, and CD33 phycoerythrin (PE)-Cy7 (all from BD Biosciences). Isotype-matched nonreactive

antibodies were used as controls. For flow cytometric analysis, monunucleated cells were washed in PBS containing 0.5% bovine serum albumin and 0.5% sodium azide (PBSA), mixed with rabbit serum to block surface Fc receptors, incubated with the antibodies for 10 minutes at 20°C in the dark, washed twice in PBSA and fixed with 0.5% formaldehyde. For intracellular markers, cells were permeabilized and fixed before exposure to antibodies using 8E, a reagent prepared in our laboratory from a proprietary formula. Measurements of antibody labeling were performed by multiparameter flow cytometry, using an LSRII flow cytometer (BD Biosciences).

[00133] Studies of MRD by flow cytometry were performed using combinations of monoclonal antibodies that identified leukemia-associated immunophenotypes determined at diagnosis. Cells staining was essentially performed as described above. Data acquisition and analysis was done as previously described, using an LSRII flow cytometer, and DIVA (BD Biosciences), and FlowJo (Tree Star, Ashland, OR) software. At least 100,000 viable mononucleated cells (up to 1,000,000) were analyzed in each sample.

Table 1. Antibodies used in this study and cell types used to test their reactivity

Specificity	**Clone**	**Fluorochrome**	**Source**	**Catalog Number**	**Positive Control**	**Negative Control (negative or dim expression)**
CD9	M-L13	FITC	BD Biosciences	341646	Monocytes	Lymphoid subset
ITGB2/ CD18	MEM-48	PE	GeneTex	GTX79945	All leukocytes	K562 cell line
IL2RA/ CD25	2A3	PE	BD Biosciences	341010	Activated lymphocytes	Resting lymphocytes
FCGR2A/ CD32	2E1	PE	Beckman Coulter	IM1935	Monocytes	Lymphoid subset
CD44	G44-26	V450	BD Biosciences	561292	All leukocytes	Jurkat cell line
CD47	B6H12	PE	BD Biosciences	556046	All leukocytes	Not known
CD52	CF1D12	FITC	Life Technologies	MHCD5201	Lymphoid	NK subset, neutrophils
ICAM1/ CD54	LB-2	PE	BD Biosciences	347977	Daudi cell line	Lymphoid subset
CD59	P282 (H19)	PE	BD Biosciences	555764	K562 cell line	Lymphocytes
FCGR1A/ CD64	10.1	V450	BD Biosciences	561202	Monocytes	Lymphocytes

CD68[1]	Y1/82A	PE	BD Biosciences	556078	Monocytes	Lymphocytes
CD86	2331 (FUN-1)	BV421	BD Biosciences	562432	Monocytes	Resting lymphocytes
CD93	VIMD2	PE	Biolegend	336108	Monocytes	Lymphocytes
CD96	6F9	PE	BD Biosciences	562379	Activated NK and T cells	Resting lymphocytes
CD97	VIM3b	FITC	BD Biosciences	555773	Monocytes	Resting lymphocytes
CD99	Tü12	PE	BD Biosciences	555689	T cell lymphoblastic leukemia cells	Granulocytes
PVR/ CD115	61708	PE	R&D Systems	FAB329P	Monocytes	Lymphocytes
IL3RA/ CD123	9F5	PE	BD Biosciences	340545	Lymphoid subset, basophils, eosinophils	Lymphoid subset
CD163	GHI/61	PE	BD Biosciences	556018	Monocytes	Lymphocytes
PRV1/ CD177	MEM-166	PE	AbD Serotec	MCA2045	Granulocytes	Lymphoid
CX3CR1/CD181	2A9-1	PE	Medical & Biological Laboratories	D070-5	Monocytes	Lymphoid subset
CD200	MRC OX-104	V450	BD Biosciences	562126	B lymphocytes	Monocytes
CD209	DCN46	V450	BD Biosciences	561275	Peripheral blood dendritic cells	Lymphocytes
IL10RA/ CD210	3F9	PE	BD Biosciences	556013	Monocytes	Lymphoid subset
CD300a	E59.126	PE	Beckman Coulter	A22328	Monocytes, lymphoid subset	Lymphoid subset
CLEC12A	50C1	PE	Biolegend	353604	Monocytes	Lymphocytes
CCL5/ Rantes[1]	21445	PE	R&D Systems	IC278P	Activated NK	Resting lymphocytes
HAVCR2/ TIM3	F38-2E2	BV421	Biolegend	345008	Monocytes	Lymphoid subset

[1] Requires membrane permeabilization

Results

Genes aberrantly expressed in AML cells and normal myeloid progenitors

[00134] To identify genes aberrantly expressed in AML, we compared global gene expression of 157 AML diagnostic samples to that of normal CD34+ myeloid progenitor cells (CD13+ and/or CD33+) purified from the bone marrow of 7 healthy donors. We found 395 probe sets that were over-expressed in AML (e.g., at least 100% higher than the highest signal measured in normal myeloid cells) and 260 that were under-expressed (e.g., at least 50% lower than the lowest normal value) in 66% or more of AML cases. Widening the inclusion criterion to genes aberrantly expressed in at least 33% of AML cases raised the numbers to 1958 and 1271, respectively (Tables 2 and 3). Therefore, the genes of Table 2 and 3 can also be useful in identifying acute myeloid leukemia and minimal residual disease in acute myeloid leukemia.

Table 2.Genes over-expressed in AML

probe	Gene	Unigene	Locus	% AML cases with overexpression
216207_x_at	IGKV1D-13	Hs.390427	28902	98.1
210972_x_at	TRA@ /// TRDV2 /// TRAV20 /// TRAJ17 /// TRAC	Hs.74647	28517	98.1
207529_at	DEFA5	Hs.72887	1670	98.1
219710_at	SH3TC2	Hs.483784	79628	98.1
217227_x_at	---	Hs.561078	---	97.5
215511_at	TCF20	Hs.475018	6942	97.5
216341_s_at	GNRHR	Hs.407587	2798	96.8
215176_x_at	---	Hs.552522	---	96.2
209057_x_at	CDC5L	Hs.485471	988	96.2
62987_r_at	CACNG4	Hs.514423	27092	95.5
201864_at	GDI1	Hs.74576	2664	95.5
221239_s_at	FCRL2	Hs.437393	79368	95.5
208013_s_at	ACRV1	Hs.169222	56	95.5
203074_at	ANXA8	Hs.463110	244	94.9
208460_at	GJA7	Hs.532593	10052	94.9
31861_at	IGHMBP2	Hs.503048	3508	94.3
71933_at	WNT6	Hs.29764	7475	94.3

probe	Gene	Unigene	Locus	% AML cases with overexpression
205758_at	CD8A	Hs.85258	925	94.3
206908_s_at	CLDN11	Hs.31595	5010	94.3
209708_at	MOXD1	Hs.6909	26002	94.3
211863_x_at	HFE	Hs.233325	3077	94.3
221943_x_at	RPL38	Hs.380953	6169	93.6
217189_s_at	C1orf16	Hs.270775	9887	93.6
206672_at	AQP2	Hs.130730	359	93.6
396_f_at	EPOR	Hs.127826	2057	93.0
217378_x_at	LOC391427	---	391427	93.0
204006_s_at	FCGR3A /// FCGR3B	Hs.372679	2214	93.0
216576_x_at	---	Hs.552522	---	93.0
211339_s_at	ITK	Hs.558348	3702	93.0
207665_at	ADAM21	Hs.178748	8747	93.0
217148_x_at	IGLV2-14	---	28815	92.4
214053_at	---	Hs.588182	---	92.4
206534_at	GRIN2A	Hs.567280	2903	92.4
211430_s_at	IGH@ /// IGHG1 /// IGHG2 /// IGHG3 /// IGHM	Hs.510635	3492	91.7
217022_s_at	IGHA1 /// IGHA2 /// MGC27165	Hs.584764	283650 /// 3493 /// 3494	91.7
205456_at	CD3E	Hs.3003	916	91.7
217157_x_at	---	Hs.556743	---	91.7
206887_at	CCBP2	Hs.24286	1238	91.7
206324_s_at	DAPK2	Hs.237886	23604	91.1
211902_x_at	TRA@	Hs.546375	6955	90.4
217430_x_at	COL1A1	Hs.172928	1277	90.4
216025_x_at	CYP2C19 /// CYP2C9	Hs.282409	1557	90.4
206948_at	NEU3	Hs.191074	10825	90.4
210148_at	HIPK3	Hs.201918	10114	90.4
208035_at	GRM6	Hs.248131	2916	89.8
48030_i_at	C5orf4	Hs.519694	10826	89.2
36564_at	IBRDC3	Hs.128366	127544	89.2
203413_at	NELL2	Hs.505326	4753	89.2
211231_x_at	CYP4A11	Hs.1645	1579	89.2
208259_x_at	IFNA7	Hs.282274	3444	89.2
213332_at	PAPPA2	Hs.187284	60676	89.2
207269_at	DEFA4	Hs.128581	1669	88.5
205445_at	PRL	Hs.1905	5617	88.5
211634_x_at	IGHM	Hs.538461	3507	88.5
211644_x_at	IGKC	Hs.449621	3514	88.5
209003_at	SLC25A11	Hs.184877	8402	88.5

probe	Gene	Unigene	Locus	% AML cases with overexpression
205291_at	IL2RB	Hs.474787	3560	88.5
212161_at	AP2A2	Hs.19121	161	88.5
208540_x_at	S100A11	Hs.417004	6282	87.9
38447_at	ADRBK1	Hs.83636	156	87.9
211900_x_at	CD6	Hs.502710	923	87.9
204443_at	ARSA	Hs.88251	410	87.9
209568_s_at	RGL1	Hs.497148	23179	87.3
211866_x_at	HFE	Hs.233325	3077	87.3
221370_at	LOC377064	Hs.556877	377064	87.3
208544_at	ADRA2B	Hs.247686	151	87.3
219112_at	RAPGEF6	---	51735	86.6
211364_at	MTAP	Hs.193268	4507	86.6
207882_at	HSAJ2425	Hs.194790	55566	86.6
221444_at	TAS2R16	Hs.272395	50833	86.6
206765_at	KCNJ2	Hs.1547	3759	86.6
202921_s_at	ANK2	Hs.567235	287	86.6
1405_i_at	CCL5	Hs.514821	6352	86.0
214777_at	---	Hs.551722	---	86.0
217480_x_at	LOC339562	Hs.449972	339562	86.0
204804_at	TRIM21	Hs.532357	6737	86.0
216292_at	PTPRM	Hs.49774	5797	86.0
208426_x_at	KIR2DL4	Hs.166085	3805	86.0
60528_at	PLA2G4B	Hs.554815	8681	85.4
36907_at	MVK	Hs.130607	4598	85.4
213823_at	HOXA11	Hs.249171	3207	85.4
216730_at	---	Hs.590753	---	85.4
211868_x_at	IGHA1 /// IGHG1 /// IGHG3	Hs.558342	3493	85.4
211661_x_at	PTAFR	Hs.77542	5724	84.7
204647_at	HOMER3	Hs.410683	9454	84.7
214470_at	KLRB1	Hs.169824	3820	84.7
209365_s_at	ECM1	Hs.81071	1893	84.7
204437_s_at	FOLR1	Hs.73769	2348	84.7
208384_s_at	MID2	Hs.12256	11043	84.7
216953_s_at	WT1	Hs.408453	7490	84.7
221910_at	ETV1	Hs.22634	2115	84.7
209138_x_at	IGLV3-25 /// DHRS4 /// IGLC2	Hs.449585 /// Hs.528385 /// Hs.584765	10901 /// 28793 /// 3538	84.1
211645_x_at	---	Hs.554197	---	84.1
33768_at	DMWD	Hs.584752	1762	84.1
219095_at	PLA2G4B	Hs.554815	8681	84.1
204837_at	MTMR9	Hs.528673	66036	84.1

probe	Gene	Unigene	Locus	% AML cases with overexpression
214070_s_at	ATP10B	Hs.109358	23120	84.1
202638_s_at	ICAM1	Hs.515126	3383	84.1
220017_x_at	CYP2C9	Hs.282624	1559	84.1
209697_at	PPP3CC	Hs.149413	5533	84.1
221332_at	BMP15	Hs.532692	9210	83.4
206227_at	CILP	Hs.442180	8483	83.4
216126_at	MGC39821	Hs.351906	284440	83.4
215241_at	TMEM16C	Hs.91791	63982	83.4
209458_x_at	HBA1 /// HBA2	Hs.449630	3039 /// 3040	82.8
205513_at	TCN1	Hs.2012	6947	82.8
64064_at	GIMAP5	Hs.412331	55340	82.8
218974_at	FLJ10159	Hs.445244	55084	82.8
216046_at	PDE8A	Hs.9333	5151	82.8
221859_at	SYT13	Hs.436643	57586	82.8
211813_x_at	DCN	Hs.156316	1634	82.8
215115_x_at	NTRK3	Hs.410969	4916	82.8
209671_x_at	TRA@ /// TRAC	Hs.74647	28755 /// 6955	82.2
205821_at	KLRK1	Hs.387787	22914	82.2
204533_at	CXCL10	Hs.413924	3627	82.2
205277_at	PRDM2	Hs.371823	7799	82.2
211590_x_at	TBXA2R	Hs.442530	6915	82.2
1494_f_at	CYP2A6	Hs.439056	1548	82.2
215622_x_at	PHF7	Hs.372719	51533	82.2
203958_s_at	ZBTB40	Hs.418966	9923	82.2
217235_x_at	IGLC2	Hs.449585	3538	81.5
217281_x_at	---	Hs.551925	---	81.5
35150_at	CD40	Hs.472860	958	81.5
201598_s_at	INPPL1	Hs.523875	3636	81.5
219697_at	HS3ST2	Hs.115830	9956	81.5
207908_at	KRT2A	Hs.707	3849	81.5
221300_at	C15orf2	Hs.451286	23742	81.5
216213_at	NEK1	Hs.481181	4750	81.5
202500_at	DNAJB2	Hs.77768	3300	81.5
211745_x_at	HBA1	Hs.449630	3039	80.9
214677_x_at	IGL@ /// IGLC1 /// IGLC2 /// IGLV3-25 /// IGLV2-14 /// IGLJ3	Hs.449585	28793 /// 28815 /// 28831 /// 3535 /// 3537 /// 3538	80.9
213539_at	CD3D	Hs.504048	915	80.9
216510_x_at	IGHA1 /// IGHD /// IGHG1 /// IGHM /// LOC390714	Hs.538461	3493 /// 3495 /// 3500 /// 3507 /// 390714	80.9
205879_x_at	RET	Hs.350321	5979	80.9

probe	Gene	Unigene	Locus	% AML cases with overexpression
206666_at	GZMK	Hs.277937	3003	80.9
206181_at	SLAMF1	Hs.523660	6504	80.9
204655_at	CCL5	Hs.514821	6352	80.3
213629_x_at	MT1F	Hs.513626	4494	80.3
204858_s_at	ECGF1	Hs.546251	1890	80.3
34846_at	CAMK2B	Hs.351887	816	80.3
210708_x_at	CASP10	Hs.5353	843	80.3
205832_at	CPA4	Hs.93764	51200	80.3
208241_at	NRG1	Hs.453951	3084	80.3
204018_x_at	HBA1 /// HBA2	Hs.449630	3039 /// 3040	79.6
211699_x_at	HBA1 /// HBA2	Hs.449630	3039 /// 3040	79.6
207563_s_at	OGT	Hs.405410	8473	79.6
58900_at	LOC222070	---	222070	79.6
221041_s_at	SLC17A5	Hs.485760	26503	79.6
206186_at	MPP3	Hs.396566	4356	79.6
59433_at	LOC286434	Hs.546700	286434	79.6
215100_at	C6orf105	Hs.126409	84830	79.6
206225_at	ZNF507	Hs.205392	22847	79.6
217414_x_at	HBA2	Hs.398636	3040	79.0
204848_x_at	HBG1 /// HBG2	Hs.567283	3047 /// 3048	79.0
209287_s_at	CDC42EP3	Hs.369574	10602	79.0
40359_at	RASSF7	Hs.72925	8045	79.0
221929_at	RBM12B	Hs.192788	389677	79.0
219400_at	CNTNAP1	Hs.408730	8506	79.0
33197_at	MYO7A	Hs.370421	4647	79.0
207192_at	DNASE1L2	Hs.103503	1775	79.0
205081_at	CRIP1	Hs.70327	1396	78.3
219962_at	ACE2	Hs.178098	59272	78.3
41386_i_at	---	---	---	78.3
203514_at	MAP3K3	Hs.29282	4215	78.3
212400_at	C9orf132	Hs.568044	399665	78.3
217342_x_at	FLJ11292	Hs.586191	55338	78.3
204227_s_at	TK2	Hs.512619	7084	78.3
215121_x_at	IGL@ /// IGLC1 /// IGLC2 /// IGLV3-25 /// IGLV2-14	Hs.449585	28793 /// 28815 /// 3535 /// 3537 /// 3538	77.7
217179_x_at	---	Hs.586050	---	77.7
209670_at	TRAC	---	28755	77.7
201087_at	PXN	Hs.446336	5829	77.7
210422_x_at	SLC11A1	Hs.471393	6556	77.7
203234_at	UPP1	Hs.488240	7378	77.7
206776_x_at	ACRV1	Hs.169222	56	77.7
204813_at	MAPK10	Hs.125503	5602	77.7

probe	Gene	Unigene	Locus	% AML cases with overexpression
216055_at	PDGFB	Hs.1976	5155	77.7
216502_at	ISG20L2	Hs.301904	81875	77.7
214768_x_at	---	Hs.534006	---	77.1
204891_s_at	LCK	Hs.470627	3932	77.1
207718_x_at	CYP2A6 /// CYP2A7 /// CYP2A7P1 /// CYP2A13	Hs.439056	1548 /// 1549 /// 1550 /// 1553	77.1
207217_s_at	NOX1	Hs.132370	27035	77.1
206281_at	ADCYAP1	Hs.531719	116	77.1
211488_s_at	ITGB8	Hs.285724	3696	77.1
211606_at	---	---	---	77.1
205925_s_at	RAB3B	Hs.123072	5865	77.1
210524_x_at	---	---	---	76.4
211395_x_at	FCGR2C	---	9103	76.4
203110_at	PTK2B	Hs.491322	2185	76.4
203111_s_at	PTK2B	Hs.491322	2185	76.4
205019_s_at	VIPR1	Hs.348500	7433	76.4
211947_s_at	BAT2D1	Hs.494614	23215	76.4
219287_at	KCNMB4	Hs.525529	27345	76.4
203370_s_at	PDLIM7	Hs.533040	9260	76.4
214128_at	C11orf11	Hs.241564	747	76.4
32699_s_at	PVR	Hs.171844	5817	76.4
213418_at	HSPA6	Hs.3268	3310	75.8
214511_x_at	FCGR1A /// LOC440607	Hs.534956	2209 /// 440607	75.8
209215_at	TETRAN	Hs.584848	10227	75.8
216984_x_at	IGLC2	Hs.449585	3538	75.8
211643_x_at	IGKC	Hs.449621	3514	75.8
90265_at	CENTA1	Hs.121593	11033	75.8
51774_s_at	LOC222070	---	222070	75.8
211067_s_at	GAS7	Hs.462214	8522	75.8
212198_s_at	TM9SF4	Hs.529360	9777	75.8
91920_at	BCAN	Hs.516904	63827	75.8
204574_s_at	MMP19	Hs.154057	4327	75.8
217541_x_at	LOC125893	Hs.446907	125893	75.8
203756_at	ARHGEF17	Hs.533719	9828	75.8
207007_at	NR1I3	Hs.349642	9970	75.8
206609_at	MAGEC1	Hs.132194	9947	75.8
205960_at	PDK4	Hs.8364	5166	75.8
204419_x_at	HBG1 /// HBG2	Hs.567283	3047 /// 3048	75.2
204561_x_at	APOC2	Hs.75615	344	75.2
204007_at	FCGR3B	---	2215	75.2
36004_at	IKBKG	Hs.43505	8517	75.2

probe	Gene	Unigene	Locus	% AML cases with overexpression
215766_at	GSTA1	Hs.446309	2938	75.2
211826_s_at	AFF1	Hs.480190	4299	75.2
219685_at	TMEM35	Hs.45140	59353	75.2
206168_at	ZC3H7B	Hs.474970	23264	75.2
216351_x_at	DAZ1 /// DAZ3 /// DAZ2 /// DAZ4	Hs.558522	1617 /// 57054 /// 57055 /// 57135	75.2
37145_at	GNLY	Hs.105806	10578	74.5
221627_at	TRIM10	Hs.274295	10107	74.5
56197_at	PLSCR3 /// MGC40107	Hs.433154	254863 /// 57048	74.5
218805_at	GIMAP5	Hs.412331	55340	74.5
221223_x_at	CISH	Hs.8257	1154	74.5
41657_at	STK11	Hs.515005	6794	74.5
214205_x_at	TXNL2	Hs.42644	10539	74.5
219716_at	APOL6	Hs.257352	80830	74.5
216036_x_at	WDTC1	Hs.469154	23038	74.5
221016_s_at	TCF7L1	Hs.516297	83439	74.5
209988_s_at	ASCL1	Hs.524672	429	74.5
221601_s_at	FAIM3	Hs.58831	9214	73.9
209031_at	IGSF4	Hs.370510	23705	73.9
204882_at	ARHGAP25	Hs.531807	9938	73.9
38149_at	ARHGAP25	Hs.531807	9938	73.9
201703_s_at	PPP1R10	Hs.106019	5514	73.9
219613_s_at	SIRT6	Hs.423756	51548	73.9
207979_s_at	CD8B1	Hs.405667	926	73.9
220158_at	LGALS14	Hs.24236	56891	73.9
205515_at	PRSS12	Hs.445857	8492	73.9
209335_at	DCN	Hs.156316	1634	73.9
211560_s_at	ALAS2	Hs.522666	212	73.2
205898_at	CX3CR1	Hs.78913	1524	73.2
216950_s_at	FCGR1A	Hs.77424	2209	73.2
218335_x_at	TNIP2	Hs.368551	79155	73.2
202197_at	MTMR3	Hs.570462	8897	73.2
215761_at	DMXL2	Hs.511386	23312	73.2
212154_at	SDC2	Hs.1501	6383	73.2
211465_x_at	FUT6	Hs.32956	2528	73.2
208591_s_at	PDE3B	Hs.445711	5140	73.2
214792_x_at	VAMP2	Hs.25348	6844	73.2
206766_at	ITGA10	Hs.158237	8515	73.2
216807_at	KIAA1751	Hs.232092	85452	73.2
217120_s_at	CRSP2	Hs.407604	9282	73.2
220991_s_at	RNF32	Hs.490715	140545	73.2
215706_x_at	ZYX	Hs.490415	7791	72.6

probe	Gene	Unigene	Locus	% AML cases with overexpression
206380_s_at	PFC	Hs.53155	5199	72.6
218888_s_at	NETO2	Hs.444046	81831	72.6
207554_x_at	TBXA2R	Hs.442530	6915	72.6
210301_at	XDH	Hs.250	7498	72.6
64899_at	LPPR2	Hs.6846	64748	72.6
206278_at	PTAFR	Hs.77542	5724	72.6
64883_at	MOSPD2	Hs.190043	158747	72.6
220009_at	LONRF3	Hs.144266	79836	72.6
215775_at	THBS1	Hs.164226	7057	72.6
214529_at	TSHB	Hs.406687	7252	72.6
210366_at	SLCO1B1	Hs.449738	10599	72.6
213515_x_at	HBG1 /// HBG2	Hs.567283	3047 /// 3048	72.0
202510_s_at	TNFAIP2	Hs.525607	7127	72.0
221067_s_at	MGC10946	Hs.130692	80763	72.0
217211_at	---	---	---	72.0
215701_at	ZNF291	Hs.458986	49855	72.0
217999_s_at	PHLDA1	Hs.484885	22822	72.0
206121_at	AMPD1	Hs.89570	270	72.0
205816_at	ITGB8	Hs.285724	3696	72.0
207796_x_at	KLRD1	Hs.524251	3824	72.0
216776_at	BCAP29	Hs.303787	55973	72.0
204385_at	KYNU	Hs.470126	8942	71.3
219992_at	TAC3	Hs.9730	6866	71.3
202637_s_at	ICAM1	Hs.515126	3383	71.3
219020_at	HS1BP3	Hs.531785	64342	71.3
209644_x_at	CDKN2A	Hs.512599	1029	71.3
202448_s_at	ZYG11BL	Hs.147950	10444	71.3
206209_s_at	CA4	Hs.89485	762	71.3
209863_s_at	TP73L	Hs.137569	8626	71.3
205695_at	SDS	Hs.439023	10993	71.3
216755_at	OSBPL10	Hs.150122	114884	71.3
206010_at	HABP2	Hs.422542	3026	71.3
221399_at	EDA2R	Hs.302017	60401	71.3
206589_at	GFI1	Hs.73172	2672	70.7
209117_at	WBP2	Hs.514489	23558	70.7
78047_s_at	LOC400843	---	400843	70.7
204445_s_at	ALOX5	Hs.89499	240	70.7
221421_s_at	ADAMTS12	Hs.481865	81792	70.7
208495_at	TLX3	Hs.249125	30012	70.7
214414_x_at	HBA2	Hs.398636	3040	70.1
200660_at	S100A11	Hs.417004	6282	70.1
214836_x_at	IGKC /// IGKV1-5	Hs.449621	28299 /// 3514	70.1
217418_x_at	MS4A1	Hs.438040	931	70.1

probe	Gene	Unigene	Locus	% AML cases with overexpression
212975_at	DENND3	Hs.18166	22898	70.1
121_at	PAX8	Hs.469728	7849	70.1
205627_at	CDA	Hs.466910	978	70.1
210184_at	ITGAX	Hs.248472	3687	70.1
214054_at	DOK2	Hs.71215	9046	70.1
211612_s_at	IL13RA1	Hs.496646	3597	70.1
206178_at	PLA2G5	Hs.319438	5322	70.1
207852_at	CXCL5	Hs.89714	6374	70.1
208092_s_at	FAM49A	Hs.467769	81553	70.1
220429_at	NDST3	Hs.480596	9348	70.1
210601_at	CDH6	Hs.171054	1004	70.1
205818_at	DBC1	Hs.532316	1620	70.1
212099_at	RHOB	Hs.502876	388	69.4
205899_at	CCNA1	Hs.417050	8900	69.4
211649_x_at	IGHM	Hs.538461	3507	69.4
215253_s_at	DSCR1	Hs.282326	1827	69.4
207044_at	THRB	Hs.187861	7068	69.4
203038_at	PTPRK	Hs.155919	5796	69.4
220533_at	---	---	---	69.4
220194_at	FLJ14001	Hs.570821	79730	69.4
211709_s_at	CLEC11A	Hs.512680	6320	68.8
214916_x_at	IGH@ /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG2 /// IGHG3 /// IGHM /// MGC27165 /// LOC390714	Hs.510635	283650 /// 3492 /// 3493 /// 3494 /// 3495 /// 3500 /// 3501 /// 3502 /// 3507 /// 390714	68.8
200808_s_at	ZYX	Hs.490415	7791	68.8
219799_s_at	DHRS9	Hs.179608	10170	68.8
214617_at	PRF1	Hs.2200	5551	68.8
210966_x_at	LARP1	Hs.292078	23367	68.8
220283_at	KIAA1822L	Hs.123515	79802	68.8
217263_x_at	RUNX1	Hs.149261	861	68.8
220161_s_at	EPB41L4B	Hs.269180	54566	68.8
222005_s_at	GNG3	Hs.179915	2785	68.8
214616_at	HIST1H3E	Hs.443021	8353	68.8
219761_at	CLEC1A	Hs.29549	51267	68.8
214225_at	PIN4	Hs.118076	5303	68.8
206831_s_at	ARSD	Hs.528631	414	68.8
206022_at	NDP	Hs.522615	4693	68.8
221651_x_at	IGKC /// IGKV1-5	Hs.449621	28299 /// 3514	68.2
64486_at	CORO1B	Hs.6191	57175	68.2
220326_s_at	FLJ10357	Hs.35125	55701	68.2

probe	Gene	Unigene	Locus	% AML cases with overexpression
207960_at	---	---	---	68.2
218937_at	ZNF434	Hs.123295	54925	68.2
207990_x_at	ACRV1	Hs.169222	56	68.2
207477_at	---	---	---	68.2
217020_at	RARB	Hs.436538	5915	68.2
37953_s_at	ACCN2	Hs.274361	41	68.2
211741_x_at	PSG3	Hs.555887	5671	68.2
205033_s_at	DEFA1 /// DEFA3	Hs.294176	1667 /// 1668	67.5
208949_s_at	LGALS3 /// GALIG	Hs.531081	3958 /// 81625	67.5
213096_at	TMCC2	Hs.6360	9911	67.5
206438_x_at	FLJ12975	Hs.167165	79867	67.5
219892_at	TM6SF1	Hs.513094	53346	67.5
209235_at	CLCN7	Hs.459649	1186	67.5
221752_at	SSH1	Hs.199763	54434	67.5
208514_at	KCNE1	Hs.121495	3753	67.5
219741_x_at	ZNF552	Hs.560727	79818	67.5
215479_at	SEMA6A	Hs.156967	57556	67.5
35147_at	MCF2L	Hs.170422	23263	67.5
204251_s_at	Cep164	Hs.504009	22897	67.5
209437_s_at	SPON1	Hs.445818	10418	67.5
207252_at	INE1	Hs.534372	8552	67.5
215796_at	TRAV20	Hs.512090	28663	67.5
205431_s_at	BMP5	Hs.296648	653	67.5
210783_x_at	CLEC11A	Hs.512680	6320	66.9
205098_at	CCR1	Hs.301921	1230	66.9
213446_s_at	IQGAP1	Hs.430551	8826	66.9
206761_at	CD96	Hs.142023	10225	66.9
206170_at	ADRB2	Hs.2551	154	66.9
214746_s_at	ZNF467	Hs.112158	168544	66.9
207704_s_at	GAS7	Hs.462214	8522	66.9
211889_x_at	CEACAM1	Hs.512682	634	66.9
215745_at	C4orf9	Hs.398178	8602	66.9
36742_at	TRIM15	Hs.309602	89870	66.9
209087_x_at	MCAM	Hs.511397	4162	66.9
205338_s_at	DCT	Hs.301865	1638	66.9
221252_s_at	GSG1	Hs.240053	83445	66.9
217048_at	---	---	---	66.9
221273_s_at	DKFZP761H1710	Hs.512767	83459	66.9
214065_s_at	CIB2	Hs.129867	10518	66.9
220378_at	TCP11	Hs.435371	6954	66.9
207446_at	TLR6	Hs.366986	10333	66.9

