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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
4 October 2012 (04.10.2012)

WIPO | PCT

(10) International Publication Number
WO 2012/134813 A1

(51) International Patent Classification:
G01N 33/574 (2006.01) *G01N 33/50* (2006.01)

(21) International Application Number:
PCT/US2012/028993

(22) International Filing Date:
14 March 2012 (14.03.2012)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/470,056 31 March 2011 (31.03.2011) US

(71) Applicant *(for all designated States except US)*: **ST. JUDE CHILDREN'S RESEARCH HOSPITAL** [US/US]; 262 Danny Thomas Place, Memphis, TN 38105-2794 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **CAMPANA, Dario** [US/SG]; 105 Clementi Road, 10-03, Block B, Kent Vale, 129789 Singapore (SG). **COUSTAN-SMITH, Elaine** [US/SG]; 105 Clementi Road, 10-03, Block B, Kent Vale, 129789 Singapore (SG).

(74) Agents: **WILLIAMSON, Kelly, J.** et al.; Alston & Bird LLP, Bank of America Plaza, 101 South Tryon Street, Suite 4000, Charlotte, NC 28280-4000 (US).

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

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*

Published:

— *with international search report (Art. 21(3))*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

— *with sequence listing part of description (Rule 5.2(a))*

(54) Title: METHODS AND COMPOSITIONS FOR IDENTIFYING MINIMAL RESIDUAL DISEASE IN ACUTE LYMPHOBLASTIC LEUKEMIA

(57) Abstract: This invention provides methods and kits for diagnosing, ascertaining the clinical course of minimal residual disease associated with acute lymphoblastic leukemia (ALL). Specifically the invention provides methods and kits useful in the diagnosis and determination of clinical parameters associated with diseases associated with ALL based on patterns of surface marker expression unique to ALL.

WO 2012/134813 A1

METHODS AND COMPOSITIONS FOR IDENTIFYING MINIMAL RESIDUAL DISEASE IN ACUTE LYMPHOBLASTIC LEUKEMIA

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

This invention was made with support under United States Government Grant CA60419 awarded by the National Institutes of Health. The United States Government has certain rights in this invention.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

The official copy of the sequence listing is submitted electronically via EFS-Web as an ASCII formatted sequence listing with a file named 415313SEQLIST.txt, created on March 6, 2012, and having a size of 225,858 bytes and is filed concurrently with the specification. The sequence listing contained in this ASCII formatted document is part of the specification and is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

This invention relates generally to the detection of minimal residual disease in patients with acute lymphoblastic leukemia (ALL) and, more specifically, to a method to improve minimal residual disease monitoring for risk assignment and selection of therapeutic regimens.

BACKGROUND OF THE INVENTION

Leukemia relapse is the major cause of treatment failure for patients with acute lymphoblastic leukemia (ALL)(Pui *et al.* (2009) *N Engl J Med.* 360:2730-2741; Gokbuget and Hoelzer (2009) *Semin.Hematol.* 46:64-75; and Faderl *et al.* (2010) *Cancer.* 116:1165-1176). Relapse originates from leukemic cells that are resistant to chemotherapy but become undetectable after initial treatment in most cases. Nevertheless, methods more sensitive than microscopic examination can demonstrate leukemic cells in a proportion of samples with no morphologic evidence of leukemia, a

finding termed "minimal residual disease (MRD)"(Campana (2009) *Hematol.Oncol Clin North Am.* 23:1083-98, vii).

MRD is currently the most powerful prognostic indicator in childhood ALL (Cave *et al.* (1998) *N Engl J Med.* 339:591-598; Coustan-Smith *et al.* (1998) *Lancet.* 351:550-554; van Dongen *et al.* (1998) *Lancet.* 352:1731-1738; Coustan-Smith *et al.* (2000) *Blood.* 96:2691-2696; Dworzak *et al.* (2002) *Blood.* 99:1952-1958; Nyvold *et al.* (2002) *Blood.* 99:1253-1258; Zhou *et al.* (2007) *Blood.* 110:1607-1611; Borowitz *et al.* (2008) *Blood.* 111:5477-5485. Basso *et al.* (2009) *J Clin Oncol.* 27:5168-5174; Conter *et al.* (2010) *Blood.* 115:3206-3214; Stow *et al.* (2010) *Blood.* 115:4657-4663). There is strong evidence supporting its prognostic significance in adult ALL (Krampera *et al.* (2003) *Br J Haematol.* 120:74-79; Vidriales , *et al.* (2003) *Blood.* 101:4695-4700; Raff *et al.* (2007) *Blood.* 109:910-915; Holowiecki *et al.* (2008) *Br.J.Haematol.* 142:227-237; Bassan *et al.* (2009) *Blood.* 113:4153-4162).

Thus, MRD monitoring has been introduced into many contemporary treatment protocols for risk assignment and selection of therapeutic regimens(Pui *et al.* (2009) *N Engl J Med.* 360:2730-2741; Gokbuget and Hoelzer. (2009) *Semin.Hematol.* 46:64-75; and Faderl *et al.* (2010) *Cancer.* 116:1165-1176). MRD measurements are also clinically useful in patients with relapsed ALL who achieve a second remission (Coustan-Smith *et al.* (2004) *Leukemia* 18:499-504; Paganin *et al.* (2008) *Leukemia.* 22:2193-2200; Raetz *et al.* (2008) *J Clin.Oncol.* 26:3971-3978), can help optimize the timing of hematopoietic stem cell transplantation (Bader *et al.* (2009) *J Clin Oncol.* 27:377-384), and guide decisions about donor lymphocyte infusion post-transplant (Lankester *et al.* (2010) *Leukemia.* 24:1462-1469).

Among methods for detecting MRD in ALL, PCR amplification of antigen-receptor genes has proven to be valuable and has been extensively standardized (Bruggemann, M., *et al.* (2010) *Leukemia.* 24:521-535) but the technical expertise and instrumentation required limit its application to specialized centers. PCR amplification of fusion transcripts may also provide useful clinical information but its applicability in ALL is restricted by the fact that molecular targets currently adaptable to routine MRD studies are present in only a minority of patients. *Id.* Flow cytometric detection of leukemia-specific markers has been shown to predict outcome in numerous clinical

correlative studies (Coustan-Smith *et al.* (1998) *Lancet.* 351:550-554; Coustan-Smith *et al.* (2000) *Blood.* 96:2691-2696; Dworzak *et al.* (2002) *Blood.* 99:1952-1958; Borowitz, *et al.* (2008) *Blood.* 111:5477-5485; Basso *et al.* (2009) *J Clin Oncol.* 27:5168-5174; Krampera *et al.* (2003) *Br J Haematol* 120:74-79; Vidriales *et al.* (2003) *Blood.* 101:4695-4700; Holowiecki *et al.* (2008) *Br.J.Haematol.* 142:227-237). The method holds potential for wider applicability than molecular techniques because flow cytometric methods for leukemia diagnosis are already established at most cancer centers worldwide (Campana (2009) *Hematol.Oncol Clin North Am.* 23:1083-98, vii).

MRD studies by flow cytometry rely on panels of antibodies to define unique immunophenotypic signatures of leukemic cells which must distinguish leukemic blasts from their normal counterparts, the CD19+ CD10+ lymphoid progenitors of the bone marrow ("hematogones")(Campana (2009) *Hematol.Oncol Clin North Am.* 23:1083-98, vii; Bruggemann *et al.* (2010) *Leukemia.* 24:521-535; McKenna *et al.* (2001) *Blood.* 98:2498-2507; Lucio *et al.* (2001) *Leukemia.* 15:1185- 1192).

Standard four-color flow cytometry can detect one leukemic cell in up to 10,000 normal bone marrow or peripheral blood cells but this task typically requires considerable interpretative expertise. Therefore, identification of new leukemia markers that are easily detectable and are stably expressed in a large proportion of ALL cases could simplify the application of MRD studies, and help extend their benefit to all patients and enhance the sensitivity of MRD detection.

BRIEF SUMMARY OF THE INVENTION

Methods and compositions are provided for identifying patients with minimal residual disease. The diagnostic methods generally comprise contacting a specimen from a patient with a plurality of probes, wherein each of said probes specifically binds to a distinct marker, wherein a first probe specifically binds to CD19, a second probe specifically binds to CD10, a third probe specifically binds to CD34, a fourth probe specifically binds to CD45, and at least two additional probes that specifically binds to any two of CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102, or CD300a. The complex formed between each of the probes and their marker is detected

and a value is generated corresponding to an expression level of each of said marker. An expression profile is generated by combining the expression level values. In such methods, the expression of CD19, CD10, CD34 and CD45 and a modulated level of at least two of CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164,CD304, CD97, CD99, CD102, or CD300a relative to a normal control is indicative of minimal residual disease in acute lymphoblastic leukemia.

Additional methods for diagnosing minimal residual disease in a subject further include obtaining a specimen from a subject. The specimen is contacted with a plurality of probes, wherein each of the probes specifically binds to a distinct marker, wherein a first probe specifically binds to CD19 and a second probe specifically binds to CD10. A CD19+/CD10+ cell is isolated from the specimen. The expression level of at least two gene products expressed in said CD19+/CD10+ cell is determined, wherein the at least two gene products encode CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a. An expression profile is generated by combining the values generated of the expression levels of the indicated markers. The expression of CD19 andCD10 and a modulated level of at least two gene products encoding CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102, or CD300a relative to a normal control is indicative of minimal residual disease in acute lymphoblastic leukemia.

Kits for practicing the diagnostic methods of the invention are also provided, as well as, kits for evaluating the efficacy of a particular therapy for a subject with ALL.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a comparison of the relative mean fluorescence intensity of immunophenotypic markers expressed in ALL cells and in $CD19^{+}CD10^{+}$ B-cell progenitors as determined by flow cytometry.

Figure 2 shows a comparison of the relative mean fluorescence intensity of immunophenotypic markers expressed in ALL cells and $CD19^{+}CD10^{+}$ B-cell progenitors as determined by flow cytometry.

Figure 3 shows a comparison of new markers to standard markers using flow cytometry.

Figure 4 graphically illustrates the expression of the new markers before, during, and at the end of remission induction therapy.

Figure 5 is a heatmap showing the percentage of cases among the main genetic subtypes of childhood ALL in which the markers studied were differentially expressed by flow cytometry.

Figure 6 is a graphic depiction of additional leukemia-associated markers that can improve resolution of MRD.

DETAILED DESCRIPTION OF THE INVENTION

The present invention will now be described more fully hereinafter with reference to the accompanying drawings, in which some, but not all embodiments of the inventions are shown. Indeed, these inventions may be embodied in many different forms and should not be construed as limited to the embodiments set forth herein; rather, these embodiments are provided so that this disclosure will satisfy applicable legal requirements. Like numbers refer to like elements throughout.

Many modifications and other embodiments of the inventions set forth herein will come to mind to one skilled in the art to which these inventions pertain having the benefit of the teachings presented in the foregoing descriptions and the associated drawings. Therefore, it is to be understood that the inventions are not to be limited to the specific embodiments disclosed and that modifications and other embodiments are intended to be included within the scope of the appended claims. Although specific terms

are employed herein, they are used in a generic and descriptive sense only and not for purposes of limitation.

Methods and compositions are provided for identifying patients with minimal residual disease in acute lymphoblastic leukemia (ALL). As discussed in further detail herein, genes expressed at different levels in ALL cells were compared to their normal counterparts. Using genome-wide gene analysis, expression profiles of 270 cases of newly diagnosed B-lineage ALL were compared to expression profiles of highly purified normal CD19+ CD10+ cells. Genes that had a substantially abnormal expression in leukemic cells were tested by flow cytometry to assess levels of protein expression. Promising molecules were examined in detail for optimization as MRD markers. Use of newly identified markers allows for the identification of unique leukemia profiles in ALL patients. Moreover, the compositions and methods disclosed herein allow for the detection of 1 leukemic cell in 100,000 normal bone marrow cells, thus significantly enhancing the power of flow cytometric monitoring of MRD in ALL.

Acute Lymphocytic Leukemia and Disease

Methods and compositions are provided herein directed to detection of minimal residual disease in acute B-lymphoblastic leukemia.

In specific methods, a specimen is taken from a subject with cancer, wherein the cancer is leukemia. Leukemia is a cancer of the bone marrow and blood. The four major types of leukemia are acute myeloid leukemia (AML), chronic myeloid leukemia (CML), acute lymphoblastic leukemia (ALL) and chronic lymphocytic leukemia (CLL). Acute leukemia is a rapidly progressing cancer that produces blood cells that are not fully developed. Acute lymphocytic leukemia is often referred to as "acute lymphoblastic leukemia" because the leukemic cell that replaces the normal marrow cell is the (leukemic) lymphoblast. There are two principal ALL subtypes including a) the B-lymphocyte subtype – identified by finding cell surface markers on the leukemic blast cells common to normal B lymphocytes; and b) the T lymphocyte subtypes – identified by finding cell surface markers on the leukemic blast cells common to normal T lymphocytes. About 15% of cases are of the T-lymphocyte, and 85% of cases are of the precursor B-cell subtype.

The effects of ALL include uncontrolled and exaggerated growth and accumulation of lymphoblasts which fail to function as normal blood cells, and blockage of the production of normal marrow cells. The lack of production of normal marrow cells often leads to a deficiency of red cells (anemia), platelets (thrombocytopenia) and normal white cells, especially neutrophils (neutropenia), in the blood. ALL progresses rapidly without treatment, therefore the methods and compositions provided herein can be employed to allow for the early detection of acute lymphocytic leukemia.

"Diagnosing ALL" 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 lymphoblastic leukemia (ALL) by identifying or detecting cells and/or cell products in specimens that are indicative of ALL, monitoring the progression of the disease, monitoring and/or detecting the recurrence of ALL disease in patients who had been previously treated for ALL, and monitoring and/or detecting minimal residual disease. The terms "diagnosing," "detecting," and "identifying" when used with acute lymphoblastic 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.

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 ALL, the absence of detectable cancer cells in the body after a course of therapy. Remission in ALL can be characterized, for example, as a lack of detectable abnormal cells in the blood, bone marrow, and/or cerebrospinal fluid, and less than 5% blast cells in the bone marrow. Embodiments of the invention 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. The methods and compositions of the instant invention can detect minimal residual disease with an incidence of less than one in 100,000 cells.

Most ALL 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 of the invention 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 of the invention 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.

In other embodiments of the invention, 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 ALL, including but not limited to chemotherapy, radiation therapy, stem cell transplantation, and biological therapy (*e.g.*, 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.

In still other embodiments of the invention, methods for evaluating the efficacy of a therapy for treating ALL in a subject are provided. Embodiments of the invention 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 of the invention 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 ALL 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 ALL and minimal residual disease is detected.

Specimens from Subjects

In embodiments of the invention, 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 of the invention, 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 of the present invention 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."

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 of the invention 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.

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.

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.

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 Specimens

In embodiments of the invention, 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 a method of the invention, 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.

In embodiments of the invention 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

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 of the invention, antibodies are used to detect marker expression at the protein level. In other aspects of the invention, marker expression is detected at the nucleic acid level.

Markers of the invention 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 ALL. In particular embodiments of the invention, markers can refer to "antigenic markers," "antigens," or "cell surface antigens," referring to proteins that are expressed on the cell surface. Combinations of markers of the invention are selective for ALL, and specifically minimal residual disease.

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.

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 modulate level of marker can include either an increase or a decrease of at least at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or higher relative to an appropriate control.

By "overexpressed" it is intended that the marker of interest is overexpressed in ALL 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 at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or higher relative to an appropriate control.

By "underexpressed" it is intended that the marker of interest is underexpressed in ALL 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 of the invention permit the differentiation of specimens indicative of an increased likelihood of minimal residual disease associated

with ALL as compared to those of normal control specimens that are indicative of nonmalignant and benign proliferation.

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 of the invention, 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). For example, in one embodiment of the invention, "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 at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or higher relative to an appropriate control or at least 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.

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 of the invention, 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). For example, in one embodiment of the invention, "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 at

least 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or lower relative to an appropriate control or at least 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.

The methods of the invention 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 ALL. Markers CD44, BCL2, HSPB1, CD73, CD24, CD123, CD72, CD86, CD200, CD79b, CD164, CD304, CD97, CD102, CD99, CD300a, CD130, PBX1, CTNNA1, ITGB7, CD69, and CD49f were analyzed and found differentially expressed in up to 81.4% of ALL cases. Embodiments of the invention can include, but are not limited to, compositions and methods related to new markers for the detection of minimal residual disease (MRD) comprising: CD44, BCL2, HSPB1, CD73, CD24, CD123, CD72, CD86, CD200, CD79b, CD164, CD304, CD97, CD102, CD99, CD300a, CD130, PBX1, CTNNA1, ITGB7, CD69, and CD49f.

In yet other embodiments, diagnosing minimal residual disease in a sample taken from a subject can comprise the detection of combinations of markers including, but not limited to markers CD19, CD10, CD34, and CD45, in combination with markers comprising: CD44, BCL2, HSPB1, CD73, CD24, CD123, CD72, CD86, CD200, CD79b, CD164, CD304, CD97, CD102, CD99, CD300a, CD130, PBX1, CTNNA1, ITGB7, CD69, or CD49f.

In yet other embodiments, diagnosing minimal residual disease in a sample taken from a subject can comprise the detection of combinations of markers including, but not limited to: CD19, CD10, CD34, and CD45, in combination with marker comprising: CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a.

The methods of the invention 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. These new markers allow MRD studies in all B-lineage ALL patients, and increase the sensitivity of detecting minimal residual disease.

Probes to Detect Markers of Minimal Residual Disease

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.

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.

Embodiments of the invention, include methods and kits comprising probes to detect markers and combinations of markers in TABLE 1 comprising genes overexpressed in B-lineage ALL.

Embodiments of the invention, include methods and kits comprising probes to detect markers and combinations of markers in TABLE 2 comprising genes underexpressed in B-lineage ALL.

Embodiments of the invention include methods and kits comprising probes to detect markers and combinations of markers comprising CD44, BCL2, HSPB1, CD73, CD24, CD123, CD72, CD86, CD200, CD79b, CD164, CD304, CD97, CD102, CD99, CD300a, CD130, PBX1, CTNNA1, ITGB7, CD69, or CD49f.

Embodiments of the invention, include methods and kits comprising a plurality of probes to detect markers and combinations of markers comprising CD19, CD10, CD34, and CD45, and any two of CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164,CD304, CD97, CD99, CD102 or CD300a (See TABLE 3).

Embodiments of the invention include methods and kits comprising contacting a specimen with a plurality of probes to detect expression levels of markers comprising CD19, CD10, CD34, and CD45, and any two of CD44, BCL2, HSPB1, CD73, CD24, CD123, CD72, CD86, CD200, CD79b, CD164, CD304, CD97, CD102, CD99, CD300a, CD130, PBX1, CTNNA1, ITGB7, CD69, or CD49f.

In one embodiment of the invention, a method comprises obtaining a specimen from a subject and contacting the specimen with plurality of probes to detect expression levels of markers. As a first step, the specimen is contacted by a plurality of probes to CD19, CD10, CD34 and CD45 wherein a first probe specifically binds to CD19, a second probe specifically binds to CD10, a third probe specifically binds to CD34, and a fourth probe specifically binds to CD45, and at least two additional probes specifically bind to any two of CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a. As a third step, at least one complex formed between each of said probes and said markers is detected and a value generated, wherein the value corresponds to an expression level of each of said marker. As a fourth step, an expression profile is

generated by combining said values generated. The expression profile displaying each of the markers from step one and those selected in step two is compared to a normal control expression profile. The expression of CD19 andCD10, a modulated level of CD34, and CD45, and a modulated level of at least one of CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a is indicative of minimal residual disease in acute lymphoblastic leukemia.

In yet another embodiment of the invention, the method further comprises contacting the specimen with at least three, four, five, six, seven, or eight additional probes to detect expression levels of markers comprising CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164,CD304, CD97, CD99, CD102 or CD300a.

In another embodiment of the invention, the method further comprises permeabilization of cells in the specimen prior to the contacting the specimen with a probe to detect expression levels of markers comprising CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164,CD304, CD97, CD99, CD102 or CD300a.

In yet another embodiment of the invention, said plurality of probes specifically bind distinct markers comprising: (a) CD10, CD19, CD34, CD45, CD38, CD24, and CD44; (b) CD10, CD19, CD34, CD45, CD38, CD58, and CD44; (c) CD10, CD19, CD34, CD45, CD38, CD73, and CD15; (d) CD10, CD19, CD34, CD45, CD38, CD200, and CD44; (e) CD10, CD19, CD34, CD45, CD66c, CD123, and CD86; (f) CD10, CD19, CD34, CD45, CD72, CD13, and CD33; or (g) CD10, CD19, CD34, CD45, CD79b, HSPB1, and Bcl-2.

In another embodiment of the invention said modulated level comprises the expression of CD34 of CD45.

In yet another embodiment of the invention said modulated level comprises the overexpression of CD44, CD58, CD73, CD200, CD86, HSPB1, BCL2, CD164, CD97, CD99, or CD300a and/or the underexpression of CD38, CD72, or CD79b, relative to a normal control.

Generating Expression Profiles

As used herein, an "expression profile" comprises one or more values corresponding to a measurement of the relative abundance of a gene expression product (i.e., 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.

In embodiments of the invention, 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.

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 according to the invention 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.

In other embodiments of the invention, 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 of the invention 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 of the invention, can include, but are not limited to, the detection of mRNA expression with probe sets shown in TABLE 1 comprising genes overexpressed in B-lineage ALL. Other embodiments of the invention, can include, but are not limited to, the detection of mRNA expression with probe sets shown in TABLE 2 comprising genes underexpressed in B-lineage ALL.

Table 1. Probe sets overexpressed in 25% of more of B-lineage ALL cases (n =270) as compared to normal bone marrow $CD19^{+}CD10^{+}$ cells from 4 healthy donors

probe set ID	CD10+ CD19+ max	CD10+ CD19+ min	ALL max	ALL min	% ALL over expressed	Title	Symbol
205270_s_at	63.1	12.7	2315.9	175.2	100.0	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	LCP2
213915_at	23.3	7.7	3934.2	11.6	98.1	natural killer cell group 7 sequence	NKG7
211745_x_at	907.2	271.5	267381.8	226.1	97.4	hemoglobin, alpha 1 /// hemoglobin, alpha 1	HBA1
214414_x_at	615.5	165.5	196027.6	18.1	97.4	hemoglobin, alpha 2 /// hemoglobin, alpha 2	HBA2
209458_x_at	1028.1	164.7	274466.9	252.3	97.0	hemoglobin, alpha 1 ///hemoglobin, alpha 2	HBA1 /// HBA2
211699_x_at	795.5	176	224904.8	286.1	97.0	hemoglobin, alpha 1 ///hemoglobin, alpha 2	HBA1 /// HBA2
215411_s_at	280	87.6	7183.4	88.9	97.0	TRAF3 interacting protein 2	TRAF3IP2
217414_x_at	445.7	33.4	158800.9	23.6	97.0	hemoglobin, alpha 2	HBA2
209116_x_at	941.1	229.3	313970.9	235.5	96.7	hemoglobin, beta	HBB
211696_x_at	1594.2	428.4	334867.9	455.7	96.7	hemoglobin, beta	HBB
204018_x_at	1005.5	299.1	283177.3	26.8	96.7	hemoglobin, alpha 1 /// hemoglobin, alpha 2	HBA1 /// HBA2
212901_s_at	47.5	36.6	930.7	44.5	96.3	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	CSTF2T
217232_x_at	1632.4	439.5	318351.3	441.5	96.3	hemoglobin, beta	HBB
212195_at	166	116.4	4130.3	211.7	95.9	MRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)	---
208469_s_at	33.4	25.9	517.3	14.1	94.8	palmitoyl-protein thioesterase 2 /// EGF-like-domain, multiple 8	PPT2 /// EGFL8
208820_at	18.3	5.4	1678	6.5	94.8	PTK2 protein tyrosine kinase 2	PTK2
212812_at	247.8	122.3	13345.6	70.7	94.8	CDNA: FLJ22642 fis, clone HSI06970	---
214617_at	130.8	94.1	6399.6	159.5	94.4	perforin 1 (pore forming protein) /// perforin 1 (pore forming protein)	PRF1
204848_x_at	50.9	16.5	120790.8	19.7	94.1	hemoglobin, gamma A /// hemoglobin, gamma G	HBG1 /// HBG2
213515_x_at	356.4	139.2	88491.2	58.9	94.1	hemoglobin, gamma A /// hemoglobin, gamma G	HBG1 /// HBG2

219243_at	37.3	8.5	3807.4	14.9	93.0	GTPase, IMAP family member 4	GIMAP4
206834_at	252.4	49.8	105121.3	49.3	92.2	hemoglobin, delta /// hemoglobin, delta	HBD
218805_at	108.4	57.2	4940.9	80.9	92.2	GTPase, IMAP family member 5 /// GTPase, IMAP family member 5	GIMAP5
215806_x_at	114.2	99.1	8980	33.2	92.2	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 ///	TRGC2 /// TRGV9 ///
204419_x_at	277.7	152.9	124214.1	48.5	92.2	hemoglobin, gamma A /// hemoglobin, gamma G	HBG1 /// HBG2
209200_at	605.5	306.8	8617.6	49.7	92.2	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C
200770_s_at	62.9	33.2	793	25.7	91.5	laminin, gamma 1 (formerly LAMB2)	LAMC1
204497_at	12.9	7.2	3587.5	8.1	91.5	adenylate cyclase 9	ADCY9
213095_x_at	40.2	29	3845.6	28	91.5	allograft inflammatory factor 1	AIF1
203745_at	132.4	83.6	1181.3	77.4	90.7	holocytochrome c synthase (cytochrome c heme-lyase)	HCCS
205950_s_at	223.3	39.9	70148.2	131	90.7	carbonic anhydrase I	CA1
210031_at	60.9	26.7	4613.9	22.6	90.7	CD3Z antigen, zeta polypeptide (TiT3 complex)	CD3Z
208923_at	349.8	238	7825.2	220.5	90.4	cytoplasmic FMR1 interacting protein 1	CYFIP1
212136_at	369.4	317.4	3062.7	228.2	90.4	ATPase, Ca++ transporting, plasma membrane 4	ATP2B4
218589_at	179.1	114.7	11915.5	71.2	90.4	purinergic receptor P2Y, G-protein coupled, 5	P2RY5
220992_s_at	63.6	42.9	664.5	16.6	90.4	chromosome 1 open reading frame 25 /// chromosome 1 open reading frame 25	C1orf25
205898_at	69.3	11.1	4165.5	6.9	90.0	chemokine (C-X3-C motif) receptor 1	CX3CR1
213539_at	160.4	53	7872.8	89.4	90.0	CD3D antigen, delta polypeptide (TiT3 complex)	CD3D
203685_at	229	149.1	5203.8	150.1	89.6	B-cell CLL/lymphoma 2	BCL2
209813_x_at	19.8	9.6	8796.6	11.2	88.9	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 ///	TRGC2 /// TRGV9 ///
205269_at	99.5	58.2	1135.6	60.5	88.5	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	LCP2
212560_at	629	507.9	13410.1	337.8	88.1	chromosome 11 open reading frame 32	C11orf32
215051_x_at	110.9	60.4	8954.9	40.8	88.1	allograft inflammatory factor 1	AIF1
218244_at	284.7	193.9	2035.2	146.7	88.1	nucleolar protein 8	NOL8
65585_at	62.8	19.8	610.3	26.2	87.8	family with sequence similarity 86, member B1	FAM86B1
205592_at	70.1	24.9	36020.7	26.5	87.4	Solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	SLC4A1

215920_s_at	46.3	21.2	631	9.7	87.4	hypothetical protein LOC283970 /// similar to nuclear pore complex interacting protein	LOC283970 /// LOC440350
213500_at	47.6	12.2	836.8	15.8	87.0	Mitochondrial ribosomal protein S22	MRPS22
201841_s_at	302	15.6	8938.9	36.4	86.7	heat shock 27kDa protein 1	HSPB1
215967_s_at	46.2	15.6	1629.1	15.5	86.7	lymphocyte antigen 9	LY9
204774_at	305.5	167.7	6766.7	297.7	86.3	ecotropic viral integration site 2A	EVI2A
202771_at	211.8	40.7	4946.6	19.9	86.3	family with sequence similarity 38, member A	FAM38A
217865_at	188.7	14.9	3581.1	11.3	85.9	ring finger protein 130	RNF130
202615_at	551.3	390.3	4195	16.1	85.9	Guanine nucleotide binding protein (G protein), q polypeptide	GNAQ
219654_at	160.3	106.9	4702.9	17.2	85.9	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	PTPLA
1405j_at	22	5.7	2700.9	7.6	85.6	chemokine (C-C motif) ligand 5	CCL5
200696_s_at	510.4	417	11239.7	359.9	84.8	gelsolin (amyloidosis, Finnish type)	GSN
204547_at	19.3	5.2	885.8	4.4	84.8	RAB40B, member RAS oncogene family	RAB40B
209901_x_at	47.7	36.8	4211	22.6	84.8	allograft inflammatory factor 1	AIF1
207643_s_at	234.7	94.4	3029.5	28	84.1	tumor necrosis factor receptor superfamily, member 1A	TNFRSF1A
210933_s_at	7.4	2.6	785.5	3.3	83.7	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	FSCN1
211821_x_at	26.2	13.7	32574.5	6.5	83.7	glycophorin A (includes MN blood group)	GYPA
32625_at	50.2	34.8	1977.7	13.2	83.7	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	NPR1
203388_at	365.8	102.9	3514.3	116.5	83.3	arrestin, beta 2	ARRB2
203372_s_at	1002.4	316.3	13986.4	31.5	83.3	suppressor of cytokine signaling 2	SOCS2
213541_s_at	631	253.7	9628.5	89.7	82.6	v-ets erythroblastosis virus E26 oncogene like (avian)	ERG
214181_x_at	171.8	56.6	11593.5	15.6	82.2	leukocyte specific transcript 1	LST1
215633_x_at	233.3	128.3	11473.5	22.7	82.2	leukocyte specific transcript 1	LST1
203373_at	1943.6	895.5	26597.2	73.1	82.2	suppressor of cytokine signaling 2	SOCS2
202594_at	453.3	354.8	2346.8	399.3	81.9	leptin receptor overlapping transcript-like 1	LEPROTL1
205173_x_at	604	304.7	7457.7	227.5	81.9	CD58 antigen, (lymphocyte function-associated antigen 3)	CD58
214761_at	244.1	157.3	3051.9	6.8	81.9	zinc finger protein 423	ZNF423
201280_s_at	16.7	7.8	647.9	7.8	81.5	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	DAB2

201906_s_at	37.3	16	2193.9	12.8	81.1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	CTDSPL
213123_at	165.8	55.4	1188.1	20.9	81.1	Microfibrillar-associated protein 3	MFAP3
201681_s_at	25.7	7.4	685.1	3.8	80.7	discs, large homolog 5 (Drosophila)	DLG5
203596_s_at	97.2	22.5	2083.3	34.8	80.7	interferon-induced protein with tetratricopeptide repeats 5	IFIT5
209409_at	203.3	102.3	2142.6	97	80.7	growth factor receptor-bound protein 10	GRB10
209933_s_at	126.1	59.1	1481.7	29.3	80.7	CD300A antigen	CD300A
218831_s_at	55.9	42.5	4423.1	18.8	80.7	Fc fragment of IgG, receptor, transporter, alpha	FCGRT
218689_at	42.1	20	997.9	13.5	80.4	Fanconi anemia, complementation group F	FANCF
202910_s_at	303.4	149.2	6537	31.5	80.4	CD97 antigen	CD97
216942_s_at	275.1	129.2	4763	48.2	80.4	CD58 antigen, (lymphocyte function-associated antigen 3)	CD58
210202_s_at	141.1	45.9	2799.5	18.1	80.4	bridging integrator 1	BIN1
202426_s_at	12.4	10.1	1492.4	6.3	80.0	retinoid X receptor, alpha	RXRA
209568_s_at	371.5	262.5	4854.8	163.5	80.0	ral guanine nucleotide dissociation stimulator-like 1	RGL1
212298_at	10.6	5.6	2155.1	3.3	80.0	neuropilin 1	NRP1
216050_at	9.3	4.5	2263.8	0.9	80.0	CDNA: FLJ20931 fis, clone ADSE01282	---
208010_s_at	15.4	6.4	550.2	2.9	80.0	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	PTPN22
215836_s_at	220.6	114.5	4999.1	75.2	79.6	protocadherin gamma subfamily A1	PCDHGA1
219777_at	45	2.4	3845.4	1.2	79.6	GTPase, IMAP family member 6	GIMAP6
221879_at	67.6	32.7	1584.5	13.1	79.6	calmodulin-like 4	CALML4
219349_s_at	123	63.1	709.7	12.8	79.6	SEC5-like 1 (S. cerevisiae)	SEC5L1
219938_s_at	67.1	43.3	1226.2	10.9	79.6	proline-serine-threonine phosphatase interacting protein 2	PSTPIP2
211582_x_at	295.3	27.2	9348.4	23.1	79.3	leukocyte specific transcript 1	LST1
212070_at	179.3	13.7	7815.2	33.7	79.3	G protein-coupled receptor 56	GPR56
203427_at	262.2	115.7	1968.9	47	79.3	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	ASF1A
201105_at	33.8	10.7	24467.4	7.8	78.9	lectin, galactoside-binding, soluble, 1 (galectin 1)	LGALS1
205099_s_at	17.7	8.1	958.1	7.1	78.9	chemokine (C-C motif) receptor 1	CCR1
202917_s_at	379.2	230.5	76685.5	107.5	78.9	S100 calcium binding protein A8 (calgranulin A)	S100A8
200953_s_at	556.9	302.6	15144.4	183.6	78.5	cyclin D2	CCND2

204563_at	415.7	288.1	16680.8	205	78.5	selectin L (lymphocyte adhesion molecule 1)	SELL
211560_s_at	32.4	17.8	59803.8	11.7	78.1	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)	ALAS2
212267_at	177.1	117.9	2050.8	127.1	78.1	KIAA0261	KIAA0261
222116_s_at	65.2	11.5	991.4	9.7	78.1	TBC1 domain family, member 16	TBC1D16
57715_at	138.8	41.2	1448.5	48.3	78.1	family with sequence similarity 26, member B	FAM26B
210916_s_at	109.2	40.8	4864.2	18.8	78.1	CD44 antigen (homing function and Indian blood group system)	CD44
209199_s_at	1762.1	1338.9	12199.4	66.6	78.1	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C
203232_s_at	7.8	4.1	916.3	4	77.8	ataxin 1	ATXN1
222061_at	60.7	6.9	864.5	13.9	77.8	CD58 antigen, (lymphocyte function-associated antigen 3)	CD58
209129_at	186.6	102.1	1556.4	77.3	77.4	thyroid hormone receptor interactor 6	TRIP6
211986_at	187.8	24.6	7591.2	30.9	77.4	AHNAK nucleoprotein (desmoyokin)	AHNAK
212135_s_at	881.2	583.9	6848.7	471.1	77.4	ATPase, Ca++ transporting, plasma membrane 4	ATP2B4
212349_at	32.2	14.1	413.8	11.1	77.4	protein O-fucosyltransferase 1	POFUT1
209163_at	64.7	37.7	1725.6	9.9	77.4	cytochrome b-561	CYB561
210164_at	56.7	5.5	1828.8	6.5	77.0	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) ///	GZMB
212602_at	79.7	18.9	1360.4	9.6	76.7	WD repeat and FYVE domain containing 3	WDFY3
200878_at	23.4	9.6	1992	6.1	76.3	endothelial PAS domain protein 1	EPAS1
209195_s_at	228.5	65.3	2349.2	62.6	76.3	adenylate cyclase 6	ADCY6
210629_x_at	374.2	216.5	6073.9	65.3	76.3	leukocyte specific transcript 1	LST1
222101_s_at	98.5	31.8	1276	15.3	76.3	dachsous 1 (Drosophila)	DCHS1
218199_s_at	72	66.6	632.1	28.1	76.3	nucleolar protein family 6 (RNA-associated)	NOL6
215543_s_at	281.3	56	1778.6	25.9	75.9	like-glycosyltransferase	LARGE
217730_at	151.8	114.9	1923.4	34.6	75.9	transmembrane BAX inhibitor motif containing 1	TMBIM1
219161_s_at	370.4	214.7	4079.9	48.4	75.9	chemokine-like factor	CKLF
201666_at	287.5	234.5	6650.2	156.8	75.6	TIMP metallopeptidase inhibitor 1	TIMP1
203186_s_at	545.5	147.1	14516.7	171.2	75.6	calvasculin, metastasin, murine placental homolog)	S100A4
203508_at	145.6	13.6	2176.2	28.1	75.6	tumor necrosis factor receptor superfamily, member 1B	TNFRSF1B
205354_at	49.1	25	799.3	13.2	75.6	guanidinoacetate N-methyltransferase	GAMT

210784_x_at	64.6	35.1	1105.8	21.4	75.6	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 /// leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	LILRB2 /// LILRB3
211744_s_at	428.3	296.5	5561.2	148.4	75.6	CD58 antigen, (lymphocyte function-associated antigen 3) /// CD58 antigen, (lymphocyte function-associated antigen 3)	CD58
219672_at	212.5	68.3	31465.9	32.8	75.6	erythroid associated factor	ERAF
202535_at	134.1	94.1	756.6	21.9	75.2	Fas (TNFRSF6)-associated via death domain	FADD
205488_at	133.2	17.6	8624.2	18.7	74.8	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	GZMA
205708_s_at	237.2	32	2798.1	131.5	74.8	transient receptor potential cation channel, subfamily M, member 2	TRPM2
214574_x_at	530.6	84	10726.8	34.4	74.8	leukocyte specific transcript 1	LST1
215177_s_at	145.9	31.5	12400.9	14.6	74.8	integrin, alpha 6	ITGA6
211101_x_at	604.8	512.8	5777.6	123.3	74.8	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	LILRA2
208634_s_at	1744.4	1323.4	8823.5	766	74.4	microtubule-actin crosslinking factor 1	MACF1
209949_at	177.6	37	3712.2	28.7	74.4	neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2)	NCF2
212678_at	181.2	55.4	902.4	70	74.4	Neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)	NF1
219837_s_at	43.5	15.8	8209.4	9.7	74.4	cytokine-like 1	CYTL1
202269_x_at	70.2	15	4634.3	4.2	74.4	guanylate binding protein 1, interferon-inducible, 67kDa /// guanylate binding protein 1, interferon-inducible, 67kDa	GBP1
202481_at	170.6	37.7	3015.7	23.6	74.1	dehydrogenase/reductase (SDR family) member 3	DHRS3
220206_at	62.6	20.4	507.2	7.4	74.1	zinc finger, MYM-type 1	ZMYM1
219753_at	462.7	331.5	29780.3	31	74.1	stromal antigen 3	STAG3
217728_at	358.4	166.7	11349.1	220.3	73.7	S100 calcium binding protein A6 (calcyclin)	S100A6
222217_s_at	459.8	324.6	4162.3	181.3	73.7	solute carrier family 27 (fatty acid transporter), member 3	SLC27A3
210146_x_at	144.2	20.9	2389.3	12.7	73.3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	LILRB2