probe	Gene	Unigene	Locus	% AML cases with overexpression
203911_at	RAP1GA1	Hs.148178	5909	66.2
207636_at	SERPINI2	Hs.445555	5276	66.2
216809_at	CYLC1	Hs.444230	1538	66.2
219579_at	RAB3IL1	Hs.13759	5866	66.2
207113_s_at	TNF	Hs.241570	7124	66.2
221866_at	TFEB	Hs.485360	7942	66.2
217629_at	---	Hs.446662	---	66.2
220944_at	PGLYRP4	Hs.58356	57115	66.2
207919_at	ART1	Hs.382188	417	66.2
215883_at	LOC401210	Hs.534797	401210	66.2
216164_at	LRRN5	Hs.26312	10446	66.2
217614_at	POLR2E	Hs.24301	5434	66.2
221394_at	TAAR2	Hs.272382	9287	66.2
213880_at	LGR5	Hs.172176	8549	66.2
221052_at	TDRKH	Hs.584859	11022	66.2
215808_at	KLK10	Hs.275464	5655	66.2
215477_at	DPY19L1P1	Hs.331147	89231	66.2
208018_s_at	HCK	Hs.126521	3055	65.6
202812_at	GAA	Hs.1437	2548	65.6
203555_at	PTPN18	Hs.516390	26469	65.6
49327_at	SIRT3	Hs.555969	23410	65.6
211641_x_at	---	Hs.64568	---	65.6
205221_at	HGD	Hs.368254	3081	65.6
211977_at	GPR107	Hs.512461	57720	65.6
220357_s_at	SGK2	Hs.472793	10110	65.6
208593_x_at	CRHR1	Hs.417628	1394	65.6
206713_at	NTNG1	Hs.143707	22854	65.6
207991_x_at	ACRV1	Hs.169222	56	65.6
44783_s_at	HEY1	Hs.234434	23462	65.6
213732_at	TCF3	Hs.371282	6929	65.6
214315_x_at	CALR	Hs.515162	811	65.0
202833_s_at	SERPINA1	Hs.525557	5265	65.0
204446_s_at	ALOX5	Hs.89499	240	65.0
204334_at	KLF7	Hs.471221	8609	65.0
213622_at	COL9A2	Hs.418012	1298	65.0
206337_at	CCR7	Hs.370036	1236	65.0
218829_s_at	CHD7	Hs.20395	55636	65.0
217580_x_at	ARL6IP2	Hs.190440	64225	65.0
207973_x_at	ACRV1	Hs.169222	56	65.0
219142_at	RASL11B	Hs.8035	65997	65.0
215126_at	---	Hs.537255	---	65.0
203700_s_at	DIO2	Hs.202354	1734	65.0
206964_at	CML2	Hs.458287	51471	65.0
212014_x_at	CD44	Hs.502328	960	64.3

probe	Gene	Unigene	Locus	% AML cases with overexpression
207152_at	NTRK2	Hs.584783	4915	64.3
205686_s_at	CD86	Hs.171182	942	64.3
210325_at	CD1A	Hs.1309	909	64.3
215822_x_at	MYT1	Hs.279562	4661	64.3
210894_s_at	CEP2	Hs.443976	11190	64.3
214759_at	WTAP	Hs.446091	9589	64.3
206032_at	DSC3	Hs.41690	1825	64.3
202150_s_at	NEDD9	Hs.37982	4739	64.3
216688_at	---	Hs.543737	---	64.3
216285_at	DGCR14	Hs.517407	8220	64.3
211429_s_at	SERPINA1	Hs.525557	5265	63.7
205131_x_at	CLEC11A	Hs.512680	6320	63.7
209906_at	C3AR1	Hs.567242	719	63.7
206177_s_at	ARG1	Hs.440934	383	63.7
204158_s_at	TCIRG1	Hs.495985	10312	63.7
212193_s_at	LARP1	Hs.292078	23367	63.7
216557_x_at	IGHA1 /// IGHG1 /// IGHG3	Hs.558342	3493 /// 3500 /// 3502	63.7
214726_x_at	ADD1	Hs.183706	118	63.7
200769_s_at	MAT2A	Hs.516157	4144	63.7
56829_at	NIBP	Hs.26814	83696	63.7
204650_s_at	APBB3	Hs.529449	10307	63.7
217117_x_at	MUC3A	Hs.554764	4584	63.7
201341_at	ENC1	Hs.104925	8507	63.7
201984_s_at	EGFR	Hs.488293	1956	63.7
209133_s_at	COMMD4	Hs.351327	54939	63.7
214081_at	PLXDC1	Hs.125036	57125	63.7
221060_s_at	TLR4	Hs.174312	7099	63.1
213826_s_at	---	---	---	63.1
209474_s_at	ENTPD1	Hs.374230	953	63.1
211413_s_at	PADI4	Hs.522969	23569	63.1
216774_at	---	---	---	63.1
207716_at	KRTHA8	Hs.248188	8687	63.1
207777_s_at	SP140	Hs.471576	11262	63.1
206309_at	LECT1	Hs.421391	11061	63.1
215167_at	CRSP2	Hs.407604	9282	63.1
214034_at	ARTS-1	Hs.436186	51752	63.1
205382_s_at	DF	Hs.155597	1675	62.4
214973_x_at	IGHD	Hs.560238	3495	62.4
211101_x_at	LILRA2	Hs.534394	11027	62.4
209498_at	CEACAM1	Hs.512682	634	62.4
209467_s_at	MKNK1	Hs.371594	8569	62.4
209002_s_at	CALCOCO1	Hs.156667	57658	62.4

probe	Gene	Unigene	Locus	% AML cases with overexpression
211881_x_at	IGLJ3	Hs.517453	28831	62.4
202723_s_at	FOXO1A	Hs.370666	2308	62.4
210031_at	CD3Z	Hs.156445	919	62.4
217269_s_at	PRSS7	Hs.149473	5651	62.4
204073_s_at	C11orf9	Hs.473109	745	62.4
216446_at	GLIS1	Hs.306691	148979	62.4
216377_x_at	ALPPL2	Hs.333509	251	62.4
214735_at	PIP3-E	Hs.146100	26034	62.4
209371_s_at	SH3BP2	Hs.167679	6452	62.4
222106_at	PRND	Hs.406696	23627	62.4
221119_at	FLJ20184	Hs.272787	54848	62.4
214610_at	CYP11B1	Hs.184927	1584	62.4
201852_x_at	COL3A1	Hs.443625	1281	62.4
211471_s_at	RAB36	Hs.369557	9609	62.4
205781_at	C16orf7	Hs.164410	9605	62.4
211203_s_at	CNTN1	Hs.567249	1272	62.4
211516_at	IL5RA	Hs.68876	3568	62.4
216539_at	ATXN3L	Hs.382641	92552	62.4
207759_s_at	DISC1 /// C1orf136	Hs.13318	27185 /// 400574	62.4
205433_at	BCHE	Hs.420483	590	62.4
212587_s_at	PTPRC	Hs.192039	5788	61.8
203332_s_at	INPP5D	Hs.262886	3635	61.8
204972_at	OAS2	Hs.584785	4939	61.8
207111_at	EMR1	Hs.2375	2015	61.8
201482_at	QSCN6	Hs.518374	5768	61.8
207643_s_at	TNFRSF1A	Hs.279594	7132	61.8
201673_s_at	GYS1	Hs.386225	2997	61.8
207376_at	VENTX	Hs.125231	27287	61.8
211883_x_at	CEACAM1	Hs.512682	634	61.8
211824_x_at	NALP1	Hs.513902	22861	61.8
208452_x_at	MYO9B	Hs.123198	4650	61.8
206520_x_at	SIGLEC6	Hs.397255	946	61.8
216034_at	SUHW1	Hs.178665	129025	61.8
214903_at	---	Hs.25422	---	61.8
213756_s_at	HSF1	Hs.530227	3297	61.8
219150_s_at	CENTA1	Hs.121593	11033	61.8
221466_at	P2RY4	Hs.533929	5030	61.8
220888_s_at	C20orf32	Hs.473144	57091	61.8
207367_at	ATP12A	Hs.147111	479	61.8
41469_at	PI3	Hs.112341	5266	61.8
203736_s_at	PPFIBP1	Hs.172445	8496	61.8
203768_s_at	STS	Hs.522578	412	61.8
215234_at	---	Hs.66185	---	61.8

probe	Gene	Unigene	Locus	% AML cases with overexpression
215489_x_at	HOMER3	Hs.410683	9454	61.1
206881_s_at	LILRA3	Hs.113277	11026	61.1
211100_x_at	LILRA2	Hs.534394	11027	61.1
211650_x_at	---	Hs.448957	---	61.1
203828_s_at	IL32	Hs.943	9235	61.1
201887_at	IL13RA1	Hs.496646	3597	61.1
219717_at	FLJ20280	Hs.518674	54876	61.1
210773_s_at	FPRL1	Hs.99855	2358	61.1
207984_s_at	MPP2	Hs.514208	4355	61.1
217024_x_at	PTPNS1	Hs.128846	140885	61.1
202885_s_at	PPP2R1B	Hs.584790	5519	61.1
215525_at	---	---	---	61.1
219792_at	AGMAT	Hs.567583	79814	61.1
217008_s_at	GRM7	Hs.475336	2917	61.1
211039_at	CHRNA1	Hs.434419	1134	61.1
204686_at	IRS1	Hs.471508	3667	61.1
221671_x_at	IGKC /// IGKV1-5	Hs.449621	28299 /// 3514	60.5
38487_at	STAB1	Hs.301989	23166	60.5
205592_at	SLC4A1	Hs.443948	6521	60.5
207459_x_at	GYPB	---	2994	60.5
215498_s_at	MAP2K3	Hs.514012	5606	60.5
217799_x_at	UBE2H	Hs.344165	7328	60.5
38710_at	OTUB1	Hs.473788	55611	60.5
207691_x_at	ENTPD1	Hs.374230	953	60.5
219991_at	SLC2A9	Hs.444612	56606	60.5
219229_at	SLCO3A1	Hs.311187	28232	60.5
211405_x_at	IFNA17	Hs.282276	3451	60.5
202895_s_at	PTPNS1	Hs.128846	140885	60.5
220951_s_at	ACF	Hs.499643	29974	60.5
213001_at	ANGPTL2	Hs.521731	23452	60.5
215057_at	---	Hs.496916	---	60.5
207093_s_at	OMG	Hs.584786	4974	60.5
211255_x_at	DEDD	Hs.517342	9191	60.5
204397_at	EML2	Hs.24178	24139	60.5
214485_at	ODF1	Hs.159274	4956	60.5
208346_at	PPBPL2	Hs.3134	10895	60.5
209840_s_at	LRRN3	Hs.3781	54674	60.5
204850_s_at	DCX	Hs.34780	1641	60.5
215379_x_at	IGL@ /// IGLC1 /// IGLC2 /// IGLV3-25 /// IGLV2-14 /// IGLJ3	Hs.449585	28793 /// 28815 /// 28831 /// 3535 /// 3537 /// 3538	59.9

probe	Gene	Unigene	Locus	% AML cases with overexpression
204745_x_at	MT1G	Hs.433391	4495	59.9
212588_at	PTPRC	Hs.192039	5788	59.9
216063_at	HBBP1	Hs.20205	3044	59.9
221747_at	TNS1	Hs.471381	7145	59.9
212969_x_at	EML3	Hs.379785	256364	59.9
216542_x_at	IGHG1 /// MGC27165	Hs.584764	283650 /// 3500	59.9
38340_at	HIP1R	Hs.524815	9026	59.9
213380_x_at	MSTP9	Hs.475654	11223	59.9
160020_at	MMP14	Hs.2399	4323	59.9
219538_at	WDR5B	Hs.567513	54554	59.9
217397_at	---	Hs.428848	---	59.9
216243_s_at	IL1RN	Hs.81134	3557	59.9
219316_s_at	C14orf58	Hs.509966	55640	59.9
33323_r_at	SFN	Hs.523718	2810	59.9
216488_s_at	ATP11A	Hs.29189	23250	59.9
219702_at	PLAC1	Hs.496811	10761	59.9
206044_s_at	BRAF	Hs.324250	673	59.9
205156_s_at	ACCN2	Hs.274361	41	59.9
211287_x_at	CSF2RA	Hs.520937	1438	59.9
210127_at	RAB6B	Hs.12152	51560	59.9
221996_s_at	CLTB	Hs.484241	1212	59.9
216851_at	IGLJ3	Hs.517453	28831	59.9
210219_at	SP100	Hs.369056	6672	59.9
215480_at	KIAA0509	Hs.554381	57242	59.9
211635_x_at	IGHV1-69	Hs.449011	28461	59.2
54970_at	DKFZp761I2123	Hs.77978	83637	59.2
216560_x_at	IGLC1 /// IGLC2	Hs.449585 /// Hs.555877	3537 /// 3538	59.2
220954_s_at	PILRB	Hs.530084	29990	59.2
64942_at	GPR153	Hs.531581	387509	59.2
219259_at	SEMA4A	Hs.408846	64218	59.2
214438_at	HLX1	Hs.74870	3142	59.2
214329_x_at	TNFSF10	Hs.478275	8743	59.2
211640_x_at	IGHV1-69	Hs.449011	28461	59.2
209436_at	SPON1	Hs.445818	10418	59.2
222329_x_at	ANKRD17	Hs.518804	26057	59.2
220375_s_at	---	---	---	59.2
207277_at	CD209	Hs.278694	30835	59.2
202409_at	LOC492304	Hs.568449	492304	59.2
34408_at	RTN2	Hs.47517	6253	59.2
216106_at	LOC145678	Hs.23777	145678	59.2
214454_at	ADAMTS2	Hs.23871	9509	59.2
220230_s_at	CYB5R2	Hs.414362	51700	59.2

probe	Gene	Unigene	Locus	% AML cases with overexpression
202192_s_at	GAS7	Hs.462214	8522	58.6
210706_s_at	RNF24	Hs.114180	11237	58.6
215116_s_at	DNM1	Hs.522413	1759	58.6
208978_at	CRIP2	Hs.534309	1397	58.6
211822_s_at	NALP1	Hs.513902	22861	58.6
205203_at	PLD1	Hs.478230	5337	58.6
220475_at	SLC28A3	Hs.584952	64078	58.6
202958_at	PTPN9	Hs.445775	5780	58.6
221082_s_at	NDRG3	Hs.437338	57446	58.6
213957_s_at	CAP350	Hs.413045	9857	58.6
219190_s_at	EIF2C4	Hs.471492	192670	58.6
220082_at	PPP1R14D	Hs.192927	54866	58.6
219746_at	DPF3	Hs.162868	8110	58.6
215524_x_at	TRA@ /// TRDV2 /// TRAV20 /// TRAJ17 /// TRAC /// MGC40069	Hs.369380	28517 /// 28663 /// 28738 /// 28755 /// 348035 /// 6955	58.6
207706_at	USH2A	Hs.232072	7399	58.6
211456_x_at	LOC440737	Hs.568244	440737	58.0
200872_at	S100A10	Hs.143873	6281	58.0
201666_at	TIMP1	Hs.522632	7076	58.0
200661_at	PPGB	Hs.517076	5476	58.0
218660_at	DYSF	Hs.252180	8291	58.0
205789_at	CD1D	Hs.1799	912	58.0
222218_s_at	PILRA	Hs.444407	29992	58.0
179_at	PMS2L11	---	441263	58.0
217493_x_at	NCR2	Hs.194721	9436	58.0
77508_r_at	RABEP2	Hs.555978	79874	58.0
221757_at	MGC17330	Hs.26670	113791	58.0
207954_at	GATA2	Hs.367725	2624	58.0
219194_at	SEMA4G	Hs.567556	57715	58.0
205294_at	BAIAP2	Hs.128316	10458	58.0
35776_at	ITSN1	Hs.160324	6453	58.0
205254_x_at	TCF7	Hs.519580	6932	58.0
204237_at	GULP1	Hs.470887	51454	58.0
221409_at	OR2S2	Hs.553540	56656	58.0
201668_x_at	MARCKS	Hs.519909	4082	58.0
215639_at	SH2D3C	Hs.306412	10044	58.0
203703_s_at	---	---	---	58.0
208121_s_at	PTPRO	Hs.160871	5800	58.0
207158_at	APOBEC1	Hs.560	339	58.0
220910_at	FRAS1	Hs.369448	80144	58.0

probe	Gene	Unigene	Locus	% AML cases with overexpression
221339_at	OR10C1	Hs.553838	442194	58.0
221034_s_at	TEX13B	Hs.333130	56156	58.0
211986_at	AHNAK	Hs.568948	79026	57.3
208248_x_at	APLP2	Hs.370247	334	57.3
216491_x_at	IGHM	Hs.538461	3507	57.3
204086_at	PRAME	Hs.30743	23532	57.3
210889_s_at	FCGR2B	Hs.492655	2213	57.3
204498_s_at	ADCY9	Hs.391860	115	57.3
211633_x_at	IGHG1	Hs.578081	3500	57.3
206011_at	CASP1	Hs.2490	834	57.3
212516_at	CENTD2	Hs.503165	116985	57.3
203233_at	IL4R	Hs.513457	3566	57.3
201802_at	SLC29A1	Hs.25450	2030	57.3
204981_at	SLC22A18	Hs.50868	5002	57.3
209060_x_at	NCOA3	Hs.382168	8202	57.3
213900_at	C9orf61	Hs.118003	9413	57.3
215521_at	PHC3	Hs.529592	80012	57.3
214421_x_at	CYP2C9	Hs.282624	1559	57.3
220288_at	MYO15A	Hs.462390	51168	57.3
207303_at	PDE1C	Hs.487897	5137	57.3
220866_at	ADAMTS6	Hs.344757	11174	57.3
213103_at	STARD13	Hs.507704	90627	57.3
207345_at	FST	Hs.9914	10468	57.3
211469_s_at	CXCR6	Hs.34526	10663	57.3
219331_s_at	FLJ10748	Hs.10414	55220	57.3
215391_at	MAP1A	Hs.194301	4130	57.3
204515_at	HSD3B1	Hs.364941	3283	57.3
211821_x_at	GYPA	Hs.434973	2993	56.7
200935_at	CALR	Hs.515162	811	56.7
206940_s_at	POU4F1	Hs.211588	5457	56.7
202878_s_at	C1QR1	Hs.97199	22918	56.7
210356_x_at	MS4A1	Hs.438040	931	56.7
210119_at	KCNJ15	Hs.411299	3772	56.7
37796_at	LRCH4	Hs.125742	4034	56.7
203561_at	FCGR2A	Hs.352642	2212	56.7
211102_s_at	LILRA2	Hs.534394	11027	56.7
208262_x_at	MEFV	Hs.173730	4210	56.7
201108_s_at	THBS1	Hs.164226	7057	56.7
201332_s_at	STAT6	Hs.524518	6778	56.7
205488_at	GZMA	Hs.90708	3001	56.7
216678_at	WDR10	Hs.477537	55764	56.7
217377_x_at	NTRK3	Hs.410969	4916	56.7
206954_at	WIT-1	Hs.567499	51352	56.7
219333_s_at	CAPN10	Hs.112218	11132	56.7

probe	Gene	Unigene	Locus	% AML cases with overexpression
218554_s_at	ASH1L	Hs.491060	55870	56.7
205374_at	SLN	Hs.334629	6588	56.7
208292_at	BMP10	Hs.158317	27302	56.7
219859_at	CLEC4E	Hs.236516	26253	56.7
205643_s_at	PPP2R2B	Hs.193825	5521	56.7
214632_at	NRP2	Hs.471200	8828	56.7
220544_at	TSKS	Hs.515858	60385	56.7
215049_x_at	CD163	Hs.504641	9332	56.1
213733_at	MYO1F	Hs.408451	4542	56.1
209166_s_at	MAN2B1	Hs.356769	4125	56.1
204774_at	EVI2A	Hs.567266	2123	56.1
210915_x_at	TRBV19 /// TRBC1	Hs.567471	28568 /// 28639	56.1
218019_s_at	PDXK	Hs.284491	8566	56.1
58367_s_at	ZNF419	Hs.98593	79744	56.1
205944_s_at	CLTCL1	Hs.368266	8218	56.1
203184_at	FBN2	Hs.519294	2201	56.1
213958_at	CD6	Hs.502710	923	56.1
206723_s_at	EDG4	Hs.122575	9170	56.1
206722_s_at	EDG4	Hs.122575	9170	56.1
210197_at	ITPK1	Hs.308122	3705	56.1
206586_at	CNR2	Hs.73037	1269	56.1
214377_s_at	CTRL	Hs.405774	1506	56.1
216294_s_at	KIAA1109	Hs.408142	84162	56.1
207330_at	PZP	Hs.480143	5858	56.1
213590_at	SLC16A5	Hs.369554	9121	56.1
207188_at	CDK3	Hs.584745	1018	56.1
212793_at	DAAM2	Hs.436590	23500	56.1
215951_at	KIAA1055	Hs.567426	23102	56.1
206199_at	CEACAM7	Hs.74466	1087	56.1
214521_at	HES2	Hs.118727	54626	56.1
213678_at	RP11-444E17.5	Hs.12840	441151	56.1
206144_at	MAGI1	Hs.567389	9223	56.1
209835_x_at	CD44	Hs.502328	960	55.4
208438_s_at	FGR	Hs.1422	2268	55.4
203665_at	HMOX1	Hs.517581	3162	55.4
216832_at	RUNX1T1	Hs.368431	862	55.4
336_at	TBXA2R	Hs.442530	6915	55.4
211668_s_at	PLAU	Hs.77274	5328	55.4
210166_at	TLR5	Hs.114408	7100	55.4
211599_x_at	MET	Hs.132966	4233	55.4
221112_at	IL1RAPL2	Hs.188763	26280	55.4
210904_s_at	IL13RA1	Hs.496646	3597	55.4
37831_at	SIPA1L3	Hs.157259	23094	55.4

probe	Gene	Unigene	Locus	% AML cases with overexpression
217563_at	CLOCK	Hs.436975	9575	55.4
209270_at	LAMB3	Hs.497636	3914	55.4
216910_at	XPNPEP2	Hs.170499	7512	55.4
212664_at	TUBB4	Hs.110837	10382	55.4
206319_s_at	SPINLW1	Hs.121084	57119	55.4
217479_at	FLJ45455	Hs.441035	388336	55.4
204122_at	TYROBP	Hs.515369	7305	54.8
204588_s_at	SLC7A7	Hs.513147	9056	54.8
218157_x_at	CDC42SE1	Hs.22065	56882	54.8
203304_at	BAMBI	Hs.533336	25805	54.8
201412_at	LRP10	Hs.525232	26020	54.8
209473_at	ENTPD1	Hs.374230	953	54.8
202897_at	PTPNS1	Hs.128846	140885	54.8
214366_s_at	ALOX5	Hs.89499	240	54.8
212252_at	CAMKK2	Hs.297343	10645	54.8
33304_at	ISG20	Hs.459265	3669	54.8
222333_at	ALS2CL	Hs.517937	259173	54.8
212818_s_at	ASB1	Hs.516788	51665	54.8
216252_x_at	FAS	Hs.244139	355	54.8
216971_s_at	PLEC1	Hs.434248	5339	54.8
205975_s_at	HOXD1	Hs.83465	3231	54.8
206574_s_at	PTP4A3	Hs.43666	11156	54.8
210883_x_at	EFNB3	Hs.26988	1949	54.8
210150_s_at	LAMA5	Hs.473256	3911	54.8
219866_at	CLIC5	Hs.485489	53405	54.8
220684_at	TBX21	Hs.272409	30009	54.8
216196_at	LOC440366	Hs.567926	440366	54.8
208585_at	BTN2A3	Hs.370522	54718	54.8
213960_at	---	Hs.149024	---	54.8
219701_at	TMOD2	Hs.513734	29767	54.8
204351_at	S100P	Hs.2962	6286	54.1
211799_x_at	HLA-C	Hs.534125	3107	54.1
205786_s_at	ITGAM	Hs.172631	3684	54.1
209892_at	FUT4	Hs.390420	2526	54.1
206697_s_at	HP	Hs.513711	3240	54.1
203548_s_at	LPL	Hs.180878	4023	54.1
205929_at	GPA33	Hs.437229	10223	54.1
216152_at	PDZRN3	Hs.434900	23024	54.1
211908_x_at	---	Hs.585642	---	54.1
219725_at	TREM2	Hs.435295	54209	54.1
214767_s_at	HSPB6	Hs.534538	126393	54.1
208156_x_at	EPPK1	Hs.200412	83481	54.1
219365_s_at	CAMKV	Hs.145156	79012	54.1
207733_x_at	PSG9	Hs.502092	5678	54.1

probe	Gene	Unigene	Locus	% AML cases with overexpression
219318_x_at	MED31	Hs.567493	51003	54.1
208004_at	PROL1	Hs.479905	58503	54.1
218692_at	FLJ20366	Hs.390738	55638	54.1
205719_s_at	PAH	Hs.325404	5053	54.1
221416_at	PLA2G2F	Hs.302034	64600	54.1
205625_s_at	CALB1	Hs.65425	793	54.1
220870_at	---	---	---	54.1
207950_s_at	ANK3	Hs.499725	288	54.1
207010_at	GABRB1	Hs.27283	2560	54.1
204150_at	STAB1	Hs.301989	23166	53.5
206050_s_at	RNH1	Hs.530687	6050	53.5
218232_at	C1QA	Hs.9641	712	53.5
218136_s_at	SLC25A37	Hs.122514	51312	53.5
205312_at	SPI1	Hs.502511	6688	53.5
208914_at	GGA2	Hs.460336	23062	53.5
200785_s_at	LRP1	Hs.162757	4035	53.5
205900_at	KRT1	Hs.80828	3848	53.5
219243_at	GIMAP4	Hs.30822	55303	53.5
41644_at	SASH1	Hs.193133	23328	53.5
218114_at	GGA1	Hs.499158	26088	53.5
214582_at	PDE3B	Hs.445711	5140	53.5
207734_at	LAX1	Hs.272794	54900	53.5
220395_at	DNAJA4	Hs.513053	55466	53.5
218030_at	GIT1	Hs.514051	28964	53.5
205170_at	STAT2	Hs.530595	6773	53.5
205708_s_at	TRPM2	Hs.369759	7226	53.5
216739_at	---	Hs.589088	---	53.5
213236_at	SASH1	Hs.193133	23328	53.5
209466_x_at	PTN	Hs.371249	5764	53.5
216973_s_at	HOXB7	Hs.436181	3217	53.5
215178_x_at	ASAHL	Hs.437365	27163	53.5
214754_at	MGC22014	Hs.516107	200424	53.5
204556_s_at	DZIP1	Hs.157002	22873	53.5
207608_x_at	CYP1A2	Hs.1361	1544	53.5
210789_x_at	CEACAM3	Hs.11	1084	53.5
215092_s_at	NFAT5	Hs.371987	10725	53.5
211916_s_at	MYO1A	Hs.5394	4640	53.5
216750_at	APBB2	Hs.479602	323	53.5
216692_at	ZNF337	Hs.213735	26152	53.5
202803_s_at	ITGB2	Hs.375957	3689	52.9
205495_s_at	GNLY	Hs.105806	10578	52.9
201234_at	ILK	Hs.5158	3611	52.9
205838_at	GYPA	Hs.434973	2993	52.9
218920_at	FLJ10404	Hs.484289	54540	52.9

probe	Gene	Unigene	Locus	% AML cases with overexpression
202436_s_at	CYP1B1	Hs.154654	1545	52.9
203668_at	MAN2C1	Hs.26232	4123	52.9
210895_s_at	CD86	Hs.171182	942	52.9
207270_x_at	CD300C	Hs.2605	10871	52.9
203516_at	SNTA1	Hs.31121	6640	52.9
220898_at	---	---	---	52.9
207051_at	SLC17A4	Hs.282931	10050	52.9
208578_at	SCN10A	Hs.250443	6336	52.9
220577_at	GVIN1	Hs.494757	387751	52.9
207705_s_at	KIAA0980	Hs.472347	22981	52.9
221631_at	CACNA1I	Hs.125116	8911	52.9
212157_at	SDC2	Hs.1501	6383	52.9
220881_at	LMO2	Hs.34560	4005	52.9
217474_at	---	Hs.569826	---	52.9
210909_x_at	LPAL2	Hs.439074	80350	52.9
203021_at	SLPI	Hs.517070	6590	52.2
38964_r_at	WAS	Hs.2157	7454	52.2
203281_s_at	UBE1L	Hs.16695	7318	52.2
216401_x_at	LOC400969 /// IGKC	Hs.429466 /// Hs.449621 /// Hs.516184 /// Hs.551722	3514 /// 400969	52.2
221565_s_at	FAM26B	Hs.241545	51063	52.2
210663_s_at	KYNU	Hs.470126	8942	52.2
204632_at	RPS6KA4	Hs.105584	8986	52.2
205926_at	IL27RA	Hs.132781	9466	52.2
215833_s_at	SPPL2B	Hs.330742	56928	52.2
217502_at	IFIT2	Hs.437609	3433	52.2
1438_at	EPHB3	Hs.2913	2049	52.2
201207_at	TNFAIP1	Hs.76090	7126	52.2
206783_at	FGF4	Hs.1755	2249	52.2
213713_s_at	LOC89944	Hs.436178	89944	52.2
205144_at	FLJ22269	Hs.567612	84179	52.2
221197_s_at	CHAT	Hs.302002	1103	52.2
218574_s_at	LMCD1	Hs.475353	29995	52.2
37793_r_at	RAD51L3	Hs.125244	5892	52.2
205503_at	PTPN14	Hs.19281	5784	52.2
201976_s_at	MYO10	Hs.481720	4651	52.2
220833_at	---	---	---	52.2
221805_at	NEFL	Hs.521461	4747	52.2
203903_s_at	HEPH	Hs.31720	9843	52.2
204489_s_at	CD44	Hs.502328	960	51.6
216268_s_at	JAG1	Hs.224012	182	51.6
203666_at	CXCL12	Hs.522891	6387	51.6

probe	Gene	Unigene	Locus	% AML cases with overexpression
202687_s_at	TNFSF10	Hs.478275	8743	51.6
210327_s_at	AGXT	Hs.144567	189	51.6
220404_at	GPR97	Hs.383403	222487	51.6
221879_at	CALML4	Hs.554828	91860	51.6
210872_x_at	GAS7	Hs.462214	8522	51.6
201625_s_at	INSIG1	Hs.520819	3638	51.6
40489_at	ATN1	Hs.143766	1822	51.6
211440_x_at	CYP3A43	Hs.306220	64816	51.6
215366_at	SNX13	Hs.487648	23161	51.6
207445_s_at	CCR9	Hs.225946	10803	51.6
219461_at	PAK6	Hs.513645	56924	51.6
206132_at	MCC	Hs.483104	4163	51.6
208524_at	GPR15	Hs.563128	2838	51.6
218892_at	DCHS1	Hs.199850	8642	51.6
222166_at	C9orf16	Hs.522412	79095	51.6
215959_at	PPFIBP2	Hs.16019	8495	51.6
216663_s_at	ZMYND10	Hs.526735	51364	51.6
221716_s_at	ACSBG2	Hs.567599	81616	51.6
204309_at	CYP11A1	Hs.303980	1583	51.6
219139_s_at	KIAA1922	Hs.436604	114819	51.6
217023_x_at	TPSAB1	---	7177	51.0
211657_at	CEACAM6	Hs.466814	4680	51.0
203104_at	CSF1R	Hs.483829	1436	51.0
219563_at	C14orf139	Hs.41502	79686	51.0
209949_at	NCF2	Hs.518604	4688	51.0
210244_at	CAMP	Hs.51120	820	51.0
218345_at	HCA112	Hs.12126	55365	51.0
210032_s_at	SPAG6	Hs.527698	9576	51.0
206057_x_at	SPN	Hs.461934	6693	51.0
210116_at	SH2D1A	Hs.349094	4068	51.0
211864_s_at	FER1L3	Hs.500572	26509	51.0
214180_at	MAN1C1	Hs.197043	57134	51.0
219257_s_at	SPHK1	Hs.68061	8877	51.0
217507_at	SLC11A1	Hs.471393	6556	51.0
201373_at	PLEC1	Hs.434248	5339	51.0
210271_at	NEUROD2	Hs.554765	4761	51.0
221643_s_at	RERE	Hs.463041	473	51.0
214928_at	OBSL1	Hs.526594	23363	51.0
205132_at	ACTC	Hs.118127	70	51.0
207597_at	ADAM18	Hs.127930	8749	51.0
219310_at	C20orf39	Hs.124638	79953	51.0
216605_s_at	CEACAM21	Hs.230424	90273	51.0
209946_at	VEGFC	Hs.435215	7424	51.0
211128_at	EDA	Hs.105407	1896	51.0