210225_x_at	74.9	39	1132.5	21.1	73.3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 /// leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	LILRB2 /// LILRB3
217188_s_at	44.3	31.3	866.3	21.9	73.3	chromosome 14 open reading frame 1	C14orf1
207338_s_at	158.2	115.3	967.9	20.4	73.3	zinc finger protein 200	ZNF200
201301_s_at	149.8	88.7	3595.6	11.2	73.3	annexin A4	ANXA4
203591_s_at	55.4	21.3	2647.9	6.6	73.0	colony stimulating factor 3 receptor (granulocyte) /// colony stimulating factor 3 receptor (granulocyte)	CSF3R
204344_s_at	60.7	28.2	753.9	24	72.6	Sec23 homolog A (S. cerevisiae)	SEC23A
212501_at	158.1	115.9	7067.4	15.6	72.6	CCAAT/enhancer binding protein (C/EBP), beta	CEBPB
204249_s_at	863.3	418.4	19159.9	415.6	71.9	LIM domain only 2 (rhombotin-like 1)	LMO2
219326_s_at	671.4	509.7	4219.2	395.1	71.9	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	B3GNT1
202894_at	182	58.6	1507.8	27.6	71.9	EPH receptor B4	EPHB4
218988_at	352.1	173.3	12424.3	59.3	71.9	solute carrier family 35, member E3	SLC35E3
209583_s_at	423.9	313.2	3955.4	42.3	71.9	CD200 antigen	CD200
213817_at	111.9	9.6	1451.4	2	71.9	MRNA; cDNA DKFZp586B0220 (from clone DKFZp586B0220)	---
208047_s_at	40.8	4	714.4	4.9	71.5	NGFI-A binding protein 1 (EGR1 binding protein 1)	NAB1
216920_s_at	169	132.3	9679.7	22.7	71.5	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9	TRGC2 /// TRGV9
204959_at	26.5	7.5	8089.4	3.1	71.5	myeloid cell nuclear differentiation antigen /// myeloid cell nuclear differentiation antigen	MNDA
204438_at	114.4	83.8	12305	5.7	71.5	mannose receptor, C type 1 /// mannose receptor, C type 1-like 1	MRC1 /// MRC1L1
203948_s_at	66.5	15.8	53188	9.1	71.1	myeloperoxidase	MPO
209365_s_at	416.3	51.2	10277.5	46.2	70.7	extracellular matrix protein 1	ECM1
214407_x_at	207	13.6	29217.6	7.7	70.7	glycophorin B (includes Ss blood group)	GYPB
221756_at	235.7	94.4	3467.9	56.7	70.7	HGFL gene /// HGFL gene	MGC17330
216511_s_at	239.9	89	2129.1	12.7	70.7	transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2
206207_at	51.8	26.6	10212	7.2	70.7	Charcot-Leyden crystal protein /// Charcot-Leyden crystal protein	CLC
210547_x_at	39.2	12.8	665.6	13.8	70.4	islet cell autoantigen 1, 69kDa	ICA1

213056_at	257.6	173.8	3516	11.2	70.4	FERM domain containing 4B	FRMD4B
219530_at	137.7	45.3	759	31.1	70.0	hypothetical protein FLJ21816	FLJ21816
222079_at	159.9	99.5	1043.2	38.1	70.0	---	---
207788_s_at	93.1	58.2	2250.2	12.5	70.0	sorbin and SH3 domain containing 3	SORBS3
212196_at	258.2	132.8	3733.9	106	69.6	MRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)	---
215844_at	21.6	10.7	305.1	7	69.6	transportin 2 (importin 3, karyopherin beta 2b)	TNPO2
215706_x_at	363.3	176.5	3611.6	78.6	69.6	zyxin	ZYX
201564_s_at	24.6	9.8	895.5	8.1	69.3	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	FSCN1
208683_at	362.3	288.9	5110.1	178	69.3	calpain 2, (m/II) large subunit	CAPN2
221861_at	202.8	34.1	1381.3	46	69.3	MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	---
200951_s_at	27.7	15.2	2127.3	6	69.3	cyclin D2	CCND2
201328_at	751.6	331.4	7886.4	286.8	68.9	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2
209344_at	630.8	208.5	7920.4	383.3	68.9	tropomyosin 4	TPM4
222303_at	604.5	422	8580.9	42	68.9	---	---
211160_x_at	41.3	19.1	1744.4	10.3	68.5	actinin, alpha 1	ACTN1
204083_s_at	84.2	9.9	1854.6	7.3	68.1	tropomyosin 2 (beta)	TPM2
211100_x_at	604.9	372.9	6014.8	326.2	68.1	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	LILRA2
221679_s_at	24.6	5.4	479	2.9	68.1	abhydrolase domain containing 6	ABHD6
218729_at	227	131.9	5414.4	61.7	68.1	latexin	LXN
221773_at	864.6	342.2	11369.1	83.4	68.1	ELK3, ETS-domain protein (SRF accessory protein 2)	ELK3
200808_s_at	336.8	99.6	3372.4	243	67.8	zyxin	ZYX
205837_s_at	18.2	1.6	5044	1.6	67.8	glycophorin A (includes MN blood group)	GYPA
222062_at	16.1	8.9	674.4	6.8	67.8	interleukin 27 receptor, alpha	IL27RA
218820_at	151	83.1	2129.3	27.9	67.8	chromosome 14 open reading frame 132	C14orf132
204648_at	71.3	15.4	1100	10	67.4	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	NPR1
205289_at	81.6	5.2	3030	5.3	67.4	bone morphogenetic protein 2	BMP2
211066_x_at	362.3	258.9	7663.5	115.2	67.4	protocadherin gamma subfamily A1	PCDHGA1
205067_at	698.3	430.6	6951.6	85.9	67.4	interleukin 1, beta	IL1B

202878_s_at	348.1	242.3	3646.4	147.1	67.0	complement component 1, q subcomponent, receptor 1	C1QR1
211581_x_at	485.2	62.8	6222.2	32.4	67.0	leukocyte specific transcript 1	LST1
212772_s_at	208.1	171.5	1656.3	86.3	67.0	ATP-binding cassette, sub-family A (ABC1), member 2	ABCA2
218522_s_at	241.8	148.4	1323.8	151.3	67.0	BPY2 interacting protein 1	BPY2IP1
221188_s_at	257.9	146.8	1620.6	76	67.0	cell death-inducing DFFA-like effector b	CIDEB
216850_at	23.1	14.9	437.5	4.5	67.0	small nuclear ribonucleoprotein polypeptide N	SNRPN
218532_s_at	220	175.4	3786.7	11.2	67.0	hypothetical protein FLJ20152	FLJ20152
203370_s_at	118.2	45.6	1223	24.7	66.7	PDZ and LIM domain 7 (enigma)	PDLIM7
206337_at	256	77.9	7065.2	126.8	66.7	chemokine (C-C motif) receptor 7 /// chemokine (C-C motif) receptor 7	CCR7
219411_at	35.5	17.4	554.2	11.3	66.7	engulfment and cell motility 3 (ced-12 homolog, C. elegans)	ELMO3
203939_at	121.1	54.3	5133.9	5	66.7	5'-nucleotidase, ecto (CD73)	NT5E
206769_at	43.1	15.2	740.5	10.2	66.3	thymosin, beta 4, Y-linked	TMSB4Y
215076_s_at	18.8	10.3	618.7	7.8	66.3	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	COL3A1
202711_at	77.2	35.2	769.5	10.5	66.3	ephrin-B1	EFNB1
201976_s_at	76.5	12	3468	10	65.9	myosin X	MYO10
209468_at	35.5	9	518.6	9.5	65.9	low density lipoprotein receptor-related protein 5	LRP5
213589_s_at	13.2	8.1	555.7	8.5	65.9	hypothetical protein LOC146712 /// UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	LOC146712 /// B3GNTL1
216352_x_at	21.4	12.4	635.4	7	65.9	protocadherin gamma subfamily A, 3	PCDHGA3
212364_at	56.6	15.9	1780.2	6.8	65.9	myosin IB	MYO1B
209101_at	428	135.6	25930.7	14.5	65.9	connective tissue growth factor	CTGF
201295_s_at	97.5	48.6	1881.2	32.4	65.6	WD repeat and SOCS box-containing 1	WSB1
203470_s_at	138.4	59.7	2050.7	27.3	65.6	pleckstrin	PLEK
209079_x_at	370.2	206.7	7185.2	78.4	65.6	protocadherin gamma subfamily A1	PCDHGA1
219539_at	116.7	24.4	771.3	10.8	65.6	gem (nuclear organelle) associated protein 6	GEMIN6
210299_s_at	280.5	132.8	4488.4	28	65.6	four and a half LIM domains 1	FHL1
210298_x_at	363.7	190.1	7144.3	24.8	65.6	four and a half LIM domains 1	FHL1

207857_at	394.5	181.8	4403.8	146.9	65.2	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	LILRA2
209930_s_at	133.8	7.8	10314	6	65.2	nuclear factor (erythroid-derived 2), 45kDa	NFE2
213694_at	301.2	211.7	3478.4	133.6	65.2	round spermatid basic protein 1	RSBN1
214880_x_at	22.8	6.3	610	3.6	65.2	caldesmon 1	CALD1
211126_s_at	411.4	157.2	4771.5	35.4	65.2	cysteine and glycine-rich protein 2	CSRP2
208146_s_at	25.5	18.8	1653.4	7.6	65.2	carboxypeptidase, vitellogenic-like /// carboxypeptidase, vitellogenic-like	CPVL
213620_s_at	983	871.1	7321.1	233.8	65.2	intercellular adhesion molecule 2	ICAM2
219667_s_at	709.4	360.7	6837.7	12.4	65.2	B-cell scaffold protein with ankyrin repeats 1	BANK1
203957_at	45.1	21.8	893.1	14.2	64.8	E2F transcription factor 6	E2F6
216035_x_at	254.4	26.8	1646.6	26.1	64.8	transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2
207827_x_at	199.3	183	30767.9	21.7	64.8	synuclein, alpha (non A4 component of amyloid precursor)	SNCA
212158_at	35.5	9.5	3320.4	4	64.8	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	SDC2
204422_s_at	9.3	6.5	388.3	2.3	64.8	fibroblast growth factor 2 (basic)	FGF2
211031_s_at	554.3	418.8	4347.1	103.8	64.8	cytoplasmic linker 2 /// cytoplasmic linker 2	CYLN2
214022_s_at	886.2	395.4	26636.7	334.7	64.4	interferon induced transmembrane protein 1 (9-27)	IFITM1
204466_s_at	374.1	223	72280.7	90.1	64.4	synuclein, alpha (non A4 component of amyloid precursor)	SNCA
204683_at	740.3	498.1	4022.8	292.4	64.1	intercellular adhesion molecule 2	ICAM2
210116_at	14.8	3.6	1595.3	4.4	64.1	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	SH2D1A
202023_at	54.6	31.9	1763.8	9.4	64.1	ephrin-A1	EFNA1
204845_s_at	23.5	5.7	406.1	1.2	64.1	glutamyl aminopeptidase (aminopeptidase A)	ENPEP
207979_s_at	120.4	38.6	2307.3	20.4	63.7	CD8 antigen, beta polypeptide 1 (p37)	CD8B1
210140_at	178.3	40.7	5369.7	30.9	63.7	cystatin F (leukocystatin)	CST7
211135_x_at	81.3	25.3	984.1	27.2	63.7	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 /// leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	LILRB2 /// LILRB3
208871_at	55.3	20.9	836.6	9.7	63.7	atrophin 1	ATN1
209683_at	217.1	49.1	2479.7	14	63.7	Family with sequence similarity 49, member A	FAM49A

201944_at	759.8	517	3132.4	663.7	63.3	hexosaminidase B (beta polypeptide)	HEXB
213103_at	56.2	12.6	763.7	10.9	63.3	START domain containing 13	STARD13
202893_at	134.7	39.5	1480.8	15.9	63.3	unc-13 homolog B (C. elegans)	UNC13B
207651_at	42.2	20.3	8734.2	8	63.3	G protein-coupled receptor 171	GPR171
207075_at	23.2	10.2	638.2	8.8	63.0	cold autoinflammatory syndrome 1	CIAS1
212728_at	85.7	26.5	958	27	63.0	discs, large homolog 3 (neuroendocrine-dlg, Drosophila)	DLG3
212063_at	733.2	361.3	15874.7	140.4	63.0	CD44 antigen (homing function and Indian blood group system)	CD44
201508_at	139.5	45.9	2084.8	20.8	63.0	insulin-like growth factor binding protein 4	IGFBP4
218025_s_at	296.9	257.9	1696.4	72.7	63.0	peroxisomal D3,D2-enoyl-CoA isomerase	PECI
202270_at	62.8	14.1	1821.4	4.4	63.0	guanylate binding protein 1, interferon-inducible, 67kDa /// guanylate binding protein 1, interferon-inducible, 67kDa	GBP1
214551_s_at	14.1	5.8	1524.8	3.8	62.6	CD7 antigen (p41)	CD7
220146_at	26.7	3.5	1010.1	2.1	62.6	toll-like receptor 7	TLR7
221786_at	214.2	173.5	1433.7	16.9	62.6	chromosome 6 open reading frame 120	C6orf120
206584_at	99.8	78.1	1102.1	13	62.6	lymphocyte antigen 96	LY96
201601_x_at	604.7	162.7	22080.6	147	62.2	interferon induced transmembrane protein 1 (9-27)	IFITM1
208130_s_at	30.5	11.4	714.8	7.5	62.2	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A)	TBXAS1
210370_s_at	193.2	9	1151.2	11.5	62.2	lymphocyte antigen 9	LY9
218607_s_at	446.2	365	1711.3	254.7	62.2	SDA1 domain containing 1	SDAD1
218613_at	251.9	109.2	2485	44.6	62.2	pleckstrin and Sec7 domain containing 3	PSD3
212975_at	687.4	618.3	10417.7	23	62.2	DENN/MADD domain containing 3	DENND3
207697_x_at	402.5	221.4	4154.4	31.9	62.2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	LILRB2
203192_at	85.8	61	1923.4	18	61.9	ATP-binding cassette, sub-family B (MDR/TAP), member 6	ABCB6
200660_at	38.2	13.9	2700.3	7.8	61.5	S100 calcium binding protein A11 (calgizzarin)	S100A11
202747_s_at	82.5	46.5	7009.4	39.7	61.5	integral membrane protein 2A	ITM2A
203061_s_at	59.9	34	667.2	17.6	61.5	mediator of DNA damage checkpoint 1	MDC1
214450_at	30.1	16.7	2250.8	16.9	61.5	cathepsin W (lymphopain) /// cathepsin W (lymphopain)	CTSW
204304_s_at	115.5	22	13206.2	6.9	61.5	prominin 1	PROM1

218999_at	116.1	33.7	811.4	10.4	61.5	hypothetical protein FLJ11000	FLJ11000
220230_s_at	162.6	11.7	7143.3	4.2	61.5	cytochrome b5 reductase 2	CYB5R2
202242_at	318.5	109	4053.5	17.3	61.5	tetraspanin 7	TSPAN7
214505_s_at	632	262.1	9639.8	188.3	61.1	four and a half LIM domains 1	FHL1
200771_at	309.6	153.2	1480.6	18.1	61.1	laminin, gamma 1 (formerly LAMB2)	LAMC1
220640_at	29.3	13.3	665.2	5.6	61.1	casein kinase 1, gamma 1	CSNK1G1
201809_s_at	398.3	237.2	7012.1	84.2	61.1	endoglin (Osler-Rendu-Weber syndrome 1)	ENG
206718_at	54.8	32.7	691	9.3	61.1	LIM domain only 1 (rhombotin 1)	LMO1
39402_at	495.8	318.6	4822.3	44.9	61.1	interleukin 1, beta	IL1B
201858_s_at	619.5	277.2	69794.9	28.2	61.1	proteoglycan 1, secretory granule	PRG1
202371_at	217.8	113.5	2896.9	9.1	61.1	transcription elongation factor A (SII)-like 4	TCEAL4
218569_s_at	54.1	43.4	610.7	21.8	60.7	kelch repeat and BTB (POZ) domain containing 4	KBTBD4
32502_at	128.3	52.3	758.7	38.5	60.7	glycerophosphodiester phosphodiesterase domain containing 5	GDPD5
218764_at	696.6	275.3	8459	79	60.7	protein kinase C, eta	PRKCH
219686_at	796.9	90	8383	15.6	60.7	serine/threonine kinase 32B	STK32B
220770_s_at	52.6	12.1	360.7	2.5	60.4	transposon-derived Buster3 transposase-like	LOC63920
202664_at	976.9	593.1	6117.3	314.8	60.0	Wiskott-Aldrich syndrome protein interacting protein	WASPIP
219865_at	142.4	71.9	1295.9	40.9	60.0	HSPC157 protein	HSPC157
202430_s_at	120.4	26.3	3812.6	8.4	60.0	phospholipid scramblase 1	PLSCR1
209234_at	97.8	28.5	926.3	9.7	60.0	kinesin family member 1B	KIF1B
222201_s_at	245.9	136.7	1241.3	48.4	60.0	CASP8 associated protein 2	CASP8AP2
209360_s_at	704.4	281	4550	124.2	60.0	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	RUNX1
210895_s_at	106.9	31.9	1392.7	13.6	60.0	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)	CD86
209035_at	195.8	41.2	4059.5	10.9	60.0	midkine (neurite growth-promoting factor 2)	MDK
208370_s_at	726.8	529.7	10489.7	85.9	60.0	Down syndrome critical region gene 1	DSCR1
203535_at	311.5	255.2	52168.5	24.2	60.0	S100 calcium binding protein A9 (calgranulin B)	S100A9
201656_at	136.6	3.2	6443.6	1.7	59.6	integrin, alpha 6	ITGA6
221523_s_at	177.2	83.5	1807.4	64.7	59.6	Ras-related GTP binding D	RRAGD
221565_s_at	167.9	33.8	1912.9	20.9	59.6	family with sequence similarity 26, member B	FAM26B
206434_at	12.7	2.4	810.5	0.7	59.6	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	SPOCK3
206506_s_at	190.3	45.2	2364.9	19	59.6	suppressor of Ty 3 homolog (S. cerevisiae)	SUPT3H

208891_at	997	526.4	13003.4	128.7	59.6	dual specificity phosphatase 6	DUSP6
207785_s_at	445.7	232.5	5173.6	231	59.3	recombining binding protein suppressor of hairless (Drosophila)	RBPSUH
212154_at	129.4	6.7	4850.1	6.7	59.3	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	SDC2
221797_at	76.7	17.6	562.9	9.9	59.3	hypothetical protein LOC339229	LOC339229
202663_at	272.6	108.1	1844.3	50.5	59.3	Wiskott-Aldrich syndrome protein interacting protein	WASPIP
206991_s_at	87.3	60.1	1388.1	29	59.3	chemokine (C-C motif) receptor 5	CCR5
207735_at	228.9	162.1	2162.1	21.7	59.3	ring finger protein 125	RNF125
211144_x_at	179.3	73.4	7308.1	11.8	59.3	T cell receptor gamma constant 2	TRGC2
201315_x_at	2600.3	1198.3	27908.8	1041.3	58.9	interferon induced transmembrane protein 2 (1-8D)	IFITM2
202524_s_at	393.7	350.1	4971.7	235	58.9	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	SPOCK2
209728_at	22	16.3	20171.1	9.5	58.9	major histocompatibility complex, class II, DR beta 4	HLA-DRB4
209892_at	228.2	110.3	3825.8	173.9	58.9	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	FUT4
212768_s_at	8.8	2.4	6175.5	1.6	58.9	olfactomedin 4	OLFM4
214966_at	42.2	11.3	563.1	5.9	58.9	glutamate receptor, ionotropic, kainate 5	GRIK5
217078_s_at	16	4.5	519.5	2.4	58.9	CD300A antigen	CD300A
206582_s_at	54.3	43.6	2710.8	14.3	58.9	G protein-coupled receptor 56	GPR56
214467_at	154.9	77.3	1080.3	55.8	58.5	G protein-coupled receptor 65	GPR65
205571_at	237.2	172.1	1201.6	71.9	58.5	lipoyltransferase 1	LIPT1
220134_x_at	84.4	22.9	803.2	9	58.5	chromosome 1 open reading frame 78	C1orf78
203680_at	168.3	39.3	2787.8	6.3	58.5	protein kinase, cAMP-dependent, regulatory, type II, beta	PRKAR2B
217800_s_at	168.2	122.5	2297.2	7.4	58.5	Nedd4 family interacting protein 1	NDFIP1
203828_s_at	18.5	8.1	3620.8	8.2	58.1	interleukin 32 /// interleukin 32	IL32
217321_x_at	11.7	3.3	310.1	2.2	58.1	Ataxin 3	ATXN3
219423_x_at	103.9	11.1	1087.9	14.1	58.1	tumor necrosis factor receptor superfamily, member 25	TNFRSF25
220187_at	6.4	3	200.6	1.7	58.1	STEAP family member 4	STEAP4
204944_at	6.1	5.3	368.8	2.2	58.1	protein tyrosine phosphatase, receptor type, G	PTPRG
204277_s_at	19.9	11.2	342.4	11.4	57.8	thymidine kinase 2, mitochondrial	TK2
205685_at	76.9	7.2	1077.2	5	57.8	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)	CD86
215933_s_at	1121.5	787.7	11058	214.8	57.8	hematopoietically expressed homeobox	HHEX

218751_s_at	339.1	208	8267.8	45	57.8	F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila)	FBXW7
211796_s_at	382.6	210.2	13295.6	10.4	57.8	T cell receptor beta variable 21-1 /// T cell receptor beta variable 19 /// T cell receptor beta variable 5-4 /// T cell receptor beta variable 3-1 /// T cell receptor beta constant 1	TRBV21-1 /// TRBV19 /// TRBV5-4 /// TRBV3-1 /// TRBC1
206666_at	123.4	33.3	5218.3	20.4	57.4	granzyme K (granzyme 3; tryptase II) /// granzyme K (granzyme 3; tryptase II)	GZMK
212671_s_at	1304.7	118.8	18591.5	149	57.4	major histocompatibility complex, class II, DQ alpha 1 /// DQ alpha 2	HLA-DQA1 /// HLA-DQA2
213262_at	154.3	93.2	1110	21.5	57.4	spastic ataxia of Charlevoix-Saguenay (sacsin)	SACS
218627_at	347.9	213.1	4194.7	69.3	57.4	hypothetical protein FLJ11259	FLJ11259
203354_s_at	37.7	20.5	814.1	8.2	57.4	pleckstrin and Sec7 domain containing 3	PSD3
217572_at	24.3	12.9	2948	4.9	57.4	Transcribed locus, strongly similar to NP_032244.1 hemoglobin alpha 1 chain [Mus musculus]	---
213993_at	15.3	8.7	815	2.8	57.4	spondin 1, extracellular matrix protein	SPON1
212170_at	164.8	106.1	770.6	12.4	57.4	RNA binding motif protein 12	RBM12
205786_s_at	168.7	50.4	5191.4	29.6	57.0	integrin, alpha M	ITGAM
221748_s_at	281.6	132.5	11141.1	85.8	57.0	tensin 1 /// tensin 1	TNS1
222155_s_at	158.3	39.8	1291.3	23.6	57.0	G protein-coupled receptor 172A	GPR172A
200665_s_at	101.3	17.2	3081.6	6.6	57.0	secreted protein, acidic, cysteine-rich (osteonectin) /// secreted protein, acidic, cysteine-rich (osteonectin)	SPARC
211795_s_at	118.4	40.8	2108	20.1	57.0	FYN binding protein (FYB-120/130)	FYB
201212_at	34.6	14.8	1137	4.4	57.0	legumain	LGMN
218695_at	49.5	32.4	816.6	13	57.0	exosome component 4	EXOSC4
208886_at	582.5	77.7	15547	11.8	57.0	H1 histone family, member 0	H1F0
218136_s_at	409	344.1	18019.6	205.2	56.7	solute carrier family 25, member 37	SLC25A37
206734_at	113.3	42.2	701.8	13.9	56.7	jerky homolog-like (mouse)	JRKL
209651_at	114.5	58	865.7	6.7	56.7	transforming growth factor beta 1 induced transcript 1	TGFB1I1
214690_at	13.1	8.5	360.6	2.8	56.7	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	TAF1B
201279_s_at	106.6	14.2	1243.9	7.6	56.3	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	DAB2

210999_s_at	224.7	70.5	3092.9	70.1	56.3	growth factor receptor-bound protein 10	GRB10
212498_at	912.7	724.8	4480.2	570.3	56.3	CDNA FLJ31636 fis, clone NT2RI2003481	---
206229_x_at	46.9	20.7	548.4	8.7	56.3	paired box gene 2	PAX2
219945_at	21.8	13.4	261.9	5.4	56.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	DDX25
206852_at	57.4	10	1522.9	1.8	56.3	EPH receptor A7	EPHA7
209485_s_at	28.9	12.4	1427.2	3.8	56.3	oxysterol binding protein-like 1A	OSBPL1A
204457_s_at	19	7.9	3486.7	4.9	55.9	growth arrest-specific 1	GAS1
206498_at	62.6	26.2	1115.7	18.8	55.9	oculocutaneous albinism II (pink-eye dilution homolog, mouse)	OCA2
209691_s_at	42.9	11	706.7	8	55.9	docking protein 4	DOK4
202446_s_at	557.8	361	16437.5	52.3	55.9	phospholipid scramblase 1	PLSCR1
206674_at	496.6	291.7	11241.8	143.6	55.9	fms-related tyrosine kinase 3	FLT3
217983_s_at	2911.2	1695.5	23933.1	798.4	55.9	ribonuclease T2	RNASET2
219812_at	398.9	90.5	5223.7	44.7	55.9	hypothetical protein MGC2463	MGC2463
205285_s_at	92.8	32.2	933.9	8.6	55.9	FYN binding protein (FYB-120/130)	FYB
202688_at	217.4	76.5	3385.9	50.9	55.6	tumor necrosis factor (ligand) superfamily, member 10	TNFSF10
202710_at	258.9	138.5	1342.8	82.5	55.6	BET1 homolog (S. cerevisiae)	BET1
204116_at	1213.2	604	8123.4	574.9	55.6	interleukin 2 receptor, gamma (severe combined immunodeficiency)	IL2RG
206332_s_at	2150.8	1433.4	10919.1	739.6	55.6	interferon, gamma-inducible protein 16	IFI16
206752_s_at	83.6	13.6	681.7	10.6	55.6	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	DFFB
208657_s_at	138.4	25.5	3249.4	25.4	55.6	septin 9	SEPT9
219487_at	59.7	1.6	551.4	3.1	55.6	hypothetical protein FLJ23560	FLJ23560
203386_at	193.2	109	1626.1	18.5	55.6	TBC1 domain family, member 4	TBC1D4
205640_at	56.9	35.6	1153	15.1	55.6	aldehyde dehydrogenase 3 family, member B1	ALDH3B1
203069_at	66.8	19	844.4	13	55.2	synaptic vesicle glycoprotein 2A	SV2A
204302_s_at	68.2	26.7	944.7	21.1	55.2	KIAA0427	KIAA0427
205290_s_at	176.5	13.9	9212	8.5	55.2	bone morphogenetic protein 2	BMP2
205881_at	117.4	11.6	790.2	25.2	55.2	zinc finger protein 74 (Cos52)	ZNF74
215574_at	78.3	19.4	2858	12.2	55.2	CDNA FLJ11454 fis, clone HEMBA1001463	---
215471_s_at	45.3	17	1245.8	15.9	54.8	microtubule-associated protein 7	MAP7
217936_at	251.3	158.7	1327.8	122.5	54.8	Rho GTPase activating protein 5	ARHGAP5
203264_s_at	75.9	25.6	513.6	9.9	54.8	Cdc42 guanine nucleotide exchange factor (GEF) 9	ARHGEF9

221058_s_at	279.4	210.1	2060.4	24.2	54.8	chemokine-like factor	CKLF
202845_s_at	663.8	459.5	2955	268.7	54.4	ralA binding protein 1	RALBP1
202931_x_at	553.1	343.6	3782.7	233.6	54.4	bridging integrator 1	BIN1
209555_s_at	81.9	8.9	8745.9	6.3	54.4	CD36 antigen (collagen type I receptor, thrombospondin receptor)	CD36
210201_x_at	795.6	608.4	5732.9	359.2	54.4	bridging integrator 1	BIN1
211627_x_at	10.8	4.1	257	2.9	54.4	estrogen receptor 1 /// estrogen receptor 1	ESR1
213193_x_at	720.7	601.7	16080.3	353.1	54.4	T cell receptor beta variable 19 /// T cell receptor beta variable 19 /// T cell receptor beta constant 1 /// T cell receptor beta constant 1	TRBV19 /// TRBC1
218510_x_at	249.7	41.2	4634.1	20.6	54.4	hypothetical protein FLJ20152	FLJ20152
218706_s_at	22.8	5.6	759.6	4	54.4	HCV NS3-transactivated protein 2	NS3TP2
212905_at	250.8	141.5	1185.6	50.5	54.4	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	CSTF2T
206234_s_at	105.2	27.5	839	12.8	54.4	matrix metallopeptidase 17 (membrane-inserted)	MMP17
203678_at	352.4	188.6	1567.1	175.4	54.1	KIAA1018 protein	KIAA1018
204720_s_at	31.5	7.3	1142.5	4.4	54.1	DnaJ (Hsp40) homolog, subfamily C, member 6	DNAJC6
210061_at	74.6	27.7	511.4	14.1	54.1	zinc finger protein 589	ZNF589
220974_x_at	30.1	15.8	1382.3	10.7	54.1	sideroflexin 3 /// sideroflexin 3	SFXN3
204067_at	191.3	43.9	958.5	21.1	54.1	sulfite oxidase	SUOX
200670_at	2422.4	1523	17638.7	508.3	54.1	X-box binding protein 1	XBP1
212731_at	220.1	158.7	830.8	14.9	54.1	ankyrin repeat domain 46	ANKRD46
221527_s_at	136.3	40.6	694.5	10.4	54.1	par-3 partitioning defective 3 homolog (C. elegans)	PARD3
211339_s_at	193	76.6	4748.8	110.2	53.7	IL2-inducible T-cell kinase	ITK
220969_s_at	122.5	79.9	614.7	58.2	53.7	---	---
219130_at	264.9	180.4	1083.9	47.7	53.7	hypothetical protein FLJ10287	FLJ10287
219335_at	165.2	77.7	1285	34.2	53.7	armadillo repeat containing, X-linked 5	ARMCX5
206275_s_at	35.9	9.6	506.5	3.2	53.7	microtubule associated monoxygenase, calponin and LIM domain containing 2	MICAL2
219871_at	36.5	11.9	819.2	4.3	53.7	hypothetical protein FLJ13197	FLJ13197
209213_at	80	41.3	944.1	8.2	53.7	carbonyl reductase 1	CBR1
210746_s_at	51.5	22.9	22040.8	16.6	53.3	erythrocyte membrane protein band 4.2 /// erythrocyte membrane protein band 4.2	EPB42
219528_s_at	139.2	37.1	1828.2	42.7	53.3	B-cell CLL/lymphoma 11B (zinc finger protein)	BCL11B

202336_s_at	22.2	10.3	4372.9	4.8	53.3	peptidylglycine alpha-amidating monooxygenase	PAM
210215_at	54.2	13.4	2653.7	5.7	53.3	transferrin receptor 2	TFR2
216321_s_at	756.7	523.2	10606.3	260.3	53.3	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NR3C1
202932_at	96.3	14	1478.6	3.4	53.3	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	YES1
221920_s_at	275.2	71.1	16582.5	15.1	53.3	solute carrier family 25, member 37	SLC25A37
208071_s_at	465.6	298.2	3598.8	36.7	53.3	leukocyte-associated Ig-like receptor 1	LAIR1
201061_s_at	426	245.6	17977.3	186.3	53.0	stomatin	STOM
212408_at	828.7	649.6	4117	668.9	53.0	torsin A interacting protein 1	TOR1AIP1
221005_s_at	38.9	14.8	491.4	11.5	53.0	phosphatidylserine synthase 2 /// phosphatidylserine synthase 2	PTDSS2
212956_at	276.4	23.5	5870	4.7	53.0	KIAA0882 protein	KIAA0882
217948_at	27.1	19.1	371.1	5.9	53.0	DKFZP564B147 protein	DKFZP564B147
216011_at	47.5	26.8	508	7.3	53.0	Solute carrier family 39 (zinc transporter), member 9	SLC39A9
202949_s_at	33.3	13.6	1345.9	7.5	52.6	four and a half LIM domains 2	FHL2
203387_s_at	266.9	209.8	1701.4	132.2	52.6	TBC1 domain family, member 4	TBC1D4
201540_at	1847.7	885.4	22279.2	224	52.6	four and a half LIM domains 1	FHL1
219315_s_at	171.4	63.4	2139.8	19.8	52.6	chromosome 16 open reading frame 30	C16orf30
205739_x_at	409.9	270.6	4446.8	95.8	52.6	zinc finger protein 588	ZNF588
211909_x_at	7.6	3.7	231	1	52.6	prostaglandin E receptor 3 (subtype EP3) /// prostaglandin E receptor 3 (subtype EP3)	PTGER3
212488_at	794.1	481.3	6100.5	39.7	52.6	collagen, type V, alpha 1	COL5A1
211368_s_at	187.8	104.4	1699.1	4.5	52.6	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1
203349_s_at	218.6	56.9	3919.9	36.4	52.2	ets variant gene 5 (ets-related molecule)	ETV5
206099_at	521.1	140.5	6649.5	98	52.2	protein kinase C, eta	PRKCH
209176_at	78.5	12.3	645.9	10.5	52.2	---	---
215111_s_at	486.3	376.5	8516	194.7	52.2	TSC22 domain family, member 1	TSC22D1
218086_at	26	10.9	3310.3	8.8	52.2	neural proliferation, differentiation and control, 1	NPDC1
217977_at	88.7	35.5	4936.5	15.4	52.2	selenoprotein X, 1	SEPX1
212473_s_at	118.4	85.5	10655.4	6.7	52.2	microtubule associated monoxygenase, calponin and LIM domain containing 2	MICAL2
205717_x_at	452.2	265.9	4246.6	159.1	51.9	protocadherin gamma subfamily A, 1	PCDHGA1

212343_at	43.5	20.4	580.2	13.2	51.9	Yip1 domain family, member 6	YIPF6
202342_s_at	66.7	9.5	492.8	3.4	51.9	tripartite motif-containing 2	TRIM2
216913_s_at	24.9	19.3	1027.2	9.6	51.9	KIAA0690	KIAA0690
211546_x_at	238.6	220.9	24574.6	38.4	51.9	synuclein, alpha (non A4 component of amyloid precursor)	SNCA
220330_s_at	76.6	55.8	1219.5	1.9	51.9	SAM domain, SH3 domain and nuclear localisation signals, 1	SAMSN1
201313_at	59.3	11.7	806.8	8.4	51.5	enolase 2 (gamma, neuronal)	ENO2
209677_at	59.3	10	494.2	6.6	51.5	protein kinase C, iota	PRKCI
208534_s_at	60.8	12.2	1464.6	6	51.5	RAS p21 protein activator 4 /// hypothetical protein FLJ21767	RASA4 /// FLJ21767
212504_at	241.7	71.4	2483.2	32	51.5	KIAA0934	KIAA0934
201329_s_at	863.4	379.9	7961	122.2	51.5	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2
209146_at	118.9	64.6	825.4	6.9	51.5	sterol-C4-methyl oxidase-like	SC4MOL
221526_x_at	245.3	109.5	1393	29.7	51.5	par-3 partitioning defective 3 homolog (C. elegans)	PARD3
214156_at	42.4	17.2	1686.2	3.8	51.5	myosin VIIA and Rab interacting protein	MYRIP
219014_at	1928.5	1774.4	18056.6	300	51.5	placenta-specific 8	PLAC8
200050_at	747.8	270.7	2799	232.9	51.1	zinc finger protein 146 /// zinc finger protein 146	ZNF146
201790_s_at	103.8	21.9	1309.1	15.1	51.1	7-dehydrocholesterol reductase	DHCR7
203611_at	1976.8	1120.4	37006.1	737.2	51.1	telomeric repeat binding factor 2	TERF2
209835_x_at	477.3	245.5	9995.9	168.9	51.1	CD44 antigen (homing function and Indian blood group system)	CD44
212183_at	100.8	17	1555.8	18.8	51.1	nudix (nucleoside diphosphate linked moiety X)-type motif 4	NUDT4
212598_at	41.3	12	536.8	6.1	51.1	WD repeat and FYVE domain containing 3	WDFY3
218113_at	229	70	1840	54.7	51.1	transmembrane protein 2	TMEM2
218486_at	132.3	10.8	3794.5	4.8	51.1	Kruppel-like factor 11	KLF11
54037_at	362.4	285.4	2749.7	98.4	51.1	Hermansky-Pudlak syndrome 4	HPS4
207813_s_at	34.9	27	288.2	8	51.1	ferredoxin reductase	FDXR
207120_at	22.2	11	322.9	2.7	51.1	zinc finger protein 667	ZNF667
214321_at	35.5	22.5	3390.7	3.4	51.1	nephroblastoma overexpressed gene	NOV
204546_at	60.8	16	772.7	8	50.7	KIAA0513	KIAA0513
205467_at	194.7	41.4	1696.3	27.4	50.7	caspase 10, apoptosis-related cysteine peptidase	CASP10

210176_at	198.1	109.2	1127.4	115.6	50.7	toll-like receptor 1	TLR1
211828_s_at	25	7.9	521.9	7.4	50.7	TRAF2 and NCK interacting kinase	TNIK
200999_s_at	220.7	113.6	3758.8	26.4	50.7	cytoskeleton-associated protein 4	CKAP4
206011_at	183.1	75.1	1908.8	12.4	50.7	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1
202517_at	273.9	170.4	6850.3	28.3	50.7	collapsin response mediator protein 1	CRMP1
204747_at	282.2	196.5	5497.8	129.3	50.4	interferon-induced protein with tetratricopeptide repeats 3	IFIT3
205838_at	28.5	9.3	8663.8	6.7	50.4	glycophorin A (includes MN blood group)	GYPA
206098_at	35.9	3.4	206	2.4	50.4	zinc finger protein 482	ZNF482
218825_at	270.2	16.8	3402.2	15.1	50.4	EGF-like-domain, multiple 7	EGFL7
209215_at	294	224.3	2545	82	50.4	tetracycline transporter-like protein	TETRAN
212077_at	70.8	60.4	5341.6	3.6	50.4	caldesmon 1	CALD1
207723_s_at	14	6.5	1469.8	3.3	50.0	killer cell lectin-like receptor subfamily C, member 3	KLRC3
219743_at	71.1	15.2	2565.5	7.9	50.0	hairy/enhancer-of-split related with YRPW motif 2	HEY2
201422_at	434.5	286.1	6636.6	46.9	50.0	interferon, gamma-inducible protein 30	IFI30
201859_at	820.4	406.8	24186.7	181.1	50.0	proteoglycan 1, secretory granule	PRG1
206232_s_at	140.2	32	1423.6	8.3	50.0	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	B4GALT6
200762_at	1427.6	1083.2	10880.8	344.9	50.0	dihydropyrimidinase-like 2	DPYSL2
209679_s_at	361	105.6	2891.8	34.3	50.0	small trans-membrane and glycosylated protein	LOC57228
203153_at	46	5.9	4357.9	7	49.6	interferon-induced protein with tetratricopeptide repeats 1	IFIT1
204310_s_at	24.1	10.3	346.6	5.8	49.6	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	NPR2
206866_at	38.8	11.3	1138.2	6	49.6	cadherin 4, type 1, R-cadherin (retinal)	CDH4
211133_x_at	167.6	48.7	831.3	33.3	49.6	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 /// leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	LILRB2 /// LILRB3
212605_s_at	456.6	387.3	2803.4	247.1	49.6	Nudix (nucleoside diphosphate linked moiety X)-type motif 3	NUDT3
213273_at	114.6	12.6	2460	10.9	49.6	odz, odd Oz/ten-m homolog 4 (Drosophila)	ODZ4
218983_at	90.8	24.9	833.9	10.5	49.6	complement component 1, r subcomponent-like	C1RL