probe	Gene	Unigene	Locus	% AML cases with overexpression
209621_s_at	PDLIM3	Hs.85862	27295	51.0
217556_at	CLCN4	Hs.495674	1183	51.0
202018_s_at	LTF	Hs.529517	4057	50.3
214407_x_at	GYPB	---	2994	50.3
200931_s_at	VCL	Hs.500101	7414	50.3
211637_x_at	---	Hs.383169	---	50.3
216153_x_at	RECK	Hs.254269	8434	50.3
213915_at	NKG7	Hs.10306	4818	50.3
205936_s_at	HK3	Hs.411695	3101	50.3
200999_s_at	CKAP4	Hs.74368	10970	50.3
212820_at	DMXL2	Hs.511386	23312	50.3
218380_at	NALP1	Hs.104305	22861	50.3
211433_x_at	KIAA1539	Hs.301696	80256	50.3
202896_s_at	PTPNS1	Hs.128846	140885	50.3
212807_s_at	SORT1	Hs.485195	6272	50.3
204436_at	pp9099	Hs.458575	80301	50.3
215037_s_at	BCL2L1	Hs.516966	598	50.3
212574_x_at	C19orf6	Hs.515003	91304	50.3
211024_s_at	TITF1	Hs.94367	7080	50.3
213633_at	SH3BP1	Hs.584875	23616	50.3
204682_at	LTBP2	Hs.512776	4053	50.3
217849_s_at	CDC42BPB	Hs.569310	9578	50.3
206248_at	PRKCE	Hs.97432	5581	50.3
206767_at	RBMS3	Hs.221436	27303	50.3
217497_at	ECGF1	Hs.546251	1890	50.3
210763_x_at	NCR3	Hs.509513	259197	50.3
206226_at	HRG	Hs.1498	3273	50.3
205368_at	KIAA0773	Hs.135343	9715	50.3
212679_at	TBL2	Hs.52515	26608	50.3
206961_s_at	TRFP	Hs.278434	9477	50.3
207039_at	CDKN2A	Hs.512599	1029	50.3
206171_at	ADORA3	Hs.281342	140	50.3
217163_at	ESR1	Hs.208124	2099	50.3
219505_at	CECR1	Hs.170310	51816	49.7
213193_x_at	TRBV19 /// TRBC1	Hs.567471	28568 /// 28639	49.7
203973_s_at	CEBPD	Hs.440829	1052	49.7
219666_at	MS4A6A	Hs.523702	64231	49.7
207697_x_at	LILRB2	Hs.534386	10288	49.7
211926_s_at	MYH9	Hs.474751	4627	49.7
222217_s_at	SLC27A3	Hs.438723	11000	49.7
210075_at	MARCH2	Hs.445113	51257	49.7
220005_at	P2RY13	Hs.546396	53829	49.7
204994_at	MX2	Hs.926	4600	49.7

probe	Gene	Unigene	Locus	% AML cases with overexpression
203065_s_at	CAV1	Hs.74034	857	49.7
214040_s_at	GSN	Hs.522373	2934	49.7
207106_s_at	LTK	Hs.434481	4058	49.7
216689_x_at	ARHGAP1	Hs.138860	392	49.7
212657_s_at	IL1RN	Hs.81134	3557	49.7
202877_s_at	C1QR1	Hs.97199	22918	49.7
209156_s_at	COL6A2	Hs.420269	1292	49.7
202801_at	PRKACA	Hs.194350	5566	49.7
212948_at	CAMTA2	Hs.373952	23125	49.7
219534_x_at	CDKN1C	Hs.106070	1028	49.7
220066_at	CARD15	Hs.135201	64127	49.7
202627_s_at	SERPINE1	Hs.414795	5054	49.7
205479_s_at	PLAU	Hs.77274	5328	49.7
208360_s_at	---	Hs.578373	---	49.7
220290_at	AIM1L	Hs.128738	55057	49.7
209594_x_at	PSG9	Hs.502092	5678	49.7
209747_at	TGFB3	Hs.2025	7043	49.7
208314_at	RRH	Hs.352262	10692	49.7
208059_at	CCR8	Hs.113222	1237	49.7
205343_at	SULT1C1	Hs.436123	6819	49.7
58916_at	KCTD14	Hs.17296	65987	49.7
206849_at	GABRG2	Hs.7195	2566	49.7
215746_at	C4orf9	Hs.398178	8602	49.7
217452_s_at	B3GALT2	Hs.518834	8707	49.7
221365_at	MLNR	Hs.248126	2862	49.7
221451_s_at	OR2W1	Hs.553526	26692	49.7
208704_x_at	APLP2	Hs.370247	334	49.0
208703_s_at	APLP2	Hs.370247	334	49.0
210629_x_at	LST1	Hs.436066	7940	49.0
203518_at	LYST	Hs.532411	1130	49.0
207076_s_at	ASS	Hs.160786	445	49.0
212765_at	CAMSAP1L1	Hs.23585	23271	49.0
203215_s_at	MYO6	Hs.149387	4646	49.0
201940_at	CPD	Hs.446079	1362	49.0
218501_at	ARHGEF3	Hs.476402	50650	49.0
214036_at	---	Hs.288741	---	49.0
206043_s_at	KIAA0703	Hs.6168	9914	49.0
216606_x_at	LYPLA2 /// LYPLA2P1 /// LOC388499	Hs.534075	11313 /// 285840 /// 388499	49.0
220483_s_at	RNF19	Hs.292882	25897	49.0
202764_at	STIM1	Hs.501735	6786	49.0
215083_at	PSPC1	Hs.213198	55269	49.0
201728_s_at	KIAA0100	Hs.151761	9703	49.0

probe	Gene	Unigene	Locus	% AML cases with overexpression
207343_at	LYZL6	Hs.97477	57151	49.0
207936_x_at	RFPL3	Hs.558455	10738	49.0
218822_s_at	NPEPL1	Hs.528513	79716	49.0
201348_at	GPX3	Hs.386793	2878	49.0
210169_at	SEC14L5	Hs.512856	9717	49.0
221453_at	G6PC2	Hs.283963	57818	49.0
217224_at	---	---	---	49.0
205152_at	SLC6A1	Hs.443874	6529	49.0
216368_s_at	COL4A3	Hs.471525	1285	49.0
220537_at	MTMR8	Hs.442892	55613	49.0
214236_at	CDC27	Hs.463295	996	49.0
205030_at	FABP7	Hs.26770	2173	49.0
220857_at	---	---	---	49.0
205108_s_at	APOB	Hs.120759	338	49.0
209631_s_at	GPR37	Hs.406094	2861	49.0
207741_x_at	TPSAB1 /// TPSB2	Hs.405479	64499 /// 7177	48.4
210004_at	OLR1	Hs.412484	4973	48.4
201350_at	FLOT2	Hs.514038	2319	48.4
205227_at	IL1RAP	Hs.478673	3556	48.4
208624_s_at	EIF4G1	Hs.433750	1981	48.4
203275_at	IRF2	Hs.374097	3660	48.4
221335_x_at	FLJ12886	Hs.466875	56006	48.4
211372_s_at	IL1R2	Hs.25333	7850	48.4
203029_s_at	PTPRN2	Hs.490789	5799	48.4
205467_at	CASP10	Hs.5353	843	48.4
201893_x_at	DCN	Hs.156316	1634	48.4
213639_s_at	ZNF500	Hs.513316	26048	48.4
206058_at	SLC6A12	Hs.437174	6539	48.4
213078_x_at	LOC254531	Hs.352614	254531	48.4
37022_at	PRELP	Hs.76494	5549	48.4
220511_s_at	DLC1	Hs.134296	10395	48.4
205411_at	STK4	Hs.472838	6789	48.4
219044_at	FLJ10916	Hs.516179	55258	48.4
218700_s_at	RAB7L1	Hs.115325	8934	48.4
217061_s_at	ETV1	Hs.22634	2115	48.4
207393_at	HCRTR2	Hs.151624	3062	48.4
213776_at	LOC157562	Hs.27371	157562	48.4
208431_s_at	TUB	Hs.568986	7275	48.4
213413_at	SBLF	---	11037	48.4
220908_at	FLJ32855	Hs.383206	80125	48.4
214597_at	SSTR2	Hs.514451	6752	48.4
210586_x_at	RHD	Hs.567331	6007	47.8
208891_at	DUSP6	Hs.298654	1848	47.8

probe	Gene	Unigene	Locus	% AML cases with overexpression
204834_at	FGL2	Hs.520989	10875	47.8
211798_x_at	IGLJ3	Hs.517453	28831	47.8
45749_at	FAM65A	Hs.152717	79567	47.8
221002_s_at	TSPAN14	Hs.568777	81619	47.8
212443_at	NBEAL2	Hs.437043	23218	47.8
204890_s_at	LCK	Hs.470627	3932	47.8
47069_at	PRR5	---	55615	47.8
216554_s_at	ENO1	Hs.517145	2023	47.8
209241_x_at	MINK1	Hs.443417	50488	47.8
211269_s_at	IL2RA	Hs.231367	3559	47.8
206513_at	AIM2	Hs.281898	9447	47.8
219657_s_at	KLF3	Hs.298658	51274	47.8
219788_at	PILRA	Hs.444407	29992	47.8
202485_s_at	MBD2	Hs.25674	8932	47.8
221851_at	LOC90379	Hs.443636	90379	47.8
204975_at	EMP2	Hs.531561	2013	47.8
212272_at	LPIN1	Hs.467740	23175	47.8
209182_s_at	C10orf10	Hs.93675	11067	47.8
211460_at	TTTY9 /// TTY9	Hs.567607	425057 /// 83864	47.8
209908_s_at	TGFB2	Hs.133379	7042	47.8
217767_at	C3	Hs.529053	718	47.8
212575_at	C19orf6	Hs.515003	91304	47.8
207863_at	ADPRH	Hs.99884	141	47.8
220565_at	CCR10	Hs.278446	2826	47.8
210644_s_at	LAIR1	Hs.467288	3903	47.1
207809_s_at	ATP6AP1	Hs.6551	537	47.1
216012_at	---	Hs.550193	---	47.1
210314_x_at	TNFSF13 /// TNFSF12-TNFSF13	Hs.54673	407977 /// 8741	47.1
207509_s_at	LAIR2	Hs.43803	3904	47.1
214298_x_at	SEPT6	Hs.496666	23157	47.1
221484_at	B4GALT5	Hs.370487	9334	47.1
219890_at	CLEC5A	Hs.446235	23601	47.1
203502_at	BPGM	Hs.198365	669	47.1
209403_at	TBC1D3 /// TBC1D3C	Hs.105891	414060 /// 84218	47.1
216052_x_at	ARTN	Hs.194689	9048	47.1
219359_at	FLJ22635	Hs.353181	80162	47.1
209370_s_at	SH3BP2	Hs.167679	6452	47.1
201798_s_at	FER1L3	Hs.500572	26509	47.1
204425_at	ARHGAP4	Hs.3109	393	47.1
209721_s_at	HOM-TES-103	Hs.15243	25900	47.1

probe	Gene	Unigene	Locus	% AML cases with overexpression
206772_at	PTHR2	Hs.159499	5746	47.1
212355_at	KIAA0323	Hs.558466	23351	47.1
204735_at	PDE4A	Hs.89901	5141	47.1
213006_at	CEBPD	Hs.440829	1052	47.1
221036_s_at	APH1B	Hs.511703	83464	47.1
220987_s_at	C11orf17 /// NUAK2	Hs.131180	56672 /// 81788	47.1
210200_at	WWP2	Hs.408458	11060	47.1
205742_at	TNNI3	Hs.512709	7137	47.1
218950_at	CENTD3	Hs.25277	64411	47.1
220032_at	FLJ21986	Hs.189652	79974	47.1
214636_at	CALCB	Hs.534305	797	47.1
50965_at	RAB26	Hs.3797	25837	47.1
209766_at	PRDX3	Hs.523302	10935	47.1
204105_s_at	NRCAM	Hs.21422	4897	47.1
220874_at	---	---	---	47.1
218272_at	FLJ20699	Hs.435832	55020	47.1
217369_at	IGHG1 /// LOC440361 /// LOC440370	Hs.512293	3500 /// 440361 /// 440370	47.1
214786_at	MAP3K1	Hs.584779	4214	47.1
207732_s_at	DLG3	Hs.522680	1741	47.1
208188_at	KRT9	Hs.2783	3857	47.1
218959_at	HOXC10	Hs.44276	3226	47.1
203180_at	ALDH1A3	Hs.459538	220	47.1
220701_at	---	---	---	47.1
206651_s_at	CPB2	Hs.512937	1361	47.1
206228_at	PAX2	Hs.155644	5076	47.1
202411_at	IFI27	Hs.532634	3429	46.5
211284_s_at	GRN	Hs.514220	2896	46.5
202295_s_at	CTSH	Hs.148641	1512	46.5
211581_x_at	LST1	Hs.436066	7940	46.5
218581_at	ABHD4	Hs.445665	63874	46.5
219528_s_at	BCL11B	Hs.510396	64919	46.5
219332_at	MICAL-L2	Hs.376617	79778	46.5
210944_s_at	CAPN3	Hs.143261	825	46.5
220751_s_at	C5orf4	Hs.519694	10826	46.5
217052_x_at	---	---	---	46.5
206515_at	CYP4F3	Hs.106242	4051	46.5
57082_at	LDLRAP1	Hs.189782	26119	46.5
203168_at	CREBL1	Hs.42853	1388	46.5
219358_s_at	CENTA2	Hs.514063	55803	46.5
216791_at	TMEM92	Hs.224630	162461	46.5
207601_at	SULT1B1	Hs.129742	27284	46.5

probe	Gene	Unigene	Locus	% AML cases with overexpression
219337_at	C1orf159	Hs.235095	54991	46.5
201333_s_at	ARHGEF12	Hs.24598	23365	46.5
213551_x_at	PCGF2	Hs.371617	7703	46.5
211810_s_at	GALC	Hs.513439	2581	46.5
207216_at	TNFSF8	Hs.494901	944	46.5
217359_s_at	NCAM1	Hs.503878	4684	46.5
206677_at	KRTHA1	Hs.41696	3881	46.5
208851_s_at	THY1	Hs.134643	7070	46.5
204751_x_at	DSC2	Hs.95612	1824	46.5
221303_at	PCDHB1	Hs.278950	29930	46.5
220574_at	SEMA6D	Hs.511265	80031	46.5
206943_at	TGFBR1	Hs.494622	7046	46.5
206888_s_at	ARHGDIG	Hs.534303	398	46.5
216474_x_at	TPSAB1	---	7177	45.9
207134_x_at	TPSAB1	---	7177	45.9
221269_s_at	SH3BGRL3	Hs.109051	83442	45.9
208450_at	LGALS2	Hs.531776	3957	45.9
216320_x_at	MST1	Hs.512587	4485	45.9
203882_at	ISGF3G	Hs.1706	10379	45.9
204320_at	COL11A1	Hs.523446	1301	45.9
204103_at	CCL4	Hs.75703	6351	45.9
207187_at	JAK3	Hs.515247	3718	45.9
220240_s_at	TMCO3	Hs.317593	55002	45.9
219428_s_at	PXMP4	Hs.368717	11264	45.9
206150_at	TNFRSF7	Hs.355307	939	45.9
212823_s_at	PLEKHG3	Hs.509637	26030	45.9
210864_x_at	HFE	Hs.233325	3077	45.9
215672_s_at	KIAA0828	Hs.195058	23382	45.9
204280_at	RGS14	Hs.9347	10636	45.9
216635_at	---	Hs.492815	---	45.9
203769_s_at	STS	Hs.522578	412	45.9
216904_at	COL6A1	Hs.474053	1291	45.9
211880_x_at	PCDHGA1	---	56114	45.9
205991_s_at	PRRX1	Hs.283416	5396	45.9
221605_s_at	PIPOX	Hs.462585	51268	45.9
222324_at	OBSCN	Hs.231655	84033	45.9
222361_at	---	Hs.551805	---	45.9
210084_x_at	TPSAB1	---	7177	45.2
205557_at	BPI	Hs.529019	671	45.2
219371_s_at	KLF2	Hs.107740	10365	45.2
201331_s_at	STAT6	Hs.524518	6778	45.2
221824_s_at	MARCH8	Hs.499489	220972	45.2
205831_at	CD2	Hs.523500	914	45.2
209286_at	CDC42EP3	Hs.369574	10602	45.2

probe	Gene	Unigene	Locus	% AML cases with overexpression
213260_at	FOXC1	Hs.348883	2296	45.2
218154_at	GSDMDC1	Hs.118983	79792	45.2
211417_x_at	GGT1	Hs.444164	2678	45.2
215364_s_at	KIAA0467	Hs.301943	23334	45.2
218148_at	FLJ13111	Hs.288382	80152	45.2
212682_s_at	BC002942	Hs.150540	91289	45.2
205238_at	CXorf34	Hs.496501	79979	45.2
210234_at	GRM4	Hs.429018	2914	45.2
218818_at	FHL3	Hs.57687	2275	45.2
221489_s_at	SPRY4	Hs.323308	81848	45.2
209695_at	PTP4A3	Hs.43666	11156	45.2
213010_at	PRKCDBP	Hs.434044	112464	45.2
208185_x_at	---	---	---	45.2
216499_at	---	Hs.409816	---	45.2
210796_x_at	SIGLEC6	Hs.397255	946	45.2
219873_at	COLEC11	Hs.32603	78989	45.2
202198_s_at	MTMR3	Hs.570462	8897	45.2
221405_at	LOC51190	---	51190	45.2
215056_at	---	Hs.498015	---	45.2
220984_s_at	SLCO5A1	Hs.443609	81796	45.2
215246_at	HDCMA18P	Hs.278635	51574	45.2
207308_at	SLCO1A2	Hs.46440	6579	45.2
217350_at	LOC160313	Hs.527883	160313	45.2
202597_at	IRF6	Hs.355827	3664	45.2
203649_s_at	PLA2G2A	Hs.466804	5320	45.2
212425_at	SCAMP1	Hs.482587	9522	45.2
221266_s_at	TM7SF4	Hs.208036	81501	45.2
206633_at	CHRNA1	Hs.434419	1134	45.2
206021_at	SCAND2	Hs.513102	54581	45.2
214079_at	DHRS2	Hs.272499	10202	45.2
203535_at	S100A9	Hs.112405	6280	44.6
215382_x_at	TPSAB1	---	7177	44.6
215806_x_at	TRGC2 /// TRGV9 /// LOC442532 /// LOC442670 /// TARP	Hs.534032	442532 /// 442670 /// 445347 /// 6967 /// 6983	44.6
200742_s_at	TPP1	Hs.523454	1200	44.6
39854_r_at	PNPLA2	Hs.118463	57104	44.6
201642_at	IFNGR2	Hs.517240	3460	44.6
203385_at	DGKA	Hs.524488	1606	44.6
205614_x_at	MST1	Hs.512587	4485	44.6
209047_at	AQP1	Hs.76152	358	44.6
40829_at	WDTC1	Hs.469154	23038	44.6

probe	Gene	Unigene	Locus	% AML cases with overexpression
213348_at	CDKN1C	Hs.106070	1028	44.6
221541_at	CRISPLD2	Hs.513779	83716	44.6
204773_at	IL11RA	Hs.558346	3590	44.6
213093_at	PRKCA	Hs.531704	5578	44.6
61874_at	C9orf7	Hs.62003	11094	44.6
202274_at	ACTG2	Hs.516105	72	44.6
209948_at	KCNMB1	Hs.484099	3779	44.6
203735_x_at	PPFIBP1	Hs.172445	8496	44.6
206105_at	AFF2	Hs.496911	2334	44.6
219255_x_at	IL17RB	Hs.558512	55540	44.6
215130_s_at	MGC35048	Hs.460217	124152	44.6
205613_at	SYT17	Hs.258326	51760	44.6
214320_x_at	CYP2A6	Hs.439056	1548	44.6
206176_at	BMP6	Hs.285671	654	44.6
220979_s_at	ST6GALNAC5	Hs.303609	81849	44.6
219225_at	PGBD5	Hs.520463	79605	44.6
207602_at	TMPRSS11D	Hs.132195	9407	44.6
210603_at	MGC10646	Hs.330986	84779	44.6
217199_s_at	STAT2	Hs.530595	6773	44.6
216472_at	ITSN1	Hs.160324	6453	44.6
221013_s_at	APOL2	Hs.474740	23780	44.6
205880_at	PRKD1	Hs.508999	5587	44.6
210072_at	CCL19	Hs.50002	6363	44.6
216230_x_at	SMPD1	Hs.498173	6609	44.6
207712_at	BAGE	Hs.545789	574	44.6
214985_at	---	Hs.44690	---	44.6
204326_x_at	MT1X	Hs.374950	4501	43.9
204620_s_at	CSPG2	Hs.443681	1462	43.9
216384_x_at	LOC440085	Hs.568172	440085	43.9
208683_at	CAPN2	Hs.350899	824	43.9
215633_x_at	LST1	Hs.436066	7940	43.9
203562_at	FEZ1	Hs.224008	9638	43.9
211426_x_at	GNAQ	Hs.269782	2776	43.9
217045_x_at	NCR2	Hs.194721	9436	43.9
214475_x_at	CAPN3	Hs.143261	825	43.9
206187_at	PTGIR	Hs.458324	5739	43.9
216981_x_at	SPN	Hs.461934	6693	43.9
209791_at	PADI2	Hs.33455	11240	43.9
210660_at	LILRA1	Hs.534393	11024	43.9
222155_s_at	GPR172A	Hs.6459	79581	43.9
217200_x_at	CYB561	Hs.355264	1534	43.9
205865_at	ARID3A	Hs.501296	1820	43.9
207458_at	C8orf51	Hs.245886	78998	43.9
209228_x_at	TUSC3	Hs.426324	7991	43.9

probe	Gene	Unigene	Locus	% AML cases with overexpression
220227_at	CDH4	Hs.473231	1002	43.9
208322_s_at	ST3GAL1	Hs.584803	6482	43.9
205285_s_at	FYB	Hs.370503	2533	43.9
203400_s_at	TF	Hs.518267	7018	43.9
217001_x_at	HLA-DOA	Hs.351874	3111	43.9
215687_x_at	PLCB1	Hs.431173	23236	43.9
217552_x_at	CR1	Hs.334019	1378	43.9
216762_at	ANKRD15	Hs.306764	23189	43.9
214072_x_at	NENF	Hs.461787	29937	43.9
207347_at	ERCC6	---	2074	43.9
216132_at	ASTN2	Hs.195633	23245	43.9
219720_s_at	C14orf118	Hs.410231	55668	43.9
206426_at	MLANA	Hs.154069	2315	43.9
214388_at	PFAAP5	Hs.507680	10443	43.9
219411_at	ELMO3	Hs.377416	79767	43.9
210816_s_at	CYB561	Hs.355264	1534	43.9
220322_at	IL1F9	Hs.211238	56300	43.9
216280_s_at	DICER1	Hs.87889	23405	43.9
213425_at	WNT5A	Hs.152213	7474	43.9
205683_x_at	TPSAB1	---	7177	43.3
212859_x_at	MT1E	Hs.534330	4493	43.3
214183_s_at	TKTL1	Hs.102866	8277	43.3
203305_at	F13A1	Hs.335513	2162	43.3
205859_at	LY86	Hs.170081	9450	43.3
204490_s_at	CD44	Hs.502328	960	43.3
209367_at	STXBP2	Hs.534352	6813	43.3
211582_x_at	LST1	Hs.436066	7940	43.3
208626_s_at	VAT1	Hs.514199	10493	43.3
219559_at	C20orf59	Hs.512686	63910	43.3
200862_at	DHCR24	Hs.498727	1718	43.3
213350_at	RPS11	Hs.433529	6205	43.3
207854_at	GYPE	Hs.371903	2996	43.3
202180_s_at	MVP	Hs.513488	9961	43.3
213198_at	ACVR1B	Hs.438918	91	43.3
221602_s_at	FAIM3	Hs.58831	9214	43.3
213110_s_at	COL4A5	Hs.369089	1287	43.3
221080_s_at	DENND1C	Hs.236449	79958	43.3
203490_at	ELF4	Hs.271940	2000	43.3
216042_at	TNFRSF25	Hs.462529	8718	43.3
209889_at	SEC31L2	Hs.18889	25956	43.3
207765_s_at	KIAA1539	Hs.301696	80256	43.3
204921_at	GAS8	Hs.431792	2622	43.3
206159_at	GDF10	Hs.2171	2662	43.3
221895_at	MOSPD2	Hs.190043	158747	43.3

probe	Gene	Unigene	Locus	% AML cases with overexpression
204841_s_at	EEA1	Hs.567367	8411	43.3
220162_s_at	CARD9	Hs.528581	64170	43.3
215995_x_at	---	---	---	43.3
209569_x_at	D4S234E	Hs.518595	27065	43.3
210185_at	CACNB1	Hs.635	782	43.3
220485_s_at	SIRPB2	Hs.22974	55423	43.3
215486_at	PRPS1L1	Hs.169284	221823	43.3
219537_x_at	DLL3	Hs.127792	10683	43.3
221367_at	MOS	Hs.533432	4342	43.3
216545_at	LOC441886	---	441886	43.3
202821_s_at	LPP	Hs.444362	4026	43.3
205206_at	KAL1	Hs.521869	3730	43.3
203862_s_at	ACTN2	Hs.498178	88	43.3
204944_at	PTPRG	Hs.146050	5793	43.3
202917_s_at	S100A8	Hs.416073	6279	42.7
206461_x_at	MT1H	Hs.438462	4496	42.7
210746_s_at	EPB42	Hs.368642	2038	42.7
211571_s_at	CSPG2	Hs.443681	1462	42.7
219777_at	GIMAP6	Hs.105468	474344	42.7
209919_x_at	GGT1	Hs.444164	2678	42.7
202250_s_at	WDR42A	Hs.492236	50717	42.7
221011_s_at	LBH	Hs.567598	81606	42.7
219868_s_at	ANKFY1	Hs.513875	51479	42.7
213716_s_at	SECTM1	Hs.558009	6398	42.7
219620_x_at	FLJ20245	Hs.495541	54863	42.7
220653_at	ZIM2	---	23619	42.7
213925_at	C1orf95	Hs.116827	375057	42.7
217033_x_at	NTRK3	Hs.410969	4916	42.7
201295_s_at	WSB1	Hs.446017	26118	42.7
201982_s_at	PAPPA	Hs.494928	5069	42.7
219388_at	GRHL2	Hs.161160	79977	42.7
203915_at	CXCL9	Hs.77367	4283	42.7
208169_s_at	PTGER3	Hs.445000	5733	42.7
215985_at	C6orf12	Hs.302037	80862	42.7
204743_at	TAGLN3	Hs.169330	29114	42.7
207687_at	INHBC	Hs.374664	3626	42.7
200795_at	SPARCL1	Hs.62886	8404	42.7
218814_s_at	C1orf75	Hs.445386	55248	42.7
204230_s_at	SLC17A7	Hs.375616	57030	42.7
214944_at	PHLPPL	Hs.531564	23035	42.7
204272_at	LGALS4	Hs.5302	3960	42.7
213783_at	MFNG	Hs.517603	4242	42.7
206704_at	CLCN5	Hs.166486	1184	42.7
205638_at	BAI3	Hs.13261	577	42.7

probe	Gene	Unigene	Locus	% AML cases with overexpression
204955_at	SRPX	Hs.15154	8406	42.7
201028_s_at	CD99	Hs.495605	4267	42.0
216833_x_at	GYPB /// GYPE	Hs.371903	2994 /// 2996	42.0
202497_x_at	SLC2A3	Hs.419240	6515	42.0
203645_s_at	CD163	Hs.504641	9332	42.0
212830_at	EGFL5	Hs.494977	1955	42.0
207675_x_at	ARTN	Hs.194689	9048	42.0
204619_s_at	CSPG2	Hs.443681	1462	42.0
211495_x_at	TNFSF13 /// TNFSF12-TNFSF13	Hs.54673	407977 /// 8741	42.0
204088_at	P2RX4	Hs.321709	5025	42.0
205798_at	IL7R	Hs.362807	3575	42.0
40850_at	FKBP8	Hs.173464	23770	42.0
219104_at	RNF141	Hs.44685	50862	42.0
211685_s_at	NCALD	Hs.492427	83988	42.0
209663_s_at	ITGA7	Hs.524484	3679	42.0
219689_at	SEMA3G	Hs.59729	56920	42.0
202695_s_at	STK17A	Hs.268887	9263	42.0
204829_s_at	FOLR2	Hs.433159	2350	42.0
207184_at	SLC6A13	Hs.504398	6540	42.0
219236_at	PAQR6	Hs.235873	79957	42.0
205636_at	SH3GL3	Hs.270055	6457	42.0
38766_at	SRCAP	Hs.584857	10847	42.0
208957_at	TXNDC4	Hs.154023	23071	42.0
220785_at	UTS2	Hs.162200	10911	42.0
212477_at	CENTB2	Hs.478746	23527	42.0
206985_at	HSD17B3	Hs.477	3293	42.0
208349_at	TRPA1	Hs.137674	8989	42.0
209683_at	FAM49A	Hs.467769	81553	42.0
205064_at	SPRR1B	Hs.1076	6699	42.0
214245_at	RPS14	Hs.381126	6208	42.0
216907_x_at	KIR3DL2	Hs.567298	3812	42.0
210533_at	MSH4	Hs.216639	4438	42.0
34063_at	RECQL5	Hs.514480	9400	42.0
214287_s_at	CDC2L5	Hs.233552	8621	42.0
210505_at	ADH7	Hs.389	131	42.0
207501_s_at	FGF12	Hs.584758	2257	42.0
216920_s_at	TRGC2 /// TRGV9 /// LOC442532 /// LOC442670 /// TARP	Hs.534032	442532 /// 442670 /// 445347 /// 6967 /// 6983	41.4
211144_x_at	TRGC2	Hs.567345	6967	41.4
206978_at	CCR2	Hs.511794	1231	41.4

probe	Gene	Unigene	Locus	% AML cases with overexpression
204961_s_at	NCF1	Hs.559477	4687	41.4
218473_s_at	GLT25D1	Hs.418795	79709	41.4
214844_s_at	DOK5	Hs.473133	55816	41.4
201276_at	RAB5B	Hs.567328	5869	41.4
200672_x_at	SPTBN1	Hs.503178	6711	41.4
206067_s_at	WT1	Hs.408453	7490	41.4
221511_x_at	CCPG1	Hs.285051	9236	41.4
201525_at	APOD	Hs.522555	347	41.4
38521_at	MAG	Hs.515354	4099	41.4
210992_x_at	FCGR2C	---	9103	41.4
220132_s_at	CLEC2D	Hs.268326	29121	41.4
205142_x_at	ABCD1	Hs.159546	215	41.4
212705_x_at	PNPLA2	Hs.118463	57104	41.4
202215_s_at	NFYC	Hs.233458	4802	41.4
206257_at	CCDC9	Hs.227782	26093	41.4
201559_s_at	CLIC4	Hs.440544	25932	41.4
203507_at	CD68	Hs.246381	968	41.4
213471_at	NPHP4	Hs.462348	261734	41.4
204819_at	FGD1	Hs.522663	2245	41.4
210130_s_at	TM7SF2	Hs.31130	7108	41.4
221857_s_at	TJAP1	Hs.520145	93643	41.4
217198_x_at	IGH@ /// IGHD /// IGHG1	Hs.567291	3492 /// 3495 /// 3500	41.4
221240_s_at	B3GNT4	Hs.363315	79369	41.4
207835_at	FBLN1	Hs.24601	2192	41.4
206663_at	SP4	Hs.88013	6671	41.4
221097_s_at	KCNMB2	Hs.478368	10242	41.4
211250_s_at	SH3BP2	Hs.167679	6452	41.4
213609_s_at	SEZ6L	Hs.194766	23544	41.4
209951_s_at	MAP2K7	Hs.531754	5609	41.4
201029_s_at	CD99	Hs.495605	4267	40.8
214669_x_at	IGKC	Hs.449621	3514	40.8
215071_s_at	HIST1H2AC	Hs.484950	8334	40.8
210786_s_at	FLI1	Hs.504281	2313	40.8
213894_at	KIAA0960	Hs.120855	23249	40.8
215214_at	IGLV3-25 /// IGLC2	Hs.449585 /// Hs.584765	28793 /// 3538	40.8
201389_at	ITGA5	Hs.505654	3678	40.8
212097_at	CAV1	Hs.74034	857	40.8
202459_s_at	LPIN2	Hs.132342	9663	40.8
215449_at	BZRPL1	Hs.357392	222642	40.8
204204_at	SLC31A2	Hs.24030	1318	40.8
212464_s_at	FN1	Hs.562079	2335	40.8
219452_at	DPEP2	Hs.372633	64174	40.8