201028_s_at	2047.8	1148.8	19384.2	325.4	49.6	CD99 antigen	CD99
211429_s_at	128.8	61.2	4692.5	21.8	49.6	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	SERPINA1
205041_s_at	8.5	3.2	1537.4	2.6	49.3	orosomucoid 1 /// orosomucoid 2	ORM1 /// ORM2
205418_at	133.4	15.3	890.2	11.3	49.3	feline sarcoma oncogene	FES
205495_s_at	165.1	14.8	3464.4	14.4	49.3	granulysin /// granulysin	GNLY
210314_x_at	176.8	16.3	1177.3	20.7	49.3	tumor necrosis factor (ligand) superfamily, member 13 /// tumor necrosis factor (ligand) superfamily, member 12-member 13	TNFSF13 /// TNFSF12-TNFSF13
209241_x_at	205.9	152.8	1195.2	26.5	49.3	misshapen-like kinase 1 (zebrafish)	MINK1
202145_at	160.4	71.4	2972.7	28.1	49.3	lymphocyte antigen 6 complex, locus E	LY6E
204352_at	516.8	346.2	3368.9	89.5	49.3	TNF receptor-associated factor 5	TRAF5
213233_s_at	508.3	399.2	2437.2	33.5	49.3	kelch-like 9 (Drosophila)	KLHL9
211367_s_at	177.9	76.1	1385.3	6.2	49.3	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1
218690_at	84	56.9	637.1	17.8	49.3	PDZ and LIM domain 4	PDLIM4
220448_at	169.6	93.8	5928.5	4.3	49.3	potassium channel, subfamily K, member 12	KCNK12
201012_at	202.4	40.4	15217.5	79.3	48.9	annexin A1	ANXA1
201325_s_at	41.6	9.2	2026.9	7.8	48.9	epithelial membrane protein 1	EMP1
206871_at	33.4	11.3	43391	8.5	48.9	elastase 2, neutrophil	ELA2
204489_s_at	491.6	46.5	6193.8	22.5	48.9	CD44 antigen (homing function and Indian blood group system)	CD44
212675_s_at	649.7	387.7	3942.6	127.4	48.9	---	---
207733_x_at	133.5	44.8	804.2	11.6	48.9	pregnancy specific beta-1-glycoprotein 9	PSG9
215469_at	9.1	6	491	2.4	48.9	CDNA FLJ11627 fis, clone HEMBA1004225	---
202052_s_at	113.2	17	783.9	9	48.5	retinoic acid induced 14	RAI14
211571_s_at	20.8	5.6	6316.7	4.8	48.5	chondroitin sulfate proteoglycan 2 (versican)	CSPG2
221942_s_at	495.9	272.4	6805.3	76.1	48.5	guanylate cyclase 1, soluble, alpha 3	GUCY1A3
208636_at	475.1	235	5700.3	22	48.5	Actinin, alpha 1	ACTN1
212503_s_at	243.6	152.1	2682.6	52.9	48.5	KIAA0934	KIAA0934
213746_s_at	181.5	133.1	2479.4	15.3	48.5	filamin A, alpha (actin binding protein 280)	FLNA
210262_at	18.9	11.2	1040.7	3.6	48.5	cysteine-rich secretory protein 2	CRISP2
206082_at	517.7	281.3	3082.3	26.6	48.5	---	---
203814_s_at	45.7	11.7	1307.6	6.4	48.1	NAD(P)H dehydrogenase, quinone 2	NQO2

207426_s_at	405.2	164.3	4003.1	88.9	48.1	tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa)	TNFSF4
217382_at	27.6	2.8	671.1	1.5	48.1	similar to Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27) (p64 CLCP) (Chloride channel ABP)	LOC390363
218152_at	397.3	264.4	2145.1	196.1	48.1	high-mobility group 20A	HMG20A
219570_at	98.5	13.1	722.8	12.4	48.1	chromosome 20 open reading frame 23	C20orf23
214439_x_at	738.3	423.3	5005.2	34.9	48.1	bridging integrator 1	BIN1
219956_at	150.6	83.3	1080.7	16.4	48.1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	GALNT6
212820_at	167.8	54.4	2069.3	11.1	48.1	Dmx-like 2	DMXL2
218694_at	175.4	122.2	1524.5	24.4	48.1	armadillo repeat containing, X-linked 1	ARMCX1
205653_at	99.7	74.7	24713.5	17	48.1	cathepsin G	CTSG
205804_s_at	239.2	196.7	1677.1	25.1	48.1	TRAF3 interacting protein 3	TRAF3IP3
203167_at	27.5	21.2	755.1	11.8	47.8	TIMP metallopeptidase inhibitor 2	TIMP2
209286_at	109.6	17.3	3085.9	13.9	47.8	CDC42 effector protein (Rho GTPase binding) 3	CDC42EP3
218758_s_at	122.6	44	901.4	17.9	47.8	DNA segment on chromosome 21 (unique) 2056 expressed sequence	D21S2056E
220618_s_at	78.8	35.1	864.5	14	47.8	zinc finger, CW type with PWWP domain 1	ZCWPW1
216056_at	37.5	20.4	1647.5	6.6	47.8	CD44 antigen (Indian blood group)	CD44
204122_at	194.7	37.7	4519.8	38.5	47.4	TYRO protein tyrosine kinase binding protein	TYROBP
211820_x_at	154	9.9	16977.4	10.9	47.4	glycophorin A (includes MN blood group)	GYPA
213975_s_at	385.3	20.4	11329.4	7.7	47.4	lysozyme (renal amyloidosis) /// leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	LYZ /// LILRB1
203305_at	477	331.4	17615.2	50.6	47.4	coagulation factor XIII, A1 polypeptide	F13A1
203923_s_at	307.5	200.6	2691.8	94.1	47.4	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	CYBB
207705_s_at	244.4	101.3	1962.5	21	47.4	KIAA0980 protein	KIAA0980
218935_at	225.6	98.8	1666.1	18.2	47.4	EH-domain containing 3	EHD3
214433_s_at	176.1	92.2	37065.6	8.9	47.4	selenium binding protein 1 /// selenium binding protein 1	SELENBP1
202382_s_at	27.2	13.3	709.5	6.9	47.0	glucosamine-6-phosphate deaminase 1	GNPDA1

210589_s_at	50.6	33.4	1138.1	22.4	47.0	glucosidase, beta; acid (includes glucosylceramidase) /// glucosidase, beta; acid, pseudogene	GBA /// GBAP
221709_s_at	59.4	16.6	632	15.8	47.0	chromosome 14 open reading frame 131 /// chromosome 14 open reading frame 131	C14orf131
218276_s_at	222.1	153.4	1251.9	51.4	47.0	salvador homolog 1 (Drosophila)	SAV1
216155_at	107.9	19	814.4	5	47.0	Neuron navigator 1	NAV1
219691_at	139	37.5	921.3	10	47.0	sterile alpha motif domain containing 9	SAMD9
215449_at	65.7	45.5	6842.1	16	47.0	benzodiazapine receptor (peripheral)-like 1	BZRPL1
201372_s_at	37.6	12.1	384.9	4.6	47.0	cullin 3	CUL3
207104_x_at	116.2	21.1	980.6	14.4	46.7	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	LILRB1
209370_s_at	401.4	81.6	4041.7	110.9	46.7	SH3-domain binding protein 2	SH3BP2
219359_at	272.8	98	4034.5	56.4	46.7	hypothetical protein FLJ22635	FLJ22635
37145_at	188.7	20.9	2719.8	16.5	46.7	granulysin	GNLY
213117_at	176.9	40.6	1268	13.6	46.7	kelch-like 9 (Drosophila)	KLHL9
210321_at	33.3	16.6	1557.9	6.2	46.7	granzyme H (cathepsin G-like 2, protein h-CCPX) /// granzyme H (cathepsin G-like 2, protein h-CCPX)	GZMH
212509_s_at	874.8	669.9	16097.8	208.4	46.7	matrix-remodelling associated 7	MXRA7
206518_s_at	35.2	14.3	1009.6	2.9	46.7	regulator of G-protein signalling 9	RGS9
205899_at	81.3	41.1	5746.4	6.7	46.7	cyclin A1	CCNA1
219952_s_at	44.5	10.4	1155.8	14.4	46.3	mucolipin 1	MCOLN1
220734_s_at	86.1	20.6	492.2	15.8	46.3	hypothetical protein MGC10334	MGC10334
221014_s_at	150.6	5.4	789.2	61.9	46.3	RAB33B, member RAS oncogene family /// RAB33B, member RAS oncogene family	RAB33B
220615_s_at	206.2	22.1	2746.1	9.3	46.3	male sterility domain containing 1	MLSTD1
200615_s_at	283.8	215.7	2222.3	31.7	46.3	adaptor-related protein complex 2, beta 1 subunit	AP2B1
218954_s_at	51.1	31.2	548.7	8	46.3	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	BRF2
221724_s_at	32.3	26.6	1445.2	9.7	46.3	C-type lectin domain family 4, member A	CLEC4A
212013_at	1198.6	779.9	6768.7	10.4	46.3	peroxidasin homolog (Drosophila)	PXDN
201060_x_at	351.6	243.5	9900.6	143.4	45.9	stomatin	STOM
204928_s_at	26.6	16.4	605.2	12.6	45.9	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	SLC10A3

205758_at	251.6	28.5	2296.3	26.2	45.9	CD8 antigen, alpha polypeptide (p32) /// CD8 antigen, alpha polypeptide (p32)	CD8A
214692_s_at	36.8	18.8	697.7	12.1	45.9	jerky homolog (mouse)	JRK
217904_s_at	54.5	20	988.3	7.2	45.9	beta-site APP-cleaving enzyme 1	BACE1
205391_x_at	97.2	24.1	5144.8	10.1	45.9	ankyrin 1, erythrocytic /// ankyrin 1, erythrocytic	ANK1
215666_at	10.4	4	4868.5	1.7	45.9	major histocompatibility complex, class II, DR beta 4	HLA-DRB4
32042_at	93.3	75.7	657	18.1	45.9	cytosolic ovarian carcinoma antigen 1	COVA1
221485_at	159.7	88.1	2565.1	13.4	45.9	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	B4GALT5
219504_s_at	74.9	32.1	647.3	5.1	45.9	chromosome 1 open reading frame 82	C1orf82
219154_at	139.2	34.7	1223.9	32.3	45.6	ras homolog gene family, member F (in filopodia)	RHOF
201964_at	592.6	317.4	2559.5	146.2	45.6	amyotrophic lateral sclerosis 4	ALS4
206414_s_at	172.8	30.4	1356.5	12.5	45.6	development and differentiation enhancing factor 2	DDEF2
209297_at	64.6	28.3	2212.4	12.9	45.6	intersectin 1 (SH3 domain protein)	ITSN1
221040_at	31.9	7.5	818.7	3.6	45.6	calpain 10	CAPN10
211474_s_at	583.1	390.7	2625.8	126.3	45.6	serpin peptidase inhibitor, clade B (ovalbumin), member 6	SERPINB6
204924_at	164.9	53.5	1519.3	16.7	45.6	toll-like receptor 2	TLR2
218625_at	309.9	197.7	7686.5	59.9	45.6	neuritin 1	NRN1
64408_s_at	69.9	34.2	431.4	7.2	45.6	calmodulin-like 4	CALML4
204030_s_at	777.4	335.9	5350.9	17.8	45.6	schwannomin interacting protein 1	SCHIP1
206048_at	26.8	6	296.3	6	45.2	ovo-like 2 (Drosophila)	OVOL2
207417_s_at	179.2	129.8	960.4	71.8	45.2	zinc finger protein 177	ZNF177
221682_s_at	55.4	3.5	615.7	2.5	45.2	protocadherin gamma subfamily B, 6	PCDHGB6
217143_s_at	148.2	47	2102.9	22.5	45.2	T cell receptor alpha locus /// T cell receptor delta locus	TRA@ /// TRD@
219200_at	193.1	136.2	791	40.9	45.2	hypothetical protein MGC5297	MGC5297
203952_at	98	67.6	671.4	26.8	45.2	activating transcription factor 6	ATF6
205878_at	39.3	19.3	420.9	6.1	45.2	POU domain, class 6, transcription factor 1	POU6F1
212062_at	18.9	10.9	2294.2	4.1	45.2	ATPase, Class II, type 9A	ATP9A
221788_at	76.1	20.4	718.2	4.8	45.2	Phosphoglucomutase 3	PGM3
207821_s_at	245.4	65	1131.2	54.3	44.8	PTK2 protein tyrosine kinase 2	PTK2
222312_s_at	50.8	9	422.6	8.3	44.8	CDNA clone IMAGE:6186815	---
207459_x_at	272.7	55.5	20138.4	19.3	44.8	glycophorin B (includes Ss blood group)	GYPB
218298_s_at	440.3	284.8	2624.6	118.3	44.8	chromosome 14 open reading frame 159	C14orf159

202202_s_at	47.6	9.8	586.4	2.7	44.8	laminin, alpha 4	LAMA4
215354_s_at	147.9	86.6	605	23.4	44.8	proline-, glutamic acid-, leucine-rich protein 1	PELP1
203355_s_at	319.3	149.7	2993.9	23.7	44.8	pleckstrin and Sec7 domain containing 3	PSD3
207030_s_at	394.1	147.2	4873.1	24.3	44.8	cysteine and glycine-rich protein 2	CSRP2
215807_s_at	69	40.2	1184.6	13.1	44.8	plexin B1	PLXNB1
212235_at	152.9	16.9	1270	13.7	44.4	plexin D1	PLXND1
218608_at	170.7	14.9	1358.1	12.8	44.4	ATPase type 13A2	ATP13A2
34726_at	210.8	91.9	901.7	87	44.4	calcium channel, voltage-dependent, beta 3 subunit	CACNB3
202201_at	261.3	56.9	23262.7	27.3	44.4	biliverdin reductase B (flavin reductase (NADPH))	BLVRB
203148_s_at	276.3	157.7	1480.8	42.5	44.4	tripartite motif-containing 14	TRIM14
215719_x_at	61.1	13.9	1175.1	5.9	44.4	Fas (TNF receptor superfamily, member 6)	FAS
222126_at	161	95	1827.7	26	44.4	Insulin receptor substrate 3-like	HRBL
212372_at	618.7	397.6	4614.1	115.8	44.4	myosin, heavy polypeptide 10, non-muscle	MYH10
221994_at	36.1	13.4	347.7	3.8	44.4	PDZ and LIM domain 5	PDLIM5
215028_at	97.8	15.6	1792.1	2.9	44.4	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	SEMA6A
212192_at	127.9	35.5	3244.7	2.6	44.4	potassium channel tetramerisation domain containing 12	KCTD12
203325_s_at	265.4	137.3	2845.4	11.5	44.4	collagen, type V, alpha 1	COL5A1
200699_at	294.6	228	1197.6	124.3	44.1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	KDELR2
218899_s_at	164.5	10.8	3140.6	10.1	44.1	brain and acute leukemia, cytoplasmic	BAALC
217519_at	30.4	4.6	285	2.2	44.1	Microtubule-actin crosslinking factor 1	MACF1
218807_at	562.5	419.2	4141.9	204.2	44.1	vav 3 oncogene	VAV3
210151_s_at	365.9	274.5	1788.9	42.5	44.1	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	DYRK3
215894_at	82.6	6.9	1987	2.1	44.1	prostaglandin D2 receptor (DP)	PTGDR
210783_x_at	163	40.1	1631.4	13	44.1	C-type lectin domain family 11, member A	CLEC11A
205154_at	38	17.4	1093.7	11.5	43.7	leucine rich repeat neuronal 5	LRRN5
210430_x_at	45.3	24.4	5655.9	16.2	43.7	Rhesus blood group, D antigen	RHD
211148_s_at	10.3	4.4	593	4.2	43.7	angiopoietin 2	ANGPT2
222144_at	28.4	13	709.7	10.4	43.7	kinesin family member 17	KIF17
210613_s_at	450.3	135.3	2720.5	25.2	43.7	synaptogyrin 1	SYNGR1
204929_s_at	343.3	181	2094.2	33.4	43.7	vesicle-associated membrane protein 5 (myobrevin)	VAMP5

201807_at	874.5	680.8	4594.7	473.5	43.3	vacuolar protein sorting 26 homolog A (yeast)	VPS26A
207846_at	9.9	1.7	407.8	0.9	43.3	POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1)	POU1F1
200923_at	674.8	262.5	6976.3	63.3	43.3	lectin, galactoside-binding, soluble, 3 binding protein	LGALS3BP
211419_s_at	38.7	9.4	731	4	43.3	chimerin (chimaerin) 2	CHN2
209582_s_at	413.4	242.1	2897.2	106.3	43.3	CD200 antigen	CD200
205131_x_at	255	36.1	2512.6	11.9	43.3	C-type lectin domain family 11, member A	CLEC11A
208322_s_at	188	60.7	2898.8	15.2	43.3	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	ST3GAL1
208198_x_at	73.6	66.4	647.4	21.5	43.3	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1	KIR2DS1
217584_at	61.9	28.2	750.6	4.8	43.3	Niemann-Pick disease, type C1	NPC1
205330_at	200.9	114.6	3525.1	24.7	43.3	meningioma (disrupted in balanced translocation) 1	MN1
214475_x_at	190.4	85.4	4205.9	10.1	43.3	calpain 3, (p94)	CAPN3
211709_s_at	559.3	441.1	5273.2	17.1	43.3	C-type lectin domain family 11, member A /// C-type lectin domain family 11, member A	CLEC11A
204032_at	75.1	13.4	409.7	7.3	43.0	breast cancer anti-estrogen resistance 3	BCAR3
205109_s_at	96.9	8.6	2788.5	5.2	43.0	Rho guanine nucleotide exchange factor (GEF) 4	ARHGEF4
218525_s_at	191.5	59.4	973.3	40.3	43.0	hypoxia-inducible factor 1, alpha subunit inhibitor	HIF1AN
221771_s_at	414.5	191.6	1621.4	150.2	43.0	M-phase phosphoprotein, mpp8	HSMPP8
221933_at	30.4	5.8	1889.4	3.6	43.0	neuroligin 4, X-linked	NLGN4X
202826_at	43.2	36.7	620.2	12.9	43.0	serine peptidase inhibitor, Kunitz type 1	SPINT1
213618_at	578.7	308	2951.3	141.6	43.0	centaurin, delta 1	CENTD1
219376_at	112.3	45.6	439	22.2	43.0	zinc finger protein 322B	ZNF322B
220986_s_at	22.1	2.9	250.7	0.9	43.0	tigger transposable element derived 6 /// tigger transposable element derived 6	TIGD6
205349_at	542.8	279.4	9728.6	79.3	43.0	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	GNA15
206001_at	1156.7	435.3	13016	73.3	43.0	neuropeptide Y	NPY
201617_x_at	30.9	6.3	1133.6	1.6	43.0	caldesmon 1	CALD1
205407_at	153.9	62.7	1103.5	6.8	43.0	reversion-inducing-cysteine-rich protein with kazal motifs	RECK
214920_at	71.5	13.9	7696.6	1	43.0	hypothetical protein LOC221981	LOC221981
203509_at	1408.7	987.3	19247.5	644.6	42.6	sortilin-related receptor, L(DLR class) A repeats-containing	SORL1

203756_at	63.4	33.9	985.4	17.2	42.6	Rho guanine nucleotide exchange factor (GEF) 17	ARHGEF17
215247_at	37	14.1	505.1	8.8	42.6	hypothetical protein LOC339692	LOC339692
204490_s_at	358.2	177	6178.3	80.2	42.6	CD44 antigen (homing function and Indian blood group system)	CD44
202990_at	129.3	80.2	2758.5	19.8	42.6	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	PYGL
209617_s_at	68.7	23.3	424.5	6	42.6	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	CTNND2
210432_s_at	126	7	8051.5	3	42.6	sodium channel, voltage-gated, type III, alpha	SCN3A
202786_at	516.7	381.8	3315.8	115.1	42.6	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	STK39
203595_s_at	211.8	106.6	2067.3	39.1	42.6	interferon-induced protein with tetratricopeptide repeats 5	IFIT5
201375_s_at	570.8	376.1	3830.3	343.5	42.2	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	PPP2CB
201640_x_at	90.8	14.3	542.2	14.8	42.2	cleft lip and palate associated transmembrane protein 1	CLPTM1
201894_s_at	782.9	494.9	3984.2	463.8	42.2	signal sequence receptor, alpha (translocon-associated protein alpha)	SSR1
210854_x_at	157.5	33	5300.7	25.1	42.2	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	SLC6A8
212014_x_at	406.8	193.4	8862.5	103.3	42.2	CD44 antigen (homing function and Indian blood group system)	CD44
212366_at	238.2	143.6	1029.8	72.6	42.2	zinc finger protein 292	ZNF292
212606_at	216.6	9.2	1437.3	6.1	42.2	WD repeat and FYVE domain containing 3	WDFY3
218676_s_at	240.6	17.7	3374.1	9.2	42.2	phosphatidylcholine transfer protein	PCTP
219485_s_at	568.5	437.9	3387.7	256.5	42.2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	PSMD10
219491_at	33.9	14	393.9	10.4	42.2	leucine rich repeat and fibronectin type III domain containing 4	LRFN4
219521_at	24.7	17.2	731.3	12.4	42.2	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	B3GAT1
49111_at	242.1	150.9	1265	107.9	42.2	MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	---

206676_at	25.6	8.4	11672.8	2.9	42.2	carcinoembryonic antigen-related cell adhesion molecule 8	CEACAM8
209970_x_at	558.3	425.2	3740.3	162.5	42.2	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1
216392_s_at	288.4	175.1	1390.9	40.1	42.2	SEC23 interacting protein	SEC23IP
201539_s_at	357.3	328.8	6236.3	98.9	42.2	four and a half LIM domains 1	FHL1
204066_s_at	99.5	53.6	13416.6	8.8	42.2	centaurin, gamma 2	CENTG2
202392_s_at	197.9	91.7	971.1	29.9	42.2	phosphatidylserine decarboxylase	PISD
204914_s_at	68	22.8	6617.3	4.2	42.2	SRY (sex determining region Y)-box 11	SOX11
213050_at	85.5	61.6	2104.7	18.4	42.2	cordon-bleu homolog (mouse)	COBL
202797_at	512.7	296.4	2519.2	230.9	41.9	SAC1 suppressor of actin mutations 1-like (yeast)	SACM1L
205844_at	44.7	3.2	2772.1	2.6	41.9	vanin 1 /// vanin 1	VNN1
221023_s_at	46.3	6	655.1	4.1	41.9	potassium voltage-gated channel, subfamily H (eag-related), member 6 /// potassium voltage-gated channel, subfamily H (eag-related), member 6	KCNH6
219799_s_at	198.1	82	2562.8	30.6	41.9	dehydrogenase/reductase (SDR family) member 9	DHRS9
202803_s_at	827.9	622.5	7958.6	236.1	41.9	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)	ITGB2
221157_s_at	25.8	14.7	294.4	5	41.9	F-box protein 24	FBXO24
202411_at	184.7	70.5	20733	10.7	41.9	interferon, alpha-inducible protein 27	IFI27
206986_at	35.2	16.2	238.3	5.6	41.9	fibroblast growth factor 18	FGF18
203550_s_at	191	73.5	1361.8	46.2	41.5	chromosome 1 open reading frame 2	C1orf2
210586_x_at	69.6	27.6	8076.6	14	41.5	Rhesus blood group, D antigen	RHD
215874_at	144.7	31.8	1354	54.7	41.5	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	ST3GAL1
219201_s_at	12.2	6.1	317.3	5.3	41.5	twisted gastrulation homolog 1 (Drosophila)	TWSG1
219363_s_at	245.9	138.9	938.5	70.7	41.5	MTERF domain containing 1	MTERFD1
222134_at	23.2	8.2	453.2	6.7	41.5	D-aspartate oxidase	DDO
202431_s_at	1088.3	130.1	8590.2	54.6	41.5	v-myc myelocytomatosis viral oncogene homolog (avian)	MYC
219913_s_at	297.8	220.7	1053.6	40.1	41.5	Crn, crooked neck-like 1 (Drosophila)	CRNKL1
202196_s_at	8.5	3.5	592.6	0.8	41.5	dickkopf homolog 3 (Xenopus laevis)	DKK3
217559_at	143.2	78.6	819.1	28.8	41.5	ribosomal protein L10-like	RPL10L
205442_at	23.3	7.8	1395.9	2.4	41.5	microfibrillar-associated protein 3-like	MFAP3L

212915_at	12	5.1	653.8	1	41.5	PDZ domain containing RING finger 3	PDZRN3
205424_at	91.1	72.1	711.9	20.3	41.5	ProSAPiP2 protein	ProSAPiP2
204288_s_at	30.9	16.4	1075.6	8.8	41.1	sorbin and SH3 domain containing 2	SORBS2
211250_s_at	123.7	10.2	1289.1	9.9	41.1	SH3-domain binding protein 2	SH3BP2
211565_at	111.6	8	1229.6	11.1	41.1	SH3-domain GRB2-like 3	SH3GL3
212759_s_at	50.3	20	1354.5	11.1	41.1	transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2
213269_at	161.6	26.4	990	13.7	41.1	zinc finger protein 248	ZNF248
202933_s_at	87.6	7.7	1307.2	3	41.1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	YES1
204319_s_at	323.1	27	3182.8	9.5	41.1	regulator of G-protein signalling 10	RGS10
206179_s_at	33.8	13.5	280.9	6.4	41.1	brain-specific protein p25 alpha	TPPP
202694_at	23.1	10.3	411.9	4.7	41.1	serine/threonine kinase 17a (apoptosis-inducing)	STK17A
213317_at	62.8	11.5	4466.4	1.6	41.1	Chloride intracellular channel 5	CLIC5
221790_s_at	153.6	46.8	3617.7	12.9	41.1	low density lipoprotein receptor adaptor protein 1	LDLRAP1
209168_at	202.8	133.5	2043.8	18.8	41.1	glycoprotein M6B	GPM6B
204430_s_at	433.8	96.8	8380.8	16.8	41.1	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	SLC2A5
203111_s_at	266.2	23.4	2421.3	22.9	40.7	PTK2B protein tyrosine kinase 2 beta	PTK2B
204011_at	238.2	32.7	4642.4	23.3	40.7	sprouty homolog 2 (Drosophila)	SPRY2
206077_at	98.8	27.1	3637.6	19.7	40.7	Kell blood group	KEL
208460_at	116.9	25.4	674.9	13.3	40.7	gap junction protein, alpha 7, 45kDa (connexin 45)	GJA7
210401_at	875.3	442.5	5542.9	273.2	40.7	purinergic receptor P2X, ligand-gated ion channel, 1	P2RX1
212186_at	66.1	36.6	986.1	28.3	40.7	acetyl-Coenzyme A carboxylase alpha	ACACA
212199_at	654.1	450.9	2384.1	261.7	40.7	Morf4 family associated protein 1-like 1	MRFAP1L1
201887_at	159.2	81.2	2829.5	30.4	40.7	interleukin 13 receptor, alpha 1	IL13RA1
205259_at	116.8	12.2	2391.5	4	40.7	nuclear receptor subfamily 3, group C, member 2	NR3C2
206150_at	440.2	65.5	5428.4	25.6	40.7	tumor necrosis factor receptor superfamily, member 7	TNFRSF7
214298_x_at	1264.2	1096.3	7522.7	184.1	40.7	septin 6	SEPT6
210390_s_at	39.8	11.9	314.9	3.3	40.7	chemokine (C-C motif) ligand 14 /// chemokine (C-C motif) ligand 15	CCL14 /// CCL15
202746_at	186.5	152.4	9006.6	24.9	40.7	integral membrane protein 2A	ITM2A
211286_x_at	39.9	21.4	331.6	7.4	40.7	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	CSF2RA
220089_at	63.8	22.6	573.9	6	40.7	L-2-hydroxyglutarate dehydrogenase	L2HGDH

200736_s_at	2887.8	1921.6	31355.7	1488.8	40.4	glutathione peroxidase 1	GPX1
204468_s_at	12.2	5.1	736.9	3.6	40.4	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	TIE1
210094_s_at	165	41.8	1041.4	27.5	40.4	par-3 partitioning defective 3 homolog (C. elegans)	PARD3
217984_at	1991.8	1242.4	15329.1	851.9	40.4	ribonuclease T2	RNASET2
219829_at	31.7	12.6	379.4	9.6	40.4	integrin beta 1 binding protein (melusin) 2	ITGB1BP2
64064_at	439.2	266.2	4543.4	171.3	40.4	GTPase, IMAP family member 5	GIMAP5
208966_x_at	3288.9	1811.3	12809.7	786.3	40.4	interferon, gamma-inducible protein 16	IFI16
213888_s_at	336	144.1	2671.9	10.8	40.4	TRAF3 interacting protein 3	TRAF3IP3
203104_at	156.1	81.9	4853.9	20.2	40.4	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog /// colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	CSF1R
202668_at	282.8	98.6	4724.3	7.1	40.4	ephrin-B2	EFNB2
203110_at	942.9	657.8	4194.4	419.8	40.0	PTK2B protein tyrosine kinase 2 beta	PTK2B
203688_at	756.1	258	5245.7	177	40.0	polycystic kidney disease 2 (autosomal dominant)	PKD2
207358_x_at	775.4	601.9	3134.2	315.2	40.0	microtubule-actin crosslinking factor 1	MACF1
209631_s_at	9.4	2.2	423.1	1.3	40.0	G protein-coupled receptor 37 (endothelin receptor type B-like)	GPR37
210066_s_at	8.2	4.2	183.1	1.1	40.0	aquaporin 4	AQP4
213848_at	330.6	78.2	2652.2	24.4	40.0	Dual specificity phosphatase 7	DUSP7
220850_at	12.6	3.9	357.8	1.1	40.0	MORC family CW-type zinc finger 1	MORC1
218816_at	33.6	13.1	422.8	6.1	40.0	leucine rich repeat containing 1	LRRC1
203817_at	196.6	124	1401.8	10.1	40.0	---	---
204915_s_at	63	13.8	2637.5	4	40.0	SRY (sex determining region Y)-box 11	SOX11
218966_at	1090.3	549.8	4844.8	343.3	39.6	myosin VC	MYO5C
51146_at	86.5	10.7	414.5	8.2	39.6	phosphatidylinositol glycan, class V	PIGV
205528_s_at	17	3.2	436	1.4	39.6	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	RUNX1T1
215388_s_at	5.7	3.2	626	1.4	39.6	complement factor H /// complement factor H-related 1	CFH /// CFHL1
215672_s_at	114.2	49	643.7	18.7	39.6	KIAA0828 protein	KIAA0828
202178_at	49.4	16.9	9160.2	6.6	39.6	protein kinase C, zeta	PRKCZ

209670_at	561.5	298	15751.4	97.6	39.6	T cell receptor alpha constant /// T cell receptor alpha constant	TRAC
200986_at	142.2	25.8	1035.7	8.5	39.6	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)	SERPING1
217440_at	26.3	4	796.2	0.5	39.6	MRNA; cDNA DKFZp566A193 (from clone DKFZp566A193)	---
213920_at	47.8	18.4	592.2	5.6	39.6	cut-like 2 (Drosophila)	CUTL2
212489_at	390.1	192	2846.1	5.9	39.6	collagen, type V, alpha 1	COL5A1
213831_at	519.5	80.8	9979.3	8.5	39.6	major histocompatibility complex, class II, DQ alpha 1	HLA-DQA1
201811_x_at	1176.8	559	14168.3	14	39.6	SH3-domain binding protein 5 (BTK-associated)	SH3BP5
203116_s_at	499.9	411.2	22232	218.8	39.3	ferrochelatase (protoporphyria)	FECH
213280_at	326	39.5	2453.6	21.7	39.3	GTPase activating Rap/RanGAP domain-like 4	GARNL4
213737_x_at	599.4	466	12405.3	237.8	39.3	hypothetical LOC283768 /// similar to hypothetical protein /// similar to hypothetical protein /// golgi autoantigen, golgin family member /// similar to hypothetical protein /// similar to hypothetical protein /// hypothetical protein DKFZp434P162	LOC283768 /// LOC388080 /// LOC388189 /// LOC390535 /// LOC400304 /// LOC440234 /// DKFZp434P162
218864_at	47.5	11.1	3993.7	10.3	39.3	tensin 1	TNS1
218980_at	24.5	6.5	632.6	5.8	39.3	formin homology 2 domain containing 3	FHOD3
208613_s_at	185.1	40.9	4202.2	15.4	39.3	filamin B, beta (actin binding protein 278)	FLNB
218536_at	202.7	131.6	826.2	7.1	39.3	MRS2-like, magnesium homeostasis factor (S. cerevisiae)	MRS2L
208303_s_at	47.2	25.1	2971.8	6.9	39.3	cytokine receptor-like factor 2	CRLF2
216620_s_at	192.7	27.7	3588.2	12.3	39.3	Rho guanine nucleotide exchange factor (GEF) 10	ARHGEF10
205715_at	26.5	18.8	1743.7	7.5	39.3	bone marrow stromal cell antigen 1	BST1
215017_s_at	148.3	71.4	866.3	2.2	39.3	formin binding protein 1-like	FNBP1L
207218_at	63	24.6	565.5	3.5	39.3	coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B)	F9
208654_s_at	1274.4	754.9	15234.8	667.6	38.9	CD164 antigen, sialomucin	CD164
209638_x_at	41.2	3.4	532.9	1.8	38.9	regulator of G-protein signalling 12	RGS12
214049_x_at	38.7	15.3	2222.3	7.7	38.9	CD7 antigen (p41)	CD7
218965_s_at	75.9	13.5	397.8	9.5	38.9	RNA binding motif protein 21	RBM21

220751_s_at	52	19.2	4567.8	11.3	38.9	chromosome 5 open reading frame 4	C5orf4
202275_at	226.8	115	4046.1	45.6	38.9	glucose-6-phosphate dehydrogenase	G6PD
219191_s_at	67.1	28.6	1955.3	9.7	38.9	bridging integrator 2	BIN2
218328_at	119.6	97.9	861.5	16.1	38.9	coenzyme Q4 homolog (yeast)	COQ4
206622_at	58.4	45.3	3374	7.6	38.9	thyrotropin-releasing hormone	TRH
203854_at	56	18.2	406.4	12.2	38.5	I factor (complement)	IF
204462_s_at	207.7	42.5	1528.7	26.5	38.5	solute carrier family 16 (monocarboxylic acid transporters), member 2	SLC16A2
218361_at	251.4	34.4	1506.7	22.1	38.5	golgi phosphoprotein 3-like	GOLPH3L
204187_at	133	21.5	10704.9	10.7	38.5	guanosine monophosphate reductase /// guanosine monophosphate reductase	GMPR
209705_at	774.4	659.1	3152.7	307.1	38.5	metal response element binding transcription factor 2	MTF2
220232_at	570.7	370.1	6663.3	133	38.5	stearoyl-CoA desaturase 5	SCD5
222273_at	172.6	109.8	752.1	30.5	38.5	poly(A) polymerase gamma	PAPOLG
200885_at	301.6	195.1	1938.3	60.7	38.5	ras homolog gene family, member C	RHOC
205372_at	87.9	9.5	860	2.2	38.5	pleiomorphic adenoma gene 1	PLAG1
215702_s_at	19	9.1	222	2.4	38.5	cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)	CFTR
216123_x_at	78.6	43.1	655.2	4.4	38.5	CDNA FLJ14096 fis, clone MAMMA1000752	---
214745_at	214.1	99.5	2085.9	2.2	38.5	phospholipase C-like 3	PLCL3
206995_x_at	112.9	6.8	541.1	6.5	38.1	scavenger receptor class F, member 1	SCARF1
210644_s_at	2023.5	1311.6	9630.6	700	38.1	leukocyte-associated Ig-like receptor 1	LAIR1
213518_at	198.1	59.3	773.3	47.3	38.1	protein kinase C, iota	PRKCI
216407_at	61.4	13.9	526.8	8.7	38.1	Vac14 homolog (S. cerevisiae)	VAC14
204297_at	424.7	357.1	9590.8	156.3	38.1	phosphoinositide-3-kinase, class 3	PIK3C3
205174_s_at	23.2	5.3	712.9	1.9	38.1	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	QPCT
218989_x_at	175.4	115	603	19.2	38.1	solute carrier family 30 (zinc transporter), member 5	SLC30A5
204759_at	484.7	307	9086.3	34.2	38.1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	RCBTB2
206479_at	17.1	5.8	214.2	1.8	38.1	transient receptor potential cation channel, subfamily M, member 1	TRPM1
214012_at	126.4	71	1014.4	7.5	38.1	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	ARTS-1