probe	Gene	Unigene	Locus	% AML cases with overexpression
212974_at	DENND3	Hs.18166	22898	40.8
210775_x_at	CASP9	Hs.329502	842	40.8
210113_s_at	NALP1	Hs.513902	22861	40.8
213119_at	SLC36A1	Hs.269004	206358	40.8
205640_at	ALDH3B1	Hs.523841	221	40.8
206377_at	FOXF2	Hs.484423	2295	40.8
201775_s_at	KIAA0494	Hs.100874	9813	40.8
204059_s_at	ME1	Hs.21160	4199	40.8
214885_at	MYST1	Hs.533803	84148	40.8
213076_at	ITPKC	Hs.515415	80271	40.8
209983_s_at	NRXN2	Hs.372938	9379	40.8
208124_s_at	SEMA4F	Hs.25887	10505	40.8
220112_at	FLJ11795	Hs.436214	79722	40.8
207537_at	PFKFB1	Hs.444304	5207	40.8
204465_s_at	INA	Hs.500916	9118	40.8
214152_at	CCPG1	Hs.285051	9236	40.8
204987_at	ITIH2	Hs.75285	3698	40.8
220334_at	RGS17	Hs.166313	26575	40.8
205157_s_at	KRT17	Hs.579174	3872	40.8
206840_at	AFM	Hs.168718	173	40.8
216530_at	---	Hs.552334	---	40.8
31835_at	HRG	Hs.1498	3273	40.8
206525_at	GABRR1	Hs.437745	2569	40.8
217423_at	TTLL2	Hs.520554	83887	40.8
207587_at	CRYGA	Hs.122566	1418	40.8
207907_at	TNFSF14	Hs.129708	8740	40.8
214087_s_at	MYBPC1	Hs.567306	4604	40.8
214069_at	LOC123876 /// ACSM2	Hs.298252	123876 /// 348158	40.8
207583_at	ABCD2	Hs.117852	225	40.8
201050_at	PLD3	Hs.257008	23646	40.1
202902_s_at	CTSS	Hs.181301	1520	40.1
209813_x_at	TRGC2 /// TRGV9 /// LOC442532 /// LOC442670 /// TARP	Hs.534032	442532 /// 442670 /// 445347 /// 6967 /// 6983	40.1
200696_s_at	GSN	Hs.522373	2934	40.1
204885_s_at	MSLN	Hs.408488	10232	40.1
220416_at	ATP8B4	Hs.511311	79895	40.1
201089_at	ATP6V1B2	Hs.295917	526	40.1
1598_g_at	GAS6	Hs.369201	2621	40.1
212509_s_at	MXRA7	Hs.250723	439921	40.1
211890_x_at	CAPN3	Hs.143261	825	40.1

probe	Gene	Unigene	Locus	% AML cases with overexpression
203567_s_at	TRIM38	Hs.584851	10475	40.1
205770_at	GSR	Hs.271510	2936	40.1
210423_s_at	SLC11A1	Hs.471393	6556	40.1
220023_at	APOB48R	Hs.200333	55911	40.1
209098_s_at	JAG1	Hs.224012	182	40.1
213296_at	PEX10	Hs.567315	5192	40.1
202807_s_at	TOM1	Hs.474705	10043	40.1
217600_at	SCUBE3	Hs.12923	222663	40.1
205949_at	CA1	Hs.23118	759	40.1
221670_s_at	LHX3	Hs.148427	8022	40.1
214971_s_at	ST6GAL1	Hs.207459	6480	40.1
203864_s_at	ACTN2	Hs.498178	88	40.1
210640_s_at	GPR30	Hs.20961	2852	40.1
216555_at	---	---	---	40.1
209807_s_at	NFIX	Hs.257970	4784	40.1
213352_at	TMCC1	Hs.477547	23023	40.1
218651_s_at	LARP6	Hs.416755	55323	40.1
214912_at	---	---	---	40.1
220805_at	HRH2	Hs.247885	3274	40.1
220791_x_at	SCN11A	Hs.186877	11280	40.1
220524_at	EPB41L4B	Hs.269180	54566	40.1
215944_at	---	Hs.568545	---	40.1
213335_s_at	ST3GAL6	Hs.148716	10402	40.1
201422_at	IFI30	Hs.14623	10437	39.5
221479_s_at	BNIP3L	Hs.131226	665	39.5
204959_at	MNDA	Hs.153837	4332	39.5
203729_at	EMP3	Hs.9999	2014	39.5
215819_s_at	RHCE /// RHD	Hs.567331	6006 /// 6007	39.5
205707_at	IL17R	Hs.129751	23765	39.5
211676_s_at	IFNGR1	Hs.520414	3459	39.5
209970_x_at	CASP1	Hs.2490	834	39.5
218589_at	P2RY5	Hs.123464	10161	39.5
218035_s_at	FLJ20273	Hs.518727	54502	39.5
220232_at	SCD5	Hs.379191	79966	39.5
209499_x_at	TNFSF13 /// TNFSF12-TNFSF13	Hs.54673	407977 /// 8741	39.5
204669_s_at	RNF24	Hs.114180	11237	39.5
202665_s_at	WASPIP	Hs.128067	7456	39.5
216541_x_at	IGHG1 /// IGHG3 /// IGHV1-69 /// MGC27165	Hs.584764	283650 /// 28461 /// 3500 /// 3502	39.5
204653_at	TFAP2A	Hs.519880	7020	39.5

probe	Gene	Unigene	Locus	% AML cases with overexpression
221530_s_at	BHLHB3	Hs.177841	79365	39.5
219277_s_at	OGDHL	Hs.17860	55753	39.5
204099_at	SMARCD3	Hs.444445	6604	39.5
211771_s_at	POU2F2	Hs.515429	5452	39.5
203868_s_at	VCAM1	Hs.109225	7412	39.5
216661_x_at	CYP2C9	Hs.282624	1559	39.5
206900_x_at	ZNF253 /// LOC114977	Hs.501796	114977 /// 56242	39.5
205819_at	MARCO	Hs.67726	8685	39.5
210239_at	IRX5	Hs.435730	10265	39.5
214397_at	MBD2	Hs.25674	8932	39.5
201265_at	---	---	---	39.5
214762_at	ATP6V1G2	Hs.249227	534	39.5
208337_s_at	NR5A2	Hs.33446	2494	39.5
207034_s_at	GLI2	Hs.111867	2736	39.5
206449_s_at	MASP1	Hs.89983	5648	39.5
205954_at	RXRG	Hs.26550	6258	39.5
215060_at	---	Hs.512643	---	39.5
220929_at	GALNT8	Hs.511985	26290	39.5
220108_at	GNA14	Hs.62697	9630	39.5
214379_at	BMX	Hs.495731	660	39.5
207503_at	TCP10	Hs.351	6953	39.5
219743_at	HEY2	Hs.144287	23493	39.5
219973_at	ARSJ	Hs.22895	79642	39.5
206164_at	CLCA2	Hs.241551	9635	39.5
200678_x_at	GRN	Hs.514220	2896	38.9
209101_at	CTGF	Hs.410037	1490	38.9
205119_s_at	FPR1	Hs.753	2357	38.9
214574_x_at	LST1	Hs.436066	7940	38.9
209806_at	HIST1H2BK	Hs.437275	85236	38.9
203388_at	ARRB2	Hs.435811	409	38.9
216250_s_at	LPXN	Hs.125474	9404	38.9
117_at	HSPA6	Hs.3268	3310	38.9
217388_s_at	KYNU	Hs.470126	8942	38.9
203508_at	TNFRSF1B	Hs.256278	7133	38.9
209288_s_at	CDC42EP3	Hs.369574	10602	38.9
211535_s_at	FGFR1	Hs.264887	2260	38.9
202621_at	IRF3	Hs.75254	3661	38.9
212002_at	C1orf144	Hs.252967	26099	38.9
221063_x_at	RNF123	Hs.553723	63891	38.9
208463_at	GABRA4	Hs.248112	2557	38.9
219946_x_at	MYH14	Hs.467142	79784	38.9
47571_at	ZNF236	Hs.189826	7776	38.9
207072_at	IL18RAP	Hs.158315	8807	38.9

probe	Gene	Unigene	Locus	% AML cases with overexpression
41856_at	UNC5B	Hs.522997	219699	38.9
219628_at	WIG1	Hs.386299	64393	38.9
221218_s_at	TPK1	Hs.490454	27010	38.9
216936_at	---	---	---	38.9
219557_s_at	NRIP3	Hs.523467	56675	38.9
213448_at	GBA	Hs.511984	2629	38.9
218749_s_at	SLC24A6	Hs.286194	80024	38.9
207185_at	SLC10A1	Hs.952	6554	38.9
215848_at	ZNF291	Hs.458986	49855	38.9
216892_at	IGHG2	Hs.510635	3501	38.9
207400_at	NPY5R	Hs.519058	4889	38.9
210716_s_at	RSN	Hs.524809	6249	38.9
221128_at	ADAM19	Hs.483944	8728	38.9
216622_at	LAMB4	Hs.62022	22798	38.9
213596_at	CASP4	Hs.138378	837	38.9
210702_s_at	PTGIS	Hs.302085	5740	38.9
216456_at	PCDH9	Hs.407643	5101	38.9
210614_at	TTPA	Hs.69049	7274	38.9
213496_at	LPPR4	Hs.13245	9890	38.9
203587_at	ARF4L	Hs.183153	379	38.9
205678_at	AP3B2	Hs.199593	8120	38.9
205764_at	---	---	---	38.9
205620_at	F10	Hs.361463	2159	38.9
221731_x_at	CSPG2	Hs.443681	1462	38.2
216041_x_at	GRN	Hs.514220	2896	38.2
209193_at	PIM1	Hs.81170	5292	38.2
214433_s_at	SELENBP1	---	8991	38.2
211820_x_at	GYPA	Hs.434973	2993	38.2
200001_at	CAPNS1	Hs.515371	826	38.2
202688_at	TNFSF10	Hs.478275	8743	38.2
208892_s_at	DUSP6	Hs.298654	1848	38.2
209500_x_at	TNFSF13 /// TNFSF12-TNFSF13	Hs.54673	407977 /// 8741	38.2
220570_at	RETN	Hs.283091	56729	38.2
212285_s_at	AGRN	Hs.273330	375790	38.2
212120_at	RHOQ	Hs.584872	23433	38.2
204328_at	EVER1	Hs.16165	11322	38.2
212090_at	GRINA	Hs.339697	2907	38.2
209822_s_at	VLDLR	Hs.370422	7436	38.2
211639_x_at	---	Hs.556320	---	38.2
213367_at	LOC155060	Hs.490512	155060	38.2
210237_at	ARTN	Hs.194689	9048	38.2
214551_s_at	CD7	Hs.36972	924	38.2

probe	Gene	Unigene	Locus	% AML cases with overexpression
211918_x_at	PAPPA2	Hs.187284	60676	38.2
212527_at	D15Wsu75e	Hs.570455	27351	38.2
216301_at	---	Hs.449575	---	38.2
210081_at	AGER	Hs.184	177	38.2
212606_at	WDFY3	Hs.480116	23001	38.2
219239_s_at	ZNF654	Hs.27595	55279	38.2
204920_at	CPS1	Hs.149252	1373	38.2
210513_s_at	VEGF	Hs.73793	7422	38.2
206087_x_at	HFE	Hs.233325	3077	38.2
211499_s_at	MAPK11	Hs.57732	5600	38.2
208099_x_at	TTLL5	Hs.200747	23093	38.2
222208_s_at	MGC13098	Hs.584991	84820	38.2
207969_x_at	ACRV1	Hs.169222	56	38.2
203892_at	WFDC2	Hs.2719	10406	38.2
211527_x_at	VEGF	Hs.73793	7422	38.2
211241_at	ANXA2P3	Hs.448622	305	38.2
211333_s_at	FASLG	Hs.2007	356	38.2
209851_at	KIAA0853	Hs.136102	23091	38.2
220957_at	CTAGE1	Hs.406709	64693	38.2
210861_s_at	WISP3	Hs.558428	8838	38.2
222082_at	ZBTB7A	Hs.465623	51341	38.2
211891_s_at	ARHGEF4	Hs.469935	50649	38.2
823_at	CX3CL1	Hs.531668	6376	38.2
210302_s_at	MAB21L2	Hs.584852	10586	38.2
220210_at	CHRNA10	Hs.157714	57053	38.2
215469_at	---	Hs.137567	---	38.2
217744_s_at	PERP	Hs.520421	64065	38.2
50277_at	GGA1	Hs.499158	26088	37.6
205922_at	VNN2	Hs.293130	8875	37.6
46256_at	SPSB3	Hs.7247	90864	37.6
208072_s_at	DGKD	Hs.471675	8527	37.6
202910_s_at	CD97	Hs.466039	976	37.6
209099_x_at	JAG1	Hs.224012	182	37.6
45526_g_at	FLJ14154	Hs.513296	79903	37.6
202363_at	SPOCK	Hs.567340	6695	37.6
39248_at	AQP3	Hs.234642	360	37.6
205568_at	AQP9	Hs.104624	366	37.6
209395_at	CHI3L1	Hs.382202	1116	37.6
221792_at	RAB6B	Hs.12152	51560	37.6
218211_s_at	MLPH	Hs.102406	79083	37.6
209295_at	TNFRSF10B	Hs.521456	8795	37.6
207700_s_at	NCOA3	Hs.382168	8202	37.6
219669_at	CD177	Hs.232165	57126	37.6
207224_s_at	SIGLEC7	Hs.274470	27036	37.6

probe	Gene	Unigene	Locus	% AML cases with overexpression
209164_s_at	CYB561	Hs.355264	1534	37.6
204044_at	QPRT	Hs.513484	23475	37.6
204021_s_at	PURA	Hs.443121	5813	37.6
206580_s_at	EFEMP2	Hs.381870	30008	37.6
213182_x_at	CDKN1C	Hs.106070	1028	37.6
208466_at	RAB3D	Hs.567397	9545	37.6
221555_x_at	CDC14B	Hs.40582	8555	37.6
216432_at	SLC28A2	Hs.367833	9153	37.6
216748_at	PYHIN1	Hs.224645	149628	37.6
203747_at	AQP3	Hs.234642	360	37.6
206934_at	SIRPB1	Hs.134565	10326	37.6
206261_at	ZNF239	Hs.25040	8187	37.6
220284_at	DKKL1	Hs.515855	27120	37.6
214064_at	TF	Hs.518267	7018	37.6
220873_at	REPS2	Hs.186810	9185	37.6
221030_s_at	ARHGAP24	Hs.444229	83478	37.6
221304_at	UGT1A10	---	54575	37.6
213952_s_at	ALOX5	Hs.89499	240	37.6
221347_at	CHRM5	Hs.584747	1133	37.6
215518_at	STXBP5L	Hs.477315	9515	37.6
205943_at	TDO2	Hs.183671	6999	37.6
208281_x_at	DAZ1 /// DAZ3 /// DAZ2 /// DAZ4	Hs.558522	1617 /// 57054 /// 57055 /// 57135	37.6
206801_at	NPPB	Hs.219140	4879	37.6
204895_x_at	MUC4	Hs.369646	4585	37.6
217165_x_at	MT1F	Hs.513626	4494	36.9
201005_at	CD9	Hs.114286	928	36.9
205147_x_at	NCF4	Hs.474781	4689	36.9
205844_at	VNN1	Hs.12114	8876	36.9
218627_at	FLJ11259	Hs.525634	55332	36.9
206120_at	CD33	Hs.83731	945	36.9
212472_at	MICAL2	Hs.501928	9645	36.9
215535_s_at	AGPAT1	Hs.409230	10554	36.9
214370_at	S100A8	Hs.416073	6279	36.9
210854_x_at	SLC6A8	Hs.540696	6535	36.9
217521_at	HAL	Hs.190783	3034	36.9
35626_at	SGSH	Hs.31074	6448	36.9
203559_s_at	ABP1	Hs.521296	26	36.9
211178_s_at	PSTPIP1	Hs.129758	9051	36.9
205566_at	ABHD2	Hs.122337	11057	36.9
205409_at	FOSL2	Hs.568265	2355	36.9
204043_at	TCN2	Hs.417948	6948	36.9
221656_s_at	ARHGEF10L	Hs.443460	55160	36.9

probe	Gene	Unigene	Locus	% AML cases with overexpression
220566_at	PIK3R5	Hs.278901	23533	36.9
206388_at	PDE3A	Hs.386791	5139	36.9
215603_x_at	GGT2	Hs.568255	2679	36.9
40020_at	CELSR3	Hs.533070	1951	36.9
218420_s_at	C13orf23	Hs.318526	80209	36.9
215557_at	SCD5	Hs.379191	79966	36.9
221294_at	GPR21	Hs.368372	2844	36.9
217428_s_at	COL10A1	Hs.520339	1300	36.9
209701_at	ARTS-1	Hs.436186	51752	36.9
204968_at	C6orf47	Hs.247323	57827	36.9
205599_at	TRAF1	Hs.531251	7185	36.9
204138_s_at	ZNF42	Hs.399810	7593	36.9
220783_at	MMP27	Hs.534479	64066	36.9
217683_at	HBE1	Hs.117848	3046	36.9
210058_at	MAPK13	Hs.178695	5603	36.9
211184_s_at	USH1C	Hs.502072	10083	36.9
214233_at	GGA2	Hs.460336	23062	36.9
206684_s_at	ATF7	Hs.12286	11016	36.9
216842_x_at	RBMY1A1 /// RBMY2FP /// RBMY1F /// RBMY1B /// RBMY1D /// RBMY1E /// RBMY1J	Hs.584735	159162 /// 159163 /// 378948 /// 378949 /// 378950 /// 378951 /// 5940	36.9
207663_x_at	GAGE3	---	2575	36.9
214520_at	FOXC2	Hs.558329	2303	36.9
210918_at	---	---	---	36.9
205931_s_at	CREB5	Hs.437075	9586	36.9
216772_at	---	---	---	36.9
209872_s_at	PKP3	Hs.534395	11187	36.9
217537_x_at	---	---	---	36.9
219115_s_at	IL20RA	Hs.445868	53832	36.9
211638_at	---	Hs.383169	---	36.9
217748_at	ADIPOR1	Hs.5298	51094	36.3
203547_at	CD4	Hs.17483	920	36.3
214875_x_at	APLP2	Hs.370247	334	36.3
208890_s_at	PLXNB2	Hs.3989	23654	36.3
202191_s_at	GAS7	Hs.462214	8522	36.3
200623_s_at	CALM3	Hs.515487	808	36.3
209179_s_at	LENG4	Hs.467279	79143	36.3
211719_x_at	FN1	Hs.203717	2335	36.3
36030_at	HOM-TES-103	Hs.15243	25900	36.3
204046_at	PLCB2	Hs.355888	5330	36.3
213607_x_at	NADK	Hs.456572	65220	36.3

probe	Gene	Unigene	Locus	% AML cases with overexpression
202650_s_at	KIAA0195	Hs.514474	9772	36.3
204914_s_at	SOX11	Hs.432638	6664	36.3
204970_s_at	MAFG	Hs.252229	4097	36.3
202761_s_at	SYNE2	Hs.525392	23224	36.3
205804_s_at	TRAF3IP3	Hs.147434	80342	36.3
32502_at	GDPD5	Hs.503297	81544	36.3
208917_x_at	NADK	Hs.456572	65220	36.3
209947_at	UBAP2L	Hs.490551	9898	36.3
202572_s_at	DLGAP4	Hs.249600	22839	36.3
215909_x_at	MINK1	Hs.443417	50488	36.3
218441_s_at	RPAP1	Hs.371045	26015	36.3
211391_s_at	ZNF278	Hs.517557	23598	36.3
206313_at	HLA-DOA	Hs.351874	3111	36.3
219722_s_at	GDPD3	Hs.289015	79153	36.3
205744_at	DOC2A	Hs.355281	8448	36.3
210247_at	SYN2	Hs.445503	6854	36.3
211726_s_at	FMO2	Hs.567271	2327	36.3
208237_x_at	ADAM22	Hs.256398	53616	36.3
209738_x_at	PSG6	Hs.466849	5675	36.3
220135_s_at	SLC7A9	Hs.408567	11136	36.3
204400_at	EFS	Hs.24587	10278	36.3
208076_at	HIST1H4D	Hs.248179	8360	36.3
207764_s_at	HIPK3	Hs.201918	10114	36.3
203963_at	CA12	Hs.210995	771	36.3
206002_at	GPR64	Hs.146978	10149	36.3
216086_at	SV2C	Hs.570933	22987	36.3
201105_at	LGALS1	Hs.445351	3956	35.7
200871_s_at	PSAP	Hs.523004	5660	35.7
205237_at	FCN1	Hs.440898	2219	35.7
219191_s_at	BIN2	Hs.14770	51411	35.7
205987_at	CD1C	Hs.1311	911	35.7
211697_x_at	LOC56902	Hs.262858	56902	35.7
205529_s_at	RUNX1T1	Hs.368431	862	35.7
218231_at	NAGK	Hs.7036	55577	35.7
212890_at	MGC15523	Hs.352240	124565	35.7
218251_at	MID1IP1	Hs.522605	58526	35.7
202284_s_at	CDKN1A	Hs.370771	1026	35.7
214032_at	ZAP70	Hs.234569	7535	35.7
213046_at	PABPN1	Hs.117176	8106	35.7
206135_at	ST18	Hs.147170	9705	35.7
213521_at	PTPN18	Hs.516390	26469	35.7
219414_at	CLSTN2	Hs.158529	64084	35.7
212171_x_at	VEGF	Hs.73793	7422	35.7
36019_at	STK19	Hs.485102	8859	35.7

probe	Gene	Unigene	Locus	% AML cases with overexpression
205059_s_at	IDUA	Hs.89560	3425	35.7
204194_at	BACH1	Hs.154276	571	35.7
205021_s_at	CHES1	Hs.567246	1112	35.7
37278_at	TAZ	Hs.409911	6901	35.7
202565_s_at	SVIL	Hs.499209	6840	35.7
205552_s_at	OAS1	Hs.524760	4938	35.7
221155_x_at	SLC25A37	Hs.122514	51312	35.7
206850_at	RRP22	Hs.73088	10633	35.7
218963_s_at	KRT23	Hs.9029	25984	35.7
212319_at	RUTBC1	Hs.513861	9905	35.7
220390_at	AGBL2	Hs.147377	79841	35.7
202928_s_at	PHF1	Hs.166204	5252	35.7
216735_x_at	HRH1	Hs.1570	3269	35.7
202509_s_at	TNFAIP2	Hs.525607	7127	35.7
207859_s_at	CHRNB3	Hs.96094	1142	35.7
214275_at	MED12	Hs.409226	9968	35.7
214293_at	SEPT11	Hs.128199	55752	35.7
218584_at	FLJ21127	Hs.211511	79600	35.7
217102_at	MAG	Hs.348346	27307	35.7
206878_at	DAO	Hs.113227	1610	35.7
215189_at	KRTHB6	Hs.278658	3892	35.7
221658_s_at	IL21R	Hs.210546	50615	35.7
205463_s_at	PDGFA	Hs.376032	5154	35.7
217375_at	---	---	---	35.7
210584_s_at	POLDIP3 /// dJ222E13.2	Hs.387850	84271 /// 91695	35.7
220519_s_at	LIM2	Hs.162754	3982	35.7
216437_at	EPC1	Hs.167805	80314	35.7
207064_s_at	AOC2	Hs.143102	314	35.7
217415_at	POLR2A	Hs.270017	5430	35.7
207214_at	SPINK4	Hs.555934	27290	35.7
206194_at	HOXC4 /// FLJ12825	Hs.350378	3221 /// 440101	35.7
220705_s_at	ADAMTS7	Hs.16441	11173	35.7
214229_at	DNAH17	Hs.464217	8632	35.7
215829_at	SHANK2	Hs.268726	22941	35.7
217270_s_at	DYRK1B	Hs.130988	9149	35.7
204129_at	BCL9	Hs.415209	607	35.7
206566_at	SLC7A1	Hs.14846	6541	35.7
208581_x_at	MT1X	Hs.374950	4501	35.0
204232_at	FCER1G	Hs.433300	2207	35.0
203591_s_at	CSF3R	Hs.524517	1441	35.0
217977_at	SEPX1	Hs.279623	51734	35.0
214084_x_at	NCF1	Hs.559477	4687	35.0

probe	Gene	Unigene	Locus	% AML cases with overexpression
204924_at	TLR2	Hs.519033	7097	35.0
211133_x_at	LILRB2 /// LILRB3	Hs.534386	10288 /// 11025	35.0
213065_at	MGC23401	Hs.527874	196441	35.0
207857_at	LILRA2	Hs.534394	11027	35.0
201364_s_at	OAZ2	Hs.74563	4947	35.0
205837_s_at	GYPA	Hs.434973	2993	35.0
220956_s_at	EGLN2	Hs.515417	112398	35.0
33322_i_at	SFN	Hs.523718	2810	35.0
211207_s_at	ACSL6	Hs.14945	23305	35.0
213326_at	VAMP1	Hs.20021	6843	35.0
209727_at	GM2A	Hs.483873	2760	35.0
203610_s_at	TRIM38	Hs.584851	10475	35.0
208106_x_at	PSG6	Hs.466849	5675	35.0
211295_x_at	CYP2A6	Hs.439056	1548	35.0
208437_at	CLCN1	Hs.121483	1180	35.0
221170_at	HRH4	Hs.287388	59340	35.0
215019_x_at	ZNF528	Hs.531612	84436	35.0
219509_at	MYOZ1	Hs.238756	58529	35.0
203458_at	SPR	Hs.301540	6697	35.0
204368_at	SLCO2A1	Hs.518270	6578	35.0
217147_s_at	TRAT1	Hs.138701	50852	35.0
211332_x_at	HFE	Hs.233325	3077	35.0
214443_at	PVR	Hs.171844	5817	35.0
204051_s_at	SFRP4	Hs.105700	6424	35.0
220853_at	GTDC1	Hs.44780	79712	35.0
210799_at	HTR1B	Hs.123016	3351	35.0
212853_at	DCUN1D4	Hs.221407	23142	35.0
210323_at	TEKT2	Hs.127111	27285	35.0
217060_at	---	Hs.521251	---	35.0
206916_x_at	TAT	Hs.161640	6898	35.0
210345_s_at	DNAH9	Hs.567259	1770	35.0
36499_at	CELSR2	Hs.57652	1952	35.0
215562_at	C1orf34	Hs.112949	22996	35.0
206280_at	CDH18	Hs.317632	1016	35.0
204509_at	CA12	Hs.210995	771	35.0
217360_x_at	IGHA1 /// IGHG1 /// IGHG3 /// MGC27165	Hs.584764	283650 /// 3493 /// 3500 /// 3502	35.0
213169_at	---	Hs.27621	---	35.0
203477_at	COL15A1	Hs.409034	1306	35.0
206165_s_at	CLCA2	Hs.241551	9635	35.0
201510_at	ELF3	Hs.67928	1999	35.0

probe	Gene	Unigene	Locus	% AML cases with overexpression
202935_s_at	SOX9	Hs.2316	6662	35.0
204688_at	SGCE	Hs.371199	8910	35.0
204471_at	GAP43	Hs.134974	2596	35.0
206482_at	PTK6	Hs.51133	5753	35.0
212843_at	NCAM1	Hs.503878	4684	34.4
206687_s_at	PTPN6	Hs.63489	5777	34.4
220088_at	C5R1	Hs.2161	728	34.4
220532_s_at	LR8	Hs.521295	28959	34.4
203615_x_at	SULT1A1	Hs.567342	6817	34.4
215047_at	TRIM58	Hs.323858	25893	34.4
221920_s_at	SLC25A37	Hs.122514	51312	34.4
38671_at	PLXND1	Hs.301685	23129	34.4
221698_s_at	CLEC7A	Hs.143929	64581	34.4
209696_at	FBP1	Hs.494496	2203	34.4
218876_at	CGI-38	Hs.534458	51673	34.4
203718_at	NTE	Hs.511760	10908	34.4
218507_at	HIG2	Hs.521171	29923	34.4
203206_at	FAM53B	Hs.129195	9679	34.4
57715_at	FAM26B	Hs.241545	51063	34.4
211610_at	KLF6	Hs.4055	1316	34.4
209582_s_at	CD200	Hs.79015	4345	34.4
211620_x_at	RUNX1	Hs.149261	861	34.4
210129_s_at	TTLL3	Hs.567445	26140	34.4
218655_s_at	FLJ20291	Hs.406223	54883	34.4
214535_s_at	ADAMTS2	Hs.23871	9509	34.4
219897_at	RNF122	Hs.151237	79845	34.4
206590_x_at	DRD2	Hs.73893	1813	34.4
215771_x_at	RET	Hs.350321	5979	34.4
220167_s_at	TP53TG3	Hs.370561	24150	34.4
214923_at	ATP6V1D	Hs.272630	51382	34.4
205058_at	SLC26A1	Hs.584858	10861	34.4
220363_s_at	ELMO2	Hs.210469	63916	34.4
209086_x_at	MCAM	Hs.511397	4162	34.4
217654_at	CFLAR	Hs.390736	8837	34.4
214969_at	MAP3K9	Hs.445496	4293	34.4
214650_x_at	MOG	Hs.141308	4340	34.4
211647_x_at	IGHM	Hs.538461	3507	34.4
212845_at	SAMD4	Hs.98259	23034	34.4
201159_s_at	NMT1	Hs.532790	4836	34.4
207394_at	ZNF137	Hs.373648	7696	34.4
203942_s_at	MARK2	Hs.567261	2011	34.4
220406_at	TGFB2	Hs.133379	7042	34.4
207052_at	HAVCR1	Hs.129711	26762	34.4
214618_at	CFLAR	Hs.390736	8837	34.4