202451_at	260.2	193.2	861.3	16.8	38.1	general transcription factor IIH, polypeptide 1, 62kDa	GTF2H1
219797_at	103.8	72.9	686.8	4.2	38.1	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme A	MGAT4A
206637_at	298.6	54.2	4668.9	1.6	38.1	purinergic receptor P2Y, G-protein coupled, 14	P2RY14
203585_at	219.3	174	2221.3	40.4	38.1	zinc finger protein 185 (LIM domain)	ZNF185
204700_x_at	158.8	78.3	747	43.7	37.8	chromosome 1 open reading frame 107	C1orf107
211924_s_at	184.9	27.2	2286.6	32.1	37.8	plasminogen activator, urokinase receptor /// plasminogen activator, urokinase receptor	PLAUR
212977_at	93.2	5	1209.6	4.3	37.8	chemokine orphan receptor 1	CMKOR1
206177_s_at	130.3	68.7	3199	26.4	37.8	arginase, liver	ARG1
201302_at	300	203.7	2835.2	21.2	37.8	annexin A4	ANXA4
208343_s_at	7.2	3	2604.5	1.1	37.8	nuclear receptor subfamily 5, group A, member 2	NR5A2
209615_s_at	92.3	24.5	507.8	6.3	37.8	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	PAK1
220646_s_at	79.7	23	801.8	5	37.8	killer cell lectin-like receptor subfamily F, member 1	KLRF1
204811_s_at	112	50.8	1771.5	12.1	37.8	calcium channel, voltage-dependent, alpha 2/delta subunit 2	CACNA2D2
205462_s_at	310.4	171.9	2565.1	18.5	37.8	hippocalcin-like 1	HPCAL1
213096_at	320.3	249.8	14744.6	27.6	37.8	transmembrane and coiled-coil domain family 2	TMCC2
217901_at	110.4	74.5	1631	5.4	37.8	Desmoglein 2	DSG2
204204_at	87.5	26.1	918.5	13.1	37.4	solute carrier family 31 (copper transporters), member 2	SLC31A2
208073_x_at	2070.2	1406.3	13227.3	1120.5	37.4	tetratricopeptide repeat domain 3	TTC3
208799_at	545.7	302.9	2235	353.8	37.4	proteasome (prosome, macropain) subunit, beta type, 5	PSMB5
214040_s_at	41.5	10.3	2140.6	9	37.4	gelsolin (amyloidosis, Finnish type)	GSN
218417_s_at	107.6	23.1	990.5	14.8	37.4	hypothetical protein FLJ20489	FLJ20489
218659_at	2636.3	1222.8	19916.5	736.9	37.4	additional sex combs like 2 (Drosophila)	ASXL2
220178_at	140.7	11.2	1510.2	11.3	37.4	chromosome 19 open reading frame 28	C19orf28
221350_at	53.8	15.1	917.6	11.3	37.4	homeo box C8	HOXC8
205945_at	97.8	7	1113.7	3.3	37.4	interleukin 6 receptor /// interleukin 6 receptor	IL6R
205614_x_at	85.9	47.3	694.9	20.6	37.4	macrophage stimulating 1 (hepatocyte growth factor-like)	MST1

202628_s_at	27.6	18.9	1056.7	8	37.4	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	SERPINE1
205952_at	88.1	19.7	2026.6	8.6	37.4	potassium channel, subfamily K, member 3	KCNK3
210504_at	181.5	109	11394.7	31.4	37.4	Kruppel-like factor 1 (erythroid)	KLF1
46665_at	83.8	45.2	1801.6	15.5	37.4	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	SEMA4C
209543_s_at	704.3	328.5	11548	98.4	37.4	CD34 antigen	CD34
205821_at	457.5	243	9684.2	45.4	37.4	killer cell lectin-like receptor subfamily K, member 1	KLRK1
206233_at	245.2	162.6	1798.1	5.9	37.4	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	B4GALT6
206574_s_at	244.7	135.8	2612.2	8.3	37.4	protein tyrosine phosphatase type IVA, member 3	PTP4A3
201363_s_at	313.2	120.7	1430.5	98.9	37.0	influenza virus NS1A binding protein	IVNS1ABP
203254_s_at	297.5	188.7	1554.2	131.8	37.0	talin 1	TLN1
206343_s_at	20.8	8.8	1783.2	5.1	37.0	neuregulin 1	NRG1
208594_x_at	398.6	305.3	3235.8	170.4	37.0	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	LILRA6
210030_at	46.4	13.8	557.9	9.9	37.0	---	---
213854_at	323.8	36.7	1730.3	26	37.0	synaptogyrin 1	SYNGR1
215299_x_at	681.9	407.1	4249.4	370.6	37.0	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	SULT1A1
220285_at	932.1	658.1	4858.2	331.9	37.0	chromosome 9 open reading frame 77	C9orf77
220684_at	244.3	156.4	1550.4	83.4	37.0	T-box 21	TBX21
221747_at	332.6	46.9	5156.1	40.1	37.0	Tensin 1 /// Tensin 1	TNS1
204513_s_at	515.9	363	4569.4	120.1	37.0	engulfment and cell motility 1 (ced-12 homolog, C. elegans)	ELMO1
208109_s_at	57.6	9.4	790.8	4.4	37.0	chromosome 15 open reading frame 5 /// chromosome 15 open reading frame 5	C15orf5
213364_s_at	220.2	97.9	1125.3	36.8	37.0	sorting nexin 1	SNX1
203949_at	269.1	88	44296	25	37.0	myeloperoxidase	MPO
201109_s_at	26.2	13.5	1803	3.3	37.0	thrombospondin 1	THBS1
205983_at	581	207.2	7380	21.6	37.0	dipeptidase 1 (renal)	DPEP1
218742_at	406.8	167.4	2459.7	21.9	37.0	nuclear prelamin A recognition factor-like	NARFL
212828_at	257.9	134.8	2422.8	27.5	37.0	synaptojanin 2	SYNJ2

209576_at	205.7	169.9	1733.8	11.3	37.0	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	GNAI1
212526_at	62.9	14.9	996.9	3	37.0	spastic paraplegia 20, spartin (Troyer syndrome)	SPG20
205463_s_at	139.4	41.4	3342.1	5.5	37.0	platelet-derived growth factor alpha polypeptide	PDGFA
203988_s_at	226.8	20	1797.6	12.4	36.7	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	FUT8
212181_s_at	595.8	508.9	7196.3	373.3	36.7	nudix (nucleoside diphosphate linked moiety X)-type motif 4	NUDT4
214255_at	161.3	24.5	2123.3	18.3	36.7	ATPase, Class V, type 10A	ATP10A
213063_at	305.7	237	1454.3	91.9	36.7	nuclear protein UKp68	FLJ11806
209210_s_at	88.1	16.6	1212.8	4.9	36.7	pleckstrin homology domain containing, family C (with FERM domain) member 1	PLEKHC1
204401_at	175.2	51.2	2120.8	12	36.7	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	KCNN4
201848_s_at	151.7	93.2	778.4	7.9	36.7	BCL2/adenovirus E1B 19kDa interacting protein 3	BNIP3
214453_s_at	296.5	109.3	6049.8	43.3	36.7	interferon-induced protein 44	IFI44
218892_at	149.5	36.5	863.8	12.8	36.7	dachsous 1 (Drosophila)	DCHS1
201324_at	94.7	14.1	3238.4	3.7	36.7	epithelial membrane protein 1	EMP1
201029_s_at	4746	2562.3	29103.9	689.6	36.7	CD99 antigen	CD99
203038_at	353	73.2	5596.8	6.7	36.7	protein tyrosine phosphatase, receptor type, K	PTPRK
218035_s_at	174.4	73.7	1360.7	16.9	36.7	RNA-binding protein	FLJ20273
203029_s_at	22.1	12.1	1684	9.2	36.3	protein tyrosine phosphatase, receptor type, N polypeptide 2	PTPRN2
203040_s_at	462.5	424.8	20562.7	233.3	36.3	hydroxymethylbilane synthase	HMBS
211876_x_at	22.8	6	700.3	5.1	36.3	protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 5 /// protocadherin gamma subfamily A, 3	PCDHGA12 /// PCDHGA11 /// PCDHGA10 /// PCDHGA6 /// PCDHGA5 /// PCDHGA3
216298_at	85.4	4	508.1	3.8	36.3	T cell receptor gamma constant 2	LOC442535
219701_at	38.1	4.3	619.8	2.4	36.3	tropomodulin 2 (neuronal)	TMOD2
221081_s_at	358	48.4	2899.8	32.4	36.3	DENN/MADD domain containing 2D	DENND2D
209963_s_at	127.9	49.4	1950.4	17.8	36.3	erythropoietin receptor	EPOR
217096_at	43	9.2	442.9	3.5	36.3	piccolo (presynaptic cytomatrix protein)	PCLO

217820_s_at	138.3	13.4	1021.9	6.3	36.3	enabled homolog (Drosophila)	ENAH
205390_s_at	29.7	26.3	3939.1	9.5	36.3	ankyrin 1, erythrocytic /// ankyrin 1, erythrocytic	ANK1
206366_x_at	44	24.7	564.3	6	36.3	chemokine (C motif) ligand 2	XCL2
211568_at	19.9	3.1	728.8	1.5	36.3	brain-specific angiogenesis inhibitor 3	BAI3
213894_at	96	24.3	2885.9	6.1	36.3	KIAA0960 protein	KIAA0960
212314_at	339.9	155.7	7986.2	55.6	36.3	KIAA0746 protein	KIAA0746
222136_x_at	519.1	310.1	2538.9	98.6	36.3	zinc finger protein 43 (HTF6)	ZNF43
205159_at	439.5	343.6	2239.7	154.7	36.3	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) /// colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	CSF2RB
220789_s_at	101.1	70.6	573.6	29	36.3	transforming growth factor beta regulator 4	TBRG4
204891_s_at	418.3	189	5581.2	30.7	36.3	lymphocyte-specific protein tyrosine kinase	LCK
212443_at	263.3	138.7	2162	17.1	36.3	neurobeachin-like 2	NBEAL2
202992_at	34.6	19.2	645.1	3.7	36.3	complement component 7	C7
210435_at	45.6	22.2	280.1	2.7	36.3	neighbor of BRCA1 gene 2	NBR2
202630_at	200.3	121.9	895.5	73	35.9	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	APPBP2
203381_s_at	29.3	10.4	1129.3	5.6	35.9	apolipoprotein E	APOE
212095_s_at	47.9	11	574.8	7.8	35.9	mitochondrial tumor suppressor 1	MTUS1
212151_at	114.4	30.4	10825.3	16.5	35.9	Pre-B-cell leukemia transcription factor 1	PBX1
213994_s_at	9.7	3.2	676	2.1	35.9	spondin 1, extracellular matrix protein	SPON1
218762_at	53.7	24.8	851.9	17.7	35.9	zinc finger protein 574	ZNF574
219149_x_at	129	42.5	571.6	38.9	35.9	debranching enzyme homolog 1 (S. cerevisiae)	DBR1
205862_at	23.7	2.3	422	1	35.9	GREB1 protein	GREB1
211450_s_at	1390	769.9	6721.5	168	35.9	mutS homolog 6 (E. coli)	MSH6
213882_at	117.5	19	636.6	5.8	35.9	TM2 domain containing 1	TM2D1
215842_s_at	43.1	5.5	1086.9	2.7	35.9	ATPase, Class VI, type 11A	ATP11A
216565_x_at	484.6	268.2	3433.7	128.6	35.9	similar to Interferon-induced transmembrane protein 3 (Interferon-inducible protein 1-8U)	LOC391020
220577_at	283.9	196.6	1308.8	83	35.9	GTPase, very large interferon inducible 1	GVIN1
207968_s_at	679.1	449.9	2961.8	79.5	35.9	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C
212761_at	621.5	511.4	4998.4	101.8	35.9	transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2

217067_s_at	20.2	4.4	741.1	1.9	35.9	dentin matrix acidic phosphoprotein	DMP1
212979_s_at	100.9	40.9	523.5	4.8	35.9	KIAA0738 gene product	KIAA0738
218402_s_at	945	647.2	5332.1	139.5	35.9	Hermansky-Pudlak syndrome 4	HPS4
219048_at	189.5	37.2	963.8	12.3	35.9	phosphatidylinositol glycan, class N	PIGN
221558_s_at	4751.5	2901.3	16261.4	242.4	35.9	lymphoid enhancer-binding factor 1	LEF1
201189_s_at	357.3	98	2314	12.8	35.9	inositol 1,4,5-triphosphate receptor, type 3	ITPR3
202540_s_at	165.2	26.9	835.4	20.7	35.6	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR
210655_s_at	89.9	21.2	6692.2	10.7	35.6	forkhead box O3A	FOXO3A
213395_at	126	7.5	1760	9.8	35.6	megalencephalic leukoencephalopathy with subcortical cysts 1	MLC1
203574_at	307.6	223.4	9812.8	43.7	35.6	nuclear factor, interleukin 3 regulated	NFIL3
210615_at	40.3	12.7	335.3	3.2	35.6	neuropilin 1	NRP1
202833_s_at	107.1	24.3	1493.7	8.1	35.6	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	SERPINA1
205098_at	220.8	141.3	2242.5	36.1	35.6	chemokine (C-C motif) receptor 1	CCR1
220922_s_at	43.1	19	1787.1	6.8	35.6	sperm protein associated with the nucleus, X-linked, family member A1 /// SPANX family, member B1 /// SPANX family, member A2 /// SPANX family, member C /// SPANX family, member B2	SPANXA1 /// SPANXB1 /// SPANXA2 /// SPANXC /// SPANXB2
218656_s_at	124.8	34.5	1094.7	9.4	35.6	lipoma HMGIC fusion partner	LHFP
201341_at	245.6	58.5	1313.2	65.5	35.2	ectodermal-neural cortex (with BTB-like domain)	ENC1
202039_at	2536.6	1152.1	12225.9	882.4	35.2	TGFB1-induced anti-apoptotic factor 1 /// myosin XVIIIA	TIAF1 /// MYO18A
202441_at	514.4	310.1	3817.2	227.7	35.2	SPFH domain family, member 1	SPFH1
204158_s_at	312.4	27.1	2026.7	13.6	35.2	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein a isoform 3	TCIRG1
204417_at	307.3	192.3	1291	152.9	35.2	galactosylceramidase (Krabbe disease)	GALC
205702_at	212.7	167	922.4	94.3	35.2	putative homeodomain transcription factor 1	PHTF1
208664_s_at	378.6	46.8	2577.1	15.2	35.2	tetratricopeptide repeat domain 3	TTC3
220024_s_at	202.4	25.4	3704.4	12.4	35.2	periaxin	PRX
204643_s_at	168.2	37.5	838.5	13.6	35.2	cytosolic ovarian carcinoma antigen 1	COVA1
213530_at	176.9	104.4	968.1	41	35.2	RAB3 GTPase activating protein subunit 1 (catalytic)	RAB3GAP1

216286_at	135.2	15.4	784.3	5.9	35.2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	B4GALT6
212641_at	243.9	104.7	1762.8	21.2	35.2	human immunodeficiency virus type I enhancer binding protein 2	HIVEP2
214752_x_at	448.9	347.9	3063.9	126.4	35.2	filamin A, alpha (actin binding protein 280)	FLNA
206032_at	133.4	56	2028.8	4.8	35.2	desmocollin 3	DSC3
213663_s_at	23.4	8.2	259.6	1.8	35.2	hypothetical LOC389275	LOC389275
219211_at	152.2	33.4	1800.2	9.8	35.2	ubiquitin specific peptidase 18	USP18
213839_at	142	94.1	2828.6	11.4	35.2	KIAA0500 protein	KIAA0500
208818_s_at	1135.7	934.7	4507	488.8	34.8	catechol-O-methyltransferase	COMT
211434_s_at	60.3	16.5	825.4	10.2	34.8	chemokine (C-C motif) receptor-like 2	CCRL2
213715_s_at	28	9.2	404.3	5.2	34.8	ankyrin repeat domain 47	ANKRD47
217542_at	143	9.9	1123.1	8.2	34.8	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	MDM2
217753_s_at	5938.3	4006.8	25428.5	2076.8	34.8	ribosomal protein S26 /// 40S ribosomal protein S26-like /// similar to 40S ribosomal protein S26	RPS26 /// RPS26L /// LOC440440
204467_s_at	171.2	51.3	13693.2	12.8	34.8	synuclein, alpha (non A4 component of amyloid precursor) /// synuclein, alpha (non A4 component of amyloid precursor)	SNCA
204712_at	14.4	5.4	195.8	1.3	34.8	WNT inhibitory factor 1	WIF1
213797_at	225.5	42.7	3486.1	14.5	34.8	radical S-adenosyl methionine domain containing 2	RSAD2
218311_at	138.3	67.8	1156.1	19.2	34.8	mitogen-activated protein kinase kinase kinase kinase 3	MAP4K3
203063_at	576.5	303.1	3994.1	63.5	34.8	protein phosphatase 1F (PP2C domain containing)	PPM1F
221221_s_at	240.4	149	1298.1	18.7	34.8	kelch-like 3 (Drosophila)	KLHL3
217110_s_at	36.7	7.1	2577.8	1.9	34.8	mucin 4, tracheobronchial	MUC4
201904_s_at	39.3	16.3	1431.6	8.9	34.4	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	CTDSPL
202017_at	94.7	21	750.8	12.3	34.4	epoxide hydrolase 1, microsomal (xenobiotic)	EPHX1
203964_at	1081	748.9	3821.7	503	34.4	N-myc (and STAT) interactor	NMI
207100_s_at	251.9	14	2082.2	22.6	34.4	vesicle-associated membrane protein 1 (synaptobrevin 1)	VAMP1

207413_s_at	92.2	21.6	661.3	11.3	34.4	sodium channel, voltage-gated, type V, alpha (long QT syndrome 3)	SCN5A
207734_at	261.8	151	1265.9	82.4	34.4	lymphocyte transmembrane adaptor 1	LAX1
221274_s_at	276.7	29	1206.4	24.3	34.4	lectin, mannose-binding 2-like /// lectin, mannose-binding 2-like	LMAN2L
208361_s_at	180.4	65.5	728.9	18.9	34.4	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa	POLR3D
210972_x_at	758.2	554.4	24206.5	214.3	34.4	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T cell receptor alpha joining 17 /// T cell receptor alpha constant	TRA@ /// TRDV2 /// TRAV20 /// TRAJ17 /// TRAC
204849_at	810.8	215	11702.5	5.4	34.4	transcription factor-like 5 (basic helix-loop-helix)	TCFL5
206400_at	31.9	13.4	575.3	5	34.4	lectin, galactoside-binding, soluble, 7 (galectin 7)	LGALS7
214667_s_at	101.6	35	998	11.4	34.4	tumor protein p53 inducible protein 11	TP53I11
220532_s_at	54.2	13.7	777.4	3.8	34.4	LR8 protein	LR8
201616_s_at	22.8	6.6	1425.1	2.1	34.4	caldesmon 1	CALD1
203910_at	179.7	83.8	10198.4	9.4	34.4	Rho GTPase activating protein 29	ARHGAP29
215761_at	164	112	967.7	19.1	34.4	Dmx-like 2	DMXL2
201579_at	158.1	58.3	5413.2	7.1	34.4	FAT tumor suppressor homolog 1 (Drosophila)	FAT
212589_at	175.6	39.9	1058.4	5.8	34.4	Sterol carrier protein 2	SCP2
210765_at	39.6	13.3	346.5	12.3	34.1	CSE1 chromosome segregation 1-like (yeast)	CSE1L
214370_at	14.7	3.3	1290.2	3.3	34.1	S100 calcium binding protein A8 (calgranulin A)	S100A8
221900_at	24.3	10.2	428.4	6.6	34.1	collagen, type VIII, alpha 2	COL8A2
203115_at	130.9	23.7	5913.7	11.8	34.1	ferrochelatase (protoporphyria)	FECH
203335_at	364.4	171.5	12858.3	46.7	34.1	phytanoyl-CoA hydroxylase (Refsum disease)	PHYH
212959_s_at	740.4	459.9	6222	203	34.1	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	GNPTAB
221182_at	23.5	5.1	327.6	1.8	34.1	chromosome 1 open reading frame 129	C1orf129
202565_s_at	206.9	161	1008.3	92.6	33.7	supervillin	SVIL
205538_at	53.5	15.2	482.7	10.8	33.7	coronin, actin binding protein, 2A	CORO2A
210904_s_at	100.9	9.1	1814.7	17.2	33.7	interleukin 13 receptor, alpha 1	IL13RA1
214094_at	57.8	25.4	508.9	17.1	33.7	far upstream element (FUSE) binding protein 1	FUBP1
216737_at	26	2.1	239.6	1.4	33.7	CDNA: FLJ20872 fis, clone ADKA02604	---

219668_at	38.9	16.6	450	8.5	33.7	ganglioside-induced differentiation-associated protein 1-like 1	GDAP1L1
202308_at	143	38	917.9	16.8	33.7	sterol regulatory element binding transcription factor 1	SREBF1
205264_at	213.8	47.3	1503.1	17.1	33.7	CD3E antigen, epsilon polypeptide associated protein	CD3EAP
207677_s_at	947.3	692.2	4262.2	272.6	33.7	neutrophil cytosolic factor 4, 40kDa /// neutrophil cytosolic factor 4, 40kDa	NCF4
208949_s_at	310.6	81.7	38822.2	26	33.7	lectin, galactoside-binding, soluble, 3 (galectin 3) /// galectin-3 internal gene	LGALS3 /// GALIG
206145_at	149.5	39.7	9642.4	9.1	33.7	Rhesus blood group-associated glycoprotein	RHAG
209570_s_at	74.1	28.9	1641.8	6	33.7	DNA segment on chromosome 4 (unique) 234 expressed sequence	D4S234E
212554_at	57.1	22.7	603.1	3.7	33.7	CAP, adenylate cyclase-associated protein, 2 (yeast)	CAP2
206650_at	41.2	15.7	306.3	8.6	33.3	IQ motif containing C	IQCC
219529_at	18.7	4.6	1679.1	3.4	33.3	chloride intracellular channel 3	CLIC3
211366_x_at	813.4	586.8	4143.1	273.4	33.3	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1
215648_at	103.5	27.2	615.5	9.1	33.3	---	---
202086_at	1340.7	562.8	24405.6	74.3	33.3	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) /// myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	MX1
205728_at	33.5	6.4	1607.1	2.1	33.3	CDNA clone IMAGE:4811759	---
211902_x_at	419.5	303.6	8249.5	116.8	33.3	T cell receptor alpha locus	TRA@
213764_s_at	5.3	2.5	694.3	0.6	33.3	microfibrillar associated protein 5	MFAP5
211102_s_at	251.5	164.5	1535.4	6.7	33.3	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	LILRA2
205573_s_at	53.1	8.9	1291.8	4.9	33.0	sorting nexin 7	SNX7
209407_s_at	339.6	126.1	1400.4	139.1	33.0	deformed epidermal autoregulatory factor 1 (Drosophila)	DEAF1
212264_s_at	284.9	94.7	1688.2	55.8	33.0	KIAA0261	KIAA0261
214567_s_at	14	5.7	436	5.5	33.0	chemokine (C motif) ligand 1 /// chemokine (C motif) ligand 2	XCL1 /// XCL2
222216_s_at	311.4	48.4	1334.9	51.3	33.0	mitochondrial ribosomal protein L17	MRPL17

203757_s_at	220.7	22.3	7715.1	10.1	33.0	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	CEACAM6
204039_at	129.9	49.4	2825.4	20.1	33.0	CCAAT/enhancer binding protein (C/EBP), alpha	CEBPA
220576_at	80.2	13.7	750.9	5.9	33.0	GPI deacylase	PGAP1
216747_at	70	20	562.1	9.1	33.0	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	APBB2
202273_at	43.6	22.7	1188.9	9	33.0	platelet-derived growth factor receptor, beta polypeptide	PDGFRB
203987_at	185.2	97.5	2062	29.6	33.0	frizzled homolog 6 (Drosophila)	FZD6
216280_s_at	47.4	17	349.9	3.5	33.0	Dicer1, Dcr-1 homolog (Drosophila)	DICER1
206831_s_at	67.5	18.8	520.8	5.7	33.0	arylsulfatase D	ARSD
200096_s_at	1044	670.1	3796	382.6	32.6	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e /// ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e	ATP6V0E
206067_s_at	24.2	4.9	1338.9	4	32.6	Wilms tumor 1	WT1
208056_s_at	1111.8	533.9	6352.1	315.6	32.6	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	CBFA2T3
209288_s_at	141.9	7.4	2379.5	6.1	32.6	CDC42 effector protein (Rho GTPase binding) 3	CDC42EP3
210915_x_at	669.4	434.1	13605.2	260.8	32.6	T cell receptor beta variable 19 /// T cell receptor beta constant 1	TRBV19 /// TRBC1
217758_s_at	636.8	342.6	3167.8	370.7	32.6	SM-11044 binding protein	SMBP
219593_at	40.1	12.7	419.5	8.4	32.6	solute carrier family 15, member 3	SLC15A3
203428_s_at	442.8	159.9	1857.4	70.3	32.6	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	ASF1A
208908_s_at	270.4	47.7	2051.6	23.8	32.6	calpastatin	CAST
218081_at	150.9	22.7	1249.2	6.8	32.6	chromosome 20 open reading frame 27	C20orf27
218660_at	151.5	37.7	2348.1	14.6	32.6	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)	DYSF
219869_s_at	393.7	317.3	2196.2	66.5	32.6	solute carrier family 39 (zinc transporter), member 8	SLC39A8
213558_at	225.6	48.5	22160	12.8	32.6	piccolo (presynaptic cytomatrix protein)	PCLO
220121_at	77.8	17.7	503.4	6.6	32.6	lines homolog 1 (Drosophila)	LINS1
65517_at	118.5	62.4	747	23.3	32.6	adaptor-related protein complex 1, mu 2 subunit	AP1M2
203450_at	161.7	73.9	561.9	19.6	32.6	PKD2 interactor, golgi and endoplasmic reticulum associated 1	PGEA1

201849_at	125.2	45.5	920.7	9.2	32.6	BCL2/adenovirus E1B 19kDa interacting protein 3	BNIP3
211626_x_at	395	173.7	1625.1	14.7	32.6	v-ets erythroblastosis virus E26 oncogene like (avian) /// v-ets erythroblastosis virus E26 oncogene like (avian)	ERG
215382_x_at	41.6	31.4	920.6	6.9	32.6	tryptase alpha/beta 1	TPSAB1
214757_at	69.6	28.4	397.8	7.6	32.6	CDNA clone IMAGE:3456494	---
202718_at	113.1	58.5	4105.7	4.9	32.6	insulin-like growth factor binding protein 2, 36kDa	IGFBP2
200979_at	323.9	250.3	1611.6	244.2	32.2	Mitogen-activated protein kinase kinase kinase 15 /// CDNA FLJ34891 fis, clone NT2NE2017562	MAP3K15
203739_at	583.5	248.5	2923	270.5	32.2	zinc finger protein 217	ZNF217
204411_at	64.1	24.9	654.9	17.7	32.2	kinesin family member 21B	KIF21B
212814_at	250.7	121.8	1055.7	132.4	32.2	KIAA0828 protein	KIAA0828
212830_at	423.1	227.3	2842.1	199.4	32.2	EGF-like-domain, multiple 5	EGFL5
217790_s_at	58.1	9	507.9	6.5	32.2	signal sequence receptor, gamma (translocon-associated protein gamma)	SSR3
219684_at	196.8	23.5	1058.6	20.7	32.2	28kD interferon responsive protein	IFRG28
221656_s_at	90.5	15.2	619	7.6	32.2	Rho guanine nucleotide exchange factor (GEF) 10-like	ARHGEF10L
221757_at	465.1	292.9	3099.8	216.1	32.2	HGFL gene /// HGFL gene	MGC17330
206127_at	356.6	70.3	1993.9	23.1	32.2	ELK3, ETS-domain protein (SRF accessory protein 2)	ELK3
216026_s_at	686	510.8	3365	21.1	32.2	polymerase (DNA directed), epsilon	POLE
220329_s_at	127.5	83.2	656.2	19.9	32.2	chromosome 6 open reading frame 96	C6orf96
202887_s_at	1419.6	658.6	11347.7	32.1	32.2	DNA-damage-inducible transcript 4	DDIT4
207621_s_at	159.4	62.9	2413.2	13.3	32.2	phosphatidylethanolamine N-methyltransferase	PEMT
209776_s_at	31	19.7	397.5	5.2	32.2	solute carrier family 19 (folate transporter), member 1	SLC19A1
204793_at	209.4	154.8	1899.3	12.8	32.2	G protein-coupled receptor associated sorting protein 1	GPRASP1
204115_at	371.9	300.5	4663.6	3.3	32.2	guanine nucleotide binding protein (G protein), gamma 11	GNG11
202948_at	47.7	6.3	591.8	3.8	31.9	interleukin 1 receptor, type I	IL1R1
205885_s_at	1000.2	455.9	5752.2	323.3	31.9	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA4 receptor)	ITGA4
206359_at	21.1	7	299.7	7.2	31.9	suppressor of cytokine signaling 3	SOCS3
1438_at	111.7	31.1	746.6	15.3	31.9	EPH receptor B3	EPHB3
208637_x_at	505.3	198.4	3743.8	95.3	31.9	actinin, alpha 1	ACTN1

209167_at	150.4	12.8	2836	5.8	31.9	glycoprotein M6B	GPM6B
211657_at	313.7	63.9	10789	22.5	31.9	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	CEACAM6
210705_s_at	189.1	119.2	849.2	12.6	31.9	tripartite motif-containing 5	TRIM5
221529_s_at	222	44.4	4666.8	13.3	31.9	plasmalemma vesicle associated protein	PLVAP
218806_s_at	287.1	204.7	1924.9	23.3	31.9	vav 3 oncogene	VAV3
202789_at	266.4	176.7	1223.4	20.9	31.9	phospholipase C, gamma 1	PLCG1
209170_s_at	197.8	44.6	3675.7	4.5	31.9	glycoprotein M6B	GPM6B
203726_s_at	56.5	18.7	2318.4	11.7	31.5	laminin, alpha 3	LAMA3
204006_s_at	166.9	19.8	2149.5	10.6	31.5	Fc fragment of IgG, low affinity IIIa, receptor (CD16a) /// Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	FCGR3A /// FCGR3B
204232_at	313.8	222.3	4420.7	144.8	31.5	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	FCER1G
219120_at	180.4	15.2	667	26.2	31.5	hypothetical protein FLJ21945	FLJ21945
219354_at	92.7	35.5	482.9	27.5	31.5	hypothetical protein FLJ11078	FLJ11078
202888_s_at	63.4	11.5	749.5	5.1	31.5	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	ANPEP
203650_at	49.3	6.5	324.9	2.7	31.5	protein C receptor, endothelial (EPCR)	PROCR
214353_at	50.1	16.6	321.3	8.2	31.5	Cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	CELSR1
212613_at	304.4	35	1511.8	8.7	31.5	butyrophilin, subfamily 3, member A2	BTN3A2
206762_at	115.6	25.7	4277.4	9.9	31.5	potassium voltage-gated channel, shaker-related subfamily, member 5	KCNA5
213218_at	166.7	123.6	656.9	19.5	31.5	zinc finger protein 187	ZNF187
218087_s_at	47.4	9.3	1490.3	0.9	31.5	sorbin and SH3 domain containing 1	SORBS1
204174_at	1237	842	13270.9	119	31.5	arachidonate 5-lipoxygenase-activating protein	ALOX5AP
217022_s_at	1283.9	273.1	35058.2	6.6	31.5	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// hypothetical protein MGC27165	IGHA1 /// IGHA2 /// MGC27165
203435_s_at	3792.8	2101.1	15156.8	14.9	31.5	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	MME

202219_at	30.5	13.8	7056.9	9.1	31.1	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	SLC6A8
202809_s_at	1265.5	710	7400.2	512	31.1	chromosome 1 open reading frame 60	C1orf60
203476_at	140.1	8.3	3079.9	12.4	31.1	trophoblast glycoprotein	TPBG
203662_s_at	44.7	19.3	3171.4	12.3	31.1	tropomodulin 1	TMOD1
213294_at	660.6	489.1	4962.7	346.1	31.1	Coiled-coil domain containing 75	CCDC75
209474_s_at	59.7	14.6	449.6	6.8	31.1	ectonucleoside triphosphate diphosphohydrolase 1	ENTPD1
211462_s_at	75.1	13.4	784.2	4.4	31.1	transducin (beta)-like 1Y-linked	TBL1Y
214277_at	21.5	2	356.2	0.5	31.1	COX11 homolog, cytochrome c oxidase assembly protein (yeast) /// COX11 homolog, cytochrome c oxidase assembly protein (yeast) pseudogene	COX11 /// COX11P
217264_s_at	72.4	31.9	487.4	9.2	31.1	sodium channel, nonvoltage-gated 1 alpha	SCNN1A
214110_s_at	28.3	16.8	809.3	6.8	31.1	Similar to lymphocyte-specific protein 1	LOC440886
202125_s_at	447.1	312.2	8793.8	278.3	30.7	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3	ALS2CR3
203972_s_at	257.9	191.8	834.8	107.8	30.7	peroxisomal biogenesis factor 3	PEX3
204655_at	243.8	157.3	2562.6	116.7	30.7	chemokine (C-C motif) ligand 5 /// chemokine (C-C motif) ligand 5	CCL5
205565_s_at	178.6	49.2	911.6	28.9	30.7	frataxin	FXN
206135_at	9.3	4.6	1153	2.3	30.7	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	ST18
206488_s_at	109.2	11.5	6444.4	9.5	30.7	CD36 antigen (collagen type I receptor, thrombospondin receptor)	CD36
210451_at	23.3	9.8	1635.2	7.6	30.7	pyruvate kinase, liver and RBC	PKLR
210703_at	51.1	8.6	287.8	8.2	30.7	---	---
212647_at	42.7	16.4	523.9	10.9	30.7	related RAS viral (r-ras) oncogene homolog	RRAS
213964_x_at	23.1	2.6	511.9	2.7	30.7	Chromosome 10 open reading frame 95	C10orf95
219360_s_at	13	7.5	2377.6	5.6	30.7	transient receptor potential cation channel, subfamily M, member 4	TRPM4
221484_at	431	310.7	4031.7	189	30.7	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	B4GALT5
222084_s_at	9.9	5.6	249.1	3.7	30.7	SET binding factor 1	SBF1
205926_at	294.3	150.8	1725.2	62.9	30.7	interleukin 27 receptor, alpha	IL27RA
206304_at	51.8	24.1	1450.1	8.8	30.7	myosin binding protein H	MYBPH

210683_at	5.9	1.7	332.1	0.6	30.7	neurturin	NRTN
215650_at	92.7	20.3	695.3	8.3	30.7	---	---
217147_s_at	63.7	6	1595.6	2.4	30.7	T cell receptor associated transmembrane adaptor 1	TRAT1
202456_s_at	40.8	21	1242.7	9.6	30.7	zyg-11 homolog B (C. elegans)-like	ZYG11BL
213012_at	202.8	116	771.6	36.3	30.7	neural precursor cell expressed, developmentally down-regulated 4	NEDD4
207513_s_at	241.5	181.8	833.3	84.5	30.7	zinc finger protein 189	ZNF189
204620_s_at	208.6	169.4	12708.4	18.5	30.7	chondroitin sulfate proteoglycan 2 (versican)	CSPG2
211574_s_at	383.8	195.8	1584.4	46.6	30.7	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)	MCP
219683_at	56.8	24.9	707.8	2.2	30.7	frizzled homolog 3 (Drosophila)	FZD3
213005_s_at	177.3	116.5	6672.7	8.4	30.7	ankyrin repeat domain 15	ANKRD15
218468_s_at	105.2	33.7	4564	4.3	30.7	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	GREM1
222154_s_at	275.4	128.6	13569	12.1	30.7	DNA polymerase-transactivated protein 6	DNAPTP6
210663_s_at	44.4	15.8	1257.6	8.7	30.4	kynureninase (L-kynurenine hydrolase)	KYNU
211600_at	5593.8	3335.9	31276.5	2421.9	30.4	---	---
212216_at	212.7	31.6	957.9	23.4	30.4	prolyl endopeptidase-like	PREPL
212848_s_at	64.8	19.9	2991.1	11.2	30.4	chromosome 9 open reading frame 3	C9orf3
213800_at	24.7	7.3	326.6	6	30.4	complement factor H	CFH
219540_at	137.6	17.3	531.1	11.2	30.4	zinc finger protein 267	ZNF267
203471_s_at	454.6	222.9	2688	73.5	30.4	pleckstrin	PLEK
204548_at	21.1	13.4	813.5	6.4	30.4	steroidogenic acute regulator	STAR
215064_at	76.1	17.5	473.1	8.3	30.4	Sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like	SC5DL
204439_at	215.3	10	10754	4.7	30.4	interferon-induced protein 44-like	IFI44L
210975_x_at	181.1	69.3	824.9	28.2	30.4	Fas-activated serine/threonine kinase	FASTK
213698_at	489.6	393.5	1567.9	83.7	30.4	zinc finger, MYM-type 6	ZMYM6
218469_at	139	97.9	4088.8	7.9	30.4	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	GREM1
201655_s_at	49.3	8.6	641.1	6.8	30.0	heparan sulfate proteoglycan 2 (perlecan)	HSPG2
210074_at	63.6	7.6	303.9	8.1	30.0	cathepsin L2	CTSL2
212466_at	26.2	5.6	657.5	4	30.0	sprouty-related, EVH1 domain containing 2	SPRED2

213521_at	776.2	547.8	4117	383.4	30.0	Protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	PTPN18
218229_s_at	435	234.6	2198.6	176.2	30.0	pogo transposable element with KRAB domain	POGK
209663_s_at	23.6	14.4	324.8	6.9	30.0	integrin, alpha 7	ITGA7
219731_at	317.6	207.2	1712.3	61.6	30.0	weakly similar to zinc finger protein 195	FLJ34077
221195_at	36	8.2	262.1	3.5	30.0	PTD016 protein	LOC51136
204276_at	105.8	23.9	706.7	6.8	30.0	thymidine kinase 2, mitochondrial	TK2
206090_s_at	176.7	107.4	666.5	50.4	30.0	disrupted in schizophrenia 1	DISC1
206618_at	45	13.6	282.2	5.2	30.0	interleukin 18 receptor 1	IL18R1
214666_x_at	123.3	45.9	565.4	9.5	30.0	iron-responsive element binding protein 2	IREB2
204821_at	222.6	133.8	1084.6	32	30.0	butyrophilin, subfamily 3, member A3	BTN3A3
47560_at	204.3	86	991.2	25.8	30.0	latrophilin 1	LPHN1
209356_x_at	118	25.8	815.1	10.6	30.0	EGF-containing fibulin-like extracellular matrix protein 2	EFEMP2
216167_at	18.5	8.4	225.8	2.6	30.0	leucine rich repeat neuronal 5	LRRN5
32402_s_at	85.9	53.2	334.4	16.9	30.0	symplekin	SYMPK
213355_at	116.3	14.9	832.8	4.9	30.0	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	ST3GAL6
37986_at	105.5	41.3	1787.6	5.1	30.0	erythropoietin receptor	EPOR
200994_at	616.5	375	2982.3	255.3	29.6	Importin 7	IPO7
202265_at	590.9	220.6	8430.4	244.1	29.6	polycomb group ring finger 4	PCGF4
211917_s_at	63.6	5.6	415.6	5.7	29.6	prolactin receptor /// prolactin receptor	PRLR
219470_x_at	154.2	87.6	1374.8	53.1	29.6	cyclin J	CCNJ
220676_at	52.2	7.7	313	4.8	29.6	ADAM metallopeptidase with thrombospondin type 1 motif, 8	ADAMTS8
200859_x_at	686.3	476.2	4868.3	194.6	29.6	filamin A, alpha (actin binding protein 280)	FLNA
200887_s_at	1051.4	588.9	8128.3	154.8	29.6	signal transducer and activator of transcription 1, 91kDa	STAT1
204150_at	216.4	53	10597.1	14.1	29.6	stabilin 1	STAB1
220396_at	197.7	48.5	1749.4	19.2	29.6	---	---
221042_s_at	100.7	16	1322	7.4	29.6	calmin (calponin-like, transmembrane)	CLMN
218686_s_at	54.6	49.1	1557.5	19.7	29.6	rhomboid family 1 (Drosophila)	RHBDF1
206682_at	78.9	23.6	445.7	6.2	29.6	C-type lectin domain family 10, member A	CLEC10A
208273_at	128.8	65.6	524.1	11.5	29.6	zinc finger protein 695	ZNF695
208614_s_at	514.9	365.6	5706.7	64.1	29.6	filamin B, beta (actin binding protein 278)	FLNB

214735_at	167.4	65.5	2571	7	29.6	phosphoinositide-binding protein PIP3-E	PIP3-E
200659_s_at	472.5	151.4	4886.9	87	29.3	prohibitin	PHB
215222_x_at	1112.1	652.9	4103.4	671.1	29.3	microtubule-actin crosslinking factor 1	MACF1
203043_at	851.8	563	4757.6	206.9	29.3	zinc finger, BED-type containing 1	ZBED1
212739_s_at	663	261.3	3017	109.5	29.3	non-metastatic cells 4, protein expressed in	NME4
219767_s_at	305.3	259.4	1419.8	86.3	29.3	crystallin, zeta (quinone reductase)-like 1	CRYZL1
209671_x_at	641.5	291.3	22825.7	60.1	29.3	T cell receptor alpha locus /// T cell receptor alpha locus /// T cell receptor alpha constant /// T cell receptor alpha constant	TRA@ /// TRAC
211597_s_at	176.8	29.1	5111.3	8.3	29.3	homeodomain-only protein /// homeodomain-only protein	HOP
221370_at	108.6	41.1	551.4	16.6	29.3	kruppel-like zinc finger factor X17	LOC377064
221641_s_at	343.8	229.3	2829.3	42.4	29.3	acyl-CoA thioesterase 9	ACOT9
212976_at	27.3	12	286.2	1.8	29.3	leucine rich repeat containing 8 family, member B	LRRC8B
207190_at	29.8	24.9	782.1	6.4	29.3	zinc finger, ZZ-type with EF-hand domain 1	ZZEF1
203434_s_at	3344.3	2134.2	13818.9	3.4	29.3	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	MME
206940_s_at	811.4	463.5	11867.2	33.2	29.3	POU domain, class 4, transcription factor 1	POU4F1
208454_s_at	166.5	23	1452.4	18.8	28.9	plasma glutamate carboxypeptidase	PGCP
211372_s_at	30.8	11.7	750.5	6.1	28.9	interleukin 1 receptor, type II	IL1R2
211743_s_at	96.8	14.7	29321.7	12.2	28.9	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein) /// proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	PRG2
216037_x_at	368.2	206.5	1613	120.8	28.9	transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2
218921_at	227.6	40.7	1358.9	53.8	28.9	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	SIGIRR
38487_at	289.4	82.3	13184.4	50.7	28.9	stabilin 1	STAB1
200813_s_at	666.6	416.6	2386	63.5	28.9	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	PAFAH1B1
219864_s_at	22.3	4.3	294.6	2	28.9	Down syndrome critical region gene 1-like 2	DSCR1L2
208680_at	8265.5	6447.7	43425.5	1422	28.9	peroxiredoxin 1	PRDX1
219451_at	178.6	31	1373.2	5.9	28.9	methionine sulfoxide reductase B2	MSRB2
204007_at	195.7	116.9	1789.5	26.7	28.9	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	FCGR3B

216333_x_at	53	28.1	1476.8	6.4	28.9	tenascin XB	TNXB
215442_s_at	12	4.8	444.7	1.5	28.9	thyroid stimulating hormone receptor	TSHR
202838_at	653.7	432.9	3736.2	70.3	28.9	fucosidase, alpha-L- 1, tissue	FUCA1
204505_s_at	315.2	265.2	13524	32.7	28.9	erythrocyte membrane protein band 4.9 (dematin)	EPB49
221912_s_at	199.3	117.4	734.2	19.8	28.9	coiled-coil domain containing 28B	CCDC28B
219564_at	103.3	17.6	1219.7	8.8	28.5	potassium inwardly-rectifying channel, subfamily J, member 16	KCNJ16
204482_at	26.5	16.4	433.9	7.7	28.5	claudin 5 (transmembrane protein deleted in velocardiofacial syndrome)	CLDN5
212486_s_at	139.3	14.3	766.1	4.1	28.5	FYN oncogene related to SRC, FGR, YES	FYN
215646_s_at	42.5	5.4	6886.2	2.5	28.5	chondroitin sulfate proteoglycan 2 (versican) /// chondroitin sulfate proteoglycan 2 (versican)	CSPG2
216833_x_at	278.3	162.2	23091.1	19.7	28.5	glycophorin B (includes Ss blood group) /// glycophorin E	GYPB /// GYPE
214945_at	97.6	72.1	821.6	4.1	28.5	NY-REN-7 antigen /// similar to KIAA0752 protein	NY-REN-7 /// LOC389347
202877_s_at	193.8	23.9	1033	19.1	28.1	complement component 1, q subcomponent, receptor 1 /// complement component 1, q subcomponent, receptor 1	C1QR1
210340_s_at	34	4.5	280.4	3.5	28.1	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	CSF2RA
221059_s_at	276.9	165.1	3040.2	105.5	28.1	coactosin-like 1 (Dictyostelium)	COTL1
203482_at	349.4	302.5	1426.7	139.9	28.1	chromosome 10 open reading frame 6	C10orf6
206023_at	13.1	6.9	366.1	3.4	28.1	neuromedin U	NMU
43511_s_at	419	243.3	1829	96.1	28.1	MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	---
204689_at	917.2	831.8	4085.4	104.7	28.1	hematopoietically expressed homeobox	HHEX
213385_at	150.6	28.5	2256.5	8	28.1	Chimerin (chimaerin) 2	CHN2
201911_s_at	120.3	20	853.8	6.4	28.1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	FARP1
213856_at	84.7	15.7	403.4	5.1	28.1	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	CD47
213953_at	49.5	15.7	693.1	3.2	28.1	keratin 20	KRT20
203139_at	746	321.6	4394	102.3	28.1	death-associated protein kinase 1	DAPK1

213451_x_at	52	41.4	1626	9	28.1	tenascin XB	TNXB
220530_at	49.1	17.1	414.9	3.7	28.1	---	---
220952_s_at	168	141.6	1240.3	6	28.1	pleckstrin homology domain containing, family A member 5	PLEKHA5
202671_s_at	203.5	102.2	2003.4	5.7	28.1	pyridoxal (pyridoxine, vitamin B6) kinase	PDXK
202665_s_at	835.1	582.7	3306.9	384.7	27.8	Wiskott-Aldrich syndrome protein interacting protein	WASPIP
204866_at	211.5	75.7	1149.8	72.8	27.8	PHD finger protein 16	PHF16
207063_at	34.8	6.4	444.4	3.7	27.8	chromosome Y open reading frame 14	CYorf14
207605_x_at	713.7	490.7	3210.3	279.1	27.8	zinc finger protein 117 (HPF9)	ZNF117
208805_at	6471.6	4957.8	25767.4	2603.4	27.8	proteasome (prosome, macropain) subunit, alpha type, 6	PSMA6
209135_at	56.4	3	536.8	2.4	27.8	aspartate beta-hydroxylase	ASPH
213696_s_at	144.5	47.7	666.6	30.8	27.8	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	MED8
216071_x_at	702.9	347	2780	381.2	27.8	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)	MED12
218181_s_at	372	256.6	1267	170.4	27.8	mitogen-activated protein kinase kinase kinase kinase 4	MAP4K4
218781_at	767.9	476.7	4153.5	332.5	27.8	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	SMC6L1
220582_at	100.2	14.2	522.5	9.2	27.8	---	---
202018_s_at	36.7	13.7	38822.7	5.7	27.8	lactotransferrin	LTF
201162_at	751	32.6	11849.6	15.7	27.8	insulin-like growth factor binding protein 7	IGFBP7
207802_at	10.5	4.1	4963.3	0.9	27.8	cysteine-rich secretory protein 3	CRISP3
220798_x_at	85.6	13.9	721.7	4.1	27.8	plasticity-related gene 2	PRG2
203411_s_at	190.1	23.1	2250.7	8.1	27.8	lamin A/C	LMNA
208862_s_at	248.5	93.1	1480.8	35.8	27.8	catenin (cadherin-associated protein), delta 1	CTNND1
217257_at	37.2	4.5	228.7	1.9	27.8	Stathmin 1/oncoprotein 18	STMN1
221352_at	80.5	23.1	489.8	8.4	27.8	DNA binding protein for surfactant protein B	HUMBINDC
201701_s_at	152.7	104.7	748.9	9.5	27.8	progesterone receptor membrane component 2	PGRMC2
218141_at	151	82.4	5427.4	15.3	27.8	likely ortholog of mouse ubiquitin-conjugating enzyme E2-230K	E2-230K
201188_s_at	243.2	136.8	1625	29.1	27.8	inositol 1,4,5-triphosphate receptor, type 3	ITPR3
208405_s_at	2539.4	1613.7	19923.7	888.6	27.4	CD164 antigen, sialomucin	CD164

211819_s_at	95	5	1000	3.4	27.4	sorbin and SH3 domain containing 1	SORBS1
213556_at	105	10.3	946.4	7.8	27.4	similar to R28379_1	LOC390940
208033_s_at	95.8	15.5	1150.3	6.3	27.4	AT-binding transcription factor 1	ATBF1
209272_at	284.7	193.5	1317.9	33.7	27.4	NGFI-A binding protein 1 (EGR1 binding protein 1)	NAB1
209604_s_at	296.1	106.9	5495.4	27.4	27.4	GATA binding protein 3	GATA3
220010_at	30.8	7.5	4146.7	3.3	27.4	KCNE1-like	KCNE1L
218017_s_at	210.9	40.1	1100.6	19.4	27.4	transmembrane protein 76	TMEM76
203398_s_at	72.1	24.1	553.6	6.4	27.4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	GALNT3
203577_at	89.1	17.9	472.5	5.5	27.4	general transcription factor IIH, polypeptide 4, 52kDa	GTF2H4
220252_x_at	399.1	132.7	2976.4	33.6	27.4	chromosome X open reading frame 21	CXorf21
204882_at	679.5	332.4	3947.9	30.2	27.4	Rho GTPase activating protein 25	ARHGAP25
205557_at	40.4	29.5	14658	6.3	27.4	bactericidal/permeability-increasing protein	BPI
202966_at	51.1	20.6	440.5	3	27.4	calpain 6	CAPN6
206761_at	182.3	81.9	2348	11.1	27.4	CD96 antigen	CD96
200931_s_at	1317.9	900.8	6524.3	471.1	27.0	vinculin	VCL
203469_s_at	47.2	16.6	512.7	11.4	27.0	cyclin-dependent kinase (CDC2-like) 10	CDK10
205987_at	249.7	16	7020.6	9.7	27.0	CD1C antigen, c polypeptide	CD1C
207668_x_at	2269.9	1931.1	10249.1	1036.8	27.0	protein disulfide isomerase family A, member 6	PDIA6
208167_s_at	54.3	6.5	1014.3	4.6	27.0	matrix metallopeptidase 16 (membrane-inserted)	MMP16
216672_s_at	12.4	6.2	212.7	4.2	27.0	myelin transcription factor 1-like	MYT1L
218275_at	99.3	19.2	384	10.7	27.0	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	SLC25A10
202169_s_at	601.6	377.7	1966.2	166.7	27.0	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	AASDHPPT
204846_at	70.3	15.1	733.6	6.7	27.0	ceruloplasmin (ferroxidase)	CP
212623_at	414.1	261	1305.9	112.5	27.0	transmembrane protein 41B	TMEM41B
214582_at	252.1	143.6	1684.1	43.7	27.0	phosphodiesterase 3B, cGMP-inhibited	PDE3B
220030_at	20.9	3.5	364.3	1.5	27.0	serine/threonine/tyrosine kinase 1	STYK1
218454_at	207.2	52.4	12684.2	21.7	27.0	hypothetical protein FLJ22662	FLJ22662
219467_at	181.6	129.5	614.8	36.9	27.0	hypothetical protein FLJ20125	FLJ20125
209122_at	542.2	267.6	8508.3	60.5	27.0	adipose differentiation-related protein	ADFP
218019_s_at	483.5	320.9	4313.3	154.2	27.0	pyridoxal (pyridoxine, vitamin B6) kinase	PDXK
216174_at	178.7	87.5	794.2	18.1	27.0	hepatocellular carcinoma-related HCRP1	HCRP1

216033_s_at	503.1	258.6	2491.8	22	27.0	FYN oncogene related to SRC, FGR, YES	FYN
206785_s_at	46.3	11.1	345.9	2.3	27.0	killer cell lectin-like receptor subfamily C, member 1 /// killer cell lectin-like receptor subfamily C, member 2	KLRC1 /// KLRC2
213712_at	86.4	15	1058.3	3	27.0	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	ELOVL2
204518_s_at	35.7	27.8	1300.7	8.2	27.0	peptidylprolyl isomerase C (cyclophilin C)	PPIC
203922_s_at	312.1	123.8	1877.8	77.6	26.7	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	CYBB
204669_s_at	173.3	18.2	2477.9	12	26.7	ring finger protein 24	RNF24
209081_s_at	26.6	7.7	800.2	5.9	26.7	collagen, type XVIII, alpha 1	COL18A1
212352_s_at	1654.9	932.1	8879.8	606.1	26.7	transmembrane emp24-like trafficking protein 10 (yeast)	TMED10
214706_at	185.9	36.8	735.8	20.7	26.7	zinc finger protein 200	ZNF200
201703_s_at	679.9	445.1	2195.6	91.2	26.7	protein phosphatase 1, regulatory subunit 10	PPP1R10
203929_s_at	85.4	34.9	576.4	17.3	26.7	microtubule-associated protein tau	MAPT
209331_s_at	583.4	270.7	2420	106.1	26.7	MYC associated factor X	MAX
209879_at	211.8	114.5	2395.8	43.1	26.7	selectin P ligand	SELPLG
212230_at	128.2	40.7	1062.4	14.4	26.7	phosphatidic acid phosphatase type 2B	PPAP2B
218904_s_at	112.6	24	782.4	11.4	26.7	chromosome 9 open reading frame 40	C9orf40
208438_s_at	186.8	44.4	2461.2	11.1	26.7	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	FGR
210222_s_at	56.5	13.7	351.5	5.1	26.7	reticulon 1	RTN1
213157_s_at	62.7	32.2	547.2	9.7	26.7	KIAA0523 protein	KIAA0523
89476_r_at	210.9	132	981.1	48.9	26.7	aminopeptidase-like 1	NPEPL1
209434_s_at	143	85.4	597.2	12.4	26.7	phosphoribosyl pyrophosphate amidotransferase	PPAT
206235_at	669.4	314.9	4071.6	82	26.7	ligase IV, DNA, ATP-dependent	LIG4
204863_s_at	160.9	119.4	837.1	8.5	26.7	interleukin 6 signal transducer (gp130, oncostatin M receptor)	IL6ST
206591_at	1526.9	1040	15016.2	19.7	26.7	recombination activating gene 1	RAG1
207339_s_at	2085.6	1712.7	24613.4	77.1	26.7	lymphotoxin beta (TNF superfamily, member 3)	LTB
202907_s_at	582.8	409.4	2160.4	481.3	26.3	nibrin	NBN
204725_s_at	425.6	347.8	1967.1	211.3	26.3	NCK adaptor protein 1	NCK1
206828_at	116.6	15.5	1426.5	10.7	26.3	TXK tyrosine kinase	TXK

209082_s_at	125.9	14.9	1409.2	12.6	26.3	collagen, type XVIII, alpha 1	COL18A1
210612_s_at	49.5	6.4	918.1	3.6	26.3	synaptojanin 2	SYNJ2
212179_at	1307.2	522	5366.7	338.9	26.3	chromosome 6 open reading frame 111	C6orf111
212268_at	550.5	299	11730.6	232.6	26.3	serpin peptidase inhibitor, clade B (ovalbumin), member 1	SERPINB1
213126_at	31.5	10.2	218.7	6.2	26.3	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	MED8
218446_s_at	129.4	15.8	573.3	14.2	26.3	family with sequence similarity 18, member B	FAM18B
220667_at	40.1	5.2	458.2	4	26.3	---	---
200827_at	111.6	46.7	675.1	21.4	26.3	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	PLOD1
203632_s_at	31	14.2	798.1	6.3	26.3	G protein-coupled receptor, family C, group 5, member B	GPRC5B
206302_s_at	441	298.4	9153.7	39.5	26.3	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	NUDT4 /// NUDT4P1
207703_at	50.8	10.5	406.9	4	26.3	neuroligin 4, Y-linked	NLGN4Y
220405_at	89.5	32.1	556.7	6.6	26.3	syntrophin, gamma 1	SNTG1
216317_x_at	150	32.7	12972.6	12.5	26.3	Rhesus blood group, CcEe antigens	RHCE
207851_s_at	108.7	26.6	679.3	8.1	26.3	insulin receptor	INSR
208492_at	60.2	22.3	287.9	7.8	26.3	regulatory factor X-associated protein	RFXAP
218232_at	91.8	45.1	1938.4	8	26.3	complement component 1, q subcomponent, alpha polypeptide	C1QA
209815_at	167.6	45	3201	3.4	26.3	patched homolog (Drosophila)	PTCH
200871_s_at	2085.5	1361.6	14505.4	683.1	25.9	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	PSAP
200889_s_at	527.4	422	2478.5	212.3	25.9	signal sequence receptor, alpha (translocon-associated protein alpha)	SSR1
207341_at	128.8	16.4	22403.2	11.7	25.9	proteinase 3 (serine proteinase, neutrophil, Wegener granulomatosis autoantigen)	PRTN3
208420_x_at	347.2	224.8	1303.3	145.3	25.9	suppressor of Ty 6 homolog (S. cerevisiae)	SUPT6H
210016_at	148.8	7.3	3757.5	6.9	25.9	myelin transcription factor 1-like	MYT1L
213435_at	36.6	5.8	4632.2	5.3	25.9	SATB family member 2	SATB2
217367_s_at	127.2	38.5	675.7	33.7	25.9	zinc fingers and homeoboxes 3	ZHX3

219346_at	56.7	4.2	502.5	4.9	25.9	leucine rich repeat and fibronectin type III domain containing 3	LRFN3
200816_s_at	1030.3	550.4	3684.2	240.8	25.9	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	PAFAH1B1
204858_s_at	143.8	32.9	992.8	16.2	25.9	endothelial cell growth factor 1 (platelet-derived)	ECGF1
214634_at	78.2	15.8	514.9	6.9	25.9	---	---
217695_x_at	114.1	25.5	1056.8	8.9	25.9	---	---
211071_s_at	904.7	682.7	4373.1	322.4	25.9	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11 /// myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	MLLT11
212895_s_at	563.7	455.4	2422.8	191.8	25.9	active BCR-related gene	ABR
206165_s_at	89.7	34.9	467.2	7.9	25.9	chloride channel, calcium activated, family member 2	CLCA2
206914_at	45.4	11.4	322.1	3.4	25.9	class-I MHC-restricted T cell associated molecule	CRTAM
221246_x_at	217.6	148.6	2307.1	20	25.9	tensin 1 /// tensin 1	TNS1
201380_at	278.8	197.5	1221	150.2	25.6	cartilage associated protein	CRTAP
216633_s_at	45	7.7	306.4	4	25.6	phospholipase C-like 3	PLCL3
221501_x_at	3049	2089.6	13557	1205	25.6	hypothetical protein LOC339047	LOC339047
45297_at	130.3	38.8	1920.1	21.3	25.6	EH-domain containing 2	EHD2
202911_at	2201.5	1372.5	8710.3	645.7	25.6	mutS homolog 6 (E. coli)	MSH6
211342_x_at	784.7	489.5	3356.7	191.2	25.6	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)	MED12
218445_at	81.9	36.9	733.8	13.2	25.6	H2A histone family, member Y2	H2AFY2
202557_at	245.1	168.8	2210.8	33.3	25.6	stress 70 protein chaperone, microsome-associated, 60kDa	STCH
200890_s_at	365.9	300.3	1698.2	54	25.6	signal sequence receptor, alpha (translocon-associated protein alpha)	SSR1
215882_at	66.6	16.5	312.9	6.9	25.6	Centrosomal protein 152kDa	CEP152
219602_s_at	160.6	75.9	1545.3	11.6	25.6	family with sequence similarity 38, member B	FAM38B
207402_at	77.6	19.7	440.4	4.3	25.6	zinc finger protein 132 (clone pHZ-12)	ZNF132
218346_s_at	682.6	523.1	11846.5	178.6	25.6	sestrin 1	SESN1
200952_s_at	210.9	49.5	3997.6	13	25.6	cyclin D2	CCND2
203608_at	957	649.2	5837.5	26.7	25.6	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	ALDH5A1

218862_at	291.5	69	2508.3	21.1	25.6	ankyrin repeat and SOCS box-containing 13	ASB13
218472_s_at	154.4	91.3	793.1	9.4	25.6	pelota homolog (Drosophila)	PELO
201743_at	67.2	16.5	1571.8	5.8	25.6	CD14 antigen /// CD14 antigen	CD14
202669_s_at	135.9	25.9	1724	10	25.6	ephrin-B2	EFNB2
218804_at	64.8	5.8	2319	0.7	25.6	transmembrane protein 16A	TMEM16A
202403_s_at	154.9	62.3	1745.3	9.2	25.6	collagen, type I, alpha 2	COL1A2
204014_at	10.9	7.3	504.9	2.6	25.6	dual specificity phosphatase 4	DUSP4
213959_s_at	69.6	41.5	719	2.8	25.6	KIAA1005 protein	KIAA1005
219759_at	415.7	208.8	3312.2	14.4	25.6	leukocyte-derived arginine aminopeptidase	LRAP
204445_s_at	613.4	374.9	3692.5	11.5	25.6	arachidonate 5-lipoxygenase	ALOX5
208542_x_at	25.5	8.2	342.1	5.1	25.2	zinc finger protein 208	ZNF208
212198_s_at	551.4	331.2	1856.6	315.1	25.2	transmembrane 9 superfamily protein member 4	TM9SF4
212203_x_at	2643.1	932.3	13245.4	931	25.2	interferon induced transmembrane protein 3 (1-8U)	IFITM3
216040_x_at	150.4	37.2	761.3	22	25.2	CDNA FLJ14073 fis, clone HEMBB1001812	---
218045_x_at	14.8	6.1	528.4	4.1	25.2	parathymosin	PTMS
218546_at	35.7	13.4	844.5	6.8	25.2	chromosome 1 open reading frame 115	C1orf115
219364_at	35.3	18	376.4	11.1	25.2	likely ortholog of mouse D11lgp2	LGP2
204413_at	67.7	31	410.9	13.9	25.2	TNF receptor-associated factor 2	TRAF2
205400_at	209.8	62.9	1064.9	26.4	25.2	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	WAS
209684_at	126.1	19.5	1033.7	9.4	25.2	Ras and Rab interactor 2	RIN2
213510_x_at	403.9	267.7	1583.6	42.9	25.2	TL132 protein	LOC220594
221584_s_at	75.5	27.7	536.4	6.7	25.2	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	KCNMA1
222078_at	51.2	19.6	743.7	7.2	25.2	Hyperpolarization activated cyclic nucleotide-gated potassium channel 3	HCN3
202687_s_at	168.8	60.4	2096	16.1	25.2	tumor necrosis factor (ligand) superfamily, member 10 /// tumor necrosis factor (ligand) superfamily, member 10	TNFSF10
203102_s_at	543.5	357	2600.5	61.1	25.2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	MGAT2
207269_at	201.2	140.2	50844.5	26.2	25.2	defensin, alpha 4, corticostatin	DEFA4
214393_at	51.3	14.2	951.1	3.8	25.2	hypothetical protein LOC284062	LOC284062
220713_at	153.5	131.7	1002	27.8	25.2	Chromosome 11 open reading frame 49	C11orf49

206983_at	98.4	40.3	1311.9	4.3	25.2	chemokine (C-C motif) receptor 6	CCR6
220416_at	88.4	44.1	3159.1	3.4	25.2	ATPase, Class I, type 8B, member 4	ATP8B4
204349_at	108	6.7	412.9	6.6	24.8	cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa	CRSP9
205718_at	208.5	12.1	3223.5	10.9	24.8	integrin, beta 7	ITGB7
210774_s_at	3772.2	3234.2	41868.2	1733.7	24.8	nuclear receptor coactivator 4	NCOA4
212552_at	1213.9	967.9	6135.2	553.6	24.8	hippocalcin-like 1	HPCAL1
202598_at	650	437.8	5525.2	129	24.8	S100 calcium binding protein A13	S100A13
204414_at	27.6	5	243.4	1.9	24.8	like-glycosyltransferase	LARGE
210128_s_at	183	38.2	1125.8	18.6	24.8	leukotriene B4 receptor	LTB4R
212217_at	273.7	155.4	836.9	60.3	24.8	prolyl endopeptidase-like	PREPL
210738_s_at	22.2	4.5	251.4	1.3	24.8	solute carrier family 4, sodium bicarbonate cotransporter, member 4	SLC4A4
202599_s_at	2080.2	919.5	11117.1	95.4	24.8	nuclear receptor interacting protein 1	NRIP1
205795_at	30.2	14.8	1096.1	2.6	24.8	neurexin 3	NRXN3
206372_at	50	23.6	1704	5.3	24.8	myogenic factor 6 (herculin)	MYF6
206231_at	289.9	145.6	1890.7	37.6	24.8	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	KCNN1
209169_at	136.9	40.3	1283.6	3.5	24.8	glycoprotein M6B	GPM6B
208981_at	738.3	406.5	5037.4	25.6	24.8	platelet/endothelial cell adhesion molecule (CD31 antigen)	PECAM1

Table 2. Probesets underexpressed in 25% of more of B-lineage ALL cases (n =270) as compared to normal bone marrow CD19+CD10+ cells from 4 healthy donors

probe set ID	CD10+ CD19+ max	CD10+ CD19+ min	ALL max	ALL min	% ALL under expressed	Title	Symbol
202388_at	29835.8	25562.5	9759.4	10.9	100	regulator of G-protein signalling 2, 24kDa	RGS2
204207_s_at	4433.5	3175.3	1223.2	332.7	100	RNA guanylyltransferase and 5'-phosphatase	RNGTT
204208_at	3110	1717.1	772.2	18.6	100	RNA guanylyltransferase and 5'-phosphatase	RNGTT
201853_s_at	12593.8	6539	3519.8	478.8	100	cell division cycle 25B	CDC25B
202626_s_at	5962.8	4459.4	4793.6	161.8	99	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	LYN

205942_s_at	2204.8	1110.2	623.9	6.3	99	acyl-CoA synthetase medium-chain family member 3	ACSM3
207540_s_at	5984.8	4323.6	2507.6	34.6	99	spleen tyrosine kinase	SYK
206046_at	1778.2	1399.6	3305.2	24.2	99	ADAM metallopeptidase domain 23	ADAM23
210377_at	1677	767.9	656.8	6.9	99	acyl-CoA synthetase medium-chain family member 3	ACSM3
210754_s_at	6524.5	5533.3	5518.6	119.3	98	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	LYN
201465_s_at	1499.1	591.2	823.4	6.2	98	v-jun sarcoma virus 17 oncogene homolog (avian)	JUN
203927_at	1369.3	1138.3	916.8	67.1	97	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	NFKBIE
211639_x_at	3276	2582.8	14470.8	9.9	97	Isolate Black93 immunoglobulin heavy chain variable region (IGVH) /// Isolate Black93 immunoglobulin heavy chain variable region (IGVH)	---
216834_at	8959.4	2947.1	7948.4	3.6	97	regulator of G-protein signalling 1	RGS1
207574_s_at	6491.2	3330.7	5589.1	23.7	96	growth arrest and DNA-damage-inducible, beta	GADD45B
209305_s_at	7175.5	3216.3	4660.8	35.8	96	growth arrest and DNA-damage-inducible, beta	GADD45B
211633_x_at	3257.1	1593.6	1815.9	9.4	96	Immunoglobulin heavy constant gamma 1	IGHG1
213419_at	1983.8	877.8	809.5	4	96	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	APBB2
217168_s_at	6948.2	4299.7	9008.6	277	96	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	HERPUD1
213808_at	1370.8	704.8	6121.1	3.6	96	ADAM metallopeptidase domain 23	ADAM23
201044_x_at	4997.4	1908.8	4534.7	6.1	96	dual specificity phosphatase 1	DUSP1
201416_at	19683.9	13224.7	36012.1	314.4	96	SRY (sex determining region Y)-box 4	SOX4
205297_s_at	17637	11257.6	8701	19.1	96	CD79B antigen (immunoglobulin-associated beta)	CD79B
221986_s_at	1516.8	1088.1	1221.8	8.2	96	kelch-like 24 (Drosophila)	KLHL24
203036_s_at	377.2	246.6	424.5	7.5	96	metastasis suppressor 1	MTSS1
209304_x_at	5576.4	2633.1	4811.7	23.5	96	growth arrest and DNA-damage-inducible, beta	GADD45B
202191_s_at	5953.1	2637.8	2695.5	15.6	95	growth arrest-specific 7	GAS7
215949_x_at	2781.1	1745.5	3036.2	10.6	95	immunoglobulin heavy constant mu	IGHM
211650_x_at	3663.2	1700.3	18473.5	9.6	95	IgG heavy chain variable region (Vh26) /// IgG heavy chain variable region (Vh26)	---
214623_at	1081.8	683.7	927	6.8	94	split hand/foot malformation (ectrodactyly) type 3 pseudogene 1	SHFM3P1
216491_x_at	7328.1	6235.1	10541.5	7.6	94	immunoglobulin heavy constant mu	IGHM

211637_x_at	6888.7	4946.8	11825.7	12.2	94	Immunoglobulin heavy chain variable region (VH IV family) from IgM rheumatoid factor	---
214522_x_at	1124.3	1009.1	1334.7	7.2	94	histone 1, H3d	HIST1H3D
40148_at	1381.9	627.4	593.3	4.4	94	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	APBB2
220668_s_at	2345.6	1514.1	5694.5	21.5	94	DNA (cytosine-5-)-methyltransferase 3 beta	DNMT3B
204730_at	4967.4	2864	8362.2	16.1	93	regulating synaptic membrane exocytosis 3	RIMS3
214916_x_at	14343.8	6892.4	17677.2	82.3	93	immunoglobulin heavy locus	IGH@
218205_s_at	19891.4	12578.8	17879.7	801.3	93	MAP kinase interacting serine/threonine kinase 2	MKNK2
202988_s_at	2636.3	560.9	2173.7	2.9	93	regulator of G-protein signalling 1	RGS1
206864_s_at	1273.7	714.7	857.8	1.8	93	harakiri, BCL2 interacting protein (contains only BH3 domain)	HRK
210150_s_at	1324.2	1056	1372.4	5	93	laminin, alpha 5	LAMA5
214973_x_at	6122	2443.4	7633.2	10.1	93	immunoglobulin heavy constant delta	IGHD
217281_x_at	3751.2	1876.2	4004.5	5.9	93	Isolate Rice94 immunoglobulin heavy chain variable region (IGVH)	---
214669_x_at	8995.8	5783	18674.6	159.4	93	immunoglobulin kappa variable 1-5	IGKC
209062_x_at	1688.2	1275.6	1789.8	32.3	92	nuclear receptor coactivator 3	NCOA3
221496_s_at	1497.2	419.1	773.1	6.1	92	transducer of ERBB2, 2	TOB2
216510_x_at	3545	1371.3	10120.1	4.8	92	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1	IGHA1 /// IGHD /// IGHG1 /// IGHM
204562_at	17170.2	7589.8	8919.6	61.1	92	interferon regulatory factor 4	IRF4
201779_s_at	4113.5	2884	2079.7	439.5	91	ring finger protein 13	RNF13
211849_s_at	1289	694.5	544.9	13	91	RNA guanylyltransferase and 5'-phosphatase	RNGTT
216986_s_at	1767	1088.9	1045.9	26.5	91	interferon regulatory factor 4	IRF4
201303_at	11275.3	6684.6	4953	869.3	91	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	DDX48
211798_x_at	3202.8	1844.7	2570.4	13	91	immunoglobulin lambda joining 3	IGLJ3
212985_at	1998.5	948.9	1367.1	5	91	Hypothetical protein FLJ14001	FLJ14001
213593_s_at	2902.3	1697.1	1429.1	15	91	Transformer-2 alpha	TRA2A
216557_x_at	4084.7	1926.7	9300.4	89.7	91	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 /// immunoglobulin heavy constant gamma 3	IGHA1 /// IGHG1 /// IGHG3

210693_at	647	223.3	700.9	6.5	91	signal peptide peptidase-like 2B	SPPL2B
217360_x_at	679	447.1	853.8	5.2	91	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 /// immunoglobulin heavy constant gamma 3	IGHA1 /// IGHG1 /// IGHG3
204440_at	4557.9	1759.5	9729.2	47.8	91	CD83 antigen (activated B lymphocytes, immunoglobulin superfamily)	CD83
203865_s_at	2572.5	1405.4	3163.5	7.1	90	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	ADARB1
215121_x_at	38082.2	24742.4	97827.3	411.9	90	immunoglobulin lambda locus	IGL@
212942_s_at	1062.1	467.7	871.1	6.3	90	KIAA1199	KIAA1199
204786_s_at	1394.1	633.2	626.5	7.3	90	interferon (alpha, beta and omega) receptor 2	IFNAR2
210172_at	2090.8	1430.9	2185.8	19.3	90	splicing factor 1	SF1
213511_s_at	8132.9	5082.3	4143.4	404.6	90	myotubularin related protein 1	MTMR1
221985_at	1969.6	1635.9	1694.5	229.7	90	kelch-like 24 (Drosophila)	KLHL24
203751_x_at	6801.2	2457.2	9483.9	3.2	89	jun D proto-oncogene	JUND
205466_s_at	456.1	371.8	864.3	2.5	89	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	HS3ST1
207993_s_at	767.8	450	542.3	9	89	calcium binding protein P22	CHP
208553_at	538.7	230	415.9	5.2	89	histone 1, H1e	HIST1H1E
213638_at	2518.5	972.3	1773.4	7.5	89	phosphatase and actin regulator 1	PHACTR1
202779_s_at	4064.5	2660.1	7091.4	94	89	ubiquitin-conjugating enzyme E2S	UBE2S
212350_at	4326.3	3443.9	2686.8	395.3	89	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	TBC1D1
214777_at	2535.8	914.1	3431.5	11	88	Ig rearranged kappa-chain mRNA V-J1-region, hybridoma AE6-5, 5' end	---
221909_at	512.9	332.3	781.3	8.1	88	hypothetical protein FLJ14627	FLJ14627
216401_x_at	2337.3	950.1	2657.3	16.9	87	Ig rearranged kappa-chain mRNA V-J1-region, hybridoma AE6-5, 5' end /// Immunoglobulin kappa constant	LOC400969 /// IGKC
219878_s_at	867.1	176.2	962.9	4.9	87	Kruppel-like factor 13	KLF13
221807_s_at	2186.5	1302.7	2491.7	10.9	87	hypothetical protein PP2447	PP2447
201668_x_at	1020.2	570.7	1370.6	10.9	87	myristoylated alanine-rich protein kinase C substrate	MARCKS
203589_s_at	901	779.9	1067.2	30.8	87	transcription factor Dp-2 (E2F dimerization partner 2)	TFDP2
219202_at	1964.6	1420.8	1763.9	17	87	rhomboid, veinlet-like 6 (Drosophila)	RHBDL6
221969_at	13313.2	10083.4	9494.5	125.3	87	Paired box gene 5 (B-cell lineage specific activator)	PAX5

211649_x_at	1586.1	762.4	1034	13.7	86	Immunoglobulin heavy constant mu /// Immunoglobulin heavy constant mu	IGHM
216095_x_at	7254.6	3992.8	3149.7	298	86	myotubularin related protein 1	MTMR1
215379_x_at	14893.2	7687.7	37246.9	354.3	86	immunoglobulin lambda locus	IGL@
214326_x_at	5238.4	1687	6719.1	4.4	86	jun D proto-oncogene	JUND
215907_at	3754.8	2954.9	4524.6	76.9	86	BTB and CNC homology 1, basic leucine zipper transcription factor 2	BACH2
202409_at	2262.9	492.3	35487.2	16.3	86	putative insulin-like growth factor II associated protein	LOC492304
216560_x_at	683.9	251.9	19290.6	10.3	86	Immunoglobulin lambda constant 1 (Mcg marker) /// Immunoglobulin lambda joining 3	IGLC1 /// IGLC2
204255_s_at	1219.3	464.5	772	11.8	86	vitamin D (1,25- dihydroxyvitamin D3) receptor	VDR
205861_at	6899.6	4313.1	13176.4	51.1	86	Spi-B transcription factor (Spi-1/PU.1 related) /// Spi-B transcription factor (Spi-1/PU.1 related)	SPIB
212451_at	1861.4	829.1	774.2	27.7	86	KIAA0256 gene product	KIAA0256
213998_s_at	1316.7	735.7	2193	5.7	86	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	DDX17
214455_at	1162.4	460.7	831.8	4.9	86	histone 1, H2bc	HIST1H2BC
213668_s_at	1789.5	1185.1	4590.5	11.1	86	SRY (sex determining region Y)-box 4	SOX4
213575_at	2193.8	846.7	1062.3	9.6	85	Transformer-2 alpha	TRA2A
216430_x_at	248.7	105	730.6	7.1	85	Immunoglobulin lambda chain variable region (IGVL gene)region, (IGL)	IGLV3-25 /// IGLC2
206641_at	318.9	157	1268	4.5	85	tumor necrosis factor receptor superfamily, member 17	TNFRSF17
220319_s_at	3796.9	2721.7	24534.1	150.8	85	myosin regulatory light chain interacting protein	MYLIP
201473_at	5254.1	1979.2	4775.3	52	84	jun B proto-oncogene	JUNB
205805_s_at	916.2	495.5	1461.5	5.1	84	receptor tyrosine kinase-like orphan receptor 1	ROR1
207521_s_at	1861	1427.3	2469.7	5.6	84	ATPase, Ca++ transporting, ubiquitous	ATP2A3
214911_s_at	5800.8	3632.4	5237.4	190.2	84	bromodomain containing 2	BRD2
219752_at	2390.6	1237.6	1756	18.2	84	RAS protein activator like 1 (GAP1 like)	RASAL1
44790_s_at	8505.4	3748.8	8257.3	6	84	chromosome 13 open reading frame 18	C13orf18
206478_at	2360.6	1769.8	5876.1	86.6	84	KIAA0125	KIAA0125
210180_s_at	2174.2	823.3	3334.9	9.1	84	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	SFRS10
217677_at	3478.3	922.5	920	20.2	84	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	PLEKHA2