probe	Gene	Unigene	Locus	% AML cases with overexpression
215430_at	GK2	Hs.98008	2712	34.4
210704_at	FEZ2	Hs.258563	9637	34.4
209116_x_at	HBB	Hs.523443	3043	33.8
217232_x_at	HBB	Hs.523443	3043	33.8
201590_x_at	ANXA2	Hs.511605	302	33.8
206676_at	CEACAM8	Hs.41	1088	33.8
208690_s_at	PDLIM1	Hs.368525	9124	33.8
212560_at	C11orf32	---	442871	33.8
202759_s_at	PALM2-AKAP2	Hs.259461	445815	33.8
218559_s_at	MAFB	Hs.169487	9935	33.8
202241_at	TRIB1	Hs.444947	10221	33.8
201040_at	GNAI2	Hs.77269	2771	33.8
212307_s_at	OGT	Hs.405410	8473	33.8
203185_at	RASSF2	Hs.379970	9770	33.8
202805_s_at	ABCC1	Hs.391464	4363	33.8
202242_at	TSPAN7	Hs.441664	7102	33.8
34206_at	CENTD2	Hs.503165	116985	33.8
210069_at	CHKB /// CPT1B	Hs.439777	1120 /// 1375	33.8
213784_at	RABL4	Hs.415172	11020	33.8
213338_at	RIS1	Hs.35861	25907	33.8
205660_at	OASL	Hs.118633	8638	33.8
212344_at	SULF1	Hs.409602	23213	33.8
34221_at	KIAA0194	Hs.586219	22993	33.8
212521_s_at	PDE8A	Hs.9333	5151	33.8
221205_at	---	---	---	33.8
217041_at	NPTXR	Hs.91622	23467	33.8
221010_s_at	SIRT5	Hs.567431	23408	33.8
203461_at	CHD2	Hs.220864	1106	33.8
208493_at	HOXA11	Hs.249171	3207	33.8
213307_at	SHANK2	Hs.268726	22941	33.8
208379_x_at	NPY2R	Hs.37125	4887	33.8
214468_at	MYH6	Hs.278432	4624	33.8
205388_at	TNNC2	Hs.182421	7125	33.8
50221_at	TFEB	Hs.485360	7942	33.8
211876_x_at	PCDHGA12 /// PCDHGA11 /// PCDHGA10 /// PCDHGA6 /// PCDHGA5 /// PCDHGA3	---	26025 /// 56105 /// 56106 /// 56109 /// 56110 /// 56112	33.8
213744_at	ATRNL1	Hs.501127	26033	33.8
207351_s_at	SH2D2A	Hs.103527	9047	33.8
207642_at	HCRT	Hs.158348	3060	33.8
207096_at	SAA4	Hs.512677	6291	33.8

probe	Gene	Unigene	Locus	% AML cases with overexpression
213807_x_at	MET	Hs.132966	4233	33.8
216219_at	AQP6	Hs.54505	363	33.8
210991_s_at	RIMS3	Hs.434924	9783	33.8
213498_at	CREB3L1	Hs.405961	90993	33.8
214598_at	CLDN8	Hs.162209	9073	33.8
211019_s_at	LSS	Hs.517366	4047	33.8
221321_s_at	KCNIP2	Hs.97044	30819	33.8
204845_s_at	ENPEP	Hs.435765	2028	33.8
208394_x_at	ESM1	Hs.129944	11082	33.8
206007_at	PRG4	Hs.432458	10216	33.8
217460_at	TNP2	Hs.513349	7142	33.8
210427_x_at	ANXA2	Hs.511605	302	33.1
218454_at	FLJ22662	Hs.131933	79887	33.1
209604_s_at	GATA3	Hs.524134	2625	33.1
218217_at	SCPEP1	Hs.514950	59342	33.1
210817_s_at	NDP52	Hs.514920	10241	33.1
204787_at	VSIG4	Hs.8904	11326	33.1
204505_s_at	EPB49	Hs.106124	2039	33.1
204912_at	IL10RA	Hs.504035	3587	33.1
221257_x_at	FBXO38	Hs.483772	81545	33.1
217743_s_at	TMEM30A	Hs.108530	55754	33.1
207651_at	GPR171	Hs.549152	29909	33.1
205076_s_at	MTMR11	Hs.425144	10903	33.1
203549_s_at	LPL	Hs.180878	4023	33.1
202869_at	OAS1	Hs.524760	4938	33.1
206522_at	MGAM	Hs.122785	8972	33.1
217184_s_at	LTK	Hs.434481	4058	33.1
211004_s_at	ALDH3B1	Hs.523841	221	33.1
64440_at	IL17RC	Hs.129959	84818	33.1
204626_s_at	ITGB3	Hs.218040	3690	33.1
219444_at	BCORL1	Hs.496748	63035	33.1
201282_at	OGDH	Hs.488181	4967	33.1
201299_s_at	MOBK1B	Hs.196437	55233	33.1
216388_s_at	LTB4R	Hs.567248	1241	33.1
219308_s_at	AK5	Hs.559718	26289	33.1
202609_at	EPS8	Hs.316997	2059	33.1
201579_at	FAT	Hs.481371	2195	33.1
205685_at	CD86	Hs.171182	942	33.1
204713_s_at	F5	Hs.30054	2153	33.1
211330_s_at	HFE	Hs.233325	3077	33.1
207813_s_at	FDXR	Hs.69745	2232	33.1
44822_s_at	KIAA1193	Hs.101891	54531	33.1
219707_at	CPNE7	Hs.461775	27132	33.1
214647_s_at	HFE	Hs.233325	3077	33.1

probe	Gene	Unigene	Locus	% AML cases with overexpression
209660_at	TTR	Hs.427202	7276	33.1
219883_at	KCNK4	Hs.97174	50801	33.1
218234_at	ING4	Hs.524210	51147	33.1
212960_at	KIAA0882	Hs.480819	23158	33.1
211789_s_at	MONDOA	Hs.437153	22877	33.1
221460_at	OR2C1	Hs.258574	4993	33.1
203910_at	ARHGAP29	Hs.483238	9411	33.1
209758_s_at	MFAP5	Hs.512842	8076	33.1
221828_s_at	C9orf28	Hs.162659	89853	33.1
207506_at	TXNL2	Hs.42644	10539	33.1
219745_at	C10orf77	Hs.309069	79847	33.1
202920_at	ANK2	Hs.567235	287	33.1
214967_at	---	---	---	33.1
215476_at	---	Hs.159157	---	33.1
221033_s_at	RNF17	Hs.333271	56163	33.1
209866_s_at	LPHN3	Hs.411097	23284	33.1
208235_x_at	GAGE7	---	2579	33.1
220887_at	C14orf162	Hs.458319	56936	33.1
216049_at	RHOBTB3	Hs.445030	22836	33.1
207500_at	CASP5	Hs.213327	838	33.1
215226_at	EXPH5	Hs.269591	23086	33.1
222167_at	---	Hs.573405	---	33.1
217026_at	CFTR	Hs.489786	1080	33.1
222075_s_at	OAZ3	Hs.144439	51686	33.1

Table 3.Genes under-expressed in AML

probe	Gene	Unigene	Locus	%AML cases with underexpression
203893_at	TAF9	Hs.248941	6880	99.4
210666_at	IDS	Hs.460960	3423	98.7
217591_at	SKIL	Hs.536655	6498	96.8
201131_s_at	CDH1	Hs.461086	999	95.5
221772_s_at	PPP2R2D	Hs.380372	55844	94.3
212224_at	ALDH1A1	Hs.76392	216	94.3
204416_x_at	APOC1	Hs.110675	341	93.6
219355_at	FLJ10178	Hs.274267	55086	93.6
210281_s_at	ZNF198	Hs.507433	7750	93.0
217975_at	WBP5	Hs.533287	51186	93.0
205830_at	CLGN	Hs.86368	1047	93.0
205239_at	AREG	Hs.270833	374	92.4
202600_s_at	NRIP1	Hs.155017	8204	92.4
203789_s_at	SEMA3C	Hs.269109	10512	92.4

probe	Gene	Unigene	Locus	%AML cases with underexpression
213553_x_at	APOC1	Hs.110675	341	91.7
209739_s_at	PNPLA4	Hs.264	8228	91.7
205767_at	EREG	Hs.115263	2069	91.7
202591_s_at	SSBP1	Hs.490394	6742	91.1
204749_at	NAP1L3	Hs.21365	4675	91.1
210054_at	C4orf15	Hs.584969	79441	90.4
209932_s_at	DUT	Hs.527980	1854	89.8
201323_at	EBNA1BP2	Hs.346868	10969	89.8
36711_at	MAFF	Hs.517617	23764	89.8
210313_at	LILRA4	Hs.406708	23547	89.8
209337_at	PSIP1	Hs.493516	11168	88.5
209507_at	RPA3	Hs.487540	6119	88.5
201465_s_at	JUN	Hs.525704	3725	88.5
206683_at	ZNF165	Hs.55481	7718	88.5
203613_s_at	NDUFB6	Hs.493668	4712	87.9
212151_at	PBX1	Hs.493096	5087	87.9
212372_at	MYH10	Hs.16355	4628	87.3
221894_at	ADCK2	Hs.534141	90956	87.3
205429_s_at	MPP6	Hs.533355	51678	87.3
208970_s_at	UROD	Hs.78601	7389	86.6
209226_s_at	TNPO1	Hs.482497	3842	86.6
203496_s_at	PPARBP	Hs.462956	5469	86.6
209524_at	HDGFRP3	Hs.513954	50810	86.6
216834_at	RGS1	Hs.75256	5996	86.6
202620_s_at	PLOD2	Hs.477866	5352	86.6
202949_s_at	FHL2	Hs.443687	2274	86.0
219855_at	NUDT11	Hs.200016	55190	86.0
208612_at	PDIA3	Hs.308709	2923	85.4
220741_s_at	PPA2	Hs.480452	27068	85.4
201138_s_at	SSB	Hs.546301	6741	85.4
205164_at	GCAT	Hs.54609	23464	85.4
217901_at	DSG2	Hs.412597	1829	85.4
202766_s_at	FBN1	Hs.146447	2200	85.4
213506_at	F2RL1	Hs.154299	2150	85.4
215691_x_at	C1orf41	Hs.525462	51668	84.7
202858_at	U2AF1	Hs.365116	7307	84.7
204616_at	UCHL3	Hs.162241	7347	84.7
203753_at	TCF4	Hs.200285	6925	84.7
208580_x_at	HIST1H4K /// HIST1H4J	Hs.278483	8362	84.7
203917_at	CXADR	Hs.473417	1525	84.7
210986_s_at	TPM1	Hs.133892	7168	84.7
213129_s_at	GCSH	Hs.546256	2653	84.1
218671_s_at	ATPIF1	Hs.241336	93974	83.4
218493_at	C16orf33	Hs.15277	79622	83.4

probe	Gene	Unigene	Locus	%AML cases with underexpression
212282_at	MAC30	Hs.199695	27346	83.4
204142_at	ENOSF1	Hs.584931	55556	83.4
211148_s_at	ANGPT2	Hs.553484	285	83.4
200748_s_at	FTH1	Hs.524910	2495	82.8
201202_at	PCNA	Hs.147433	5111	82.8
205345_at	BARD1	Hs.54089	580	82.8
205262_at	KCNH2	Hs.188021	3757	82.8
204720_s_at	DNAJC6	Hs.584843	9829	82.8
201586_s_at	SFPQ	Hs.355934	6421	82.2
39729_at	PRDX2	Hs.432121	7001	82.2
206494_s_at	ITGA2B	Hs.411312	3674	82.2
215908_at	MARCH6	Hs.432862	10299	82.2
216956_s_at	ITGA2B	Hs.411312	3674	82.2
204004_at	PAWR	Hs.406074	5074	82.2
210215_at	TFR2	Hs.544932	7036	81.5
202555_s_at	MYLK	Hs.477375	4638	81.5
203628_at	IGF1R	Hs.20573	3480	81.5
220418_at	UBASH3A	Hs.473912	53347	81.5
218883_s_at	MLF1IP	Hs.481307	79682	80.9
211569_s_at	HADHSC	Hs.438289	3033	80.9
202691_at	SNRPD1	Hs.464734	6632	80.9
206493_at	ITGA2B	Hs.411312	3674	80.9
208029_s_at	LAPTM4B	Hs.492314	55353	80.9
220085_at	HELLS	Hs.463677	3070	80.9
221606_s_at	NSBP1	Hs.282204	79366	80.9
211784_s_at	SFRS1	Hs.68714	6426	80.3
217802_s_at	NUCKS1	Hs.213061	64710	80.3
206207_at	CLC	Hs.889	1178	80.3
221884_at	EVI1	Hs.165830	2122	80.3
201839_s_at	TACSTD1	Hs.692	4072	80.3
202890_at	MAP7	Hs.486548	9053	80.3
202988_s_at	RGS1	Hs.75256	5996	80.3
206770_s_at	SLC35A3	Hs.567432	23443	79.6
201690_s_at	TPD52	Hs.368433	7163	79.6
221496_s_at	TOB2	Hs.474978	10766	79.6
203680_at	PRKAR2B	Hs.433068	5577	79.6
204753_s_at	HLF	Hs.196952	3131	79.6
211734_s_at	FCER1A	Hs.897	2205	79.6
203138_at	HAT1	Hs.470611	8520	79.0
211074_at	LOC441762	Hs.532675	441762	79.0
214039_s_at	LAPTM4B	Hs.492314	55353	79.0
203856_at	VRK1	Hs.422662	7443	79.0
203815_at	GSTT1	Hs.268573	2952	79.0
204775_at	CHAF1B	Hs.75238	8208	79.0
211700_s_at	TRO	Hs.434971	7216	79.0

probe	Gene	Unigene	Locus	%AML cases with underexpression
222258_s_at	SH3BP4	Hs.516777	23677	79.0
208638_at	PDIA6	Hs.212102	10130	78.3
200612_s_at	AP2B1	Hs.514819	163	78.3
216449_x_at	TRA1	Hs.192374	7184	78.3
221270_s_at	QTRT1	Hs.323084	81890	78.3
218894_s_at	FLJ10292	Hs.104650	55110	78.3
214682_at	PKD1 /// NPIP /// LOC339047 /// LOC399491	Hs.546868	339047	78.3
222078_at	HCN3	Hs.284171	57657	78.3
209388_at	PAPOLA	Hs.253726	10914	77.7
202340_x_at	NR4A1	Hs.524430	3164	77.7
220377_at	C14orf110	Hs.395486	29064	77.7
219550_at	ROBO3	Hs.435621	64221	77.7
205691_at	SYNGR3	Hs.435277	9143	77.7
202839_s_at	NDUFB7	Hs.532853	4713	77.1
201599_at	OAT	Hs.523332	4942	77.1
221777_at	FLJ14827	Hs.524762	84934	77.1
212382_at	TCF4	Hs.200285	6925	77.1
206023_at	NMU	Hs.418367	10874	77.1
220520_s_at	FLJ20130	Hs.163629	54830	77.1
202393_s_at	KLF10	Hs.435001	7071	76.4
204071_s_at	TOPORS	Hs.535961	10210	76.4
207895_at	NAALADL1	Hs.13967	10004	76.4
217617_at	PBX1	Hs.493096	5087	76.4
218885_s_at	GALNT12	Hs.47099	79695	76.4
215164_at	TCF4	Hs.200285	6925	76.4
215203_at	GOLGA4	Hs.344151	2803	75.8
212386_at	TCF4	Hs.200285	6925	75.8
219555_s_at	BM039	Hs.584937	55839	75.8
212291_at	HIPK1	Hs.532363	204851	75.8
214295_at	KIAA0485	---	57235	75.8
203465_at	MRPL19	Hs.44024	9801	75.8
210612_s_at	SYNJ2	Hs.434494	8871	75.8
207469_s_at	PIR	Hs.495728	8544	75.8
201215_at	PLS3	Hs.496622	5358	75.8
207335_x_at	ATP5I	Hs.85539	521	75.2
209267_s_at	SLC39A8	Hs.288034	64116	75.2
205176_s_at	ITGB3BP	Hs.166539	23421	75.2
203099_s_at	CDYL	Hs.269092	9425	75.2
203565_s_at	MNAT1	Hs.509523	4331	75.2
211743_s_at	PRG2	Hs.512633	5553	75.2
201291_s_at	TOP2A	Hs.156346	7153	75.2
219201_s_at	TWSG1	Hs.514685	57045	75.2
214829_at	AASS	Hs.433075	10157	75.2

probe	Gene	Unigene	Locus	%AML cases with underexpression
205967_at	HIST1H4C	Hs.46423	8364	74.5
221021_s_at	CTNNBL1	Hs.472667	56259	74.5
205159_at	CSF2RB	Hs.285401	1439	74.5
218741_at	C22orf18	Hs.208912	79019	74.5
213693_s_at	MUC1	Hs.89603	4582	74.5
210387_at	HIST1H2BG	Hs.240135	8339	74.5
203497_at	PPARBP	Hs.462956	5469	73.9
201369_s_at	ZFP36L2	Hs.503093	678	73.9
217408_at	MRPS18B	Hs.274417	28973	73.9
203347_s_at	MTF2	Hs.31016	22823	73.9
202889_x_at	MAP7	Hs.486548	9053	73.9
215296_at	CDC42BPA	Hs.35433	8476	73.9
213415_at	CLIC2	Hs.54570	1193	73.9
213092_x_at	DNAJC9	Hs.59125	23234	73.2
212190_at	SERPINE2	Hs.38449	5270	73.2
202840_at	TAF15	Hs.402752	8148	73.2
211828_s_at	TNIK	Hs.34024	23043	73.2
203577_at	GTF2H4	Hs.485070	2968	73.2
214043_at	PTPRD	Hs.567325	5789	73.2
207332_s_at	TFRC	Hs.529618	7037	72.6
212855_at	DCUN1D4	Hs.221407	23142	72.6
211596_s_at	LRIG1	Hs.518055	26018	72.6
209167_at	GPM6B	Hs.495710	2824	72.6
205706_s_at	ANKRD26	Hs.361041	22852	72.6
212281_s_at	MAC30	Hs.199695	27346	72.0
209526_s_at	HDGFRP3	Hs.513954	50810	72.0
206116_s_at	TPM1	Hs.133892	7168	72.0
218320_s_at	NDUFB11	Hs.521969	54539	71.3
215380_s_at	C7orf24	Hs.530024	79017	71.3
209790_s_at	CASP6	Hs.3280	839	71.3
219598_s_at	RWDD1	Hs.532164	51389	71.3
216060_s_at	DAAM1	Hs.19156	23002	71.3
203764_at	DLG7	Hs.77695	9787	71.3
203382_s_at	APOE	Hs.515465	348	71.3
203381_s_at	APOE	Hs.515465	348	71.3
214769_at	CLCN4	Hs.495674	1183	71.3
206693_at	IL7	Hs.536926	3574	71.3
214464_at	CDC42BPA	Hs.35433	8476	71.3
203543_s_at	KLF9	Hs.150557	687	71.3
200647_x_at	EIF3S8	Hs.567374	8663	70.7
202887_s_at	DDIT4	Hs.523012	54541	70.7
201904_s_at	CTDSPL	Hs.475963	10217	70.7
203203_s_at	HRB2	Hs.584861	11103	70.7
208576_s_at	HIST1H3B	Hs.533292	8358	70.7
219479_at	KDELC1	Hs.408629	79070	70.7

probe	Gene	Unigene	Locus	%AML cases with underexpression
213241_at	PLXNC1	Hs.584845	10154	70.1
215785_s_at	CYFIP2	Hs.519702	26999	70.1
206310_at	SPINK2	Hs.98243	6691	70.1
204126_s_at	CDC45L	Hs.474217	8318	70.1
221406_s_at	MSH5	Hs.371225	4439	70.1
210487_at	DNTT	Hs.534206	1791	70.1
201242_s_at	ATP1B1	Hs.291196	481	70.1
215096_s_at	ESD	Hs.432491	2098	69.4
202557_at	STCH	Hs.352341	6782	69.4
210802_s_at	HSA9761	Hs.533222	27292	69.4
210180_s_at	SFRS10	Hs.533122	6434	69.4
218694_at	ARMCX1	Hs.9728	51309	69.4
203708_at	PDE4B	Hs.198072	5142	69.4
212148_at	PBX1	Hs.493096	5087	69.4
201905_s_at	CTDSPL	Hs.475963	10217	69.4
217593_at	ZNF447	Hs.235390	65982	69.4
204755_x_at	HLF	Hs.196952	3131	69.4
209160_at	AKR1C3	Hs.78183	8644	69.4
205390_s_at	ANK1	Hs.491558	286	68.8
218816_at	LRRC1	Hs.485581	55227	68.8
209493_at	PDZK3	Hs.481819	23037	68.8
201689_s_at	TPD52	Hs.368433	7163	68.8
213954_at	KIAA0888	Hs.91662	26049	68.8
214943_s_at	RBM34	Hs.535224	23029	68.8
215230_x_at	EIF3S8	Hs.567374	8663	68.2
205644_s_at	SNRPG	Hs.6454	6637	68.2
202427_s_at	BRP44	Hs.517768	25874	68.2
201014_s_at	PAICS	Hs.518774	10606	68.2
218585_s_at	DTL	Hs.126774	51514	68.2
214316_x_at	CALR	Hs.515162	811	68.2
206306_at	RYR3	Hs.369250	6263	68.2
203352_at	ORC4L	Hs.558364	5000	68.2
212062_at	ATP9A	Hs.368002	10079	68.2
209994_s_at	ABCB1 /// ABCB4	Hs.489033	5243	68.2
203053_at	BCAS2	Hs.22960	10286	67.5
202705_at	CCNB2	Hs.194698	9133	67.5
202388_at	RGS2	Hs.78944	5997	67.5
203209_at	RFC5	Hs.506989	5985	67.5
208657_s_at	SEPT9	Hs.440932	10801	67.5
213668_s_at	SOX4	Hs.357901	6659	67.5
221349_at	VPREB1	Hs.247979	7441	67.5
207120_at	ZNF667	Hs.433473	63934	67.5
208767_s_at	LAPTM4B	Hs.492314	55353	66.9
205677_s_at	DLEU1	Hs.584850	10301	66.9

probe	Gene	Unigene	Locus	%AML cases with underexpression
205178_s_at	RBBP6	Hs.188553	5930	66.9
203448_s_at	TERF1	Hs.584810	7013	66.9
202942_at	ETFB	Hs.74047	2109	66.9
213896_x_at	KIAA0974	Hs.408577	317662	66.9
216620_s_at	ARHGEF10	Hs.98594	9639	66.9
208790_s_at	PTRF	Hs.437191	284119	66.9
204709_s_at	KIF23	Hs.270845	9493	66.9
222313_at	CNOT2	Hs.133350	4848	66.9
207781_s_at	ZNF6	Hs.326801	7552	66.9
218194_at	REXO2	Hs.7527	25996	66.2
218611_at	IER5	Hs.15725	51278	66.2
210504_at	KLF1	Hs.37860	10661	66.2
221896_s_at	HIGD1A	Hs.7917	25994	66.2
213891_s_at	TCF4	Hs.200285	6925	66.2
217963_s_at	NGFRAP1	Hs.448588	27018	66.2
206660_at	IGLL1	Hs.348935	3543	66.2
208789_at	PTRF	Hs.437191	284119	66.2
219237_s_at	DNAJB14	Hs.512743	79982	66.2
203294_s_at	LMAN1	Hs.465295	3998	66.2
219790_s_at	NPR3	Hs.237028	4883	66.2
201466_s_at	JUN	Hs.525704	3725	66.2
204621_s_at	NR4A2	Hs.165258	4929	66.2
207871_s_at	ST7	Hs.368131	7982	66.2
202619_s_at	PLOD2	Hs.477866	5352	66.2
215474_at	MGC39581	Hs.130177	257062	66.2
212952_at	CALR	Hs.515162	811	65.6
206283_s_at	TAL1	Hs.73828	6886	65.6
204057_at	IRF8	Hs.137427	3394	65.6
205909_at	POLE2	Hs.162777	5427	65.6
212385_at	TCF4	Hs.200285	6925	65.6
41577_at	PPP1R16B	Hs.45719	26051	65.6
206470_at	PLXNC1	Hs.584845	10154	65.6
200985_s_at	CD59	Hs.278573	966	65.6
213684_s_at	PDLIM5	Hs.480311	10611	65.6
202503_s_at	KIAA0101	Hs.81892	9768	65.0
222103_at	ATF1	Hs.435267	466	65.0
201890_at	RRM2	Hs.226390	6241	65.0
207655_s_at	BLNK	Hs.444049	29760	65.0
205624_at	CPA3	Hs.646	1359	65.0
213758_at	COX4I1	Hs.433419	1327	65.0
201602_s_at	PPP1R12A	Hs.49582	4659	65.0
221024_s_at	SLC2A10	Hs.305971	81031	65.0
202882_x_at	NOL7	Hs.549161	51406	64.3
201274_at	PSMA5	Hs.485246	5686	64.3
218350_s_at	GMNN	Hs.234896	51053	64.3

probe	Gene	Unigene	Locus	%AML cases with underexpression
213229_at	DICER1	Hs.87889	23405	64.3
214710_s_at	CCNB1	Hs.23960	891	64.3
219819_s_at	MRPS28	Hs.521124	28957	64.3
201043_s_at	ANP32A	Hs.458747	8125	64.3
204441_s_at	POLA2	Hs.201897	23649	64.3
207883_s_at	TFR2	Hs.544932	7036	64.3
206702_at	TEK	Hs.89640	7010	64.3
200891_s_at	SSR1	Hs.114033	6745	63.7
208971_at	UROD	Hs.78601	7389	63.7
214214_s_at	C1QBP	Hs.555866	708	63.7
208078_s_at	SNF1LK	Hs.282113	150094	63.7
219311_at	C18orf9	Hs.236940	79959	63.7
214623_at	SHFM3P1	---	26226	63.7
209170_s_at	GPM6B	Hs.495710	2824	63.7
220900_at	FLJ12078	Hs.584973	80042	63.7
219117_s_at	FKBP11	Hs.438695	51303	63.1
219551_at	EAF2	Hs.477325	55840	63.1
218762_at	ZNF574	Hs.13323	64763	63.1
215471_s_at	MAP7	Hs.486548	9053	63.1
213549_at	SLC18A2	Hs.369009	6571	63.1
201462_at	SCRN1	Hs.520740	9805	63.1
220432_s_at	CYP39A1	Hs.387367	51302	63.1
221475_s_at	RPL15	Hs.381219	6138	62.4
202268_s_at	APPBP1	Hs.460978	8883	62.4
200596_s_at	EIF3S10	Hs.523299	8661	62.4
202020_s_at	LANCL1	Hs.13351	10314	62.4
214182_at	ARF6	Hs.525330	382	62.4
207983_s_at	STAG2	Hs.496710	10735	62.4
218339_at	MRPL22	Hs.483924	29093	62.4
210028_s_at	ORC3L	Hs.410228	23595	62.4
219498_s_at	BCL11A	Hs.370549	53335	62.4
218609_s_at	NUDT2	Hs.493767	318	62.4
203092_at	TIMM44	Hs.465784	10469	62.4
219407_s_at	LAMC3	Hs.201805	10319	62.4
220012_at	ERO1LB	Hs.558519	56605	62.4
201691_s_at	TPD52	Hs.368433	7163	62.4
221691_x_at	NPM1	Hs.557550	4869	61.8
200853_at	H2AFZ	Hs.119192	3015	61.8
201970_s_at	NASP	Hs.319334	4678	61.8
202345_s_at	FABP5	Hs.408061	2171	61.8
215111_s_at	TSC22D1	Hs.507916	8848	61.8
211727_s_at	COX11	Hs.96530	1353	61.8
206102_at	PSF1	Hs.360033	9837	61.8
202900_s_at	NUP88	Hs.584784	4927	61.8
210036_s_at	KCNH2	Hs.188021	3757	61.8

probe	Gene	Unigene	Locus	%AML cases with underexpression
205097_at	SLC26A2	Hs.302738	1836	61.8
219203_at	C14orf122	Hs.271614	51016	61.8
204238_s_at	C6orf108	Hs.109752	10591	61.8
202779_s_at	UBE2S	Hs.396393	27338	61.8
219258_at	FLJ20516	Hs.426696	54962	61.8
204412_s_at	NEFH	Hs.198760	4744	61.8
203213_at	CDC2	Hs.334562	983	61.8
208820_at	PTK2	Hs.395482	5747	61.8
209922_at	BRAP	Hs.530940	8315	61.8
219651_at	DPPA4	Hs.317659	55211	61.8
203667_at	TBCA	Hs.291212	6902	61.1
202854_at	HPRT1	Hs.412707	3251	61.1
213535_s_at	UBE2I	Hs.302903	7329	61.1
205961_s_at	PSIP1	Hs.493516	11168	61.1
202484_s_at	MBD2	Hs.25674	8932	61.1
203097_s_at	RAPGEF2	Hs.113912	9693	61.1
1053_at	RFC2	Hs.139226	5982	61.1
209585_s_at	MINPP1	Hs.121260	9562	61.1
200832_s_at	SCD	Hs.558396	6319	61.1
33767_at	NEFH	Hs.198760	4744	61.1
205731_s_at	NCOA2	Hs.446678	10499	61.1
213194_at	ROBO1	Hs.13640	6091	61.1
200826_at	SNRPD2	Hs.515472	6633	60.5
209104_s_at	NOLA2	Hs.27222	55651	60.5
201897_s_at	CKS1B	Hs.374378	1163	60.5
202983_at	SMARCA3	Hs.3068	6596	60.5
213685_at	---	Hs.15535	---	60.5
211721_s_at	ZNF551	Hs.184846	90233	60.5
211013_x_at	PML	Hs.526464	5371	60.5
209905_at	HOXA9	Hs.127428	3205	60.5
202085_at	TJP2	Hs.50382	9414	60.5
205472_s_at	DACH1	Hs.129452	1602	60.5
206999_at	IL12RB2	Hs.479347	3595	60.5
212981_s_at	KIAA0738	Hs.406492	9747	60.5
204559_s_at	LSM7	Hs.512610	51690	59.9
203721_s_at	WDR50	Hs.463465	51096	59.9
201593_s_at	LEREPO4	Hs.368598	55854	59.9
201263_at	TARS	Hs.481860	6897	59.9
212057_at	KIAA0182	Hs.461647	23199	59.9
221520_s_at	CDCA8	Hs.524571	55143	59.9
202201_at	BLVRB	Hs.515785	645	59.9
221709_s_at	C14orf131	Hs.106005	55778	59.9
218086_at	NPDC1	Hs.105547	56654	59.9
219088_s_at	ZNF576	Hs.11110	79177	59.9
205471_s_at	DACH1	Hs.129452	1602	59.9

probe	Gene	Unigene	Locus	%AML cases with underexpression
200602_at	APP	Hs.434980	351	59.9
211755_s_at	ATP5F1	Hs.514870	515	59.2
214431_at	GMPS	Hs.546324	8833	59.2
213302_at	PFAS	Hs.370336	5198	59.2
203773_x_at	BLVRA	Hs.488143	644	59.2
214953_s_at	APP	Hs.434980	351	59.2
204300_at	PET112L	Hs.119316	5188	59.2
205769_at	SLC27A2	Hs.11729	11001	59.2
211597_s_at	HOP	Hs.121443	84525	59.2
36830_at	MIPEP	Hs.507498	4285	59.2
219789_at	NPR3	Hs.237028	4883	59.2
204304_s_at	PROM1	Hs.479220	8842	59.2
214223_at	---	---	---	59.2
219703_at	MNS1	Hs.444483	55329	59.2
209781_s_at	KHDRBS3	Hs.444558	10656	59.2
205572_at	ANGPT2	Hs.553484	285	59.2
214469_at	HIST1H2AE	Hs.121017	3012	59.2
210574_s_at	NUDC	Hs.263812	10726	58.6
212943_at	KIAA0528	Hs.271014	9847	58.6
211729_x_at	BLVRA	Hs.488143	644	58.6
205981_s_at	ING2	Hs.107153	3622	58.6
206146_s_at	RHAG	Hs.120950	6005	58.6
208950_s_at	ALDH7A1	Hs.483239	501	58.6
209485_s_at	OSBPL1A	Hs.370725	114876	58.6
214651_s_at	HOXA9	Hs.127428	3205	58.6
202690_s_at	SNRPD1	Hs.464734	6632	58.0
214700_x_at	RIF1	Hs.536537	55183	58.0
218729_at	LXN	Hs.478067	56925	58.0
222146_s_at	TCF4	Hs.200285	6925	58.0
203771_s_at	BLVRA	Hs.488143	644	58.0
215526_at	WWOX	Hs.461453	51741	58.0
213939_s_at	RIPX	Hs.7972	22902	58.0
213094_at	GPR126	Hs.318894	57211	58.0
208956_x_at	DUT	Hs.527980	1854	57.3
202567_at	SNRPD3	Hs.356549	6634	57.3
213097_s_at	ZRF1	Hs.558476	27000	57.3
203351_s_at	ORC4L	Hs.558364	5000	57.3
210425_x_at	GOLGA8B	Hs.356225	440270	57.3
201948_at	GNL2	Hs.75528	29889	57.3
212533_at	WEE1	Hs.249441	7465	57.3
205419_at	EBI2	Hs.784	1880	57.3
208352_x_at	ANK1	Hs.491558	286	57.3
37986_at	EPOR	Hs.127826	2057	57.3
210115_at	RPL39L	Hs.478582	116832	57.3
216373_at	FLJ90013	Hs.479223	202018	57.3

probe	Gene	Unigene	Locus	%AML cases with underexpression
211955_at	RANBP5	Hs.513057	3843	56.7
201846_s_at	RYBP	Hs.7910	23429	56.7
203690_at	TUBGCP3	Hs.224152	10426	56.7
218529_at	CD320	Hs.558499	51293	56.7
205193_at	MAFF	Hs.517617	23764	56.7
203228_at	PAFAH1B3	Hs.466831	5050	56.7
210446_at	GATA1	Hs.765	2623	56.7
208353_x_at	ANK1	Hs.491558	286	56.7
213616_at	C18orf10	Hs.558473	25941	56.7
220010_at	KCNE1L	Hs.522753	23630	56.7
209774_x_at	CXCL2	Hs.75765	2920	56.7
203817_at	---	---	---	56.7
202599_s_at	NRIP1	Hs.155017	8204	56.7
214331_at	TSFM	Hs.505784	10102	56.7
203316_s_at	SNRPE	Hs.334612	6635	56.1
221452_s_at	TMEM14B	Hs.273077	81853	56.1
202467_s_at	COPS2	Hs.369614	9318	56.1
208910_s_at	C1QBP	Hs.555866	708	56.1
218188_s_at	TIMM13	Hs.75056	26517	56.1
206555_s_at	THUMPD1	Hs.460232	55623	56.1
203794_at	CDC42BPA	Hs.35433	8476	56.1
219546_at	BMP2K	Hs.146551	55589	56.1
221286_s_at	PACAP	Hs.409563	51237	56.1
214045_at	LIAS	Hs.550502	11019	56.1
205984_at	CRHBP	Hs.115617	1393	56.1
217538_at	RUTBC1	Hs.513861	9905	56.1
217818_s_at	ARPC4	Hs.323342	10093	56.1
203895_at	PLCB4	Hs.472101	5332	56.1
217889_s_at	CYBRD1	Hs.221941	79901	56.1
222348_at	---	---	---	56.1
222378_at	FLJ43663	Hs.150556	378805	56.1
209290_s_at	NFIB	Hs.370359	4781	56.1
219174_at	CCDC2	Hs.145402	80173	56.1
204115_at	GNG11	Hs.83381	2791	56.1
200750_s_at	RAN	Hs.10842	5901	55.4
219192_at	UBAP2	Hs.493739	55833	55.4
217979_at	TSPAN13	Hs.364544	27075	55.4
201569_s_at	SAMM50	Hs.505824	25813	55.4
218711_s_at	SDPR	Hs.26530	8436	55.4
204030_s_at	SCHIP1	Hs.134665	29970	55.4
205240_at	GPSM2	Hs.584901	29899	55.4
208791_at	CLU	Hs.436657	1191	55.4
215779_s_at	HIST1H2BG	Hs.240135	8339	55.4
214815_at	TRIM33	Hs.568681	51592	55.4
215402_at	APPBP2	Hs.84084	10513	55.4

probe	Gene	Unigene	Locus	%AML cases with underexpression
204005_s_at	PAWR	Hs.406074	5074	55.4
218981_at	ACN9	Hs.42785	57001	55.4
200786_at	PSMB7	Hs.213470	5695	54.8
208993_s_at	PPIG	Hs.470544	9360	54.8
201764_at	MGC5576	Hs.103834	79022	54.8
202780_at	OXCT1	Hs.278277	5019	54.8
219658_at	PTCD2	Hs.126906	79810	54.8
219918_s_at	ASPM	Hs.121028	259266	54.8
215054_at	EPOR	Hs.127826	2057	54.8
213550_s_at	---	---	---	54.8
209129_at	TRIP6	Hs.534360	7205	54.8
210254_at	MS4A3	Hs.99960	932	54.8
216022_at	WNK1	Hs.504432	65125	54.8
207056_s_at	SLC4A8	Hs.370636	9498	54.8
209669_s_at	SERBP1	Hs.530412	26135	54.1
201459_at	RUVBL2	Hs.515846	10856	54.1
203391_at	FKBP2	Hs.227729	2286	54.1
212005_at	C1orf144	Hs.252967	26099	54.1
205086_s_at	hCAP-H2	Hs.180903	29781	54.1
209516_at	SMYD5	Hs.516095	10322	54.1
207877_s_at	NVL	Hs.497867	4931	54.1
218856_at	TNFRSF21	Hs.443577	27242	54.1
213844_at	HOXA5	Hs.37034	3202	54.1
210758_at	PSIP1	Hs.493516	11168	54.1
221841_s_at	KLF4	Hs.376206	9314	54.1
217787_s_at	GALNT2	Hs.567272	2590	54.1
208963_x_at	FADS1	Hs.503546	3992	54.1
216813_at	---	---	---	54.1
201427_s_at	SEPP1	Hs.275775	6414	54.1
205711_x_at	ATP5C1	Hs.271135	509	53.5
217774_s_at	HSPC152	Hs.333579	51504	53.5
212780_at	SOS1	Hs.278733	6654	53.5
210793_s_at	NUP98	Hs.524750	4928	53.5
211302_s_at	PDE4B	Hs.198072	5142	53.5
209531_at	GSTZ1	Hs.26403	2954	53.5
219961_s_at	C20orf19	Hs.187635	55857	53.5
222154_s_at	DNAPTP6	Hs.120323	26010	53.5
218435_at	DNAJC15	Hs.438830	29103	53.5
213067_at	MYH10	Hs.16355	4628	53.5
216248_s_at	NR4A2	Hs.165258	4929	53.5
205372_at	PLAG1	Hs.14968	5324	53.5
207879_at	---	---	---	53.5
213224_s_at	LOC92482	Hs.192249	92482	52.9
218049_s_at	MRPL13	Hs.333823	28998	52.9
201292_at	TOP2A	Hs.156346	7153	52.9

probe	Gene	Unigene	Locus	%AML cases with underexpression
202468_s_at	CTNNAL1	Hs.58488	8727	52.9
201830_s_at	NET1	Hs.25155	10276	52.9
203821_at	HBEGF	Hs.799	1839	52.9
202095_s_at	BIRC5	Hs.514527	332	52.9
212263_at	QKI	Hs.510324	9444	52.9
214724_at	DIXDC1	Hs.116796	85458	52.9
203532_x_at	CUL5	Hs.440320	8065	52.9
217684_at	TYMS	Hs.369762	7298	52.9
206669_at	GAD1	Hs.420036	2571	52.9
214130_s_at	PDE4DIP	Hs.584841	9659	52.9
215330_at	FLJ43663	Hs.150556	378805	52.9
214167_s_at	RPLP0 /// RPLP0-like	Hs.448226	220717	52.2
212694_s_at	PCCB	Hs.63788	5096	52.2
209049_s_at	PRKCBP1	Hs.446240	23613	52.2
212368_at	ZNF292	Hs.485892	23036	52.2
204976_s_at	AMMECR1	Hs.211021	9949	52.2
203068_at	KLHL21	Hs.7764	9903	52.2
205453_at	HOXB2	Hs.514289	3212	52.2
205046_at	CENPE	Hs.75573	1062	52.2
204766_s_at	NUDT1	Hs.534331	4521	52.2
216650_at	LOC283412 /// LOC442165	Hs.531538	283412	52.2
215200_x_at	VIL2	Hs.487027	7430	52.2
218128_at	NFYB	Hs.84928	4801	52.2
213122_at	TSPYL5	Hs.173094	85453	52.2
219341_at	CLN8	Hs.127675	2055	52.2
220602_s_at	FLJ22795 /// LOC388152 /// LOC388161	Hs.405809	388152	52.2
201506_at	TGFBI	Hs.369397	7045	52.2
210691_s_at	CACYBP	Hs.508524	27101	52.2
200876_s_at	PSMB1	Hs.352768	5689	51.6
221532_s_at	WDR61	Hs.513055	80349	51.6
200783_s_at	STMN1	Hs.209983	3925	51.6
203196_at	ABCC4	Hs.508423	10257	51.6
218456_at	C1QDC1	Hs.234355	65981	51.6
221685_s_at	FLJ20364	Hs.368710	54908	51.6
219837_s_at	CYTL1	Hs.13872	54360	51.6
202237_at	NNMT	Hs.503911	4837	51.6
201367_s_at	ZFP36L2	Hs.503093	678	51.6
222326_at	PDE4B	Hs.198072	5142	51.6
209314_s_at	HBS1L	Hs.378532	10767	51.6
208646_at	RPS14	Hs.381126	6208	51.0
201901_s_at	YY1	Hs.388927	7528	51.0

probe	Gene	Unigene	Locus	%AML cases with underexpression
202469_s_at	CPSF6	Hs.369606	11052	51.0
219030_at	CGI-121	Hs.157401	51002	51.0
202309_at	MTHFD1	Hs.435974	4522	51.0
221932_s_at	C14orf87	Hs.532683	51218	51.0
219067_s_at	C10orf86	Hs.258798	54780	51.0
221652_s_at	C12orf11	Hs.505077	55726	51.0
201377_at	UBAP2L	Hs.490551	9898	51.0
218025_s_at	PECI	Hs.15250	10455	51.0
202732_at	PKIG	Hs.472831	11142	51.0
212692_s_at	LRBA	Hs.480938	987	51.0
210762_s_at	DLC1	Hs.134296	10395	51.0
202339_at	SYMPK	Hs.515475	8189	51.0
208792_s_at	CLU	Hs.436657	1191	51.0
208178_x_at	TRIO	Hs.130031	7204	51.0
201688_s_at	TPD52	Hs.368433	7163	51.0
217876_at	GTF3C5	Hs.495417	9328	51.0
212463_at	CD59	Hs.278573	966	51.0
219264_s_at	PPP2R3B	Hs.124942	28227	51.0
210882_s_at	TRO	Hs.434971	7216	51.0
220298_s_at	SPATA6	Hs.408467	54558	51.0
64900_at	CHST5 /// MGC15429	Hs.420796	23563	51.0
221618_s_at	TAF9L	Hs.567505	51616	51.0
214143_x_at	RPL24 /// SLC36A2	Hs.483877	153201	50.3
200642_at	SOD1	Hs.443914	6647	50.3
219041_s_at	REPIN1	Hs.521289	29803	50.3
205133_s_at	HSPE1	Hs.1197	3336	50.3
201501_s_at	GRSF1	Hs.309763	2926	50.3
212594_at	PDCD4	Hs.232543	27250	50.3
221007_s_at	FIP1L1	Hs.518760	81608	50.3
212629_s_at	PKN2	Hs.440833	5586	50.3
219247_s_at	ZDHHC14	Hs.187459	79683	50.3
212396_s_at	KIAA0090	Hs.439200	23065	50.3
216804_s_at	PDLIM5	Hs.480311	10611	50.3
206726_at	PGDS	Hs.128433	27306	50.3
214051_at	MGC39900	Hs.496530	286527	50.3
203212_s_at	MTMR2	Hs.181326	8898	50.3
204307_at	KIAA0329	Hs.195667	9895	50.3
203072_at	MYO1E	Hs.370392	4643	50.3
204979_s_at	SH3BGR	Hs.473847	6450	50.3
216027_at	TXNDC13	Hs.169358	56255	50.3
207855_s_at	CLCC1	Hs.554803	23155	50.3
215388_s_at	CFH /// CFHL1	Hs.154224	3075	50.3
200679_x_at	HMGB1	Hs.434102	3146	49.7

probe	Gene	Unigene	Locus	%AML cases with underexpression
202589_at	TYMS	Hs.369762	7298	49.7
201273_s_at	SRP9	Hs.511425	6726	49.7
208787_at	MRPL3	Hs.205163	11222	49.7
218003_s_at	FKBP3	Hs.509226	2287	49.7
201275_at	FDPS	Hs.335918	2224	49.7
202347_s_at	HIP2	Hs.50308	3093	49.7
206061_s_at	DICER1	Hs.87889	23405	49.7
217739_s_at	PBEF1	Hs.489615	10135	49.7
203049_s_at	KIAA0372	Hs.482868	9652	49.7
209340_at	UAP1	Hs.492859	6675	49.7
202861_at	PER1	Hs.445534	5187	49.7
201283_s_at	OIP106	Hs.535711	22906	49.7
213789_at	---	---	---	49.7
203542_s_at	KLF9	Hs.150557	687	49.7
212813_at	JAM3	Hs.150718	83700	49.7
210415_s_at	ODF2	Hs.129055	4957	49.7
205673_s_at	ASB9	Hs.19404	140462	49.7
204627_s_at	ITGB3	Hs.218040	3690	49.7
213610_s_at	KLHL23	---	151230	49.7
215339_at	NKTR	Hs.529509	4820	49.7
211969_at	HSPCA	Hs.525600	3320	49.0
211713_x_at	KIAA0101	Hs.81892	9768	49.0
222035_s_at	PAPOLA	Hs.253726	10914	49.0
218654_s_at	MRPS33	Hs.83006	51650	49.0
206364_at	KIF14	Hs.3104	9928	49.0
208935_s_at	LGALS8	Hs.4082	3964	49.0
209318_x_at	PLAGL1	Hs.444975	5325	49.0
204444_at	KIF11	Hs.8878	3832	49.0
218886_at	PAK1IP1	Hs.310231	55003	49.0
219251_s_at	WDR60	Hs.389945	55112	49.0
221586_s_at	E2F5	Hs.445758	1875	49.0
202855_s_at	SLC16A3	Hs.500761	9123	49.0
208814_at	HSPA4	Hs.90093	3308	49.0
215931_s_at	ARFGEF2	Hs.62578	10564	49.0
211506_s_at	IL8	Hs.624	3576	49.0
218656_s_at	LHFP	Hs.507798	10186	49.0
215016_x_at	DST	Hs.485616	667	49.0
215720_s_at	NFYA	Hs.10441	4800	49.0
216765_at	MAP2K5	Hs.114198	5607	49.0
208672_s_at	SFRS3	Hs.572089	6428	48.4
203133_at	SEC61B	Hs.191887	10952	48.4
211761_s_at	CACYBP	Hs.508524	27101	48.4
202911_at	MSH6	Hs.445052	2956	48.4
221570_s_at	METTL5	Hs.470553	29081	48.4
215780_s_at	SET ///	Hs.436687	389168	48.4

probe	Gene	Unigene	Locus	%AML cases with underexpression
	LOC389168			
201464_x_at	JUN	Hs.525704	3725	48.4
202048_s_at	CBX6	Hs.511952	23466	48.4
209299_x_at	PPIL2	Hs.438587	23759	48.4
209196_at	WDR46	Hs.520063	9277	48.4
209605_at	TST	Hs.474783	7263	48.4
204825_at	MELK	Hs.184339	9833	48.4
212750_at	PPP1R16B	Hs.45719	26051	48.4
205155_s_at	SPTBN2	Hs.26915	6712	48.4
209406_at	BAG2	Hs.55220	9532	48.4
215248_at	GRB10	Hs.164060	2887	48.4
207057_at	SLC16A7	Hs.439643	9194	48.4
213150_at	HOXA10	Hs.110637	3206	48.4
212489_at	COL5A1	Hs.210283	1289	48.4
222364_at	SLC44A1	Hs.494700	23446	48.4
216278_at	KIAA0256	Hs.9997	9728	48.4
207721_x_at	HINT1	Hs.483305	3094	47.8
208691_at	TFRC	Hs.529618	7037	47.8
212036_s_at	PNN	Hs.409965	5411	47.8
200790_at	ODC1	Hs.467701	4953	47.8
212055_at	C18orf10	Hs.558473	25941	47.8
209662_at	CETN3	Hs.128073	1070	47.8
209759_s_at	DCI	Hs.403436	1632	47.8
213147_at	HOXA10	Hs.110637	3206	47.8
219737_s_at	PCDH9	Hs.407643	5101	47.8
205393_s_at	CHEK1	Hs.24529	1111	47.8
221900_at	COL8A2	Hs.353001	1296	47.8
220302_at	MAK	Hs.446125	4117	47.8
211136_s_at	CLPTM1	Hs.444441	1209	47.8
207550_at	MPL	Hs.82906	4352	47.8
211549_s_at	HPGD	Hs.77348	3248	47.8
212182_at	NUDT4	Hs.506325	11163	47.8
208368_s_at	BRCA2	Hs.34012	675	47.8
215567_at	C14orf111	Hs.343173	51077	47.8
214712_at	---	---	---	47.8
208753_s_at	NAP1L1	Hs.524599	4673	47.1
216237_s_at	MCM5	Hs.517582	4174	47.1
221829_s_at	TNPO1	Hs.482497	3842	47.1
208661_s_at	TTC3	Hs.368214	7267	47.1
202947_s_at	GYPC	Hs.59138	2995	47.1
221847_at	LOC440123	Hs.585252	440123	47.1
201123_s_at	EIF5A	Hs.534314	1984	47.1
211028_s_at	KHK	Hs.567297	3795	47.1
203264_s_at	ARHGEF9	Hs.54697	23229	47.1
218976_at	DNAJC12	Hs.260720	56521	47.1

probe	Gene	Unigene	Locus	%AML cases with underexpression
206298_at	ARHGAP22	Hs.435063	58504	47.1
207124_s_at	GNB5	Hs.155090	10681	47.1
215992_s_at	RAPGEF2	Hs.113912	9693	47.1
206698_at	XK	Hs.78919	7504	47.1
211840_s_at	PDE4D	Hs.117545	5144	47.1
207798_s_at	ATXN2L	Hs.460499	11273	47.1
214422_at	RAD23B /// LOC131185	Hs.521640	131185	47.1
203913_s_at	HPGD	Hs.77348	3248	47.1
208805_at	PSMA6	Hs.446260	5687	46.5
211936_at	HSPA5	Hs.522394	3309	46.5
200806_s_at	HSPD1	Hs.567290	3329	46.5
213655_at	YWHAE	Hs.513851	7531	46.5
215416_s_at	STOML2	Hs.3439	30968	46.5
210983_s_at	MCM7	Hs.438720	4176	46.5
209153_s_at	TCF3	Hs.371282	6929	46.5
219076_s_at	PXMP2	Hs.430299	5827	46.5
215223_s_at	SOD2	Hs.487046	6648	46.5
203061_s_at	MDC1	Hs.433653	9656	46.5
213593_s_at	TRA2A	Hs.445652	29896	46.5
203114_at	SSSCA1	Hs.534388	10534	46.5
204833_at	ATG12	Hs.264482	9140	46.5
212070_at	GPR56	Hs.513633	9289	46.5
204162_at	KNTC2	Hs.414407	10403	46.5
212229_s_at	FBXO21	Hs.159699	23014	46.5
222180_at	---	---	---	46.5
212529_at	FLJ30656	Hs.355570	124801	46.5
204717_s_at	SLC29A2	Hs.32951	3177	46.5
215440_s_at	BEXL1	Hs.184736	56271	46.5
209488_s_at	RBPMS	Hs.334587	11030	46.5
207850_at	CXCL3	Hs.89690	2921	46.5
206864_s_at	HRK	Hs.87247	8739	46.5
215846_at	CDC42SE2	Hs.508829	56990	46.5
219148_at	PBK	Hs.104741	55872	46.5
210662_at	KYNU	Hs.470126	8942	46.5
211987_at	TOP2B	Hs.475733	7155	45.9
200969_at	SERP1	Hs.518326	27230	45.9
202078_at	COPS3	Hs.6076	8533	45.9
202396_at	TCERG1	Hs.443465	10915	45.9
218450_at	HEBP1	Hs.294133	50865	45.9
201540_at	FHL1	Hs.435369	2273	45.9
206478_at	KIAA0125	Hs.584844	9834	45.9
218452_at	SMARCAL1	Hs.516674	50485	45.9
202478_at	TRIB2	Hs.467751	28951	45.9
216614_at	ITPR2	Hs.512235	3709	45.9

probe	Gene	Unigene	Locus	%AML cases with underexpression
204881_s_at	UGCG	Hs.304249	7357	45.9
212758_s_at	TCF8	Hs.124503	6935	45.9
221071_at	---	---	---	45.9
206847_s_at	HOXA7	Hs.446318	3204	45.9
201044_x_at	DUSP1	Hs.171695	1843	45.9
219990_at	E2F8	Hs.523526	79733	45.9
215002_at	LOC23117 /// DKFZp547E087 /// LOC348162 /// LOC388221 /// LOC440345 /// LOC440354 /// LOC613037	Hs.444600	23117	45.9
206637_at	P2RY14	Hs.2465	9934	45.9
222320_at	CDC73	Hs.378996	79577	45.9
204386_s_at	MRP63	Hs.458367	78988	45.2
208758_at	ATIC	Hs.90280	471	45.2
200658_s_at	PHB	Hs.514303	5245	45.2
208843_s_at	GORASP2	Hs.431317	26003	45.2
209014_at	MAGED1	Hs.5258	9500	45.2
217848_s_at	PPA1	Hs.437403	5464	45.2
217814_at	GK001	Hs.202011	57003	45.2
212508_at	MOAP1	Hs.24719	64112	45.2
213227_at	PGRMC2	Hs.507910	10424	45.2
204299_at	FUSIP1	Hs.3530	10772	45.2
59644_at	BMP2K	Hs.146551	55589	45.2
203989_x_at	F2R	Hs.482562	2149	45.2
207194_s_at	ICAM4	Hs.386467	3386	45.2
204962_s_at	CENPA	Hs.1594	1058	45.2
221690_s_at	NALP2	Hs.369279	55655	45.2
218430_s_at	RFXDC2	Hs.282855	64864	45.2
205391_x_at	ANK1	Hs.491558	286	45.2
207232_s_at	DZIP3	Hs.409210	9666	45.2
214255_at	ATP10A	Hs.128041	57194	45.2
203533_s_at	CUL5	Hs.440320	8065	45.2
204195_s_at	PKNOX1	Hs.431043	5316	45.2
207532_at	CRYGD	Hs.546247	1421	45.2
212715_s_at	MICAL3	Hs.528024	57553	45.2
221187_s_at	FLJ22688	Hs.288800	80199	45.2
220171_x_at	KIAA1704	Hs.507922	55425	45.2
214637_at	OSM	Hs.248156	5008	45.2
202371_at	TCEAL4	Hs.194329	79921	45.2
203987_at	FZD6	Hs.292464	8323	45.2
205122_at	TMEFF1	Hs.336224	8577	45.2
202144_s_at	ADSL	Hs.75527	158	44.6

probe	Gene	Unigene	Locus	%AML cases with underexpression
202001_s_at	NDUFA6	Hs.274416	4700	44.6
201931_at	ETFA	Hs.39925	2108	44.6
217745_s_at	MAK3	Hs.269528	80218	44.6
210093_s_at	MAGOH	Hs.421576	4116	44.6
209680_s_at	KIFC1	Hs.436912	3833	44.6
222209_s_at	FLJ22104	Hs.188591	65084	44.6
204622_x_at	NR4A2	Hs.165258	4929	44.6
209035_at	MDK	Hs.82045	4192	44.6
202336_s_at	PAM	Hs.369430	5066	44.6
222375_at	PPIG	Hs.470544	9360	44.6
203865_s_at	ADARB1	Hs.474018	104	44.6
204524_at	PDPK1	Hs.459691	5170	44.6
205628_at	PRIM2A	Hs.485640	5558	44.6
203325_s_at	COL5A1	Hs.210283	1289	44.6
202760_s_at	AKAP2 /// PALM2-AKAP2	Hs.259461	11217	44.6
219650_at	FLJ20105	Hs.47558	54821	44.6
218087_s_at	SORBS1	Hs.38621	10580	44.6
201134_x_at	COX7C	Hs.430075	1350	43.9
201277_s_at	HNRPAB	Hs.248746	3182	43.9
203345_s_at	MTF2	Hs.31016	22823	43.9
209330_s_at	HNRPD	Hs.480073	3184	43.9
217028_at	CXCR4	Hs.421986	7852	43.9
202232_s_at	hfl-B5	Hs.502244	10480	43.9
201197_at	AMD1	Hs.159118	262	43.9
203048_s_at	KIAA0372	Hs.482868	9652	43.9
205964_at	ZNF426	Hs.567574	79088	43.9
209865_at	SLC35A3	Hs.567432	23443	43.9
206655_s_at	GP1BB	Hs.517410	2812	43.9
204317_at	GTSE1 /// LOC440834	Hs.386189	440834	43.9
209081_s_at	COL18A1	Hs.517356	80781	43.9
205857_at	---	---	---	43.9
220593_s_at	FLJ20753	Hs.202542	55036	43.9
205413_at	MPPED2	Hs.289795	744	43.9
208826_x_at	HINT1	Hs.483305	3094	43.3
202857_at	TMEM4	Hs.8752	10330	43.3
202431_s_at	MYC	Hs.202453	4609	43.3
201880_at	ARIH1	Hs.268787	25820	43.3
200965_s_at	ABLIM1	Hs.438236	3983	43.3
205051_s_at	KIT	Hs.479754	3815	43.3
211464_x_at	CASP6	Hs.3280	839	43.3
214579_at	NPAL3	Hs.523442	57185	43.3
219188_s_at	LRP16	Hs.502814	28992	43.3
204558_at	RAD54L	Hs.523220	8438	43.3

probe	Gene	Unigene	Locus	%AML cases with underexpression
213566_at	RNASE6	Hs.23262	6039	43.3
219661_at	RANBP17	Hs.410810	64901	43.3
206871_at	ELA2	Hs.99863	1991	43.3
208937_s_at	ID1	Hs.504609	3397	43.3
205937_at	CGREF1	Hs.159525	10669	43.3
208499_s_at	DNAJC3	Hs.59214	5611	43.3
212775_at	OBSL1	Hs.526594	23363	43.3
204141_at	TUBB2	Hs.512712	7280	43.3
213714_at	CACNB2	Hs.59093	783	43.3
203434_s_at	MME	Hs.307734	4311	43.3
215578_at	---	---	---	43.3
213619_at	HNRPH1	Hs.202166	3187	42.7
209492_x_at	ATP5I	Hs.85539	521	42.7
40189_at	SET	Hs.436687	6418	42.7
209118_s_at	TUBA3	Hs.524395	7846	42.7
210097_s_at	NOL7	Hs.549161	51406	42.7
203362_s_at	MAD2L1	Hs.559215	4085	42.7
203373_at	SOCS2	Hs.485572	8835	42.7
200983_x_at	CD59	Hs.278573	966	42.7
201067_at	PSMC2	Hs.437366	5701	42.7
222186_at	ZA20D3	Hs.306329	54469	42.7
218237_s_at	SLC38A1	Hs.533770	81539	42.7
205653_at	CTSG	Hs.421724	1511	42.7
204917_s_at	MLLT3	Hs.493585	4300	42.7
219094_at	ARMC8	Hs.266826	25852	42.7
213012_at	NEDD4	Hs.1565	4734	42.7
203467_at	PMM1	Hs.75835	5372	42.7
219922_s_at	LTBP3	Hs.289019	4054	42.7
204112_s_at	HNMT	Hs.42151	3176	42.7
204468_s_at	TIE1	Hs.78824	7075	42.7
214804_at	FSHPRH1	Hs.348920	2491	42.7
202269_x_at	GBP1	Hs.62661	2633	42.7
210466_s_at	SERBP1	Hs.530412	26135	42.0
218462_at	BXDC5	Hs.481202	80135	42.0
217836_s_at	YY1AP1	Hs.584927	55249	42.0
212160_at	XPOT	Hs.85951	11260	42.0
201737_s_at	MARCH6	Hs.432862	10299	42.0
218662_s_at	HCAP-G	Hs.567567	64151	42.0
203787_at	SSBP2	Hs.102735	23635	42.0
221599_at	PTD015	Hs.503357	28971	42.0
208501_at	GFI1B	Hs.118539	8328	42.0
218930_s_at	FLJ11273	Hs.396358	54664	42.0
205521_at	ENDOGL1	Hs.517897	9941	42.0
205997_at	ADAM28	Hs.174030	10863	42.0
217259_at	MTMR7	Hs.584834	9108	42.0

probe	Gene	Unigene	Locus	%AML cases with underexpression
221027_s_at	PLA2G12A	Hs.480519	81579	42.0
213478_at	KIAA1026	Hs.368823	23254	42.0
209914_s_at	NRXN1	Hs.468505	9378	42.0
218801_at	UGCGL2	Hs.193226	55757	42.0
215392_at	MINPP1	Hs.121260	9562	42.0
213088_s_at	DNAJC9	Hs.59125	23234	41.4
200984_s_at	CD59	Hs.278573	966	41.4
203560_at	GGH	Hs.78619	8836	41.4
207165_at	HMMR	Hs.72550	3161	41.4
207828_s_at	CENPF	Hs.497741	1063	41.4
220040_x_at	KIAA1166	Hs.28249	55906	41.4
218397_at	FANCL	Hs.411433	55120	41.4
212949_at	BRRN1	Hs.308045	23397	41.4
217858_s_at	ARMCX3	Hs.172788	51566	41.4
213420_at	DHX57	Hs.468226	90957	41.4
210139_s_at	PMP22	Hs.372031	5376	41.4
214126_at	MCART1	Hs.118394	92014	41.4
207892_at	CD40LG	Hs.652	959	41.4
209204_at	LMO4	Hs.436792	8543	41.4
211267_at	HESX1	Hs.171980	8820	41.4
218045_x_at	PTMS	Hs.504613	5763	41.4
207110_at	KCNJ12	Hs.200629	3768	41.4
220004_at	DDX43	Hs.125507	55510	41.4
218395_at	ACTR6	Hs.115088	64431	40.8
201565_s_at	ID2	Hs.180919	3398	40.8
220007_at	FLJ13984	Hs.135146	79828	40.8
212599_at	AUTS2	Hs.21631	26053	40.8
219733_s_at	SLC27A5	Hs.309583	10998	40.8
221922_at	GPSM2	Hs.584901	29899	40.8
208788_at	ELOVL5	Hs.520189	60481	40.8
204306_s_at	CD151	Hs.512857	977	40.8
209094_at	DDAH1	Hs.379858	23576	40.8
211182_x_at	RUNX1	Hs.149261	861	40.8
219497_s_at	BCL11A	Hs.370549	53335	40.8
206877_at	MXD1	Hs.468908	4084	40.8
204430_s_at	SLC2A5	Hs.530003	6518	40.8
209764_at	MGAT3	Hs.276808	4248	40.8
209372_x_at	TUBB2 /// TUBB-PARALOG	Hs.512712	347733 /// 7280	40.8
205352_at	SERPINI1	Hs.478153	5274	40.8
208403_x_at	MAX	Hs.285354	4149	40.8
209763_at	CHRDL1	Hs.496587	91851	40.8
207341_at	PRTN3	Hs.928	5657	40.8
202110_at	COX7B	Hs.522699	1349	40.1