221671_x_at	31680.7	22551	62604.2	824.8	84	immunoglobulin kappa constant /// immunoglobulin kappa variable 1-5	IGKC /// IGKV1-5
211644_x_at	3855.6	1621.8	10586.8	15.6	84	immunoglobulin kappa constant /// immunoglobulin kappa constant	IGKC
203796_s_at	1878.7	1512.3	1760.6	15	83	B-cell CLL/lymphoma 7A	BCL7A
209398_at	16587.4	5879.3	9073.2	152.8	83	histone 1, H1c	HIST1H1C
214975_s_at	2134.4	976.2	807.9	12.8	83	myotubularin related protein 1	MTMR1
216984_x_at	2571.9	1074.1	61397.8	14.5	83	Immunoglobulin lambda joining 3	IGLC2
213811_x_at	9733.6	8324.7	8071.1	756.7	83	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3
214472_at	2531.2	829.1	2678.5	4.6	83	histone 1, H3d	HIST1H3D
209457_at	1335.3	711.6	3666.5	15.2	83	dual specificity phosphatase 5	DUSP5
203588_s_at	1599.5	1292.4	3992.3	37.4	83	transcription factor Dp-2 (E2F dimerization partner 2)	TFDP2
201022_s_at	2376.3	1884.5	4537.8	55.5	83	destrin (actin depolymerizing factor)	DSTN
204642_at	1707.9	798.1	1750.6	10.6	83	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	EDG1
221651_x_at	33345.6	22787.2	65363	833.2	83	immunoglobulin kappa constant /// immunoglobulin kappa variable 1-5	IGKC /// IGKV1-5
205967_at	35751.3	3512.1	6722.1	343.1	82	histone 1, H4c	HIST1H4C
209138_x_at	29357.3	20677.1	73861.4	288.6	82	Immunoglobulin lambda constant 1 (Mcg marker) /// Dehydrogenase/reductase (SDR family) member 4 like 2 /// Immunoglobulin lambda joining 3	IGLV3-25 /// DHRS4 /// IGLC2
220377_at	1115.8	527	2828.2	5.7	82	chromosome 14 open reading frame 110	C14orf110
201464_x_at	6805.8	3623.7	8372.6	35.1	82	v-jun sarcoma virus 17 oncogene homolog (avian)	JUN
209558_s_at	2068	1613.9	2686.7	18.5	82	huntingtin interacting protein-1-related	HIP1R
204254_s_at	659.8	405.3	772.8	11.3	81	vitamin D (1,25- dihydroxyvitamin D3) receptor	VDR
217783_s_at	13626.2	9959.4	22889.8	1046.7	81	yippee-like 5 (Drosophila)	YPEL5
218611_at	3234.4	2084.7	3865.3	198.3	81	immediate early response 5	IER5
201670_s_at	1189.3	856.9	1989.8	3.5	81	myristoylated alanine-rich protein kinase C substrate	MARCKS
211641_x_at	3555.3	1451.3	3293	36.3	81	Isolate Middle91 immunoglobulin heavy chain variable region (IGVH) /// Isolate Middle91 immunoglobulin heavy chain variable region (IGVH)	---
211643_x_at	1996.9	1433.2	2681	50.1	81	Immunoglobulin kappa variable 1-5 /// Immunoglobulin kappa variable 1-5	IGKC

211881_x_at	2614.2	1336	2124.8	29.4	81	immunoglobulin lambda joining 3	IGLJ3
216365_x_at	631.9	215.9	904.6	7.3	81	Immunoglobulin lambda constant 1 (Mcg marker)	IGLV3-25
208195_at	1294.9	882	2851.1	26.5	81	titin	TTN
214768_x_at	1795.5	1077.9	8676.1	16.2	81	(clone TR1.6VL) anti-thyroid peroxidase monoclonal autoantibody IgK chain, V region	---
201466_s_at	921.5	787.4	2738.4	9.6	81	v-jun sarcoma virus 17 oncogene homolog (avian)	JUN
221841_s_at	2789.2	1790.2	11750.7	11.4	81	Kruppel-like factor 4 (gut)	KLF4
216576_x_at	1975.4	979.2	3352.2	16.5	81	Immunoglobulin kappa light chain variable region (IGKV gene), clone 25	---
211655_at	212	201.8	745.9	3.1	81	Immunoglobulin lambda joining 3	IGLC2
203973_s_at	1408.8	859.5	4658	6.9	81	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD
204315_s_at	946.5	492.1	525.7	8.3	80	G-2 and S-phase expressed 1	GTSE1
222045_s_at	857.3	586.8	1247.2	11.5	80	chromosome 20 open reading frame 67	C20orf67
201462_at	414.5	295.2	1052.3	7.3	80	secernin 1	SCRN1
221766_s_at	790.1	490.7	5906.8	5	80	family with sequence similarity 46, member A	FAM46A
208937_s_at	968.9	404.1	1480.6	6.7	80	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	ID1
209374_s_at	37136	23220	48689.7	660.5	80	immunoglobulin heavy constant mu	IGHM
219517_at	1979.2	948.8	1150.7	14.8	80	elongation factor RNA polymerase II-like 3	ELL3
214677_x_at	32140.2	22901.4	67468.9	346.5	80	immunoglobulin lambda locus	IGL@
211199_s_at	334.7	174.5	751.5	5.8	80	inducible T-cell co-stimulator ligand	ICOSLG
210776_x_at	13331.7	9144.1	9907.6	669.1	80	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3
218473_s_at	5608.8	4109.8	8071.8	522.8	80	glycosyltransferase 25 domain containing 1	GLT25D1
221239_s_at	1531.7	693	3556	18	80	Fc receptor-like 2 /// Fc receptor-like 2	FCRL2
217258_x_at	1046.5	523.9	4342.2	8.9	80	Clone ds1-1 immunoglobulin lambda chain VJ region, (IGL)	---
205148_s_at	385.7	200.8	687.1	7	79	chloride channel 4	CLCN4
219463_at	3214.4	1350.9	13373	14.1	79	chromosome 20 open reading frame 103	C20orf103
200920_s_at	38532.8	16690.7	33740.6	861.8	79	B-cell translocation gene 1, anti-proliferative	BTG1
216356_x_at	631.4	390.7	536.4	12.7	79	BAI1-associated protein 3	BAIAP3
222044_at	1249.2	664	2083.4	26.9	79	---	---
202946_s_at	2248.1	1707.1	6129.4	60.2	79	BTB (POZ) domain containing 3	BTBD3

207038_at	281.4	238.9	300.4	6.2	79	solute carrier family 16 (monocarboxylic acid transporters), member 6	SLC16A6
207237_at	956.6	465.4	1294	12.3	79	potassium voltage-gated channel, shaker-related subfamily, member 3	KCNA3
217384_x_at	612.4	304.7	911.3	4.8	79	similar to immunoglobulin M chain	LOC388255
209324_s_at	2041.9	708.8	6688.9	12.5	79	regulator of G-protein signalling 16	RGS16
204121_at	408.3	367.7	1061.5	6	79	growth arrest and DNA-damage-inducible, gamma	GADD45G
203942_s_at	361	171.6	475.7	4.3	78	MAP/microtubule affinity-regulating kinase 2	MARK2
222313_at	349.6	202.6	841.7	2.6	78	CCR4-NOT transcription complex, subunit 2	CNOT2
219978_s_at	4662.1	2406.5	3581.7	46.1	78	nucleolar and spindle associated protein 1	NUSAP1
213931_at	1964.2	1049.6	5069	8.8	78	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein	ID2 /// ID2B
206394_at	389.7	292.1	888.7	5.1	78	myosin binding protein C, fast type	MYBPC2
202625_at	2660.4	1441.8	2664.1	42.3	77	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog /// v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	LYN
209795_at	7502.8	6458.6	16301.1	31.6	77	CD69 antigen (p60, early T-cell activation antigen)	CD69
204165_at	4862.1	2495.5	6203	70.3	77	WAS protein family, member 1	WASF1
219041_s_at	5504.4	3685.5	4616.5	468.6	77	replication initiator 1	REPIN1
219471_at	12565.2	5971.3	13508.4	33.2	77	chromosome 13 open reading frame 18	C13orf18
220066_at	375.4	86.3	382.2	2.5	77	caspase recruitment domain family, member 15	CARD15
212575_at	144.6	44.4	292.7	3.8	77	chromosome 19 open reading frame 6	C19orf6
212970_at	2128.3	1091.9	1609.5	75.3	77	Hypothetical protein FLJ14001	FLJ14001
219518_s_at	1488.3	893.3	1512	9.8	77	elongation factor RNA polymerase II-like 3	ELL3
222015_at	633	193.6	914.6	21.6	77	Casein kinase 1, epsilon	CSNK1E
209579_s_at	3990.3	2660.8	3384	170.6	76	methyl-CpG binding domain protein 4	MBD4
210024_s_at	2119.7	1680.2	3640.3	12.3	76	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	UBE2E3
216542_x_at	2645.8	1678.4	2673.3	163.1	76	immunoglobulin heavy constant gamma 1 (G1m marker) /// hypothetical protein MGC27165	IGHG1 /// MGC27165
219396_s_at	5460.4	2755.9	13298.1	16.4	76	nei endonuclease VIII-like 1 (E. coli)	NEIL1
205413_at	743.7	198.2	2539.4	1.6	76	metallophosphoesterase domain containing 2	MPPED2

204936_at	372.7	152.6	479	8.4	76	mitogen-activated protein kinase kinase kinase kinase 2	MAP4K2
211640_x_at	1068.2	595	957.6	5.2	76	Immunoglobulin heavy variable 1-69 /// Immunoglobulin heavy variable 1-69	IGHV1-69
219474_at	738.5	237.1	669.4	4.3	76	TPA-induced transmembrane protein	TTMP
215918_s_at	559.5	394.8	1953.4	7	76	spectrin, beta, non-erythrocytic 1	SPTBN1
208549_x_at	18830.4	15231.4	27927.9	3006.9	75	prothymosin, alpha	PTMA
204004_at	706.5	501.8	1864.2	8.2	75	PRKC, apoptosis, WT1, regulator	PAWR
212225_at	5240.5	2651.9	5996.8	16.3	75	eukaryotic translation initiation factor 1	EIF1
209994_s_at	625.3	379	769.6	6.1	74	ATP-binding cassette, sub-family B (MDR/TAP), member 1 /// ATP-binding cassette, sub-family B (MDR/TAP), member 4	ABCB1 /// ABCB4
204621_s_at	690.7	254.2	6807.8	3.7	74	nuclear receptor subfamily 4, group A, member 2	NR4A2
203749_s_at	1201.3	388.8	736.1	6.7	74	retinoic acid receptor, alpha	RARA
208610_s_at	3729.1	1815	3999.5	60.7	74	serine/arginine repetitive matrix 2	SRRM2
210282_at	261.2	213.2	366.3	1	74	zinc finger protein 198	ZNF198
214860_at	430.9	222.1	490	4.6	74	solute carrier family 9 (sodium/hydrogen exchanger), member 7	SLC9A7
217227_x_at	1602.6	756.2	2441.6	23	74	Rearranged Humigla1L1 gene encoding IgG light chain	---
201951_at	279.8	226.8	738.3	2.9	74	activated leukocyte cell adhesion molecule	ALCAM
205692_s_at	4324.2	2887.3	3686	27.6	74	CD38 antigen (p45)	CD38
213986_s_at	841.4	593.5	1076.9	4.5	74	chromosome 19 open reading frame 6	C19orf6
211634_x_at	5224.7	1694.7	4720.7	20.3	73	immunoglobulin heavy constant mu /// immunoglobulin heavy constant mu	IGHM
81737_at	646.3	446.2	770.6	7.4	73	SLC7A5 pseudogene /// Hypothetical protein LOC440345 /// Homo sapiens, clone IMAGE:4271781	LOC388221 /// LOC440345
202083_s_at	317.7	183.4	1605	2.4	73	SEC14-like 1 (S. cerevisiae)	SEC14L1
219737_s_at	11684.4	7378.4	14726.6	16.7	73	protocadherin 9	PCDH9
220719_at	1481	469.5	797	6.9	73	hypothetical protein FLJ13769	FLJ13769
208785_s_at	4134.8	3677.7	13593.6	594.9	73	microtubule-associated protein 1 light chain 3 beta	MAP1LC3B
209191_at	2880.1	1467.9	6610.5	8.6	73	tubulin, beta 6	TUBB6
217148_x_at	4052.1	2173.6	58163.1	58	73	immunoglobulin lambda variable 2-14	IGLV2-14

210130_s_at	974.7	577.8	889.6	18.4	73	transmembrane 7 superfamily member 2	TM7SF2
213311_s_at	1408	1130.2	1200.8	15.6	73	KIAA1049 protein	KIAA1049
205484_at	938.8	533	2842.4	25	73	signaling threshold regulating transmembrane adaptor 1	SIT1
218857_s_at	1156.2	560.9	1331.2	15.2	72	asparaginase like 1	ASRGL1
219692_at	551	246	718.4	9.5	72	kringle containing transmembrane protein 2	KREMEN2
201041_s_at	31896.4	27090.3	35352.9	639.6	72	dual specificity phosphatase 1	DUSP1
201353_s_at	1792.5	1125.4	1363.6	42.7	72	bromodomain adjacent to zinc finger domain, 2A	BAZ2A
209876_at	1164.7	741.6	933.9	25.3	72	G protein-coupled receptor kinase interactor 2	GIT2
211908_x_at	840.4	383.1	1279.8	10.5	72	IgG heavy chain variable region (Vh26) /// IgG heavy chain variable region (Vh26)	---
213309_at	2887.6	2012.8	3909	51.6	72	phospholipase C-like 2	PLCL2
215176_x_at	5352.9	2060.8	9753.4	29.7	72	Immunoglobulin kappa light chain variable region (IGKV gene), clone 25	---
222158_s_at	1538.1	1024.4	8371.1	33.7	72	chromosome 1 open reading frame 121	C1orf121
214696_at	673.2	368	3256.6	4.3	72	hypothetical protein MGC14376	MGC14376
212886_at	3206.4	1651.1	5457.4	89.7	71	DKFZP434C171 protein	DKFZP434C171
222145_at	925.4	605.5	1445	7.4	71	Hypothetical protein LOC440345	LOC440345
215692_s_at	715.3	222.9	1591.7	3.7	71	metallophosphoesterase domain containing 2	MPPED2
218319_at	1039.6	480.7	2475.8	2.4	71	pellino homolog 1 (Drosophila)	PELI1
201738_at	4836.6	3578.5	6966.7	648.1	71	translation factor sui1 homolog	GC20
202165_at	1200.4	799.6	1456	40.8	71	protein phosphatase 1, regulatory (inhibitor) subunit 2	PPP1R2
202283_at	2098.9	1138.5	3262.7	13.2	71	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	SERPINF1
208621_s_at	4972.8	2805.7	15342.9	32.8	71	villin 2 (ezrin)	VIL2
213394_at	1188.9	875	6923.8	15.5	71	mitogen activated protein kinase binding protein 1	MAPKBP1
213718_at	834.5	527.1	1336.4	14.3	70	RNA binding motif protein 4	RBM4
222258_s_at	686	179	908.7	4.5	70	SH3-domain binding protein 4	SH3BP4
202241_at	1454.6	748.6	2493.8	15.4	70	tribbles homolog 1 (Drosophila)	TRIB1
208616_s_at	10243.9	8059.5	9030.6	2120.1	70	protein tyrosine phosphatase type IVA, member 2	PTP4A2
210281_s_at	603	419.9	1173.4	10.5	70	zinc finger protein 198	ZNF198
221755_at	619.1	525.1	1257	7.8	70	EH domain binding protein 1-like 1	EHBP1L1

222315_at	717.8	189.5	3569.7	7.5	70	Potassium inwardly-rectifying channel, subfamily J, member 15	KCNJ15
201961_s_at	409.1	306.2	506	10.4	70	ring finger protein 41	RNF41
202864_s_at	2177.6	1438.3	2327.6	71.3	70	nuclear antigen Sp100	SP100
204681_s_at	1024.3	453.5	1395.2	8.1	70	Rap guanine nucleotide exchange factor (GEF) 5	RAPGEF5
208018_s_at	4580.1	1787.4	3725.6	34.5	70	hemopoietic cell kinase	HCK
208078_s_at	7552.5	1852.9	12086.4	22	70	SNF1-like kinase /// SNF1-like kinase	SNF1LK
211635_x_at	5284	1353.9	4018.2	17.2	70	Immunoglobulin heavy variable 1-69 /// Immunoglobulin heavy variable 1-69	IGHV1-69
212827_at	26342.6	20722.2	42899.7	451.6	70	immunoglobulin heavy constant mu /// immunoglobulin heavy constant mu	IGHM
91703_at	987.4	806.9	1421.1	18.6	70	EH domain binding protein 1-like 1	EHBP1L1
202082_s_at	736.6	531.1	1740.6	7.7	70	SEC14-like 1 (S. cerevisiae)	SEC14L1
209711_at	2282.7	1650.5	4802	123.6	70	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	SLC35D1
209765_at	1649	1006.1	1671.7	25	69	ADAM metallopeptidase domain 19 (meltrin beta)	ADAM19
209189_at	18298	8625.6	23154.4	27.1	69	v-fos FBJ murine osteosarcoma viral oncogene homolog	FOS
214836_x_at	6042.5	2307.2	9640.9	95.8	69	immunoglobulin kappa constant /// immunoglobulin kappa variable 1-5	IGKC /// IGKV1-5
211645_x_at	4806.7	1366.1	6733.2	32.1	69	Immunoglobulin kappa light chain (IGKV) mRNA variable region, joining region, and constant region /// Immunoglobulin kappa light chain (IGKV) mRNA variable region, joining region, and constant region	---
220046_s_at	9791.7	5330.2	18566.8	700.8	69	cyclin L1	CCNL1
222067_x_at	5113.8	2281.1	5150.2	71	69	histone 1, H2bd	HIST1H2BD
201739_at	1031.8	566.7	15238.3	9.4	69	serum/glucocorticoid regulated kinase	SGK
201792_at	3894.1	2225.8	6769.2	32.7	68	AE binding protein 1	AEBP1
213476_x_at	4760.7	3613.7	8249	538.4	68	tubulin, beta 3	TUBB3
214290_s_at	37691.1	15264.6	33965.1	608.2	68	histone 2, H2aa	HIST2H2AA
214708_at	244.2	114.9	451.8	4.4	68	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	SNTB1
218612_s_at	1028.2	575	970.5	27.3	68	tumor suppressing subtransferable candidate 4	TSSC4
218696_at	3446.9	3255.1	8935	148.1	68	eukaryotic translation initiation factor 2-alpha kinase 3	EIF2AK3

200846_s_at	6661.4	5681.8	8018	491.9	68	protein phosphatase 1, catalytic subunit, alpha isoform	PPP1CA
201392_s_at	1306	739.6	1220.5	7	68	insulin-like growth factor 2 receptor	IGF2R
208576_s_at	282.8	114.3	298.8	3.6	68	histone 1, H3b	HIST1H3B
204192_at	13251.7	5624.7	10302.9	225.6	67	CD37 antigen	CD37
208091_s_at	4116.6	2073.2	3069.3	124.4	67	EGFR-coamplified and overexpressed protein /// EGFR-coamplified and overexpressed protein	ECOP
215214_at	1058.7	400.8	17480.7	5	67	Immunoglobulin lambda constant 1 (Mcg marker) /// Immunoglobulin lambda joining 3	IGLV3-25 /// IGLC2
217378_x_at	2616.1	1178.5	7662.5	21	67	similar to Ig kappa chain precursor V region (orphon V108) - human (fragment)	LOC391427
207704_s_at	1084.8	780.1	1241.6	15.7	67	growth arrest-specific 7	GAS7
218100_s_at	1189.7	690.8	2508	51.4	67	estrogen-related receptor beta like 1	ESRRBL1
202147_s_at	1318.9	508.9	1610.5	9.8	67	interferon-related developmental regulator 1	IFRD1
208727_s_at	9260.1	1361	4138.1	45.2	67	cell division cycle 42 (GTP binding protein, 25kDa)	CDC42
216706_x_at	207	79.7	368.5	6.9	67	Active Ig mu-chain mRNA V-region (VDJ), 5' end, clone mu-11-8	---
219751_at	310.6	231.6	420.2	5.3	67	hypothetical protein FLJ21148	FLJ21148
215092_s_at	361.3	186.8	1137.8	11.4	67	nuclear factor of activated T-cells 5, tonicity-responsive	NFAT5
219577_s_at	1163.9	833.6	3119.6	54.9	67	ATP-binding cassette, sub-family A (ABC1), member 7	ABCA7
202733_at	4530.6	1589.5	2513.1	12.8	66	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	P4HA2
207819_s_at	806.5	550.4	1100.7	8	66	ATP-binding cassette, sub-family B (MDR/TAP), member 4	ABCB4
211944_at	1418.4	805	1310.1	17.6	66	BAT2 domain containing 1	BAT2D1
200702_s_at	1386.6	561.8	1982.9	16.2	66	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	DDX24
203752_s_at	21461.8	16988.4	36043.8	2627.2	66	jun D proto-oncogene	JUND
210640_s_at	260.5	106.6	2653.6	8.5	66	G protein-coupled receptor 30	GPR30
217320_at	311.9	147.1	738.6	3.4	66	Ig rearranged gamma-chain mRNA V-region, 5' end of cds (from clone S9P16)	---
205780_at	605.3	143	1884.3	6.7	66	BCL2-interacting killer (apoptosis-inducing)	BIK
202844_s_at	853.6	453	685.1	11.7	66	ralA binding protein 1	RALBP1

217198_x_at	779.9	452.7	1188.6	8.5	66	immunoglobulin heavy locus /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker)	IGH@ /// IGHD /// IGHG1
218404_at	346	122.8	533.2	7.7	66	sorting nexin 10	SNX10
209372_x_at	576.3	131.3	1377.7	9.4	66	tubulin, beta 2	TUBB2
202719_s_at	545	356.5	1245.4	9.5	66	testis derived transcript (3 LIM domains)	TES
207535_s_at	658.4	446.7	721.3	6.6	65	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NFKB2
208523_x_at	1864.9	1135.7	2759	62.3	65	histone 1, H2bi	HIST1H2BI
210240_s_at	3675.6	1394.4	1846.6	53.4	65	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	CDKN2D
	739.8	222	515.3	5.6	65	immunoglobulin kappa constant /// similar to Ig kappa chain	IGKC /// LOC339562
216066_at	391.6	229.2	542.8	11.9	65	ATP-binding cassette, sub-family A (ABC1), member 1	ABCA1
211226_at	100.1	57.9	246.2	3.5	65	galanin receptor 2	GALR2
204215_at	4073.8	3830.3	3926.3	401.2	64	chromosome 7 open reading frame 23	C7orf23
219341_at	430.1	138.9	707.8	4.9	64	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	CLN8
220603_s_at	1196.8	787.4	1233.3	44.1	64	multiple C2-domains with two transmembrane regions 2	MCTP2
201669_s_at	1969.4	891	4075.8	3.3	64	myristoylated alanine-rich protein kinase C substrate	MARCKS
202819_s_at	986.9	863.2	2552.4	30.6	64	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	TCEB3
201243_s_at	300.7	171.1	474.3	8.1	64	ATPase, Na+/K+ transporting, beta 1 polypeptide	ATP1B1
209154_at	4487.1	1728.6	2541.9	178.4	64	Tax1 (human T-cell leukemia virus type I) binding protein 3	TAX1BP3
215946_x_at	8832.4	6771.2	13320.6	297.3	64	similar to omega protein	LOC91353
217179_x_at	1514.4	959	1819.1	28.8	64	(clone 9F2L) Ig rearranged L-chain mRNA V-region, 5' end	---
201021_s_at	1894.7	1359.4	4252.5	62.6	64	destrin (actin depolymerizing factor)	DSTN
204005_s_at	231.6	143.2	471.2	1.6	64	PRKC, apoptosis, WT1, regulator	PAWR
217963_s_at	1003.1	479	7490.1	17.3	64	nerve growth factor receptor (TNFRSF16) associated protein 1	NGFRAP1

201917_s_at	2035.5	1564.9	2933.3	216.1	64	solute carrier family 25, member 36	SLC25A36
208490_x_at	2965.2	2315	4156.3	66.3	64	histone 1, H2bf	HIST1H2BF
211868_x_at	1153.8	685.2	2705.6	16.7	64	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker)	IGHA1 /// IGHG1 /// IGHG3
206865_at	544.2	280.4	1736.8	8.4	64	Harakiri, BCL2 interacting protein (contains only BH3 domain)	HRK
202354_s_at	635.7	559.8	888.1	10.2	63	general transcription factor IIF, polypeptide 1, 74kDa	GTF2F1
203505_at	2678.1	1046.2	2299.6	7.7	63	ATP-binding cassette, sub-family A (ABC1), member 1	ABCA1
212574_x_at	1371.7	942.4	1732.6	23.8	63	chromosome 19 open reading frame 6	C19orf6
212826_s_at	19729.1	15012.9	19642.3	1648.1	63	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	SLC25A6
222024_s_at	1582.5	1143.2	5119	28.3	63	A kinase (PRKA) anchor protein 13	AKAP13
202166_s_at	2057.9	1473.3	1443	170.4	63	protein phosphatase 1, regulatory (inhibitor) subunit 2	PPP1R2
207492_at	1232.9	853.9	975.7	44.3	63	N-glycanase 1	NGLY1

215777_at	634.9	229.3	19107.3	4.6	63	IgV lambda [human, chronic lymphocytic leukemia case P87, mRNA Partial Mutant, 237 nt]	---
205734_s_at	1450.1	47.1	593	2.8	62	AF4/FMR2 family, member 3	AFF3
208244_at	651	427.8	885.3	13.6	62	bone morphogenetic protein 3 (osteogenic)	BMP3
208685_x_at	5013.2	3634.6	4652.7	168.3	62	bromodomain containing 2	BRD2
209020_at	3058.3	1661.5	4878.3	377.5	62	chromosome 20 open reading frame 111	C20orf111
209761_s_at	4503.7	3048.2	3929.8	514.6	62	SP110 nuclear body protein	SP110
213002_at	730.9	613.7	1010.8	24.9	62	Myristoylated alanine-rich protein kinase C substrate	MARCKS
215785_s_at	6233.1	4436.7	6694.4	199.8	62	cytoplasmic FMR1 interacting protein 2	CYFIP2
216971_s_at	371.8	154.2	741.3	4.4	62	plectin 1, intermediate filament binding protein 500kDa	PLEC1
38340_at	3343.8	2368.3	4903.3	346.7	62	huntingtin interacting protein-1-related	HIP1R
202723_s_at	6466.6	4219.6	17277.3	134	62	forkhead box O1A (rhabdomyosarcoma)	FOXO1A
201235_s_at	2025.4	1288.6	2444	15.1	62	BTG family, member 2	BTG2
205655_at	403.5	276.4	727.1	3.4	62	Mdm4, transformed 3T3 cell double minute 4, p53 binding protein (mouse)	MDM4
219505_at	2737.3	2243.7	4093.5	42.1	62	cat eye syndrome chromosome region, candidate 1	CECR1
215621_s_at	1006.6	621.9	5610.5	9.2	62	immunoglobulin heavy constant delta	IGHD
200790_at	8522.6	5203	11216.3	281.2	61	ornithine decarboxylase 1	ODC1
216541_x_at	892.6	313.8	927.6	7	61	immunoglobulin heavy constant gamma 1 /// immunoglobulin heavy constant gamma 3	IGHG1 /// IGHG3
202503_s_at	11012.2	8769.1	10879.3	475.6	61	KIAA0101	KIAA0101
204081_at	717.2	168.4	1091.9	14.4	61	neurogranin (protein kinase C substrate, RC3)	NRGN
207838_x_at	981.8	649.4	1635	10.6	61	pre-B-cell leukemia transcription factor interacting protein 1	PBXIP1
209682_at	2478.1	1025.2	2193.7	129.8	61	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	CBLB
202773_s_at	431.4	216.8	451.7	5.7	61	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	SFRS8
214469_at	1051.2	408.8	2077.8	6.9	61	histone 1, H2ae	HIST1H2AE
218302_at	925.2	657.8	1130.3	10.9	61	presenilin enhancer 2 homolog (C. elegans)	PSENEN
201688_s_at	2138.1	1206.6	7186	9	61	tumor protein D52	TPD52
204961_s_at	2274	1590.8	2420.1	6.6	60	neutrophil cytosolic factor 1 (47kDa, chronic granulomatous disease, autosomal 1)	NCF1

208527_x_at	2428.2	1698.4	3233.1	139.5	60	histone 1, H2be	HIST1H2BE
218280_x_at	14912.4	4785.1	11736.4	394.9	60	histone 2, H2aa	HIST2H2AA
220085_at	1071.5	318.2	880.2	5.2	60	helicase, lymphoid-specific	HELLS
215498_s_at	5844.5	3004.3	21628.8	326.9	60	mitogen-activated protein kinase kinase 3 /// mitogen-activated protein kinase kinase 3	MAP2K3
204152_s_at	1746.6	983.2	1317.7	9.3	60	manic fringe homolog (Drosophila)	MFNG
204790_at	1686.5	945.9	2070.3	17.7	60	SMAD, mothers against DPP homolog 7 (Drosophila)	SMAD7
210594_x_at	1508.6	819.7	1369.8	61	60	myelin protein zero-like 1	MPZL1
212587_s_at	7477.2	2952.5	8415.8	35.6	60	protein tyrosine phosphatase, receptor type, C	PTPRC
213015_at	2233.4	966.7	1632.3	119.4	60	Bobby sox homolog (Drosophila)	BBX
215908_at	637.4	160.6	619	6.2	60	Membrane-associated ring finger (C3HC4) 6	MARCH6
205666_at	525.6	174.3	567.5	9.9	60	flavin containing monooxygenase 1	FMO1
209760_at	6164.9	4460.5	9469.1	632	60	KIAA0922 protein	KIAA0922
212487_at	1468.3	1046.3	1280	61.7	60	KIAA0553 protein	KIAA0553
214084_x_at	2283.5	1604.9	2794.8	21.7	60	neutrophil cytosolic factor 1 (47kDa, chronic granulomatous disease, autosomal 1)	NCF1
216300_x_at	400.9	157	421	6.3	60	retinoic acid receptor, alpha	RARA
216503_s_at	373	304.1	446.9	10	60	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	MLLT10
220369_at	473.2	186.1	566.3	18.4	60	KIAA2010	KIAA2010
216853_x_at	771.7	402.8	3033.3	17.9	60	Immunoglobulin lambda joining 3	IGLJ3
209318_x_at	773.2	451.5	845.6	6.2	59	pleiomorphic adenoma gene-like 1	PLAGL1
217184_s_at	719.1	381.7	1070.9	10.8	59	leukocyte tyrosine kinase	LTK
217975_at	407.1	252.5	1308.6	5	59	WW domain binding protein 5	WBP5
201291_s_at	4378.2	1215.3	2993.2	12.6	59	topoisomerase (DNA) II alpha 170kDa	TOP2A
208900_s_at	2917.2	890.6	2375.6	13.1	59	topoisomerase (DNA) I	TOP1
215224_at	345.8	184.4	398.1	7	59	ribosomal protein L23	RPL23
216027_at	257.2	92.1	269.6	2.5	59	thioredoxin domain containing 13	TXNDC13
202768_at	5278.9	656.8	12292.3	16	59	FBJ murine osteosarcoma viral oncogene homolog B	FOSB
201216_at	10786	7362.1	9271.5	913.1	59	endoplasmic reticulum protein 29	ERP29
209715_at	658.5	505.7	607	27	59	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	CBX5
221520_s_at	1580.8	714	2876.9	23.1	59	cell division cycle associated 8	CDCA8
201690_s_at	1828.9	1315	5834.8	18.5	59	tumor protein D52	TPD52
201890_at	3517.3	1900	4008	18.4	58	ribonucleotide reductase M2 polypeptide	RRM2

209204_at	276.6	190.6	497.6	7	58	LIM domain only 4	LMO4
215589_at	174.9	104.6	490.4	2.4	58	SMAD specific E3 ubiquitin protein ligase 1	SMURF1
216054_x_at	1967	1230.6	11056.3	205	58	myosin, light polypeptide 4, alkali; atrial, embryonic	MYL4
200917_s_at	548.2	419.2	713	5.3	58	signal recognition particle receptor ('docking protein')	SRPR
202332_at	2393.6	1053.4	1876.3	54.6	58	casein kinase 1, epsilon	CSNK1E
205548_s_at	1716.9	1128.9	3271.5	10.1	58	BTG family, member 3	BTG3
205511_at	431.6	250.6	588.5	4	57	hypothetical protein FLJ10038	FLJ10038
205735_s_at	350.5	129.7	531.1	5.4	57	AF4/FMR2 family, member 3	AFF3
221234_s_at	7856.5	4916.3	9481.1	67.1	57	BTB and CNC homology 1, basic leucine zipper transcription factor 2 /// BTB and CNC homology 1, basic leucine zipper transcription factor 2	BACH2
216905_s_at	170.4	52.4	353.3	2.2	57	suppression of tumorigenicity 14 (colon carcinoma, matriptase, epithin)	ST14
202340_x_at	1678.5	281.2	5316.6	16.4	57	nuclear receptor subfamily 4, group A, member 1	NR4A1
215108_x_at	104.7	27.2	980.8	1	57	trinucleotide repeat containing 9	TNRC9
220331_at	469.3	340.8	1727.5	10.2	57	cytochrome P450, family 46, subfamily A, polypeptide 1	CYP46A1
210656_at	195.3	105.3	313	2.4	57	embryonic ectoderm development	EED
210872_x_at	1054.2	636.6	910.4	15.6	57	growth arrest-specific 7	GAS7
212430_at	3874.3	2227.6	7014.2	368	57	RNA-binding region (RNP1, RRM) containing 1 /// RNA-binding region (RNP1, RRM) containing 1	RNPC1
213517_at	1773.3	845.4	1174.7	110.1	57	Poly(rC) binding protein 2	PCBP2
215925_s_at	4238.1	1888.1	4968.5	9.1	57	CD72 antigen	CD72
203725_at	1583.5	1262.3	6711.6	30.6	57	growth arrest and DNA-damage-inducible, alpha	GADD45A
212113_at	899.1	423.6	830.4	18.9	56	hypothetical LOC552889	LOC552889
213502_x_at	10063.7	7408.9	8939.7	480.7	56	similar to bK246H3.1 (immunoglobulin lambda-like polypeptide 1, pre-B-cell specific)	LOC91316
215078_at	455.7	188.4	853.5	4.3	56	superoxide dismutase 2, mitochondrial	SOD2
216969_s_at	816.1	494	706.4	7.2	56	kinesin family member 22	KIF22
203290_at	583.9	388.9	21095.6	8.8	56	major histocompatibility complex, class II, DQ alpha 1 /// major histocompatibility complex, class II, DQ alpha 1	HLA-DQA1
218002_s_at	198.9	94	1519.6	3.1	56	chemokine (C-X-C motif) ligand 14	CXCL14
212130_x_at	31870.8	22675.5	92658.7	4959.1	56	eukaryotic translation initiation factor 1	EIF1

212016_s_at	2144.1	2025.9	3775	76.9	56	polypyrimidine tract binding protein 1	PTBP1
216997_x_at	1772.9	1068.2	5808.1	4.3	56	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	TLE4
210088_x_at	1798.2	1214.4	12113	204	56	myosin, light polypeptide 4, alkali; atrial, embryonic	MYL4
205347_s_at	1244.6	606	5245.4	39.6	56	thymosin-like 8	TMSL8
201876_at	484.2	398.4	5375.3	7.9	56	paraoxonase 2	PON2
206459_s_at	211.3	121.1	330.1	8.5	55	wingless-type MMTV integration site family, member 2B	WNT2B
206555_s_at	2931.4	1311.7	1416.1	161.1	55	THUMP domain containing 1	THUMPD1
208702_x_at	2780.2	2063.1	4542.2	112.7	55	amyloid beta (A4) precursor-like protein 2	APLP2
215513_at	257.1	198.6	438.5	9	55	hydatidiform mole associated and imprinted	HYMAI
215635_at	149.7	90.2	256.5	1.1	55	Phosphodiesterase 8A	PDE8A
219437_s_at	1153.5	478.4	1406	14.9	55	ankyrin repeat domain 11	ANKRD11
208960_s_at	3772.2	1315.2	23071.2	15.1	55	Kruppel-like factor 6	KLF6
203037_s_at	3407.9	1492.7	5965.9	63.7	55	metastasis suppressor 1	MTSS1
205449_at	708.6	491.4	845.1	8	55	SAC3 domain containing 1	SAC3D1
208615_s_at	4008.2	2618.2	3219.2	469.2	55	protein tyrosine phosphatase type IVA, member 2	PTP4A2
217591_at	922.4	388	1491	11.9	55	SKI-like	SKIL
222238_s_at	700.1	271.8	1836.4	12.1	55	polymerase (DNA directed), mu	POLM
218856_at	2635.9	933.8	6067.9	16.2	55	tumor necrosis factor receptor superfamily, member 21	TNFRSF21
201996_s_at	1068.9	397.4	809.9	12.1	54	spen homolog, transcriptional regulator (Drosophila)	SPEN
209069_s_at	36623.3	24646.6	44984.8	3477.8	54	H3 histone, family 3B (H3.3B)	H3F3B
209262_s_at	502.8	224.7	533.8	9.3	54	nuclear receptor subfamily 2, group F, member 6	NR2F6
213730_x_at	5090.4	3880.5	4655.5	407.8	54	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3
213742_at	887.4	515.1	1080.7	24.7	54	splicing factor, arginine/serine-rich 11	SFRS11
221586_s_at	766.3	451.4	862.6	4.3	54	E2F transcription factor 5, p130-binding	E2F5
209773_s_at	4102.1	2963.2	9386.6	273.9	54	ribonucleotide reductase M2 polypeptide	RRM2
205931_s_at	126.3	78.6	567.7	5.1	54	cAMP responsive element binding protein 5	CREB5
215223_s_at	1802.3	683.2	13374.5	24.7	54	superoxide dismutase 2, mitochondrial	SOD2
212094_at	298.8	175.7	14501.7	3.3	54	paternally expressed 10	PEG10
204794_at	978.6	131	765.5	9.1	54	dual specificity phosphatase 2	DUSP2
207186_s_at	3198.9	2048.3	3694.6	175.4	54	fetal Alzheimer antigen	FALZ