probe	Gene	Unigene	Locus	%AML cases with underexpression
201381_x_at	CACYBP	Hs.508524	27101	40.1
201143_s_at	EIF2S1	Hs.151777	1965	40.1
201829_at	NET1	Hs.25155	10276	40.1
218710_at	FLJ20272	Hs.468125	55622	40.1
204146_at	RAD51AP1	Hs.504550	10635	40.1
204028_s_at	RABGAP1	Hs.271341	23637	40.1
215338_s_at	NKTR	Hs.529509	4820	40.1
209304_x_at	GADD45B	Hs.110571	4616	40.1
205394_at	CHEK1	Hs.24529	1111	40.1
219054_at	FLJ14054	Hs.13528	79614	40.1
210377_at	ACSM3	Hs.160976	6296	40.1
201996_s_at	SPEN	Hs.558463	23013	40.1
204069_at	MEIS1	Hs.526754	4211	40.1
208813_at	GOT1	Hs.500756	2805	40.1
210868_s_at	ELOVL6	Hs.412939	79071	40.1
205190_at	PLS1	Hs.203637	5357	40.1
219135_s_at	FLJ12681	Hs.71912	64788	40.1
218051_s_at	FLJ12442	Hs.84753	64943	40.1
203836_s_at	MAP3K5	Hs.186486	4217	40.1
219785_s_at	FBXO31	Hs.567582	79791	40.1
215850_s_at	NDUFA5	Hs.83916	4698	40.1
210734_x_at	MAX	Hs.285354	4149	40.1
201334_s_at	ARHGEF12	Hs.24598	23365	40.1
205253_at	PBX1	Hs.493096	5087	40.1
219976_at	HOOK1	Hs.378836	51361	40.1
205407_at	RECK	Hs.388918	8434	40.1
219871_at	FLJ13197	Hs.29725	79667	40.1
219688_at	BBS7	Hs.58974	55212	40.1
209803_s_at	PHLDA2	Hs.154036	7262	40.1
201947_s_at	CCT2	Hs.189772	10576	39.5
200085_s_at	TCEB2	Hs.172772	6923	39.5
202501_at	MAPRE2	Hs.532824	10982	39.5
206052_s_at	SLBP	Hs.298345	7884	39.5
211653_x_at	AKR1C2	Hs.567256	1646	39.5
202391_at	BASP1	Hs.201641	10409	39.5
201397_at	PHGDH	Hs.487296	26227	39.5
213008_at	FLJ10719	Hs.513126	55215	39.5
207000_s_at	PPP3CC	Hs.149413	5533	39.5
207949_s_at	ICA1	Hs.487561	3382	39.5
212891_s_at	GADD45GIP1	Hs.515164	90480	39.5
203960_s_at	C1orf41	Hs.525462	51668	39.5
221908_at	TMEM118	Hs.437195	84900	39.5
202711_at	EFNB1	Hs.144700	1947	39.5
201923_at	PRDX4	Hs.83383	10549	39.5
205389_s_at	ANK1	Hs.491558	286	39.5

probe	Gene	Unigene	Locus	%AML cases with underexpression
217486_s_at	ZDHHC17	Hs.4014	23390	39.5
214966_at	GRIK5	Hs.367799	2901	39.5
216228_s_at	WDHD1	Hs.385998	11169	39.5
210012_s_at	EWSR1	Hs.374477	2130	39.5
215653_at	GPC5	Hs.567269	2262	39.5
200840_at	KARS	Hs.3100	3735	38.9
201584_s_at	DDX39	Hs.311609	10212	38.9
202824_s_at	TCEB1	Hs.554594	6921	38.9
208795_s_at	MCM7	Hs.438720	4176	38.9
201478_s_at	DKC1	Hs.4747	1736	38.9
203137_at	WTAP	Hs.446091	9589	38.9
209181_s_at	RABGGTB	Hs.78948	5876	38.9
201326_at	CCT6A	Hs.82916	908	38.9
218680_x_at	SERF2 /// HYPK	Hs.424126	10169 /// 25764	38.9
212279_at	MAC30	Hs.199695	27346	38.9
209219_at	RDBP	Hs.423935	7936	38.9
217956_s_at	MASA	Hs.18442	58478	38.9
205339_at	SIL	Hs.525198	6491	38.9
215215_s_at	LOC81691	Hs.177926	81691	38.9
221521_s_at	Pfs2	Hs.433180	51659	38.9
219000_s_at	DCC1	Hs.315167	79075	38.9
202283_at	SERPINF1	Hs.532768	5176	38.9
209750_at	NR1D2	Hs.37288	9975	38.9
219213_at	JAM2	Hs.517227	58494	38.9
202806_at	DBN1	Hs.130316	1627	38.9
202479_s_at	TRIB2	Hs.467751	28951	38.9
216983_s_at	ZNF224	Hs.549077	7767	38.9
213556_at	LOC390940	Hs.22049	390940	38.9
214146_s_at	PPBP	Hs.2164	5473	38.9
207087_x_at	ANK1	Hs.491558	286	38.9
220221_at	VPS13D	Hs.439381	55187	38.9
204149_s_at	GSTM4	Hs.348387	2948	38.9
205808_at	ASPH	Hs.332422	444	38.9
210368_at	PCDHGB4 /// PCDHGA8	---	8641 /// 9708	38.9
214405_at	CUGBP2	Hs.309288	10659	38.9
209967_s_at	CREM	Hs.200250	1390	38.9
209900_s_at	SLC16A1	Hs.75231	6566	38.9
214393_at	LOC284062	Hs.436395	284062	38.9
210997_at	HGF	Hs.396530	3082	38.9
213591_at	ALDH7A1	Hs.483239	501	38.9
207717_s_at	PKP2	Hs.164384	5318	38.9
200705_s_at	EEF1B2	Hs.421608	1933	38.2
208808_s_at	HMGB2	Hs.434953	3148	38.2
207585_s_at	RPL36AL	Hs.444749	6166	38.2

probe	Gene	Unigene	Locus	%AML cases with underexpression
201892_s_at	IMPDH2	Hs.476231	3615	38.2
201317_s_at	PSMA2	Hs.333786	5683	38.2
217725_x_at	SERBP1	Hs.530412	26135	38.2
206445_s_at	HRMT1L2	Hs.20521	3276	38.2
217679_x_at	---	Hs.573462	---	38.2
219105_x_at	ORC6L	Hs.49760	23594	38.2
209122_at	ADFP	Hs.3416	123	38.2
203224_at	RFK	Hs.37558	55312	38.2
216212_s_at	DKC1	Hs.4747	1736	38.2
218857_s_at	ASRGL1	Hs.535326	80150	38.2
213007_at	FLJ10719	Hs.513126	55215	38.2
208158_s_at	OSBPL1A	Hs.370725	114876	38.2
220688_s_at	C1orf33	Hs.463797	51154	38.2
203590_at	DNCLI2	Hs.369068	1783	38.2
205667_at	WRN	Hs.567358	7486	38.2
213899_at	METAP2	Hs.444986	10988	38.2
219242_at	Cep63	Hs.443301	80254	38.2
212387_at	---	---	---	38.2
216591_s_at	SDHC	Hs.444472	6391	38.2
204928_s_at	SLC10A3	Hs.522826	8273	38.2
203069_at	SV2A	Hs.516153	9900	38.2
203662_s_at	TMOD1	Hs.404289	7111	38.2
209528_s_at	KIAA0683	Hs.271044	9894	38.2
218663_at	HCAP-G	Hs.567567	64151	38.2
218707_at	ZNF444	Hs.24545	55311	38.2
220183_s_at	NUDT6	Hs.558459	11162	38.2
219742_at	PRR7	Hs.534492	80758	38.2
203891_s_at	DAPK3	Hs.233308	1613	38.2
214764_at	KIAA0507	Hs.552801	57241	38.2
204113_at	CUGBP1	Hs.530727	10658	38.2
214452_at	BCAT1	Hs.438993	586	38.2
218901_at	PLSCR4	Hs.477869	57088	38.2
213793_s_at	HOMER1	Hs.129051	9456	38.2
215457_at	ARPC1A	Hs.124126	10552	38.2
219380_x_at	POLH	Hs.439153	5429	38.2
201226_at	NDUFB8	Hs.523215	4714	37.6
208796_s_at	CCNG1	Hs.79101	900	37.6
218447_at	DC13	Hs.388255	56942	37.6
204023_at	RFC4	Hs.518475	5984	37.6
203675_at	NUCB2	Hs.128686	4925	37.6
204516_at	ATXN7	Hs.476595	6314	37.6
201055_s_at	HNRPA0	Hs.96996	10949	37.6
222240_s_at	ISYNA1	Hs.405873	51477	37.6
209704_at	MTF2	Hs.31016	22823	37.6
219217_at	FLJ23441	Hs.503389	79731	37.6

probe	Gene	Unigene	Locus	%AML cases with underexpression
204531_s_at	BRCA1	Hs.194143	672	37.6
202859_x_at	IL8	Hs.624	3576	37.6
222303_at	---	---	---	37.6
217776_at	RDH11	Hs.226007	51109	37.6
202747_s_at	ITM2A	Hs.17109	9452	37.6
212186_at	ACACA	Hs.160556	31	37.6
205008_s_at	CIB2	Hs.129867	10518	37.6
201841_s_at	HSPB1	Hs.520973	3315	37.6
218756_s_at	MGC4172	Hs.462859	79154	37.6
214095_at	SHMT2	Hs.75069	6472	37.6
215224_at	RPL23	Hs.406300	9349	37.6
204182_s_at	ZNF297B	Hs.355581	23099	37.6
219386_s_at	SLAMF8	Hs.438683	56833	37.6
214472_at	HIST1H3D	Hs.532144	8351	37.6
210506_at	FUT7	Hs.457	2529	37.6
207808_s_at	PROS1	Hs.64016	5627	37.6
205292_s_at	HNRPA2B1	Hs.487774	3181	36.9
200807_s_at	HSPD1	Hs.567290	3329	36.9
212426_s_at	YWHAQ	Hs.74405	10971	36.9
220647_s_at	CHCHD8	Hs.475387	51287	36.9
201091_s_at	CBX3	Hs.381189	11335	36.9
222266_at	C19orf2	Hs.466391	8725	36.9
209795_at	CD69	Hs.208854	969	36.9
203285_s_at	HS2ST1	Hs.48823	9653	36.9
203189_s_at	NDUFS8	Hs.90443	4728	36.9
204947_at	E2F1	Hs.96055	1869	36.9
217919_s_at	MRPL42	Hs.199579	28977	36.9
202536_at	CHMP2B	Hs.476930	25978	36.9
208269_s_at	ADAM28	Hs.174030	10863	36.9
213989_x_at	C21orf18	Hs.473727	54093	36.9
210157_at	C19orf2	Hs.466391	8725	36.9
206233_at	B4GALT6	Hs.464848	9331	36.9
219412_at	RAB38	Hs.283148	23682	36.9
202871_at	TRAF4	Hs.8375	9618	36.9
215509_s_at	BUB1	Hs.469649	699	36.9
209213_at	CBR1	Hs.88778	873	36.9
209917_s_at	TP53AP1	Hs.274329	11257	36.9
220038_at	SGK3	Hs.380877	23678	36.9
217071_s_at	MTHFR	Hs.214142	4524	36.9
209576_at	GNAI1	Hs.134587	2770	36.9
203803_at	PCYOX1	Hs.567502	51449	36.9
207030_s_at	CSRP2	Hs.530904	1466	36.9
221802_s_at	KIAA1598	Hs.501140	57698	36.9
208515_at	HIST1H2BM	Hs.182432	8342	36.9
203222_s_at	TLE1	Hs.197320	7088	36.9

probe	Gene	Unigene	Locus	%AML cases with underexpression
209487_at	RBPMS	Hs.334587	11030	36.9
202244_at	PSMB4	Hs.89545	5692	36.3
215171_s_at	TIMM17A	Hs.20716	10440	36.3
217845_x_at	HIGD1A	Hs.7917	25994	36.3
217933_s_at	LAP3	Hs.479264	51056	36.3
201093_x_at	SDHA	Hs.440475	6389	36.3
218708_at	NXT1	Hs.516933	29107	36.3
202416_at	DNAJC7	Hs.500156	7266	36.3
201614_s_at	RUVBL1	Hs.272822	8607	36.3
209543_s_at	CD34	Hs.374990	947	36.3
218285_s_at	DHRS6	Hs.567972	56898	36.3
208886_at	H1F0	Hs.226117	3005	36.3
212183_at	NUDT4	Hs.506325	11163	36.3
81737_at	LOC388221 /// LOC440345	Hs.348979 /// Hs.444600 /// Hs.587880	388221 /// 440345	36.3
218264_at	BCCIP	Hs.370292	56647	36.3
202648_at	RPS19	Hs.438429	6223	36.3
201640_x_at	CLPTM1	Hs.444441	1209	36.3
213638_at	PHACTR1	Hs.436996	221692	36.3
204794_at	DUSP2	Hs.1183	1844	36.3
221224_s_at	FLJ22955	Hs.463148	79877	36.3
206500_s_at	C14orf106	Hs.437941	55320	36.3
215757_at	PRKDC	Hs.491682	5591	36.3
202773_s_at	SFRS8	Hs.308171	6433	36.3
207521_s_at	ATP2A3	Hs.513870	489	36.3
213082_s_at	SLC35D2	Hs.494556	11046	36.3
211200_s_at	EFCAB2	Hs.134857	84288	36.3
211085_s_at	STK4	Hs.472838	6789	36.3
206906_at	ICAM5	Hs.465862	7087	36.3
203165_s_at	SLC33A1	Hs.478031	9197	36.3
214918_at	HNRPM	Hs.465808	4670	36.3
219166_at	C14orf104	Hs.231761	55172	36.3
212466_at	SPRED2	Hs.59332	200734	36.3
202270_at	GBP1	Hs.62661	2633	36.3
215212_at	---	Hs.127737	---	36.3
203830_at	NJMU-R1	Hs.462754	64149	36.3
214715_x_at	ZNF160	Hs.467236	90338	35.7
218334_at	NIF3L1BP1	Hs.288151	80145	35.7
208662_s_at	TTC3	Hs.368214	7267	35.7
218039_at	NUSAP1	Hs.511093	51203	35.7
203011_at	IMPA1	Hs.492120	3612	35.7
201036_s_at	HADHSC	Hs.438289	3033	35.7
201017_at	EIF1AX	Hs.522590	1964	35.7
218858_at	DEPDC6	Hs.303788	64798	35.7

probe	Gene	Unigene	Locus	%AML cases with underexpression
213357_at	GTF2H5	Hs.356224	404672	35.7
201083_s_at	BCLAF1	Hs.486542	9774	35.7
218620_s_at	HEMK1	Hs.517987	51409	35.7
218236_s_at	PRKD3	Hs.173536	23683	35.7
204695_at	CDC25A	Hs.1634	993	35.7
221248_s_at	WHSC1L1	Hs.32099	54904	35.7
210547_x_at	ICA1	Hs.487561	3382	35.7
203955_at	KIAA0649	Hs.533260	9858	35.7
203919_at	TCEA2	Hs.505004	6919	35.7
45633_at	FLJ13912	Hs.47125	64785	35.7
203627_at	IGF1R	Hs.20573	3480	35.7
215288_at	TRPC2	Hs.131910	7221	35.7
203715_at	TBCE	Hs.498143	6905	35.7
219327_s_at	GPRC5C	Hs.446438	55890	35.7
212019_at	RSL1D1	Hs.401842	26156	35.7
211548_s_at	HPGD	Hs.77348	3248	35.7
215942_s_at	GTSE1	Hs.386189	51512	35.7
211280_s_at	NRF1	Hs.298069	4899	35.7
216254_at	PARVB	Hs.475074	29780	35.7
205063_at	SIP1	Hs.533862	8487	35.7
201951_at	ALCAM	Hs.150693	214	35.7
210875_s_at	TCF8	Hs.124503	6935	35.7
220474_at	SLC25A21	Hs.134544	89874	35.7
201922_at	TINP1	Hs.482526	10412	35.0
201432_at	CAT	Hs.502302	847	35.0
200959_at	FUS	Hs.513522	2521	35.0
203538_at	CAMLG	Hs.529846	819	35.0
218256_s_at	NUP54	Hs.430435	53371	35.0
209678_s_at	PRKCI	Hs.478199	5584	35.0
203177_x_at	TFAM	Hs.559835	7019	35.0
209250_at	DEGS1	Hs.299878	8560	35.0
204504_s_at	HIRIP3	Hs.567370	8479	35.0
213134_x_at	BTG3	Hs.473420	10950	35.0
219553_at	NME7	Hs.567487	29922	35.0
202188_at	NUP93	Hs.276878	9688	35.0
211962_s_at	ZFP36L1	Hs.85155	677	35.0
221809_at	RANBP10	Hs.368569	57610	35.0
219156_at	SYNJ2BP	Hs.443661	55333	35.0
205398_s_at	SMAD3	Hs.555881	4088	35.0
213701_at	DKFZp434N2030	Hs.494204	91298	35.0
219769_at	INCENP	Hs.142179	3619	35.0
207206_s_at	ALOX12	Hs.422967	239	35.0
210830_s_at	PON2	Hs.530077	5445	35.0
221760_at	MAN1A1	Hs.102788	4121	35.0
212013_at	PXDN	Hs.332197	7837	35.0

probe	Gene	Unigene	Locus	%AML cases with underexpression
216850_at	SNRPN	Hs.564847	6638	35.0
204439_at	IFI44L	Hs.389724	10964	35.0
205768_s_at	SLC27A2	Hs.11729	11001	35.0
212979_s_at	KIAA0738	Hs.406492	9747	35.0
207996_s_at	C18orf1	Hs.149363	753	35.0
220809_at	FLJ14327	---	79972	35.0
216113_at	ABI2	Hs.471156	10152	35.0
214807_at	---	Hs.99472	---	35.0
207286_at	CEP4	Hs.518767	9662	35.0
200022_at	RPL18	Hs.515517	6141	34.4
217724_at	SERBP1	Hs.530412	26135	34.4
217809_at	BZW2	Hs.487635	28969	34.4
200818_at	ATP5O	Hs.409140	539	34.4
208246_x_at	TK2	Hs.512619	7084	34.4
202330_s_at	UNG	Hs.191334	7374	34.4
207405_s_at	RAD17	Hs.16184	5884	34.4
212677_s_at	KIAA0582	Hs.146007	23177	34.4
218349_s_at	ZWILCH	Hs.21331	55055	34.4
214048_at	MBD4	Hs.35947	8930	34.4
40472_at	LOC254531	Hs.352614	254531	34.4
202894_at	EPHB4	Hs.437008	2050	34.4
204663_at	ME3	Hs.199743	10873	34.4
208146_s_at	CPVL	Hs.233389	54504	34.4
220589_s_at	MDS028	Hs.446098	55846	34.4
220266_s_at	KLF4	Hs.376206	9314	34.4
218899_s_at	BAALC	Hs.533446	79870	34.4
218927_s_at	CHST12	Hs.213088	55501	34.4
217555_at	SMC1L1	Hs.211602	8243	34.4
202260_s_at	STXBP1	Hs.288229	6812	34.4
215630_at	---	---	---	34.4
205215_at	RNF2	Hs.124186	6045	34.4
210024_s_at	UBE2E3	Hs.470804	10477	34.4
209480_at	HLA-DQB1	Hs.409934	3119	34.4
207115_x_at	MBTD1	Hs.369586	54799	34.4
220549_at	FSBP	---	10646	34.4
201171_at	ATP6V0E	Hs.484188	8992	34.4
207737_at	---	---	---	34.4
209067_s_at	HNRPDL	Hs.527105	9987	33.8
212593_s_at	PDCD4	Hs.232543	27250	33.8
213649_at	SFRS7	Hs.309090	6432	33.8
204905_s_at	EEF1E1	Hs.88977	9521	33.8
205353_s_at	PBP	Hs.433863	5037	33.8
204949_at	ICAM3	Hs.353214	3385	33.8
202534_x_at	DHFR	Hs.83765	1719	33.8
201139_s_at	SSB	Hs.546301	6741	33.8

probe	Gene	Unigene	Locus	%AML cases with underexpression
206111_at	RNASE2	Hs.728	6036	33.8
207769_s_at	PQBP1	Hs.534384	10084	33.8
214349_at	LOC388388	Hs.464404	388388	33.8
48808_at	DHFR	Hs.83765	1719	33.8
203095_at	MTIF2	Hs.149894	4528	33.8
213311_s_at	KIAA1049	Hs.415342	22980	33.8
205548_s_at	BTG3	Hs.473420	10950	33.8
217370_x_at	FUS	Hs.513522	2521	33.8
219037_at	CGI-115	Hs.408101	51018	33.8
219212_at	HSPA14	Hs.534169	51182	33.8
221582_at	HIST3H2A	Hs.26331	92815	33.8
202918_s_at	PREI3	Hs.205173	25843	33.8
201767_s_at	ELAC2	Hs.434232	60528	33.8
207011_s_at	PTK7	Hs.90572	5754	33.8
213599_at	OIP5	Hs.567421	11339	33.8
207104_x_at	LILRB1	Hs.149924	10859	33.8
213286_at	ZFR	Hs.435231	51663	33.8
217974_at	TM7SF3	Hs.438641	51768	33.8
207574_s_at	GADD45B	Hs.110571	4616	33.8
212497_at	C14orf32	Hs.437831	93487	33.8
201425_at	ALDH2	Hs.436437	217	33.8
214757_at	---	Hs.533128	---	33.8
204643_s_at	COVA1	Hs.171458	10495	33.8
201876_at	PON2	Hs.530077	5445	33.8
219254_at	FLJ22222	Hs.567578	79701	33.8
212254_s_at	DST	Hs.485616	667	33.8
212478_at	FLJ13910	Hs.75277	64795	33.8
201743_at	CD14	Hs.163867	929	33.8
205762_s_at	DUS4L	Hs.97627	11062	33.8
204083_s_at	TPM2	Hs.300772	7169	33.8
210299_s_at	FHL1	Hs.435369	2273	33.8
211407_at	NDUFB7	Hs.532853	4713	33.8
206112_at	ANKRD7	Hs.371820	56311	33.8
212287_at	SUZ12	Hs.462732	23512	33.1
212773_s_at	TOMM20	Hs.533192	9804	33.1
203346_s_at	MTF2	Hs.31016	22823	33.1
215438_x_at	GSPT1	Hs.528780	2935	33.1
217266_at	RPL15 /// LOC136321 /// LOC402694	Hs.381219	136321 /// 402694 /// 6138	33.1
203474_at	IQGAP2	Hs.291030	10788	33.1
208822_s_at	DAP3	Hs.516746	7818	33.1
218011_at	UBL5	Hs.534477	59286	33.1
203358_s_at	EZH2	Hs.444082	2146	33.1
220668_s_at	DNMT3B	Hs.251673	1789	33.1

probe	Gene	Unigene	Locus	%AML cases with underexpression
217841_s_at	PME-1	Hs.503251	51400	33.1
200894_s_at	FKBP4	Hs.524183	2288	33.1
210829_s_at	SSBP2	Hs.102735	23635	33.1
212060_at	SR140	Hs.529577	23350	33.1
218487_at	ALAD	Hs.1227	210	33.1
218865_at	MOSC1	Hs.497816	64757	33.1
215587_x_at	DHRS8	Hs.282984	51170	33.1
218957_s_at	WDR71	Hs.525017	80227	33.1
211855_s_at	SLC25A14	Hs.194686	9016	33.1
204824_at	ENDOG	Hs.224137	2021	33.1
203341_at	CEBPZ	Hs.135406	10153	33.1
210298_x_at	FHL1	Hs.435369	2273	33.1
205136_s_at	NUFIP1	Hs.525006	26747	33.1
209811_at	CASP2	Hs.368982	835	33.1
201906_s_at	CTDSPL	Hs.475963	10217	33.1
208719_s_at	DDX17	Hs.528305	10521	33.1
215029_at	---	---	---	33.1
213479_at	NPTX2	Hs.3281	4885	33.1
218404_at	SNX10	Hs.520714	29887	33.1
206145_at	RHAG	Hs.120950	6005	33.1
214930_at	SLITRK5	Hs.508337	26050	33.1
219663_s_at	MGC4659	Hs.157527	80757	33.1
220348_at	KBTBD9	Hs.130593	114818	33.1
32088_at	BLZF1	Hs.130746	8548	33.1

[00135] Among the differentially expressed genes, some has been previously shown to be aberrantly expressed in AML. These included WT1 (over-expressed in 84.7% of cases) (33, 34), CD56 (46.5%) (35), CD7 (38.2%) (36, 37), CD33 (36.9%) (38), CD4 (36.3%) (39), CD14 (30.6%) (38), and CD19 (28.0%) (39), while CD34 was under-expressed (36.3%) (40). Interestingly, genes previously reported to be "leukemia stem cell-specific" had also been shortlisted in our screening. This included 18 of the 25 genes reported by Saito et al. (41) to be over-expressed in CD34+CD38- AML cells; the remaining 7 were either over-expressed in <25% of cases (n = 4) or not probed by the HG-U133A array (n = 3). Similarly, we identified 16 of the 21 genes associated with AML stem cells by Kikushige et al. (42); the remaining 5 were either over-expressed in <25% of cases (n = 3) or not probed by our array (n = 2). In sum, of the 35 probed genes previously found to be over-expressed in "leukemia stem cells" (6 were listed by both Saito and Kikushige), 28 were also found to be over-expressed in our analysis (including all 6 common genes) (Table 4).

Table 4. Genes overexpressed in AML "stem cells" according to previous studies and their overexpression in AML according to the present analysis

Gene overexpressed in AML stem cells according to Saito et al. (41)	**Gene overexpressed in AML stem cells according to Kikushige et al. (42)**	**AML cases with overexpression in this study (%)**
WT1		84.7
FCGR2C, CD32	FCGR2C, CD32	76.4
DOK2		70.1
	CD96	66.9
HCK		65.6
CD86	CD86	64.3
	CD44	64.3
C1QR1, CD93		56.7
ITGB2, CD18	ITGB2, CD18	52.9
	CSF1R, CD115	51.0
IL2RA, CD25	IL2RA, CD25	47.8
LY86		43.3
IL7R, CD127		42.0
	CD99	42.0
	IL17R	39.5
CD97	CD97	37.6
CD33	CD33	36.9
	CD9	36.9
CD1C		35.7
AK5		33.1
BIK		31.2
	CD47	30.6
TNFRSF4, CD134		29.3
	CD84	29.3
IL2RG, CD132		27.4
	ITGB7	27.4
CEACAM6, CD66c		26.8
	FLT3	25.5
CD180		<25
CTSC		<25
PDE9A		<25
CD24		<25
	CD36	<25
	CD123	<25
	ITGAE	<25
LRG1		Not on HG-U133A array
SUCNR1		Not on HG-U133A array
TNFSF13B		Not on HG-U133A array

	CLL-1	Not on HG-U133A array
	TIM-3	Not on HG-U133A array

[a]Gene expression was studied by HG-U133A oligonucleotide microarrays in157 AML samples and 7 samples of normal CD34+ myeloid progenitors. Shown is the percentage of AML cases with expression signals higher than 2-fold of the highest value obtained among normal CD34+ myeloid cells

Flow cytometric analysis of proteins encoded by aberrantly expressed genes

[00136] Some of genes differentially expressed by gene array analysis (e.g., CD7, CD19, CD56) encoded proteins already used as flow cytometric markers for MRD studies (8, 20, 21, 24, 25, 28, 31, 35, 43, 44), suggesting that mining the microarray data might uncover other useful markers. For further studies, we prioritized genes that were a) differentially expressed in at least 33% of cases of AML; b) over-expressed by at least 5-fold of the maximum value in normal cells, or under-expressed by at least 5-fold of the minimum value; c) targetable by commercially available, fluorochrome-conjugated, antibodies. We selected 24 genes (22 over-expressed in AML, 1 under-expressed, and 1 over-expressed in some cases and under-expressed in others) (Table 5). To these, we added *CD47*, *CD123, TIM3*, and *CLEC12A (CLL-1)*, which had been previously associated with AML stem-cells (42, 45-47). In our gene expression analysis, *CD47* and *CD123* were overexpressed in <33% of cases and had not met our selection criteria; *TIM3* and *CLEC12A (CLL-1)* were not probed by the HG-U133A oligonucleotide microarray.

Table 5. Differentially expressed markers according to gene array analysis selected for further studies

Probe	**Symbol and/or common name**	**% of AML cases with differential expression[a]**
Overexpressed in AML		
202638_s_at	ICAM1, CD54	84.1
204655_at	CCL5, RANTES	80.3
211395_x_at	FCGR2C, CD32	76.4
214511_x_at	FCGR1A, CD64	75.8
205898_at	CX3CR1	73.2
206761_at	CD96	66.9
205686_s_at	CD86	64.3
212014_x_at	CD44	64.3

207277_at	CD209	59.2
202878_s_at	C1QR1, CD93	56.7
215049_x_at	CD163	56.1
202803_s_at	ITGB2, CD18	52.9
207270_x_at	CD300C	52.9
203104_at	CSF1R, CD115	51.0
211269_s_at	IL2RA, CD25	47.8
201028_s_at	CD99	42.0
203507_at	CD68	41.4
202910_s_at	CD97	37.6
219669_at	CD177	37.6
201005_at	CD9	36.9
209582_s_at	CD200	34.4
204912_at	IL10RA, CD210	33.1
204661_at	CD52	28.7
Underexpressed in AML		
200985_s_at	CD59	65.6
34210_at	CD52	28.0

[a]Gene expression was studied by HG-U133A oligonucleotide microarrays in 157 AML samples and 7 samples of normal CD34+ myeloid progenitors. Shown is the percentage of AML cases with expression signals higher than 2-fold of the highest value obtained among normal CD34+ myeloid cells ("overexpressed in AML") or at least 50% lower than the lowest signal among the normal CD34+ myeloid cells ("underexpressed in AML").

[00137] After confirming the specificity of the antibodies with positive and negative target cells (Table 1), we tested the expression of the 28 selected markers in 191 AML and 63 leukemia-free bone marrow samples. These were from either healthy donors (n = 23) or children with leukemia on therapy and MRD-negative (n = 40); many of the latter samples contained high proportions of regenerating $CD34^+$ myeloid progenitors. Six of the 28 markers (CD115, CD163, CD177, CD209, CD210, and CCL5/Rantes) were expressed in AML cells at levels too low to allow reliable MRD studies and were excluded from further studies. Among the remaining 22 markers, expression in AML was significantly different ($P<0.01$) for 16: CD9, CD32, CD44, CD52, CD54, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CX3CR1, and Tim-3 were predominantly over-expressed, while CD59 was predominantly under-expressed, in agreement with the gene array result (FIG. 1). For the other 6 markers, differences between leukemic and normal cells were either not statistically

significant (CD18, CD47, CD200, and CLEC12A; P > 0.1), or yielded a higher P value (CD25, P = 0.049; CD300a, P = 0.020). Regardless, some AML cases had clear over- or under-expression (FIG. 2), suggesting their potential as markers for MRD studies.

[00138] For each of the 22 markers, we determined the number of AML cases that expressed them at a median fluorescence intensity (MFI) higher than the maximum level seen among normal CD34+ myeloid cells plus 1 standard deviation (SD), or lower than the lowest value minus 1 SD. By these criteria, the 22 markers were differentially expressed in 14.8%-57.3% (median, 36.5%) of cases (Table 6). Interestingly, several (CD18, CD44, CD47, CD52, CD59, CD97, CD123, CD200, and CD300a) were over-expressed in some cases and under-expressed in others.