208515_at	273.2	147.1	314.1	2.7	54	histone 1, H2bm	HIST1H2BM
216278_at	693.4	224.7	773.7	8.1	54	KIAA0256 gene product	KIAA0256
201689_s_at	1240	836.8	3977.5	5.6	54	tumor protein D52	TPD52
208547_at	214.9	70.7	717.9	4.1	54	histone 1, H2bb	HIST1H2BB
202021_x_at	31691.4	21494.7	85265.8	4111	54	eukaryotic translation initiation factor 1	EIF1
211789_s_at	1245.2	392.4	2084.4	3.9	54	MondoA	MONDOA
216211_at	706.9	446.7	969.5	4.1	54	Chromosome 10 open reading frame 18	C10orf18
216855_s_at	762.9	453.7	745.5	9.6	54	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	HNRPU
217729_s_at	4929.7	2647.3	3119.9	82.2	54	amino-terminal enhancer of split	AES
205398_s_at	853.6	471.2	2255.6	15.6	54	SMAD, mothers against DPP homolog 3 (Drosophila)	SMAD3
219582_at	1125.1	657.8	2626.9	26	54	opioid growth factor receptor-like 1	OGFRL1
221658_s_at	346.4	188.1	872.7	10.9	54	interleukin 21 receptor	IL21R
201101_s_at	3208.5	2063.6	5635	67	53	BCL2-associated transcription factor 1	BCLAF1
209759_s_at	615.2	547.2	916.5	19.2	53	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	DCI
213134_x_at	2196	1367.7	3628.9	34.2	53	BTG family, member 3	BTG3
213973_at	550.6	326.5	905.3	23	53	ribosome binding protein 1 homolog 180kDa (dog)	RRBP1
218247_s_at	1742.4	1256.3	2236.9	23.3	53	ring finger and KH domain containing 2	RKHD2
220084_at	64.6	18.9	377.2	0.9	53	chromosome 14 open reading frame 105	C14orf105
205020_s_at	673.7	395.9	7567.1	10.8	53	ADP-ribosylation factor-like 4	ARL4
203431_s_at	811.1	664	1444.9	5	53	Rho GTPase-activating protein	RICS
203647_s_at	1905.8	1751.4	2621.7	99.7	53	ferredoxin 1	FDX1
206967_at	509.1	418.5	824.2	16.3	53	cyclin T1	CCNT1
211067_s_at	1610.4	1150.4	2029.1	14.7	53	growth arrest-specific 7 /// growth arrest-specific 7	GAS7
219079_at	1986.5	1349.2	2656.5	282.9	53	cytochrome b5 reductase 4	CYB5R4
200796_s_at	824.2	351.7	2316.3	7.2	53	myeloid cell leukemia sequence 1 (BCL2-related)	MCL1
206885_x_at	754.9	476.8	2066.3	16.3	53	growth hormone 1	GH1
215499_at	3466.8	2239.5	12058.5	356.5	53	mitogen-activated protein kinase kinase 3 /// mitogen-activated protein kinase kinase 3	MAP2K3
209774_x_at	167.5	75.2	481.9	5.5	53	chemokine (C-X-C motif) ligand 2	CXCL2
210830_s_at	331	242.4	5046.2	7.2	53	paraoxonase 2	PON2
208580_x_at	822	213.3	1069.5	7.8	53	histone 1, H4k /// histone 1, H4j	HIST1H4J

210450_at	1833.4	612.6	1191.4	5.2	53	hypothetical protein LOC90925	LOC90925
213649_at	5388.1	2999.2	6475.2	472.9	53	splicing factor, arginine/serine-rich 7, 35kDa	SFRS7
220012_at	781.5	388.1	895	12.3	53	ERO1-like beta (S. cerevisiae)	ERO1LB
201502_s_at	17163.8	10773.5	46569.3	853.9	53	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NFKBIA
202818_s_at	1643	1085.6	4783.7	230.2	53	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	TCEB3
214007_s_at	517.6	394.4	1224.7	16.4	53	PTK9 protein tyrosine kinase 9	PTK9
219057_at	364	227.5	767.7	21.2	53	rabaptin, RAB GTPase binding effector protein 2	RABEP2
213566_at	684.1	410.2	4352.6	6.8	53	ribonuclease, RNase A family, k6 /// ribonuclease, RNase A family, k6	RNASE6
201242_s_at	194.3	113.3	318.9	2	52	ATPase, Na+/K+ transporting, beta 1 polypeptide	ATP1B1
213042_s_at	1042.3	539.7	1179.2	4.5	52	ATPase, Ca++ transporting, ubiquitous	ATP2A3
214095_at	257.5	138.9	356.9	7.2	52	serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2
219555_s_at	830	381.5	1573.2	14	52	uncharacterized bone marrow protein BM039	BM039
217276_x_at	863.2	308.8	1969.2	9.4	52	serine hydrolase-like 2	SERHL2
204141_at	1257.3	269.4	15893	2.8	52	tubulin, beta 2	TUBB2
203504_s_at	1918.4	1199.3	2847.2	124.2	52	ATP-binding cassette, sub-family A (ABC1), member 1	ABCA1
208930_s_at	2787.7	728.6	3337.9	10.9	52	interleukin enhancer binding factor 3, 90kDa	ILF3
209088_s_at	1844.7	948.9	2377.1	140.9	52	ubinuclein 1	UBN1
211899_s_at	588.9	278.8	1062.4	11.9	52	TNF receptor-associated factor 4	TRAF4
214308_s_at	241.8	183.2	350.9	11.2	52	homogentisate 1,2-dioxygenase (homogentisate oxidase)	HGD
219179_at	562.2	418	933.6	4.7	52	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	DACT1
213345_at	540.7	335.9	1086.5	12.4	52	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	NFATC4
216248_s_at	910.5	287.2	10463.2	5	52	nuclear receptor subfamily 4, group A, member 2	NR4A2
210395_x_at	2016.7	1139	13375.5	213.8	52	myosin, light polypeptide 4, alkali; atrial, embryonic	MYL4
211138_s_at	1347.3	650.6	2154.6	40.2	51	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	KMO
215392_at	411.6	224.1	466	1.2	51	Multiple inositol polyphosphate histidine phosphatase, 1	MINPP1

215623_x_at	607.6	323.7	813.1	5.5	51	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	SMC4L1
218033_s_at	461.4	291.7	498.6	14.3	51	stannin	SNN
214464_at	199.1	35.8	733.4	2.9	51	CDC42 binding protein kinase alpha (DMPK-like)	CDC42BPA
216373_at	190.6	96.3	404.2	1.2	51	Hypothetical protein FLJ90013	FLJ90013
200712_s_at	2609.1	2080.3	3286.1	434.4	51	microtubule-associated protein, RP/EB family, member 1	MAPRE1
203919_at	814.8	488.1	776.7	5.8	51	transcription elongation factor A (SII), 2	TCEA2
209750_at	673.3	407.6	807.5	22.5	51	nuclear receptor subfamily 1, group D, member 2	NR1D2
212774_at	5871.1	4225.9	6384.8	284.6	51	zinc finger protein 238	ZNF238
218260_at	865.6	711.8	2892	20.5	51	cross-immune reaction antigen PCIA1	PCIA1
205671_s_at	689	503.6	2229.6	8.3	51	major histocompatibility complex, class II, DO beta	HLA-DOB
201846_s_at	2714	1876.5	4890.4	179.1	51	RING1 and YY1 binding protein	RYBP
202076_at	2724	2258.9	4525.3	417.2	51	baculoviral IAP repeat-containing 2	BIRC2
202782_s_at	2320.6	1102	1432.9	118.5	51	skeletal muscle and kidney enriched inositol phosphatase	SKIP
208077_at	930.8	569.3	1293.3	14.6	51	chromosome 9 open reading frame 38	C9orf38
215188_at	589.7	221	424.2	4.9	51	serine/threonine kinase 24 (STE20 homolog, yeast)	STK24
218811_at	699.2	349.3	916.1	7.5	51	chromosome 7 open reading frame 19	C7orf19
220937_s_at	1450	620.9	2138.9	14.3	51	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	ST6GALNAC4
203243_s_at	262.6	108.2	615.8	1.5	51	PDZ and LIM domain 5	PDLIM5
221551_x_at	987.7	682.4	2015.3	21.6	51	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	ST6GALNAC4
217234_s_at	7979	3102	19092.8	29.1	51	villin 2 (ezrin)	VIL2
208069_x_at	577.9	384.2	1644.2	10.1	51	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// chorionic somatomammotropin hormone-like 1 /// growth hormone 1 /// growth hormone 2	CSH1 /// CSH2 /// CSHL1 /// GH1 /// GH2
200648_s_at	1761.8	951.5	5262.9	3	51	glutamate-ammonia ligase (glutamine synthetase)	GLUL
210889_s_at	343.6	180	1849.1	7.1	51	Fc fragment of IgG, low affinity IIb, receptor (CD32)	FCGR2B
203628_at	410.3	208.3	1386.3	5.2	51	insulin-like growth factor 1 receptor	IGF1R

201793_x_at	690.1	311.4	855.6	12.2	50	chromosome 1 open reading frame 16	C1orf16
215357_s_at	706.9	619	983.5	23.8	50	polymerase (DNA-directed), delta interacting protein 3	POLDIP3
201925_s_at	1190.3	834.1	2621.5	29	50	decay accelerating factor for complement (CD55, Cromer blood group system)	DAF
213747_at	217.4	155.9	505.8	5.6	50	---	---
213122_at	1063.7	507	4660.5	12.5	50	TSPY-like 5	TSPYL5
200783_s_at	3283.3	2555.7	3636.6	276.3	50	stathmin 1/oncoprotein 18	STMN1
209713_s_at	309.2	247.8	624.8	8.5	50	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	SLC35D1
206675_s_at	117.8	82.7	259.1	2	50	SKI-like	SKIL
205397_x_at	380.7	98.7	1241	10.8	50	SMAD, mothers against DPP homolog 3 (Drosophila)	SMAD3
209151_x_at	1522.5	934.4	1986	8	50	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3
218724_s_at	1079.1	581.3	1009.7	20.5	50	TGFB-induced factor 2 (TALE family homeobox)	TGIF2
219990_at	521.6	393.4	1001	5.4	50	E2F transcription factor 8	E2F8
216412_x_at	475	198.6	1291.7	9.7	50	Clone ds1-1 immunoglobulin lambda chain VJ region, (IGL)	---
202393_s_at	3382	1512.9	8593.5	160.2	50	Kruppel-like factor 10	KLF10
214826_at	216.5	166.3	473.3	6	50	2'-phosphodiesterase	2'-PDE
202464_s_at	625.6	494.3	4013.6	9	50	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	PFKFB3
206195_x_at	230	164.5	436.5	8.5	49	growth hormone 2	GH2
210448_s_at	6937.5	1830	13603.4	33.3	49	purinergic receptor P2X, ligand-gated ion channel, 5	P2RX5
214516_at	260	99.8	440.2	4.6	49	histone 1, H4b	HIST1H4B
207106_s_at	519.4	285.3	1063.1	6.8	49	leukocyte tyrosine kinase	LTK
208046_at	274	104.8	701.7	7.9	49	histone 1, H4a	HIST1H4A
215284_at	406.3	296.3	1224.3	7.9	49	Sorting nexin 9	SNX9
204285_s_at	3741	3031.1	25815.9	127.7	49	phorbol-12-myristate-13-acetate-induced protein 1	PMAIP1
201499_s_at	6299	4419.1	7502.7	892.6	49	ubiquitin specific peptidase 7 (herpes virus-associated)	USP7
202240_at	964.4	607.7	1358.9	23.8	49	polo-like kinase 1 (Drosophila)	PLK1
213887_s_at	1776	1213.9	1430.7	56.8	49	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	POLR2E
214056_at	550.7	294.7	690.3	7.3	49	Myeloid cell leukemia sequence 1 (BCL2-related)	MCL1

217230_at	471.6	59.2	695.4	7	49	villin 2 (ezrin)	VIL2
203391_at	497.4	170.6	1012.4	17.2	49	FK506 binding protein 2, 13kDa	FKBP2
219681_s_at	487.9	328.9	1101	4.4	49	RAB11 family interacting protein 1 (class I)	RAB11FIP1
210387_at	3080.5	1587.3	7883.1	12.2	49	histone 1, H2bg	HIST1H2BG
219839_x_at	442.9	211.3	1486.8	7.6	49	T-cell leukemia/lymphoma 1B /// T-cell leukemia/lymphoma 6	TCL1B /// TCL6
206413_s_at	1611.3	892.6	34444.7	23.8	49	T-cell leukemia/lymphoma 1B /// T-cell leukemia/lymphoma 6	TCL1B /// TCL6
208546_x_at	1652.9	954.3	1981.3	32.4	49	histone 1, H2bh	HIST1H2BH
209753_s_at	1802.8	1211.1	2265.4	188.5	49	thymopoietin	TMPO
214712_at	364	86.8	327.1	1.6	49	---	---
216207_x_at	4775.2	3222.6	9161.2	398.9	49	immunoglobulin kappa variable 1D-13	IGKV1D-13
219961_s_at	434.9	261.5	641.1	16.1	49	chromosome 20 open reading frame 19	C20orf19
220987_s_at	1908.9	838.2	1462.1	109.5	49	chromosome 11 open reading frame 17 /// chromosome 11 open reading frame 17 /// NUAK family, SNF1-like kinase, 2 /// NUAK family, SNF1-like kinase, 2	C11orf17 /// NUAK2
219659_at	126.6	72.7	996.1	5.9	49	ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2	ATP8A2
202379_s_at	5195.1	2436.4	4839.2	148.8	48	natural killer-tumor recognition sequence	NKTR
210791_s_at	793	342.6	1070.1	8.1	48	Rho GTPase-activating protein	RICS
212665_at	1742.4	925.9	2080.5	229.1	48	TCDD-inducible poly(ADP-ribose) polymerase	TIPARP
206660_at	14361.7	8315	29213.3	26.9	48	immunoglobulin lambda-like polypeptide 1	IGLL1
220400_at	220.9	123.3	457.5	5.5	48	vacuolar protein sorting 13B (yeast)	VPS13B
202014_at	2765	1272.3	17225.8	37.9	48	protein phosphatase 1, regulatory (inhibitor) subunit 15A	PPP1R15A
212611_at	1669.7	1156.8	8728.6	150.2	48	deltex 4 homolog (Drosophila)	DTX4
205769_at	310.3	192.6	1536.6	4.7	48	solute carrier family 27 (fatty acid transporter), member 2	SLC27A2
209269_s_at	1196.2	890	1180.9	131.4	48	Spleen tyrosine kinase	SYK
209469_at	217.3	34	256.4	2.1	48	glycoprotein M6A	GPM6A
213939_s_at	619.7	451.4	1008	6.7	48	rap2 interacting protein x	RIPX
215338_s_at	1640.9	956.8	1577.3	16.6	48	natural killer-tumor recognition sequence	NKTR
216645_at	600.6	427.4	745.3	24.2	48	---	---

219340_s_at	689.7	323.6	994.5	9.6	48	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	CLN8
221004_s_at	3633.1	1929.3	6469.8	15.2	48	integral membrane protein 2C /// integral membrane protein 2C	ITM2C
206665_s_at	477.7	197.9	4662.1	3.4	48	BCL2-like 1	BCL2L1
206255_at	1042.3	700	3332.5	7.8	48	B lymphoid tyrosine kinase	BLK
202208_s_at	548.3	385.1	2457.6	10.6	48	ADP-ribosylation factor-like 7	ARL7
201236_s_at	5477.4	4515.7	4123.8	551.1	47	BTG family, member 2	BTG2
207002_s_at	378.3	188.2	433.3	2	47	pleiomorphic adenoma gene-like 1	PLAGL1
207798_s_at	201.9	76	526.5	2.7	47	ataxin 2-like	ATXN2L
214554_at	396.1	163.7	871.2	3.2	47	histone 1, H2al	HIST1H2AL
220001_at	284.9	175.2	4940.2	8	47	peptidyl arginine deiminase, type IV	PADI4
212457_at	667.9	310.9	1110	18.1	47	transcription factor binding to IGHM enhancer 3	TFE3
213061_s_at	953.9	821.8	1418.2	114.7	47	N-terminal asparagine amidase	NTAN1
218529_at	515.8	310.3	522.9	27.8	47	CD320 antigen	CD320
202871_at	481.2	246.6	1360.7	14.4	47	TNF receptor-associated factor 4	TRAF4
215891_s_at	318.1	138.6	781.1	5.9	47	GM2 ganglioside activator	GM2A
215200_x_at	1026.2	273.1	4081.9	12.7	47	Villin 2 (ezrin)	VIL2
206342_x_at	481.2	311.1	3521.6	8.3	47	iduronate 2-sulfatase (Hunter syndrome)	IDS
202479_s_at	707.8	486.7	5353.1	9.3	47	tribbles homolog 2 (Drosophila)	TRIB2
217849_s_at	141.2	44	919.4	3.9	47	CDC42 binding protein kinase beta (DMPK-like)	CDC42BPB
210506_at	134.1	84.3	855.2	5.1	47	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	FUT7
205023_at	205.3	58.5	370.3	4.3	47	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	RAD51
206632_s_at	937.4	353	856.9	2.9	47	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	APOBEC3B
211947_s_at	1169	170.5	1508.8	10.9	47	BAT2 domain containing 1	BAT2D1
206314_at	158.9	90	323.8	4.4	47	zinc finger protein 167	ZNF167
219313_at	154.4	116.7	380.8	4.8	47	hypothetical protein DKFZp434C0328	DKFZp434C0328
205544_s_at	215.9	129	5833.9	10.1	47	complement component (3d/Epstein Barr virus) receptor 2	CR2
206951_at	606.2	340.8	663.5	12.3	46	histone 1, H4e	HIST1H4E
212620_at	509.8	199.8	1165.4	15	46	zinc finger protein 609	ZNF609

212240_s_at	2426.9	1923.9	8975.2	277.2	46	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	PIK3R1
205425_at	861.5	365.5	1018.8	4.3	46	huntingtin interacting protein 1	HIP1
217390_x_at	755	553.5	779.3	23.7	46	---	---
220609_at	617	260.1	601.4	4.7	46	hypothetical protein LOC202181	LOC202181
221491_x_at	1553.3	699.6	2570	2.5	46	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 4	HLA-DRB1 /// HLA-DRB3 /// HLA-DRB4
217536_x_at	136.5	46.7	276.9	0.9	46	---	---
212227_x_at	30362	21224.4	93725.6	4332.2	46	eukaryotic translation initiation factor 1	EIF1
205922_at	313.3	65.8	1335.5	6.8	46	vanin 2 /// vanin 2	VNN2
204684_at	476.7	190.9	3423.4	8.5	46	neuronal pentraxin I	NPTX1
214786_at	427.6	294.4	1480.2	7.1	46	mitogen-activated protein kinase kinase kinase 1	MAP3K1
215721_at	375.9	288.8	1301.2	5.2	46	immunoglobulin heavy constant gamma 1 (G1m marker)	IGHG1
205768_s_at	175.3	98.1	836.9	3.6	46	solute carrier family 27 (fatty acid transporter), member 2	SLC27A2
201397_at	1061.9	740.9	1765.5	23.8	46	phosphoglycerate dehydrogenase	PHGDH
211022_s_at	375.1	227.3	427.8	6.7	46	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	ATRX
220797_at	216.3	169.9	429.9	3.8	46	hypothetical protein MGC3329	MGC3329
208705_s_at	6796.1	6040.4	20022	1065.6	46	eukaryotic translation initiation factor 5	EIF5
213780_at	134.2	77.1	476.5	5.7	46	Full-length cDNA clone CS0DI027YJ05 of Placenta Cot 25-normalized of Homo sapiens (human)	---
216456_at	667.5	279	2544.7	3.1	46	Protocadherin 9	PCDH9
37028_at	5364.5	1966.1	20132.4	281	46	protein phosphatase 1, regulatory (inhibitor) subunit 15A	PPP1R15A
219855_at	691.1	115.1	1950.7	15	46	nudix (nucleoside diphosphate linked moiety X)-type motif 11	NUDT11

201411_s_at	805.9	399.3	863.9	7.5	45	pleckstrin homology domain containing, family B (evectins) member 2	PLEKHB2
201926_s_at	1353.7	877.4	2551.7	26.8	45	decay accelerating factor for complement (CD55, Cromer blood group system)	DAF
202095_s_at	1357.7	1007.1	2523.9	21.7	45	baculoviral IAP repeat-containing 5 (survivin)	BIRC5
207904_s_at	448.8	304.7	583.5	9.7	45	leucyl/cystinyl aminopeptidase	LNPEP
211865_s_at	349.3	223.2	651.6	6.6	45	fizzy/cell division cycle 20 related 1 (Drosophila)	FZR1
213281_at	841.7	540.7	984.3	28.2	45	---	---
214108_at	510.5	345.5	990.6	23.5	45	MYC associated factor X	MAX
219709_x_at	423	326.4	666.2	6.8	45	chromosome 16 open reading frame 24	C16orf24
219996_at	424	247.1	427.5	7.9	45	ankyrin repeat and SOCS box-containing 7	ASB7
220220_at	321.7	221.7	595.8	3.4	45	hypothetical protein FLJ10120	FLJ10120
222263_at	512.1	304.2	770.4	17.1	45	solute carrier family 35, member E1	SLC35E1
209193_at	3851.9	2313.1	9601.8	305.9	45	pim-1 oncogene /// pim-1 oncogene	PIM1
208786_s_at	5397.9	3573.9	16076.1	661.2	45	microtubule-associated protein 1 light chain 3 beta	MAP1LC3B
209325_s_at	875.7	433.6	2078.9	10.7	45	regulator of G-protein signalling 16	RGS16
221054_s_at	405.2	125.6	890.2	2.4	45	T-cell leukemia/lymphoma 6	TCL6
203954_x_at	112.4	104	394.1	9.6	45	claudin 3	CLDN3
205214_at	696.7	515.9	3489	16.2	45	serine/threonine kinase 17b (apoptosis-inducing)	STK17B
201393_s_at	1577.7	1059.6	1740.6	12.7	45	insulin-like growth factor 2 receptor	IGF2R
212027_at	1333	485.9	996.2	18.9	45	RNA binding motif protein 25	RBM25
213669_at	844.5	573.2	991	8.8	45	FCH domain only 1	FCHO1
214542_x_at	506.2	283.5	898.1	10.8	45	histone 1, H2ai	HIST1H2AI
217236_x_at	710.2	459.7	761.3	23.6	45	Immunoglobulin heavy constant gamma 1 (G1m marker)	IGHG1
205901_at	667.9	295.2	1655.3	15.2	45	prepronociceptin	PNOC
212291_at	925.7	468.1	1971.1	11.8	45	homeodomain interacting protein kinase 1	HIPK1
205803_s_at	161.9	108.6	503.3	2.2	45	transient receptor potential cation channel, subfamily C, member 1	TRPC1
220266_s_at	900.9	355.1	6496.8	11.3	45	Kruppel-like factor 4 (gut)	KLF4
215330_at	211.7	109.6	776.5	5.7	45	Hypothetical protein FLJ43663	FLJ43663
214043_at	266.7	154.3	3097.2	5.6	45	Protein tyrosine phosphatase, receptor type, D	PTPRD
201979_s_at	812.1	513.7	906.9	9.9	44	protein phosphatase 5, catalytic subunit	PPP5C
203479_s_at	588.2	244.4	715.9	15.1	44	OTU domain containing 4	OTUD4
204908_s_at	1879.3	431.4	2716.8	7.4	44	B-cell CLL/lymphoma 3	BCL3

209559_at	347.6	145.1	483.7	8.8	44	huntingtin interacting protein-1-related	HIP1R
209718_at	483	361.1	707.2	9.7	44	kleisin beta	hCAP-H2
212588_at	3482.7	2298.1	6552	94.9	44	protein tyrosine phosphatase, receptor type, C	PTPRC
218434_s_at	956.1	383.5	3026.3	9.4	44	acetoacetyl-CoA synthetase	AACS
214581_x_at	729.6	320.5	3228.7	3.1	44	tumor necrosis factor receptor superfamily, member 21	TNFRSF21
213172_at	108.6	53.6	428.6	3.8	44	tetratricopeptide repeat domain 9	TTC9
202478_at	1685.6	710.2	14010.6	14.2	44	tribbles homolog 2 (Drosophila)	TRIB2
218523_at	1581.8	585.8	2999.4	34.4	44	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	LHPP
220324_at	121.8	96.4	227.5	2.6	44	chromosome 6 open reading frame 155	C6orf155
203320_at	2769.4	1553.3	5905.3	148.9	44	lymphocyte adaptor protein	LNK
216518_at	205.1	116.7	515.1	4.4	44	MRNA; cDNA DKFZp564E233 (from clone DKFZp564E233)	---
220809_at	135.3	66.2	449.4	3.5	44	hypothetical protein FLJ14327	FLJ14327
206802_at	233.8	138.6	478	10.2	44	paired box gene 5 (B-cell lineage specific activator)	PAX5
212478_at	661.4	318.8	1868.1	9.3	44	hypothetical protein FLJ13910	FLJ13910
217209_at	165.2	118.6	446.2	12.2	44	---	---
204719_at	102.2	52.9	338	1.8	44	ATP-binding cassette, sub-family A (ABC1), member 8	ABCA8
209982_s_at	155.3	109.2	1350.3	4.7	44	neurexin 2	NRXN2
201780_s_at	1014	631.5	772.5	40.1	44	ring finger protein 13	RNF13
209153_s_at	12253.8	5691	8812.5	552.7	44	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3
209754_s_at	1401.8	705.4	1593.9	16.7	44	thymopoietin	TMPO
211404_s_at	1362.9	833	2347.3	22.9	44	amyloid beta (A4) precursor-like protein 2	APLP2
212073_at	730.4	433.9	766.1	8.7	44	casein kinase 2, alpha 1 polypeptide	CSNK2A1
214190_x_at	591	240.2	730.7	5.6	44	golgi associated, gamma adaptin ear containing, ARF binding protein 2	GGA2
214422_at	250.7	58.5	306.9	2.1	44	RAD23 homolog B (S. cerevisiae)	RAD23B
215083_at	681.3	386.7	923.9	9.7	44	Paraspeckle component 1	PSPC1
216067_at	321.2	122	372.9	4.1	44	---	---
216218_s_at	1014.3	670.8	1657.5	30.6	44	phospholipase C-like 2	PLCL2
222309_at	281.3	147	1126.8	2.9	44	Chromosome 6 open reading frame 62	C6orf62
210993_s_at	4684	2723.7	16961	7.3	44	SMAD, mothers against DPP homolog 1 (Drosophila)	SMAD1

200916_at	5108.1	1744.3	6584.8	62.5	43	transgelin 2	TAGLN2
208947_s_at	452.8	239.9	528.5	9.1	43	regulator of nonsense transcripts 1	RENT1
210717_at	366.1	204.6	486.9	4.4	43	Ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	UBE2D2
217284_x_at	1056.8	484.7	2082.6	16.8	43	serine hydrolase-like	SERHL
217684_at	311.6	169.8	536.7	12.3	43	thymidylate synthetase	TYMS
218435_at	1320.3	790.5	1286.5	9.1	43	DnaJ (Hsp40) homolog, subfamily C, member 15	DNAJC15
219279_at	952.4	771.3	2004.7	24.3	43	dedicator of cytokinesis 10	DOCK10
222337_at	144.1	74.4	405.1	7.2	43	Nardilysin (N-arginine dibasic convertase)	NRD1
203896_s_at	116.5	34.3	890.2	2.2	43	phospholipase C, beta 4	PLCB4
201072_s_at	973.3	734.6	1263	53.5	43	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	SMARCC1
204269_at	1830.9	1064.3	3312.7	151.8	43	pim-2 oncogene	PIM2
208795_s_at	4268.9	3568.4	4893.9	592.1	43	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	MCM7
212345_s_at	2299.8	1709.5	2604.3	251.9	43	cAMP responsive element binding protein 3-like 2	CREB3L2
215164_at	965.1	508.4	1611.4	4.7	43	Transcription factor 4	TCF4
218927_s_at	1032.4	762.2	1817.1	17.2	43	carbohydrate (chondroitin 4) sulfotransferase 12	CHST12
217274_x_at	1238.9	796.9	3380	97.2	43	myosin, light polypeptide 4, alkali; atrial, embryonic	MYL4
205620_at	173.8	72.8	322.8	6.7	43	coagulation factor X	F10
208583_x_at	1234.3	766.5	1297.9	37.6	43	histone 1, H2aj	HIST1H2AJ
211921_x_at	47312.2	33664.3	58378.1	7053.1	43	prothymosin, alpha (gene sequence 28) /// prothymosin, alpha (gene sequence 28)	PTMA
219072_at	480.8	422.9	746.5	26	43	B-cell CLL/lymphoma 7C	BCL7C
216466_at	87.7	47.4	333.5	1.6	43	neuron navigator 3	NAV3
214774_x_at	114.6	17.3	1325.4	0.6	43	trinucleotide repeat containing 9	TNRC9
200681_at	5619.1	3222.4	4088.7	914.8	42	glyoxalase I	GLO1
202825_at	566.4	326.3	1090.4	12.8	42	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	SLC25A4
216508_x_at	5910.3	3567.4	6310.2	494.6	42	high-mobility group box 1	HMGB1
220764_at	195.7	132.2	293.8	6.7	42	protein phosphatase 4, regulatory subunit 2	PPP4R2
212420_at	2900.9	2182.6	6708	168.7	42	E74-like factor 1 (ets domain transcription factor)	ELF1
212758_s_at	646.9	184.1	1585.5	9	42	transcription factor 8 (represses interleukin 2 expression)	TCF8

220374_at	339.7	241.8	682.4	12.6	42	BTB (POZ) domain containing 5	BTBD5
200616_s_at	946	343.2	927.7	12.4	42	KIAA0152	KIAA0152
205205_at	982.8	305.4	1182.4	10.7	42	v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (avian)	RELB
207943_x_at	543	330.3	625.4	8.5	42	pleiomorphic adenoma gene-like 1	PLAGL1
209038_s_at	345	152.6	668	8.1	42	EH-domain containing 1	EHD1
210666_at	372.9	43.1	289.3	10.2	42	iduronate 2-sulfatase (Hunter syndrome)	IDS
212122_at	182.5	81.3	264	3	42	ras homolog gene family, member Q	RHOQ
212684_at	397	337.6	629.4	14.1	42	zinc finger protein 3 (A8-51)	ZNF3
215269_at	990.5	519.8	1185.3	15.4	42	transmembrane protein 1	TMEM1
216422_at	274	122.3	399.5	6.9	42	proliferation-associated 2G4, 38kDa	PA2G4
221043_at	524.2	318.4	711.7	12.9	42	---	---
221952_x_at	17836.4	16373.5	17116.4	2216.8	42	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	TRMT5
203590_at	680.5	506.9	1718.3	21.6	42	dynein, cytoplasmic, light intermediate polypeptide 2	DNCLI2
208703_s_at	1557.7	1261.2	3450.2	133.7	42	amyloid beta (A4) precursor-like protein 2	APLP2
210362_x_at	328.4	126.9	723.2	5.6	42	promyelocytic leukemia	PML
214852_x_at	154.4	107.8	362.4	6	42	vacuolar protein sorting 13A (yeast)	VPS13A
217418_x_at	4552.9	1979.4	25689	63.2	42	membrane-spanning 4-domains, subfamily A, member 1	MS4A1
202192_s_at	3906.7	2433.3	4114.9	274.1	41	growth arrest-specific 7	GAS7
203376_at	3692.7	2663	3142.2	506	41	cell division cycle 40 homolog (yeast)	CDC40
209470_s_at	212.6	93.7	341.2	1.4	41	glycoprotein M6A	GPM6A
212529_at	297.1	117	559.5	8.7	41	hypothetical protein FLJ30656	FLJ30656
215159_s_at	466	342.8	742.5	6.5	41	NAD kinase	NADK
201565_s_at	5880.2	1727.4	19822.8	47.1	41	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	ID2
213299_at	179.6	60.8	529.2	4.1	41	zinc finger and BTB domain containing 7A	ZBTB7A
208245_at	104.5	67	842.3	1.6	41	RAB9, member RAS oncogene family, pseudogene 1	RAB9P1
204346_s_at	1584.9	1272.1	2423.3	129.2	41	Ras association (RalGDS/AF-6) domain family 1	RASSF1
209478_at	1031.7	918	1260.3	41.6	41	stimulated by retinoic acid 13 homolog (mouse)	STRA13
210115_at	633.5	354.8	928.7	9	41	ribosomal protein L39-like	RPL39L
210218_s_at	510.7	252.4	430.8	8.7	41	nuclear antigen Sp100	SP100

210407_at	483.2	237.4	667	4.8	41	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	PPM1A
212026_s_at	384.9	198.5	582.4	10.9	41	exocyst complex component 7	EXOC7
218401_s_at	959	552.1	927.4	73.5	41	zinc finger protein 281	ZNF281
222378_at	210.6	121.7	441.6	5.2	41	Hypothetical protein FLJ43663	FLJ43663
207631_at	165.8	85.7	337	7.7	41	neighbor of BRCA1 gene 2	NBR2
211151_x_at	667.6	384.3	2032.1	6	41	growth hormone 1	GH1
43427_at	201.2	143.7	621.5	9.3	41	acetyl-Coenzyme A carboxylase beta	ACACB
216361_s_at	279.2	87.6	690.4	2	41	MYST histone acetyltransferase (monocytic leukemia) 3	MYST3
219135_s_at	356.2	262.9	1031.1	9.5	41	hypothetical protein FLJ12681	FLJ12681
208476_s_at	185.2	147.7	735.6	6.5	41	FERM domain containing 4A	FRMD4A
213954_at	101	74.4	325.1	3.3	41	KIAA0888 protein	KIAA0888
212592_at	806.3	485.3	15583.5	8.7	41	Immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	IGJ
202005_at	443.9	239.8	814	25.5	41	suppression of tumorigenicity 14 (colon carcinoma, matriptase, epithin)	ST14
202487_s_at	9563.8	8094.3	9690.7	1623.9	41	H2A histone family, member V	H2AFV
204484_at	3918.2	2035.4	3075.3	59.7	41	phosphoinositide-3-kinase, class 2, beta polypeptide	PIK3C2B
206707_x_at	3161.2	1759	4423.4	183.3	41	chromosome 6 open reading frame 32	C6orf32
214243_s_at	993.5	280.2	1457.1	10	41	serine hydrolase-like	SERHL
214481_at	430	143.5	665.5	3.9	41	histone 1, H2am	HIST1H2AM
217576_x_at	630.6	373	947.5	13.1	41	son of sevenless homolog 2 (Drosophila)	SOS2
222322_at	254.5	79.2	429.9	1.6	41	Transcribed locus	---
203833_s_at	873.1	695.6	1838	91.8	41	trans-golgi network protein 2	TGOLN2
200719_at	1366.7	1017.2	3859	22.4	41	S-phase kinase-associated protein 1A (p19A)	SKP1A
216277_at	135.1	67.5	619.8	5	41	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1
200772_x_at	41243	33563.5	53587.8	7692.7	40	prothymosin, alpha (gene sequence 28)	PTMA
204048_s_at	369	251.6	684.4	6.3	40	phosphatase and actin regulator 2	PHACTR2
204074_s_at	1098.2	494.2	737.2	17.2	40	glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein	GlyBP
208719_s_at	2411.4	187.5	3784	6.1	40	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	DDX17
214743_at	2864.9	2185.8	3477.7	461.9	40	cut-like 1, CCAAT displacement protein (Drosophila)	CUTL1

214834_at	152.8	61.7	287.8	2.7	40	HBII-437 C/D box snoRNA /// HBII-13 snoRNA	HBII-437 /// HBII-13
215802_at	699.1	240.8	742.6	5	40	Transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	TLE1
203233_at	1017	703	2086.3	21.8	40	interleukin 4 receptor	IL4R
220879_at	356.5	218.2	837.1	28.7	40	---	---
201283_s_at	289.1	87.5	329	6.7	40	OGT(O-Glc-NAc transferase)-interacting protein 106 KDa	OIP106
203395_s_at	309	220.9	380.9	8.2	40	hairy and enhancer of split 1, (Drosophila)	HES1
204524_at	692.2	215.4	649.7	9.2	40	3-phosphoinositide dependent protein kinase-1	PDPK1
215615_x_at	217.3	119	406.9	4.4	40	---	---
217650_x_at	526.7	320	665.4	16.1	40	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	ST3GAL2
218039_at	4736	3722.1	7499	402.9	40	nucleolar and spindle associated protein 1	NUSAP1
221654_s_at	2225.9	1866.2	3238.5	454.2	40	ubiquitin specific peptidase 3	USP3
205193_at	417.5	181	1462.3	21.6	40	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	MAFF
206100_at	490.7	264.8	1235.7	8.9	40	carboxypeptidase M	CPM
219703_at	211.4	170.9	493.9	3.6	40	meiosis-specific nuclear structural 1	MNS1
206204_at	74.9	46.7	814.1	1.8	40	growth factor receptor-bound protein 14	GRB14
204115_at	371.9	300.5	4663.6	3.3	40	guanine nucleotide binding protein (G protein), gamma 11	GNG11
202879_s_at	768.3	396.1	815.9	10.9	40	pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1)	PSCD1
205346_at	310.7	138.4	420.8	8.9	40	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	ST3GAL2
213940_s_at	1325.5	781.7	2148.6	5.4	40	formin binding protein 1	FNBP1
214030_at	552.5	218.8	766.3	9.2	40	hypothetical protein DKFZp667G2110	DKFZp667G2110
219312_s_at	287.3	230	531.5	5.7	40	zinc finger and BTB domain containing 10	ZBTB10
219534_x_at	307.9	42	561.3	3.2	40	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	CDKN1C
221848_at	429.1	362.1	661.7	24.7	40	zinc finger, CCCH-type with G patch domain	ZGPAT
203467_at	368	154.2	751.9	8	40	phosphomannomutase 1	PMM1
205024_s_at	1179.4	755.8	1567.1	28.5	39	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	RAD51
208808_s_at	14054.5	11679.2	14451.9	1436.6	39	high-mobility group box 2	HMGB2

208928_at	387.9	161.8	547.1	9.6	39	P450 (cytochrome) oxidoreductase	POR
209447_at	1248.8	638.5	1546.1	14.3	39	spectrin repeat containing, nuclear envelope 1	SYNE1
212105_s_at	1088.6	498.6	1463.7	13.4	39	DEAH (Asp-Glu-Ala-His) box polypeptide 9	DHX9
214665_s_at	3166	2307.8	3142.1	334.7	39	calcium binding protein P22	CHP
221628_s_at	326.8	98.4	548.3	8.3	39	cytokine-like nuclear factor n-pac	N-PAC
204646_at	418.5	299.3	1102.6	6.2	39	dihydropyrimidine dehydrogenase	DPYD
205081_at	1999.9	1137.4	6452.3	8.4	39	cysteine-rich protein 1 (intestinal)	CRIP1
206877_at	122	40.9	918.6	6	39	MAX dimerization protein 1	MXD1
212651_at	285.2	84.9	1297.4	4.8	39	Rho-related BTB domain containing 1	RHOBTB1
214251_s_at	603.2	285.5	1741.8	4.1	39	nuclear mitotic apparatus protein 1	NUMA1
201962_s_at	1277.2	637.4	1078.3	24.4	39	ring finger protein 41	RNF41
204183_s_at	383.8	245.7	428	9.8	39	adrenergic, beta, receptor kinase 2	ADRBK2
205267_at	12559.7	5949	10129.5	195.1	39	POU domain, class 2, associating factor 1	POU2AF1
209501_at	706.2	547.4	1404.7	21.9	39	cerebellar degeneration-related protein 2, 62kDa	CDR2
215779_s_at	1882.7	716.6	3292.8	15.4	39	histone 1, H2bg	HIST1H2BG
219507_at	748.8	521.7	755.7	23	39	arginine/serine-rich coiled-coil 1	RSRC1
221908_at	523.4	234.3	943.1	13.8	39	Transmembrane protein 118	TMEM118
208325_s_at	664.6	384.2	1413.3	12.8	39	A kinase (PRKA) anchor protein 13	AKAP13
209803_s_at	109.2	47.7	258.5	1.7	39	pleckstrin homology-like domain, family A, member 2	PHLDA2
7592_s_at	106	47.9	252.5	4.4	39	hyperpolarization activated cyclic nucleotide-gated potassium channel 2	HCN2
205489_at	1211.9	581.2	3410.5	45.9	39	crystallin, mu	CRYM
202102_s_at	4917.3	2139.9	4161.3	206.4	39	bromodomain containing 4	BRD4
209461_x_at	392	219.8	510.5	10.2	39	WD repeat domain 18	WDR18
210778_s_at	746.7	571.2	1009.9	9.4	39	MAX dimerization protein 4	MXD4
213062_at	944.9	662	1245.4	21.2	39	N-terminal asparagine amidase	NTAN1
213996_at	1935.9	1006.9	1599.5	31.4	39	yippee-like 1 (Drosophila)	YPEL1
55583_at	356.5	228.2	491.2	34.9	39	dedicator of cytokinesis 6	DOCK6
217626_at	183.5	73.9	598.9	8.1	39	aldo-keto reductase family 1, member C1 /// aldo-keto reductase family 1, member C2	AKR1C1 /// AKR1C2
219951_s_at	175.7	117.5	603	6.9	39	chromosome 20 open reading frame 12	C20orf12
205830_at	121.3	64	421.7	2.2	39	calmegin	CLGN