Table 6. Expression of the new markers in AML cells relative to their expression in non-leukemia bone marrow $CD34^+$ cells expressing CD13 and/or CD33 as determined by flow cytometry

Marker	Number of AML cases studied	Number of non-leukemic bone marrow studied	Number of AML cases with over-expression [a]	Number of AML cases with under-expression [b]	% AML cases with over- or under-expression
CD18	82	15	15	32	57.3
CD54	142	33	79	0	55.6
CD52	96	16	34	17	53.1
CD97	96	29	50	0	52.1
CD96	65	14	32	0	49.2
CD59	146	33	7	63	47.9
CD200	132	18	25	35	45.5
CD44	148	38	53	12	43.9
CX3CR1	99	18	43	0	43.4
TIM-3	98	27	40	0	40.8
CD300a	145	27	26	28	37.2
CD86	123	25	44	0	35.8
CD123	93	11	29	4	35.5
CD32	87	13	27	0	31.0
CD9	98	28	28	0	28.6
CD99	95	20	25	0	26.3
CD64	146	22	43	0	29.5
CLEC12A	68	9	15	0	22.1
CD47	67	11	7	7	20.9
CD68	139	21	24	0	17.3
CD25	87	13	14	0	16.1
CD93	88	13	13	0	14.8

[a] Number of AML cases that expressed the indicated marker at levels higher than the highest mean fluorescence intensity (MFI) value (+1 SD) recorded among normal CD34+ myeloid progenitors.

[b] Number of AML cases that expressed the indicated marker at levels lower than the lowest MFI (- 1 SD) measured in normal CD34+ myeloid progenitors.

The new markers persist at relapse and are expressed on AML with stem cell features

[00139] Leukemia subclones at diagnosis may become predominant at relapse, resulting in immunophenotypic shifts (25). We determined the prevalence of expression shifts using paired samples collected at diagnosis and relapse from 16 AML patients, for a total of 168 tests. As shown in FIG. 3A, in 146 of the 168 (86.9%) tests, a new marker was aberrantly expressed at diagnosis and remained aberrantly expressed at relapse. In an additional 13 (7.7%) tests, a new marker not present at diagnosis was detected at relapse. In only 9 (5.4%) tests, an aberrantly expressed marker at diagnosis reverted to normal range at relapse. Importantly, in all 16 patients studied, markers aberrantly expressed at diagnosis in more than 50% of blasts remained abnormally expressed at relapse (FIG. 7). Thus, the new markers remained prevalently expressed at relapse, indicating that their aberrant expression extended to virtually all sub-clones within the leukemic cell populations.

[00140] The potential usefulness of the new markers was further corroborated by studies of marker expression in AML cells with phenotypic features associated with leukemia stem-cells, e.g., CD34-positive, CD38-dim/negative. We studied 12 diagnostic samples containing 13% to 65% (median, 27%) AML stem cells. Collectively, the new markers were aberrantly expressed in these cells and in the more mature CD38-bright cells in 48 tests (43 over-expressed in both subsets, 5 under-expressed in both subsets) while in an additional 12, clear aberrant expression was confined to the stem cell subset. In only 5 tests, the markers were aberrantly expressed in the more mature cells but were within the normal range in the stem cell population. Although variations in expression intensity among AML subsets with different maturity features were observed, marker expression largely overlapped: median MFI for the overexpressed markers in AML stem cells was 104% (27% to 597%) of that in more mature cells (FIGs. 3B, 3C, and 8).

Validation of the new markers for MRD detection

[00141] The above results indicated that the new markers should allow reliable detection of MRD. This assumption was tested in 190 bone marrow and 18 peripheral blood samples which were collected from 52 patients with AML (35 children and 17 adults) during treatment (68 at the end of the first or second cycle of remission induction therapy, and 140 collected subsequently), for a total of 720 tests. In all 52 patients, at least one of the new markers had been found to be abnormally expressed at diagnosis. We used 8-marker panels including CD34, CD117, CD45 and CD33 in addition to the new markers.

[00142] By standard flow cytometric methods (Table 7) (24, 27), 54 of the 208 samples studied had 0.01% or more leukemic cells (0.01% to <0.1%, 7; ≥ 0.1%, 47), and 154 had no detectable leukemic cells. There was an excellent correlation between these results and those obtained with the new marker combinations (FIG. 4A). All 54 specimens with MRD according to the standard method also had MRD by the new markers, with levels of MRD estimated by the two sets of markers generally matching (Spearman r = 0.9816, P <0.0001). Moreover, in 3 samples where the standard MRD markers failed to detect residual leukemic cells, the new markers revealed the presence of 0.10%, 0.19% and 0.28% leukemic cells (FIG. 4A).

[00143] To be useful for MRD studies, leukemia markers should persist despite exposure to chemotherapy. To this end, we measured levels of expression in leukemic cells of 27 patients who had MRD ≥0.1% during treatment according to standard flow cytometric methods (Table 7). FIG. 4B shows data obtained for 6 markers; data for 13 additional markers are shown in FIG. 9. Overall, expression levels remained beyond the threshold of the maximum normal value (or minimum for CD59) plus 1 SD; in only 4 of 175 (2.3%) MRD tests (one each for CD54, CD59, CD97 and TIM3), the marker's mean fluorescence intensity crossed that threshold. Thus, exposure to chemotherapy is unlikely to cause false-negative results in MRD studies with these markers.

Table 7. Standard marker panel for MRD studies in AML

FITC	PE	PerCP	APC	PECy7	APCH7	BV421	BV510 or v500
CD13	CD133	CD34	CD117	CD33	CD45	CD38	anti-HLA-Dr
CD15	CD56	CD34	CD117	CD33	CD45	CD19	CD4
CD7	NG2 (7.1)	CD34	CD117	CD33	CD45	CD11b	anti-HLA-Dr
IgG2a	IgG1	CD34	CD117	CD33	CD45	CD41a	IgG2a

The following antibodies were used: CD13 (WM-47) from Merck; CD15 (MMA), CD56 (NCM16.2), CD34 (8G12), CD33 (P67.6), CD41a (HIP8), CD19 (HIB19), anti-HLA-Dr (G46-6), Mouse IgG1 (X40), Mouse IgG2a (X39), Mouse IgG2a (G155-178), from BD Biosciences; CD38 (HIT2), CD11b (ICRF44), CD4 (OKT4) from Biolegend; CD133 (AC133/1), CD117 (A3C6E2) from Miltenyi Biotec; CD7 (4H9) from eBioscience; NG2 (7.1) from Beckman Coulter.

Association of the new markers with AML subtypes

[00144] We determined whether expression of the new markers identified in this study was associated with clinically relevant features of AML, including *RUNX1-RUNX1T1, CBFB-MYH11*, *MLL* gene rearrangements, *BCR-ABL*, *NPM1* mutations, *FLT3* internal tandem duplications (ITD), monosomy 7, or M7 morphology with or without t(1;22)(p13;q13). We found that aberrant expression of some of the markers was more prevalent in some AML subtypes (FIGs. 5 and 10). Thus, among *RUNX1-RUNX1T1* cases there was a significantly higher prevalence of CD52 ($P < 0.0001$ by Fisher's exact test), CD96 ($P = 0.0012$), CD200 ($P = 0.0002$), CLEC12A ($P = 0.0029$) and TIM3 ($P = 0.0018$) over-expression, while CD59 ($P = 0.0015$) and CD300a ($P < 0.0001$) were particularly under-expressed. Cases with *CBFB-MYH11* commonly over-expressed CD54 ($P = 0.0009$), and CD93 ($P = 0.0016$), those with *MLL* gene rearrangements CD18 ($P = 0.0009$), CD64 ($P < 0.0001$) and CD68 ($P = 0.0090$), and those with *FLT3* ITD CD25 ($P = 0.0047$). Finally, AML M7 cases show a higher prevalence of CD44 ($P < 0.0001$) and CD200 ($P = 0.0002$) under-expression, regardless of whether the t(1;22)(p13;q13) was present or not.

Application of the new markers for MRD monitoring

[00145] Among the 191 AML cases studied for marker expression, 34 (17.8%) had less than 25% leukemic cells expressing CD34. A sub-analysis of the 22 selected markers in these cases was performed, comparing their expression to that of CD117+ CD33+ cells from non-leukemic bone marrow samples, including maturing myeloid cells, monoblasts and erythroblasts, and excluding mature monocytes and granulocytes. As shown in FIG. 11, expression in this subset of AML was significantly different ($P < 0.001$) for 6 of the markers (CD9, CD44, CD86, CD97, CD99, and CX3CR1). For another 8 markers (CD32, CD54, CD59, CD64, CD68, CD123, CD200, CD300a/c) comparisons yielded a higher P value (< 0.05 but > 0.01). For the remaining 8 markers, the differences were not significant ($P > 0.05$), although some AML cases had clear over- or under-expression.

[00146] To visualize how the new leukemia-associated markers could improve the resolution of leukemic and normal cells, artificial mixtures containing various proportions of AML cells and normal bone marrow mononucleated cells (from 2 healthy donors and 2 MRD-negative children with ALL regenerating after chemotherapy) were prepared. The individual samples had been labelled with either the most distinctive set of standard markers

(CD13, CD133 and CD38) or the most distinctive new markers (CD9, CD44, CD54) identified in the AML cells; both standard and new markers had been combined with CD34, CD117, CD45 and CD33, which identified immature myeloid cells. All flow cytometric files were merged, and analyzed by using t-Distributed Stochastic Neighbor Embedding (t-SNE) machine learning algorithm (48). As shown in FIG. 12, the new markers provided a clear separation between AML and normal cells, whereas these overlapped with the best standard markers. FIG. 6C illustrates an experiment in which data from 10 non-leukemic bone marrow samples were superimposed and either analyzed alone or with the addition of data from a diagnostic AML specimen at different concentrations. After conventional gating of CD34, CD33 and CD117 viable single cells, we applied t-SNE. Event at 1 in 100,000 frequency AML cells were clearly distinguishable as separate cluster; a subsequent analysis of the cluster demonstrated the predicted AML marker profile.

[00147] Next, tSNE was used to visualize data from bone marrow samples collected during therapy from two patients with AML in morphologic remission. In one of the samples, one aliquot was labelled with the 4 best available standard markers (CD38, CD133, CD7, and anti-HLA-Dr) and the other with 2 new markers (CD52 and CD47), in addition to CD34, CD117, CD45 and CD33. As shown in FIG. 13, there was considerable overlap between the cells identified as AML and normal immature myeloid cells despite the use of 4 standard MRD markers. By contrast, the cell populations were clearly distinct with the new markers and MRD 0.05% could be unequivocally identified. The second sample illustrates the advantage of adding a new marker (CD96) to standard marker (CD7); addition of CD96 improved the discrimination of MRD, estimated at 0.04%.

[00148] The availability of additional markers should allow MRD studies in patients lacking suitable leukemia-associated immunophenotypes by traditional methods. By improving the resolution of leukemic and normal cells, the sensitivity of the test should also increase. To test these predictions, we applied 8-10-antibody panels including the new markers to 129 consecutive samples obtained from 118 patients with AML at diagnosis and 11 at relapse. FIG. 6A shows the percentage of cases studies with each marker. The immunophenotype of the individual cases is summarized in FIG. 14. The new markers allowed the definition of an aberrant profile for MRD monitoring in all 129 cases. By contrast, panels composed only by traditional markers (Table 7) could not identify an aberrant immunophenotype in 14 of the 129 cases (10.8%). Comparisons between the immunophenotype of AML cells to that of normal hematopoietic cells indicated that the new

markers would allow a sensitivity of MRD detection of 0.01% or better in all 129 cases (0.001% in 52 cases, 40.3%). Sensitivity with the standard markers, however, was limited to 0.1% in 52 (40.3%); in 53 (41.1%) extended to 0.01%, and only in 10 (7.8%) 0.001% could be achieved (FIG. 6B). Hence, the new markers expand the possibility of MRD studies by flow cytometry and increase their sensitivity.

[00149] In 37 children and adolescents with AML treated according to the Malaysia-Singapore AML 2006 protocol after the first course of remission induction therapy, the new markers were used to detect MRD (≥0.01%) in 22 patients, while 15 were MRD negative. As shown in FIG. 15, absence of detectable MRD was associated with a significantly more favorable outcome (P=0.010).

Additional marker combinations

[00150] Table 8 identifies three panels that are combinations of markers.

Table 8

Antibody panel	Established markers to identify immature myeloid cells				New markers to distinguish normal from AML				
1	CD 34	CD 117	CD 33	CD 45	CD 52	CD59 or CD96 or CD300a	TIM3	CD200	CD123
2	CD 34	CD 117	CD 33	CD 45	CD 9	CD93 or CD99 or CLEC12 A	CD44	CD32	CD25
3	CD 34	CD 117	CD 33	CD 45	CD 97	CD54 or CD68 or CX3CR1	CD64	CD86	CD47

[00151] CD34 (8G12), PerCP Cy5.5, BD Biosciences

[00152] CD117 (A3C6E2), APC, Miltenyi Biotec

[00153] CD33 (P67.6), PE-Cy7, BD Biosciences

[00154] CD45 (2D1), APC-H7, Miltenyi Biotec

[00155] CD52 (CF1D12), FITC, Life Technologies

[00156] CD59 (P282; H19), PE, BD Biosciences

[00157] CD96 (6F9), PE, BD Biosciences

[00158] CD300a (E59.126), PE, Beckman Coulter

[00159] TIM3/CD366 (F38-2E2), BV421, Biolegend

[00160] CD200(MRC OX-104), BV510, BD Biosciences

[00161] CD123 (9F5), BV786, BD Biosciences

[00162] CD9 (M-L13), FITC, BD Biosciences

[00163] CD93 (VIMD2), PE, Biolegend

[00164] CD99 (Tü12), PE, BD Biosciences

[00165] CLEC12A/CD371 (50C1), PE, Biolegend

[00166] CD44 (G44-26), BV450, BD Biosciences

[00167] CD32 (FL18.26), BV510, BD Biosciences

[00168] CD25 (2A3), BV786, BD Biosciences

[00169] CD97 (VIM3b), FITC, BD Biosciences

[00170] CD54 (LB-2), PE, BD Biosciences

[00171] CD68 (Y1/82A), PE, BD Biosciences

[00172] CX3CR1/CD181 (2A9-1), PE, Medical & Biological Laboratories

[00173] CD64 (10.1), V450, BD Biosciences

[00174] CD86 (FUN-1), BV510, BD Biosciences

[00175] CD47 (B6H12), BV786, BD Biosciences

[00176] CD18, MEM-48, PE, GeneTex

Discussion

[00177] Sequential measurement of treatment response and, hence, MRD monitoring are essential for a “precision medicine” approach to the clinical management of AML. The only option to monitor MRD in the majority of patients with AML is flow cytometric detection of markers aberrantly expressed in leukemic cells. The soundness of this approach depends entirely on the identification of cell marker profiles that are unequivocally distinct from those expressed by normal hematopoietic cells. In this study, we used genome-wide gene expression analysis to uncover differences between AML cells and CD34+ myeloid hematopoietic cells, which are the most challenging cells to distinguish from AML blasts by flow cytometry because of their close immunophenotypic resemblance (49). The results of

this analysis, enriched by genes previously reported to be differentially expressed in leukemic and normal hematopoietic stem cells, led us to the identification of 22 promising markers which reliably detected MRD in follow-up samples of patients with AML. By expanding the range of markers, the identification of AML cells in the background of normal hematopoiesis was greatly improved. With antibodies panels targeting the new markers, unique leukemia profiles could be defined in all 129 consecutive diagnostic AML samples studied, and the potential sensitivity of MRD detection increased to 1 leukemic cell in 10,000 normal bone marrow cells or greater for all cases. Thus, it is now possible to implement highly sensitive and reliable assays to monitor MRD in all patients with AML.

[00178] Leukemia-associated markers currently used for MRD studies in AML had been identified empirically, primarily by observing flow cytometric data obtained during the process of leukemia diagnosis (49). Instead, our starting point was an unbiased and wide-ranging comparison of gene expression in normal and leukemic cells, an approach that had previously led us to discover new markers for MRD studies in ALL (30). It might be argued that differential expression at mRNA level cannot predict protein expression levels, but the flow cytometric data in our study generally reflected the differences emerging from the gene array comparisons. Mirkowska et al. (50) used mass spectrometry to study protein expression on the surface of ALL cells and amplified leukemic samples through xenograft models to obtain sufficient cell quantities. It is possible that this approach could also be used to discover new markers for AML. To this end, the database that we generated for gene expression of CD34+ normal myeloid cells could also be a useful reference for studies attempting to define the surfaceome of AML by mass spectrometry. Although our gene expression analysis relied on a database of pediatric AML, the immunophenotypic aberrations that we observed extended to adult AML cases. We noted, however, that some markers were particularly prevalent in cases with specific genetic features. For example, cases with *RUNX1-RUNXT1*, an abnormality more common in pediatric than adult AML (51, 52), often had abnormal expression of CD52, CD59, CD96, CD200, CD300a, CLEC12A and TIM3, whereas CD25 was more frequently over-expressed in cases with *FLT3* ITD, more common in adults (53).

[00179] Gene expression differences between normal and leukemic stem cells had been previously noted (41, 42). Our gene-expression results and the immunophenotypic studies of cell subsets within the AML populations study suggest that these differences extend to most leukemic cells, regardless of their stem cell status. Saito et al. (41) used the immunophenotype CD34+ CD38- to sort “leukemia stem cells” from 21 AML samples;

corresponding cells from 5 cord blood or bone marrow samples served as a normal control. Using a similar approach, Kikushige et al. (42) analyzed gene expression of "leukemia stem cells" from 12 AML samples and 5 normal bone marrow samples. Collectively, the two studies identified 40 genes over-expressed in "leukemia stem cells", 35 of which were probed by our HG-U133 array. Surprisingly, all 35 were also found to be overexpressed in our analysis. We tested 5 of these by flow cytometry found that 3 (CD32, CD96 and CD97) were also significantly overexpressed at the protein level, while CD18 and CD25 were less consistently overexpressed. Another marker recently reported to be associated with leukemia stem cells, CD99 (54), was also over-expressed in AML cells according to both our gene expression analysis and subsequent flow cytometric validation. It is noteworthy that CD99 has been proposed to be a targetable marker for immunotherapy (54), and CD123, another marker over-expressed in our group, is being targeted by antibodies and chimeric antigen receptor-T cells for the treatment of AML (46, 55). While the focus of our study was the identification of new markers of AML to track MRD, our database warrant further exploration for targetable markers preferentially expressed in AML cells.

[00180] In patients with AML, a better assessment of treatment response should help predicting relapse and optimize therapy. Therefore, measuring MRD levels at key points during chemotherapy can help steering decisions about intensity of subsequent chemotherapy, eligibility for allogeneic hematopoietic stem cell transplantation, or experimental therapy (1, 56). The markers identified in this study were generally stable during chemotherapy and remained expressed at relapse. MRD levels measured using these markers correlated well with those detectable by standard methods, but the new approach significantly improved sensitivity and allowed MRD measurement in all patients. A limitation of MRD monitoring by flow cytometry has been the requirement for an expert operator to interpret the complex patterns. As demonstrated in this study, the combination of the new markers with contemporary analytical tools, should significantly clarify the distinction between normal and leukemic cells, mitigate the risk of incorrect interpretation, and facilitate the implementation of response-directed therapy in AML.

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INCORPORATION BY REFERENCE AND EQUIVALENTS

[00181] The teachings of all patents, published applications and references cited herein are incorporated by reference in their entirety.

[00182] While example embodiments have been particularly shown and described, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the embodiments encompassed by the appended claims.

CLAIMS

What is claimed is:

1. A method of detecting an expression level of a plurality of markers in a subject, the method comprising:
    a) contacting a sample from the subject with a plurality of probes, wherein:
        i) each probe specifically binds to a single marker;
        ii) the markers are two or more of CD9, CD18, CD25, CD32, CD44, CD47, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CD200, CD300a, CLEC12A, CX3CR1 and Tim-3; and
    b) detecting a complex formed between each probe and corresponding marker in a), wherein a value is generated corresponding to an expression level of each of the markers.

2. A method of diagnosing and treating acute myeloid leukemia in a subject, the method comprising:
    a) contacting a sample from the subject with a plurality of probes, wherein:
        i) each probe specifically binds to a single marker;
        ii) the markers are two or more of of CD9, CD18, CD25, CD32, CD44, CD47, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CD200, CD300a, CLEC12A, CX3CR1 and Tim-3;
    b) detecting a complex formed between each probe and corresponding marker in a), wherein a value is generated corresponding to an expression level of each of the markers;
    c) diagnosing whether the subject has acute myeloid leukemia based on the generated values corresponding to the expression level of the markers; and
    d) administering to the subject diagnosed with acute myeloid leukemia an effective amount of a therapy for treating acute myeloid leukemia.

3. A method of diagnosing acute myeloid leukemia in a subject, the method comprising:
    a) contacting a sample from the subject with a plurality of probes, wherein:

i) each probe specifically binds to a single marker;

ii) the markers are two or more of CD9, CD18, CD25, CD32, CD44, CD47, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CD200, CD300a, CLEC12A, CX3CR1 and Tim-3;

b) detecting a complex formed between each probe and corresponding marker in a), wherein a value is generated corresponding to an expression level of each of the markers; and

c) diagnosing whether the subject has acute myeloid leukemia based on the generated values corresponding to the expression level of the markers.

4. The method of any one of Claims 1-3, wherein the markers are two or more of CD9, CD32, CD44, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CX3CR1 and Tim-3.

5. The method of any one of Claims 1-3, wherein the markers are CD54, CD18, CD96, CD97 and CD99.

6. The method of any one of Claims 1-3, wherein the markers are CD44, CD54, CD18, CD96, CD97 and CD99.

7. The method of any one of Claims 1-3, wherein the plurality of probes is a first set of probes that specifically bind to:

a) CD52;

b) CD59, CD96, or CD300a;

c) TIM3;

d) CD200; and

e) CD123; and

further comprising a second set of probes that specifically bind to:

a) CD34;

b) CD117;

c) CD33; and

d) CD45.

8. The method of any one of Claims 1-3, wherein the plurality of probes is a first set of probes that specifically bind to:

a) CD9;

b) CD93, CD99, or CLEC12A;

c) CD44;

d) CD32; and

e) CD25; and

further comprising a second set of probes that specifically bind to:

a) CD34;

b) CD117;

c) CD33; and

d) CD45.

9. The method of any one of Claims 1-3, wherein the plurality of probes is a first set of probes that specifically bind to:

a) CD97;

b) CD54, CD68, or CXCR1;

c) CD64;

d) CD86; and

e) CD47; and

further comprising a second set of probes that specifically bind to:

a) CD34;

b) CD117;

c) CD33; and

d) CD45.

10. The method of any one of Claims 1-3, wherein the plurality of probes is a first set of probes that specifically bind to:

a) CD54;

b) CD18;

c) CD96;

d) CD97; and

e) CD99; and

further comprising a second set of probes that specifically bind to:

a) CD34;
b) CD117;
c) CD33; and
d) CD45.

11. The method of any one of Claims 1-3, wherein the plurality of probes is a first set of probes that specifically bind to:
a) CD44;
b) CD54;
c) CD18;
d) CD96; and
e) CD97 and CD99; and
further comprising a second set of probes that specifically bind to:
a) CD34;
b) CD117;
c) CD33; and
d) CD45.

12. The method of any one of Claims 1-3, wherein one or more of the probes is an antibody that specifically binds to a single marker.

13. The method of any one of Claims 1-3, wherein contacting the sample from the subject with a plurality of probes comprises subjecting the sample to flow cytometry.

14. The method of any one of Claims 1-3, wherein the value generated is fluorescence intensity.

15. The method of any one of Claims 1-3, wherein the value generated is mean fluorescence intensity or median fluorescence intensity.

16. The method of any one of Claims 1-3, further comprising contacting the sample with an agent that permeabilizes a cell membrane prior to contacting the sample from the subject with a plurality of probes.

17. The method of any one of Claims 1-3, wherein the sample comprises one or more of blood cells, bone marrow, and cellular products derived from blood cells or bone marrow cells.

18. The method of any one of Claims 1-3, wherein the sample is a bone marrow sample.

19. The method of any one of Claims 1-3, wherein the subject has been diagnosed previously with acute myeloid leukemia.

20. The method of any one of Claims 1-3, wherein the acute myeloid leukemia is minimal residual disease in acute myeloid leukemia.

21. The method of any one of Claims 1-3, further comprising contacting the sample with one or more probes that specifically detect one or more genes of Table 2 or Table 3.

22. A method of detecting an expression level of a plurality of markers in a subject, the method comprising:

a) contacting a sample from the subject with a first set of one or more probes and with a second set of one or probes, wherein:

i) each probe of the first set of one or more probes specifically binds to a single marker, wherein the markers to which the first set of probes binds are selected from the group consisting of CD9, CD18, CD25, CD32, CD44, CD47, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CD200, CD300a, CLEC12A, CX3CR1 and Tim-3; and

ii) each probe of the second set of one or more probes specifically binds to a single marker, wherein the markers to which the second set of probes binds are selected from the group consisting of CD45, CD34, CD33, and CD117; and

b) detecting a complex formed between each probe and corresponding marker in a), wherein a value is generated corresponding to an expression level of each of the markers.

23. A method of detecting an expression level of a plurality of markers in a subject, the method comprising:

a) contacting a sample from the subject with a first set of one or more probes and with a second set of one or more probes, wherein:

i) each probe of the first set of one or more probes specifically binds to a single marker, wherein the markers to which the first set of probes binds are selected from the group consisting of CD9, CD18, CD25, CD32, CD44, CD47, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CD200, CD300a, CLEC12A, CX3CR1 and Tim-3; and

ii) each probe of the second set of one or more probes specifically binds to a single marker, wherein the markers to which the second set of probes binds are selected from the group consisting of CD34, CD13 and CD33; and

b) detecting a complex formed between each probe and corresponding marker in a), wherein a value is generated corresponding to an expression level of each of the markers.

24. The method of any one of Claims 22 and 23, wherein:

the first set of probes comprises probes that specifically bind to:

a) CD52;

b) CD59, CD96, or CD300a;

c) TIM3;

d) CD200; and

e) CD123; and

further comprising a second set of probes that specifically bind to:

a) CD34;

b) CD117;

c) CD33; and

d) CD45.

25. The method of any one of Claims 22 and 23, wherein:

the first set of probes comprises probes that specifically bind to:

a) CD9;

b) CD93, CD99, or CLEC12A;

c) CD44;

d) CD32; and

e) CD25; and

the second set of probes comprises probes that specifically bind to:

a) CD34;

b) CD117;

c) CD33; and

d) CD45.

26. The method of any one of Claims 22 and 23, wherein:

the first set of probes comprises probes that specifically bind to:

a) CD97;

b) CD54, CD68, or CXCR1;

c) CD64;

d) CD86; and

e) CD47; and

the second set of probes comprises probes that specifically bind to:

a) CD34;

b) CD117;

c) CD33; and

d) CD45.

27. The method of any one of Claims 22 and 23, wherein

the first set of probes comprises probes that specifically bind to:

a) CD54;

b) CD18;

c) CD96;

d) CD97; and

e) CD99; and

further comprising a second set of probes that specifically bind to:

a) CD34;

b) CD117;

c) CD33; and

d) CD45.

28. The method of any one of Claims 22 and 23, wherein
the first set of probes comprises probes that specifically bind to:
    a) CD44;
    b) CD54;
    c) CD18;
    d) CD96; and
    e) CD97 and CD99; and
further comprising a second set of probes that specifically bind to:
    a) CD34;
    b) CD117;
    c) CD33; and
    d) CD45.

29. The method any one of Claims 22 and 23, wherein one or more of the probes is an antibody that specifically binds to a single marker.

30. The method any one of Claims 22 and 23, wherein contacting the sample from the subject with probes comprises subjecting the sample to flow cytometry.

31. The method any one of Claims 22 and 23, wherein the value generated is fluorescence intensity.

32. The method of any one of Claims 22 and 23, wherein the value generated is mean fluorescence intensity or median fluorescence intensity

33. The method any one of Claims 22 and 23, further comprising contacting the sample with an agent that permeabilizes a cell membrane prior to contacting the sample from the subject with a plurality of probes.

34. The method any one of Claims 22 and 23, wherein the sample comprises one or more of blood cells, bone marrow, and cellular products derived from blood cells or bone marrow cells.

35. The method any one of Claims 22 and 23, wherein the sample is a bone marrow sample.

36. The method any one of Claims 22 and 23, wherein the subject has been diagnosed previously with acute myeloid leukemia.

37. The method of Claims 22 and 23, wherein the acute myeloid leukemia is minimal residual disease in acute myeloid leukemia.

38. The method of any one of Claims 22 and 23, further comprising contacting the sample with one or more probes that specifically detect one or more genes of Table 2 or Table 3.

39. A kit for detecting an expression level of a plurality of markers in a subject, the kit comprising a plurality of probes, wherein:
    a) each of the plurality of probes specifically binds to a single marker; and
    b) the markers are two or more of CD9, CD18, CD25, CD32, CD44, CD47, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CD200, CD300a, CLEC12A, CX3CR1 and Tim-3.

40. A kit for detecting an expression level of a plurality of markers in a subject, the kit comprising a first set of one or more probes and a second set of one or more probes, wherein:
    a) each probe of the first set of one or more probes specifically binds to a single marker, wherein the markers to which the first set of probes binds are selected from the group consisting of CD9, CD18, CD25, CD32, CD44, CD47, CD52, CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CD200, CD300a, CLEC12A, CX3CR1 and Tim-3; and
    b) each probe of the second set of one or more probes specifically binds to a single marker, wherein the markers to which the second set of probes binds are selected from the group consisting of CD45, CD34, CD33 and CD117.

41. A kit for detecting an expression level of a plurality of markers in a subject, the kit comprising a first set of one or more probes and a second set of one or more probes, wherein:
    a) each probe of the first set of one or more probes specifically binds to a single marker, wherein the markers to which the first set of probes binds are selected from the group consisting of CD9, CD18, CD25, CD32, CD44, CD47, CD52,

CD54, CD59, CD64, CD68, CD86, CD93, CD96, CD97, CD99, CD123, CD200, CD300a, CLEC12A, CX3CR1 and Tim-3; and

b) each probe of the second set of one or more probes specifically binds to a single marker, wherein the markers to which the second set of probes binds are selected from the group consisting of CD34, CD13 and CD33.

42. A device for monitoring expression levels of a plurality of markers in a subject, the device comprising:

a) an input member that receives digital representations of a subject sample, the digital representations including flow cytometry outputs corresponding to a plurality of markers;

b) a processor engine coupled to receive from the input member the digital representations, the processor engine responsive to the digital representations and determining parameter values corresponding to an expression level of a marker in the subject sample;

c) a graphics memory module communicatively coupled to the processor engine and transforming the determined parameter values into a graphical representation indicative of expression levels of the plurality of markers in the subject; and

d) a display monitor coupled to the graphics memory module rendering the graphical representation as generated by the graphics memory module.

43. The device of Claim 42, wherein the processor engine applies a t-Distributed Stochastic Neighbor Embedding (tSNE) machine learning algorithm to determine the parameter values in a manner enabling generation of the graphical representation.

44. A processor-based method for monitoring acute myeloid leukemia, the method comprising:

a) receiving by a digital processor flow cytometry output representative of a plurality of markers of a subject sample;

b) in the processor, in response to the flow cytometry output, determining parameter values corresponding to an expression level of a marker in the subject sample, and transforming the parameter values into a graphical representation;

c) outputting the graphical representation to a graphics memory module; and

d) rendering on a display monitor the graphical representation by the graphics memory module.

45. The method of Claim 44, wherein determining parameter values comprises applying a t-Distributed Stochastic Neighbor Embedding (tSNE) machine learning algorithm to transform the values corresponding to an expression level of a marker into a graphical representation.