213156_at	498.5	259.4	517.5	4	38	MRNA; cDNA DKFZp586B211 (from clone DKFZp586B211) /// Homo sapiens, clone IMAGE:4214654, mRNA	---
216621_at	567.5	296.2	664.1	12.4	38	Rho-associated, coiled-coil containing protein kinase 1	ROCK1
217268_at	92.9	29	371.7	0.8	38	RAB7, member RAS oncogene family	RAB7
210491_at	137.5	98.5	538.1	3.2	38	---	---
203126_at	439.7	366.7	1524.8	6	38	inositol(myo)-1(or 4)-monophosphatase 2	IMPA2
212254_s_at	162	121.3	552.2	4.5	38	dystonin	DST
202146_at	882.7	430.7	853.4	27.8	38	interferon-related developmental regulator 1	IFRD1
204975_at	1069.6	427.3	1016.3	13	38	epithelial membrane protein 2	EMP2
205426_s_at	453.2	267.2	650.8	11.7	38	huntingtin interacting protein 1	HIP1
209182_s_at	993.6	330.7	1620.7	9.7	38	chromosome 10 open reading frame 10	C10orf10
218194_at	5628.1	2372.6	5536	376.4	38	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	REXO2
217204_at	190.3	82.6	408.3	2.2	38	Mitochondrial translational release factor 1-like	MTRF1L
219922_s_at	331	157.2	854.4	3.2	38	latent transforming growth factor beta binding protein 3	LTBP3
213537_at	2955.4	1564.6	10603.5	32.8	38	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1
214230_at	333.3	172.9	3101.8	6.6	38	cell division cycle 42 (GTP binding protein, 25kDa)	CDC42
209156_s_at	133.3	51.3	605.9	4.2	38	collagen, type VI, alpha 2	COL6A2
205306_x_at	1281.1	521.1	1837.7	62.9	37	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	KMO
208184_s_at	1225.2	677	1209.5	24.7	37	transmembrane protein 1	TMEM1
212492_s_at	1554.5	674.1	1671.1	79.6	37	jumonji domain containing 2B	JMJD2B
213106_at	1975.6	946.3	1743.3	150.2	37	ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1	ATP8A1
219286_s_at	1929.7	1420.7	2353.4	39	37	RNA binding motif protein 15	RBM15

204840_s_at	116.6	22.2	405.6	0.4	37	early endosome antigen 1, 162kD	EEA1
219651_at	158	50.8	472.4	3.7	37	developmental pluripotency associated 4	DPPA4
210356_x_at	4859.8	2065.7	27465.2	118.8	37	membrane-spanning 4-domains, subfamily A, member 1	MS4A1
201367_s_at	3841.3	440.5	3294.3	4.4	37	zinc finger protein 36, C3H type-like 2	ZFP36L2
205436_s_at	5772.5	3401.4	8416.8	129.1	37	H2A histone family, member X	H2AFX
211672_s_at	1173.9	986.1	1802.1	18.1	37	actin related protein 2/3 complex, subunit 4, 20kDa /// actin related protein 2/3 complex, subunit 4, 20kDa	ARPC4
212459_x_at	788.8	562.7	1530.9	53.5	37	succinate-CoA ligase, GDP-forming, beta subunit	SUCLG2
212520_s_at	2137.8	1356.8	2927.7	140.6	37	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	SMARCA4
215169_at	403.8	77.6	459.2	3.4	37	solute carrier family 35, member E2	SLC35E2
215781_s_at	303.2	111.1	458.5	4.7	37	topoisomerase (DNA) III beta	TOP3B
220589_s_at	302.3	168.9	504.6	10.4	37	uncharacterized hematopoietic stem/progenitor cells protein MDS028	MDS028
222001_x_at	1020.4	723	2006.4	11	37	LOC440669	LOC440669
205423_at	1750.2	1333.8	3693.6	144.7	37	adaptor-related protein complex 1, beta 1 subunit	AP1B1
219371_s_at	8724.6	5051.9	18217	451.6	37	Kruppel-like factor 2 (lung)	KLF2
205471_s_at	235.8	104.3	1645.6	3.7	37	dachshund homolog 1 (Drosophila)	DACH1
36711_at	454.5	125.8	4719.8	2.7	37	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	MAFF
209184_s_at	3447.1	1380.2	19735.9	185.2	37	insulin receptor substrate 2	IRS2
216080_s_at	1763.4	1541.1	12130.1	26.7	37	fatty acid desaturase 3	FADS3
206551_x_at	1941.3	1090.3	1840.1	94.2	37	kelch-like 24 (Drosophila)	KLHL24
209118_s_at	6782.7	4027.8	10974.1	496.1	37	tubulin, alpha 3	TUBA3
209592_s_at	1061.5	830.1	1149.1	63.4	37	WD repeat domain 68	WDR68
211997_x_at	55066.4	40842.6	74824.4	4914.8	37	H3 histone, family 3B (H3.3B)	H3F3B
204680_s_at	531.6	492.2	1100	70.2	37	Rap guanine nucleotide exchange factor (GEF) 5	RAPGEF5
210360_s_at	351.1	241.1	706	6	37	metastasis suppressor 1	MTSS1
219995_s_at	67.8	22.6	234.6	0.4	37	hypothetical protein FLJ13841	FLJ13841
211141_s_at	113.6	76.1	433.7	4	37	CCR4-NOT transcription complex, subunit 3	CNOT3

204244_s_at	989.7	431.6	816	5.8	36	activator of S phase kinase	ASK
207740_s_at	1081.5	677	1204.7	20.3	36	nucleoporin 62kDa	NUP62
209235_at	934.8	339.2	1405.7	21.7	36	chloride channel 7	CLCN7
214829_at	520.5	150.3	618.9	2	36	aminoadipate-semialdehyde synthase	AASS
216012_at	3285.1	822.5	2116.6	164.8	36	Unidentified mRNA, partial sequence	---
208579_x_at	6232.3	2992.5	13423.9	240.5	36	H2B histone family, member S	H2BFS
212609_s_at	309.3	116.3	677.5	5.3	36	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AKT3
215768_at	206.3	134.9	520.2	5.6	36	SRY (sex determining region Y)-box 5	SOX5
216224_s_at	227.1	178.7	506	12.9	36	histone deacetylase 6	HDAC6
220297_at	133.8	90.5	314	8.7	36	BTB (POZ) domain containing 7	BTBD7
218785_s_at	120.6	74.9	459.4	3.1	36	RAB, member RAS oncogene family-like 5	RABL5
217263_x_at	190	129.4	767.3	9.1	36	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	RUNX1
201629_s_at	1512.1	1043.6	2486.8	52.9	36	acid phosphatase 1, soluble	ACP1
201679_at	514.4	351.2	759.1	8.6	36	arsenate resistance protein ARS2	ARS2
201745_at	908.2	601.1	1718.6	130.1	36	PTK9 protein tyrosine kinase 9	PTK9
202870_s_at	2228.1	1100.3	4341.3	56.3	36	CDC20 cell division cycle 20 homolog (S. cerevisiae)	CDC20
208107_s_at	594.2	283.2	834.1	11.6	36	exonuclease NEF-sp /// exonuclease NEF-sp	LOC81691
209257_s_at	2342.4	961.4	2637.3	83.1	36	chondroitin sulfate proteoglycan 6 (bamacan)	CSPG6
213810_s_at	392.9	168.6	563.2	11	36	Chromosome 6 open reading frame 166	C6orf166
213947_s_at	1435.9	1019.4	2459.7	55.1	36	nucleoporin 210kDa	NUP210
214160_at	213.7	108.9	377.8	7	36	---	---
215720_s_at	432.1	288.8	825	6.5	36	nuclear transcription factor Y, alpha	NFYA
217785_s_at	386.1	113.6	458.8	7	36	SNARE protein Ykt6	YKT6
207057_at	275.7	163.6	909.8	5.2	36	solute carrier family 16 (monocarboxylic acid transporters), member 7	SLC16A7
209446_s_at	190	110.3	394.6	4.8	36	---	---
201482_at	401	314.2	1198.1	30.8	36	quiescin Q6	QSCN6
214242_at	128.5	56.6	458	4.8	36	Mannosidase, alpha, class 1A, member 2	MAN1A2
219208_at	114.6	37.6	281	3.8	36	F-box protein 11	FBXO11

221125_s_at	479.4	282.6	2029.4	22.5	36	potassium large conductance calcium-activated channel, subfamily M beta member 3	KCNMB3
211884_s_at	433.9	339.7	719.6	10	36	class II, major histocompatibility complex, transactivator	CIITA
219646_at	607	193.7	653.3	10	36	hypothetical protein FLJ20186	FLJ20186
204198_s_at	1516.7	621.8	4598.1	16	36	runt-related transcription factor 3	RUNX3
220958_at	245.4	213.8	499	8.5	36	unc-51-like kinase 4 (C. elegans)	ULK4
222179_at	238.6	189	550.6	10.6	36	---	---
212249_at	431.4	395.5	1226.3	13.1	36	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	PIK3R1
208518_s_at	126.8	86.6	604.3	7.5	36	period homolog 2 (Drosophila)	PER2
211238_at	102.8	72.7	447	3.6	36	ADAM metallopeptidase domain 7	ADAM7
200706_s_at	2637	1168.1	2666	19.5	35	lipopolysaccharide-induced TNF factor	LITAF
200921_s_at	12107.4	6043.1	18371.2	274.8	35	B-cell translocation gene 1, anti-proliferative	BTG1
202705_at	2491.5	1661.2	4425.3	26.5	35	cyclin B2	CCNB2
207078_at	466.5	233.5	708.3	4.5	35	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	MED6
207522_s_at	6423.6	2981.6	5910.6	75.5	35	ATPase, Ca++ transporting, ubiquitous	ATP2A3
209464_at	1253.5	825.7	1454.9	84.5	35	aurora kinase B	AURKB
211647_x_at	501.3	285.6	536.8	8.4	35	Immunoglobulin heavy constant mu /// Immunoglobulin heavy constant mu	IGHM
211998_at	10496.3	4591.7	15151.5	702.8	35	H3 histone, family 3B (H3.3B)	H3F3B
212142_at	1054.9	612.5	1543.4	69.3	35	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	MCM4
213691_at	365.7	283.3	623.9	24.4	35	---	---
200810_s_at	4607	3204.4	9656.1	380.4	35	cold inducible RNA binding protein	CIRBP
201006_at	375.3	235.7	940.5	8.9	35	peroxiredoxin 2	PRDX2
208704_x_at	3138	2390.2	6336.7	329	35	amyloid beta (A4) precursor-like protein 2	APLP2
214970_s_at	151.6	83.9	396.6	3.1	35	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	ST6GAL1
41577_at	756.4	535.7	4896.8	15.2	35	protein phosphatase 1, regulatory (inhibitor) subunit 16B	PPP1R16B

200853_at	11838.3	7861.6	13501	1153	35	H2A histone family, member Z	H2AFZ
204612_at	578.4	413.9	864.9	14.9	35	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	PKIA
205406_s_at	280.5	215.1	477.6	4.1	35	sperm autoantigenic protein 17	SPA17
208918_s_at	1625.2	1160.2	1821	66.2	35	NAD kinase	NADK
212700_x_at	382.6	287.1	543.5	19.2	35	pleckstrin homology domain containing, family M (with RUN domain) member 1	PLEKHM1
213229_at	1470.2	945.1	2296.5	38.7	35	Dicer1, Dcr-1 homolog (Drosophila)	DICER1
214405_at	299.6	112.6	432.8	3.9	35	CUG triplet repeat, RNA binding protein 2	CUGBP2
215984_s_at	360.6	181.1	484.1	9.6	35	ADP-ribosylation factor related protein 1	ARFRP1
216101_at	338.3	223.6	553.7	12.7	35	Hypothetical protein LOC283755	LOC283755
222366_at	1123.1	633.7	1108.5	107.5	35	Activity-dependent neuroprotector	ADNP
209053_s_at	1604.8	927.6	3584.9	27.4	35	Wolf-Hirschhorn syndrome candidate 1	WHSC1
217784_at	442.5	209.6	2269.5	16.8	35	SNARE protein Ykt6	YKT6
210279_at	1545.9	595.5	3675	9.7	35	G protein-coupled receptor 18	GPR18
219785_s_at	152.6	84.4	584.7	3.9	35	F-box protein 31	FBXO31
41397_at	321.1	264.6	939.1	12.2	35	hypothetical protein LOC55565	LOC55565
220799_at	139.2	44.1	500.8	2.7	35	glial cells missing homolog 2 (Drosophila)	GCM2
208072_s_at	4341.9	2975.7	14061.5	145.3	35	diacylglycerol kinase, delta 130kDa	DGKD
213580_at	96	72.6	341.5	3	35	---	---
220842_at	104.2	82.3	458.1	4.6	35	Abelson helper integration site	AHI1
220450_at	706.7	410.9	2373.9	13	35	---	---
210932_s_at	157.8	61.9	314.6	3	34	ring finger protein (C3H2C3 type) 6	RNF6
212079_s_at	714.5	393.5	900.7	6.9	34	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	MLL
213036_x_at	6399.2	4049.5	6841.1	79.3	34	ATPase, Ca++ transporting, ubiquitous	ATP2A3
213726_x_at	7796.1	5120	13306.9	910.2	34	tubulin, beta, 2	TUBB2
214041_x_at	6122.7	1995.5	4462.5	365.8	34	Ribosomal protein L37a	RPL37A
214463_x_at	1049.2	311	1545.7	16.6	34	histone 1, H4k /// histone 1, H4j	HIST1H4K /// HIST1H4J
214557_at	170.5	55.5	277.9	2.4	34	pituitary tumor-transforming 2	PTTG2

215339_at	149.9	25.5	249.9	1.4	34	natural killer-tumor recognition sequence	NKTR
222352_at	327.4	242.8	480.9	12.4	34	F-box protein 31	FBXO31
205003_at	222.6	145.7	554.2	3.2	34	dedicator of cytokinesis 4	DOCK4
210610_at	235.6	157	554.7	15.4	34	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	CEACAM1
212019_at	180.4	108.3	415.5	2.8	34	ribosomal L1 domain containing 1	RSL1D1
213674_x_at	2559.9	1457.1	7346.2	20.9	34	immunoglobulin heavy constant delta	IGHD
217697_at	169	105.4	535.4	2.7	34	FYN oncogene related to SRC, FGR, YES	FYN
205301_s_at	112.2	99.8	329.2	6.8	34	8-oxoguanine DNA glycosylase	OGG1
218949_s_at	3172.1	2003.8	7319.2	179.9	34	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	QRSL1
201498_at	2576.2	1649.1	2581.9	338	34	Unknown protein	USP7
201678_s_at	3884.7	2665.8	3904	398.1	34	DC12 protein	DC12
215581_s_at	554.5	340.7	728.1	5.6	34	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	MCM3AP
220018_at	412.3	263.1	462.6	4.9	34	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	CBLL1
220286_at	354.5	271	686.7	18.3	34	myotubularin related protein 10	MTMR10
222150_s_at	3354	1546.8	3922.1	23.6	34	hypothetical protein LOC54103	LOC54103
66053_at	271.2	83.3	409.2	4.2	34	heterogeneous nuclear ribonucleoprotein U-like 2	HNRPUL2
204947_at	723.2	647	1959.6	45.5	34	E2F transcription factor 1	E2F1
215006_at	1050.5	675.3	2162	55.9	34	---	---
220328_at	168.9	122.6	339.6	4.4	34	polyhomeotic like 3 (Drosophila)	PHC3
221976_s_at	149.4	108.1	825.1	5.5	34	Hepatoma-derived growth factor, related protein 3	HDGFRP3
202387_at	1578.7	1163.7	8122.2	230.8	34	BCL2-associated athanogene /// BCL2-associated athanogene	BAG1
203760_s_at	923.5	364.7	2249.3	14.1	34	Src-like-adaptor /// Src-like-adaptor	SLA
204324_s_at	181.4	92.4	623	7.3	34	golgi phosphoprotein 4	GOLPH4
221276_s_at	163.9	135.8	455.1	4.3	34	syncoilin, intermediate filament 1 /// syncoilin, intermediate filament 1	SYNC1
215407_s_at	96.3	67.7	288.5	4.4	34	astrotactin 2	ASTN2

210393_at	418.7	136.2	3640.2	12.5	34	leucine-rich repeat-containing G protein-coupled receptor 5	LGR5
200671_s_at	1392.9	702.6	2278.6	8.7	34	spectrin, beta, non-erythrocytic 1	SPTBN1
202589_at	17240.3	13462.3	20596.6	380.9	34	thymidylate synthetase	TYMS
203742_s_at	743	677.9	1213.6	7	34	thymine-DNA glycosylase	TDG
219624_at	223.1	129.3	345.4	5.6	34	BCL2-associated athanogene 4	BAG4
76897_s_at	236.7	80.5	371.7	3.4	34	KIAA0674	KIAA0674
204826_at	534.2	443.9	1446.3	37.3	34	cyclin F	CCNF
210517_s_at	3300.7	1353.1	9242.7	11	34	A kinase (PRKA) anchor protein (gravin) 12	AKAP12
211039_at	168.1	70.9	868.7	7	34	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) /// cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	CHRNA1
219778_at	102.8	76.6	310.6	2.8	34	zinc finger protein, multitype 2	ZFPM2
207573_x_at	11632.8	10131.6	12633.1	2167.8	33	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	ATP5L
211919_s_at	29614.3	23208.6	54252.2	1497.1	33	chemokine (C-X-C motif) receptor 4 /// chemokine (C-X-C motif) receptor 4	CXCR4
211936_at	9520.1	4084.9	9404.7	325.9	33	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	HSPA5
219876_s_at	314.1	140	513.2	9	33	hypothetical protein DKFZp434M0331	DKFZp434M0331
221557_s_at	728.3	173.4	1429.9	6.4	33	lymphoid enhancer-binding factor 1	LEF1
201085_s_at	3189.8	1357.3	13637.2	73	33	SON DNA binding protein	SON
201586_s_at	8569.9	5652.5	17622.8	1201.6	33	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	SFPQ
212733_at	2061.3	1548.7	5477	216.4	33	KIAA0226	KIAA0226
217930_s_at	284.2	214.8	636.1	9.5	33	toll interacting protein	TOLLIP
202509_s_at	258	105.5	790.5	11.1	33	tumor necrosis factor, alpha-induced protein 2	TNFAIP2
209936_at	357.6	274.7	869.6	6.4	33	RNA binding motif protein 5	RBM5
214284_s_at	193	132	753.1	5.6	33	Fibroblast growth factor 18	FGF18
215820_x_at	210.4	160	460.9	5.9	33	sorting nexin 13	SNX13

206700_s_at	1479.6	229	4109.1	15.1	33	Smcy homolog, Y-linked (mouse)	SMCY
204262_s_at	194	123.5	506.5	7.3	33	presenilin 2 (Alzheimer disease 4)	PSEN2
204049_s_at	168.2	135.5	479.6	7.5	33	phosphatase and actin regulator 2	PHACTR2
207781_s_at	194.5	118.1	751	1.1	33	zinc finger protein 6 (CMPX1)	ZNF6
205712_at	235.6	181	1105.9	6.4	33	protein tyrosine phosphatase, receptor type, D	PTPRD
204114_at	864.4	304.3	4631.7	12	33	nidogen 2 (osteonidogen)	NID2
202412_s_at	2463.6	945.5	1998.4	58.6	33	ubiquitin specific peptidase 1	USP1
202575_at	280.6	207.3	482	13.4	33	cellular retinoic acid binding protein 2	CRABP2
205249_at	225.3	75.4	367.7	11.7	33	early growth response 2 (Krox-20 homolog, Drosophila)	EGR2
219237_s_at	509.8	349.6	583.8	10	33	DnaJ (Hsp40) homolog, subfamily B, member 14	DNAJB14
203331_s_at	1079.1	847.9	2665.7	30.2	33	inositol polyphosphate-5-phosphatase, 145kDa	INPP5D
214615_at	257.5	190.8	516.5	7.4	33	purinergic receptor P2Y, G-protein coupled, 10	P2RY10
205632_s_at	1124.2	750.9	2645.1	88.4	33	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	PIP5K1B
214984_at	147.5	93.4	521.2	2	33	PI-3-kinase-related kinase SMG-1	SMG1
202732_at	876.3	589.3	2260.7	28.7	33	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	PKIG
213538_at	2967.3	1774.4	9703.8	472.3	33	SON DNA binding protein	SON
210592_s_at	4102.2	3018.5	15575.9	276.3	33	spermidine/spermine N1-acetyltransferase	SAT
214254_at	118.5	73.8	391.7	4.1	33	melanoma antigen family A, 4	MAGEA4
209465_x_at	88.2	60.5	352.3	3.3	33	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	PTN
221980_at	140	114.6	428.9	12.9	33	Elastin microfibril interfacer 2	EMILIN2
205617_at	348.8	147.5	454.9	6.4	33	proline rich Gla (G-carboxyglutamic acid) 2	PRRG2
212382_at	4841.3	2575.4	7602.8	80.3	33	Transcription factor 4	TCF4
213146_at	580.7	260.3	1033.7	9.3	33	---	---
215016_x_at	293	100.3	581.8	4.1	33	dystonin	DST
215464_s_at	1495.7	546	891	15.1	33	Tax1 (human T-cell leukemia virus type I) binding protein 3	TAX1BP3
219233_s_at	742.2	542	1209.2	18.8	33	gasdermin-like	GSDML

220843_s_at	286.7	139.9	402.3	5.6	33	WD repeats and SOF1 domain containing	WDSOF1
206566_at	139.4	84.4	328.6	3.9	33	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	SLC7A1
209037_s_at	441.2	245.2	1038.9	9.6	33	EH-domain containing 1	EHD1
204525_at	119.9	94.7	373.2	1.3	33	PHD finger protein 14	PHF14
207604_s_at	498.4	299.6	1302.9	6	33	solute carrier family 4, sodium bicarbonate cotransporter, member 7	SLC4A7
218480_at	322.2	291.5	680.8	22.7	33	hypothetical protein FLJ21839	FLJ21839
215112_x_at	62.4	14.6	597.2	0.3	33	MCF.2 cell line derived transforming sequence-like 2	MCF2L2
207462_at	263	165.5	1053.3	5.7	33	glycine receptor, alpha 2	GLRA2
207334_s_at	239.9	113.8	971.7	5.8	33	transforming growth factor, beta receptor II (70/80kDa)	TGFBR2
220570_at	180.4	89.6	3075.1	7	33	resistin	RETN
213745_at	87.6	50.3	363.4	2.4	33	attractin-like 1	ATRNL1
202533_s_at	711	317.8	704.1	12.5	32	dihydrofolate reductase	DHFR
203795_s_at	3293	2438.1	5241.7	239.2	32	B-cell CLL/lymphoma 7A	BCL7A
211200_s_at	374.4	97.7	390.5	4.4	32	EF-hand calcium binding domain 2	EFCAB2
212629_s_at	983.6	762.4	1470.6	49.1	32	protein kinase N2	PKN2
218262_at	765.3	563.6	1191.6	48.3	32	hypothetical protein FLJ22318	FLJ22318
218802_at	2316.7	1822.3	2483.5	42.4	32	hypothetical protein FLJ20647	FLJ20647
222032_s_at	461.1	241.6	508.1	13.7	32	Unknown protein	USP7
206997_s_at	210.7	71.6	498.5	7.4	32	heparan sulfate 6-O-sulfotransferase 1	HS6ST1
213922_at	481.2	199.2	1028.1	2.3	32	tau tubulin kinase 2	TTBK2
60084_at	281	130	624.4	5	3	cylindromatosis (turban tumor syndrome)	CYLD
207712_at	163	88	395.3	4	3	B melanoma antigen	BAGE
216709_at	153.8	103.2	482.7	6.5	3	Hypothetical gene supported by BC013370; BC034583	LOC400655
205385_at	124.8	79.1	691.4	8.7	3	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	MDM2
209524_at	432.4	154.3	1100.3	3.9	3	hepatoma-derived growth factor, related protein 3	HDGFRP3
204688_at	283.8	139.5	1709.8	5.6	3	sarcoglycan, epsilon	SGCE
212092_at	323.4	177.7	27725.6	6.4	3	paternally expressed 10	PEG10

203317_at	1832.1	859.6	1426.6	133.2	3	pleckstrin and Sec7 domain containing 4	PSD4
204335_at	487.2	62.9	856	8.4	3	hypothetical protein FLJ10374	FLJ10374
208548_at	162.5	66.9	324.4	3.4	3	interferon, alpha 6	IFNA6
208608_s_at	337.6	133.3	587.1	10.4	3	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	SNTB1
214305_s_at	4659	3426.8	5099.6	498.5	3	splicing factor 3b, subunit 1, 155kDa	SF3B1
214744_s_at	279.8	117.4	349.2	7.6	3	Similar to Zgc:73149 protein	LOC442209
219814_at	450.4	149.4	788.7	10	3	muscleblind-like 3 (Drosophila)	MBNL3
205840_x_at	798.1	421.9	2064.1	14.2	3	growth hormone 1	GH1
210961_s_at	171.3	91.8	415.9	3.7	3	adrenergic, alpha-1D-, receptor	ADRA1D
211192_s_at	431	237.8	881.3	8.3	3	CD84 antigen (leukocyte antigen)	CD84
213799_s_at	370.5	198.3	755	14.3	3	protein tyrosine phosphatase, receptor type, A	PTPRA
220729_at	151.5	60.7	336.3	2.6	3	---	---
207238_s_at	2281.5	1823	5647.1	43.2	3	protein tyrosine phosphatase, receptor type, C	PTPRC
214971_s_at	275.6	125.8	787.6	7.8	3	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	ST6GAL1
213988_s_at	943.7	577.2	4736.9	24.4	3	spermidine/spermine N1-acetyltransferase	SAT
201584_s_at	5701.3	3803.1	5988.4	552.8	3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	DDX39
205308_at	426.6	135.5	505.4	3.9	3	chromosome 8 open reading frame 70	C8orf70
208977_x_at	9681.2	5369.7	14888.5	972	3	tubulin, beta, 2	TUBB2
210466_s_at	5244.2	3388	6177	820.6	3	SERPINE1 mRNA binding protein 1	SERBP1
213725_x_at	1418.9	780.6	1815.3	69.9	3	hypothetical protein LOC283824	LOC283824
218176_at	1009.6	548.2	1460.3	10.6	3	melanoma antigen family F, 1	MAGEF1
41037_at	189.6	101.1	356.3	6.6	3	TEA domain family member 4	TEAD4
207470_at	181.1	83.8	435.3	3.2	3	hypothetical protein DKFZp566H0824	DKFZp566H0824
209083_at	3910.9	3369.5	9674.6	516.6	3	coronin, actin binding protein, 1A	CORO1A
210741_at	116	54.2	258.8	2.9	3	Rho guanine nucleotide exchange factor (GEF) 12	ARHGEF12
219106_s_at	83.2	24.4	781.6	1.2	3	kelch repeat and BTB (POZ) domain containing 10	KBTBD10
33646_g_at	325.7	251.1	1119.4	4.5	3	GM2 ganglioside activator	GM2A

215002_at	116.2	32	583.2	2	31	KIAA0220-like protein /// hypothetical gene LOC283846 /// hypothetical protein 348162 /// NPIP-like locus /// hypothetical protein LOC440345 /// PI-3-kinase-related kinase SMG-1 pseudogene	LOC23117 /// DKFZp547E087 /// LOC348162 /// LOC388221 /// LOC440345 /// LOC440354
209526_s_at	622.2	426.6	1995	9.3	31	hepatoma-derived growth factor, related protein 3	HDGFRP3
201005_at	6598.1	4694.1	25569.7	11.4	31	CD9 antigen (p24)	CD9
206247_at	1394.4	1038.9	1334.3	166.5	31	MHC class I polypeptide-related sequence B	MICB
212315_s_at	453.7	257.2	856.9	11.4	31	nucleoporin 210kDa	NUP210
215855_s_at	732.8	504.4	1338.6	36.5	31	TATA element modulatory factor 1	TMF1
218992_at	547.1	338.7	925.8	19.4	31	chromosome 9 open reading frame 46	C9orf46
222023_at	270	146.6	382	3.6	31	A kinase (PRKA) anchor protein 13	AKAP13
207829_s_at	305.8	252.4	665.6	31.3	31	BCL2/adenovirus E1B 19kDa interacting protein 1	BNIP1
215728_s_at	353.9	258.2	713.1	16.8	31	acyl-CoA thioesterase 7	ACOT7
218279_s_at	217.1	138.9	700.8	3.3	31	histone 2, H2aa	HIST2H2AA
220623_s_at	152.1	108.2	339.2	4.7	31	testis specific, 10	TSGA10
203245_s_at	253.2	176	590.9	10.2	31	FLJ35348	FLJ35348
203298_s_at	2224.3	1657	4931.3	308.5	31	Jumonji, AT rich interactive domain 2	JARID2
208622_s_at	8534.4	2241.9	17271.3	137.7	31	villin 2 (ezrin)	VIL2
209388_at	861.1	717.7	2495.3	65.9	31	poly(A) polymerase alpha	PAPOLA
222074_at	197.2	71.6	1101.8	2.2	31	uroporphyrinogen decarboxylase	UROD
211299_s_at	235.5	221.3	561.1	9.5	31	flotillin 2	FLOT2
214240_at	152.7	133.8	416.1	9.6	31	galanin	GAL
215037_s_at	900.5	530.2	6759	19.6	31	BCL2-like 1	BCL2L1
215163_at	177.2	41.2	971.9	4.6	31	---	---

215694_at	113.4	92.2	345	3.2	31	spermatogenesis associated 5-like 1	SPATA5L1
219073_s_at	282.2	200.3	1001.9	3.4	31	oxysterol binding protein-like 10	OSBPL10
214337_at	63.6	30.2	363.5	1.6	31	coatomer protein complex, subunit alpha	COPA
207339_s_at	2085.6	1712.7	24613.4	77.1	31	lymphotoxin beta (TNF superfamily, member 3)	LTB
201580_s_at	1692.5	1189.9	1675.7	160.3	31	thioredoxin domain containing 13	TXNDC13
201694_s_at	2112.8	467.7	3888.6	23.7	31	early growth response 1	EGR1
207999_s_at	667.3	514.6	836	69.8	31	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	ADARB1
212744_at	279.5	267	498.4	11	31	Bardet-Biedl syndrome 4	BBS4
212810_s_at	873.7	577.3	931.9	28.4	31	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	SLC1A4
217203_at	192.4	68.4	327.3	3.5	31	---	---
217893_s_at	1798.4	767.9	2805.8	20.5	31	chromosome 1 open reading frame 108	C1orf108
220529_at	580.9	275.3	598.2	22.9	31	hypothetical protein FLJ11710	FLJ11710
221436_s_at	693.1	377.3	1276.4	10	31	cell division cycle associated 3 /// cell division cycle associated 3	CDCA3
206919_at	185.6	109.2	552.5	3	31	ELK4, ETS-domain protein (SRF accessory protein 1)	ELK4
210928_at	179.2	64.4	491.1	6.8	31	CCR4-NOT transcription complex, subunit 2	CNOT2
217602_at	183	98.6	704.3	3.7	31	peptidylprolyl isomerase A (cyclophilin A)	PPIA
213523_at	555.5	373.4	1967.5	13.8	31	cyclin E1	CCNE1
204362_at	872	628.3	3033.3	9.9	31	src family associated phosphoprotein 2	SCAP2
204686_at	255	163.7	1166.5	5.3	31	insulin receptor substrate 1	IRS1
214627_at	398	173.9	5293.7	16.9	31	eosinophil peroxidase	EPX
215139_at	95.2	54.9	314.1	3.6	31	Rho guanine nucleotide exchange factor (GEF) 10	ARHGEF10
215767_at	119	73.9	582.8	4.6	31	chromosome 2 open reading frame 10	C2orf10
203827_at	148.4	66.5	727	3.9	31	WD40 repeat protein Interacting with phosphoInositides of 49kDa	WIPI49
201364_s_at	1746.5	1321.7	2921.9	120.9	30	ornithine decarboxylase antizyme 2	OAZ2
202413_s_at	4532.3	3194.3	4483.5	763.6	30	ubiquitin specific peptidase 1	USP1
202971_s_at	851	538	1188.6	8.7	30	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	DYRK2

205367_at	2237.6	1328.9	3421.3	68.2	30	adaptor protein with pleckstrin homology and src homology 2 domains	APS
208076_at	558.8	407.3	705.1	12.5	30	histone 1, H4d	HIST1H4D
209152_s_at	3493.2	1505.9	2674.6	248.4	30	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3
212525_s_at	908.7	543.6	1204.8	13.5	30	H2A histone family, member X	H2AFX
215024_at	355.8	228.8	464.7	9	30	chromosome 7 open reading frame 28B	C7orf28B
219426_at	570	329.1	586.4	42.2	30	eukaryotic translation initiation factor 2C, 3	EIF2C3
222349_x_at	185.8	110.7	350.5	8.6	30	ring finger protein 126 pseudogene 1	RNF126P1
204935_at	112.6	32.6	258.5	1.9	30	protein tyrosine phosphatase, non-receptor type 2	PTPN2
215992_s_at	226.5	128.2	899.5	7.8	30	Rap guanine nucleotide exchange factor (GEF) 2	RAPGEF2
209967_s_at	134.8	43	415.7	5.5	30	cAMP responsive element modulator	CREM
204286_s_at	1054.4	645.4	6785.1	27	30	phorbol-12-myristate-13-acetate-induced protein 1	PMAIP1
206390_x_at	349.1	275	5566.7	21.4	30	platelet factor 4 (chemokine (C-X-C motif) ligand 4)	PF4
220270_at	142.4	102.5	516.2	5.9	30	tudor domain containing 4	TDRD4
204396_s_at	363.5	249.8	3619.7	4.4	30	G protein-coupled receptor kinase 5	GRK5
202305_s_at	1106	859.8	1483.6	59.9	30	fasciculation and elongation protein zeta 2 (zygin II)	FEZ2
203297_s_at	3578.4	2269.2	4416	249.5	30	Jumonji, AT rich interactive domain 2	JARID2
203311_s_at	1645.4	1021.3	3135	78.6	30	ADP-ribosylation factor 6	ARF6
206965_at	214.2	122.3	370.6	3.3	30	Kruppel-like factor 12	KLF12
208903_at	848.2	783.6	1237.4	131.2	30	Ribosomal protein S28	RPS28
210050_at	282.7	138	358.7	6.7	30	triosephosphate isomerase 1	TPI1
214656_x_at	1723.7	865.9	1324.6	76.4	30	myosin IC	MYO1C
218913_s_at	1248	564.4	1373.8	39.5	30	GEM interacting protein	GMIP
219840_s_at	837.2	186.2	1234.8	8	30	T-cell leukemia/lymphoma 6	TCL6
205350_at	194.6	78.9	417.2	8.8	30	cellular retinoic acid binding protein 1	CRABP1
206886_x_at	816.4	315.5	2779.8	7.6	30	growth hormone 1	GH1
218851_s_at	212	137	784.1	12.2	30	WD repeat domain 33	WDR33
201593_s_at	2313.4	2053.5	5467.5	439.2	30	likely ortholog of mouse immediate early response, erythropoietin 4	LEREPO4
215212_at	272	129.7	714.5	3.1	30	CDNA FLJ12091 fis, clone HEMBB1002582	---

206361_at	220.1	126	661.1	13	30	G protein-coupled receptor 44	GPR44
206489_s_at	121.6	61.4	543.2	4.5	30	discs, large (Drosophila) homolog-associated protein 1	DLGAP1
202576_s_at	828.5	524.2	1222.5	32.9	30	DEAD (Asp-Glu-Ala-As) box polypeptide 19B /// DEAD (Asp-Glu-Ala-As) box polypeptide 19A /// DDX19-DDX19L protein	DDX19B /// DDX19A /// DDX19-DDX19L
204982_at	759.2	306.6	1312	18.5	30	G protein-coupled receptor kinase interactor 2	GIT2
209181_s_at	2471.5	1445.1	3301	370.2	30	Rab geranylgeranyltransferase, beta subunit	RABGGTB
212119_at	1486.3	1058.8	1840.8	181.7	30	ras homolog gene family, member Q	RHOQ
213971_s_at	1705.5	1190	1646.9	278	30	suppressor of zeste 12 homolog (Drosophila)	SUZ12
214314_s_at	247.2	109.9	261.2	1.5	30	eukaryotic translation initiation factor 5B	EIF5B
217914_at	795.6	473.5	1574.4	36.4	30	two pore segment channel 1	TPCN1
219537_x_at	612.7	151.4	710.1	10.7	30	delta-like 3 (Drosophila)	DLL3
219892_at	406.1	301.3	693.9	12.7	30	transmembrane 6 superfamily member 1	TM6SF1
200906_s_at	196.9	84.1	443.8	5.7	30	palladin	KIAA0992
213963_s_at	296.6	119.6	722.2	9.6	30	Sin3A-associated protein, 30kDa	SAP30
33148_at	202.2	153.4	456.9	5.9	30	zinc finger RNA binding protein	ZFR
212715_s_at	313	179.1	744.1	6.8	30	microtubule associated monoxygenase, calponin and LIM domain containing 3	MICAL3
203845_at	1062.2	644.3	5682	75.2	30	p300/CBP-associated factor	PCAF
216961_s_at	162.2	126	401	11.5	30	RPA interacting protein	RIP
219841_at	178.9	78.2	389.7	4.2	30	activation-induced cytidine deaminase	AICDA
216065_at	170.2	63.4	574.6	4.9	30	---	---
220602_s_at	180	97.5	579.2	6.4	30	hypothetical protein FLJ22795 /// hypothetical protein FLJ90297 /// LOC388161	FLJ22795 /// LOC388152 /// LOC388161
202391_at	2179.6	964.3	13386.3	154.3	30	brain abundant, membrane attached signal protein 1	BASP1
216260_at	100.5	73.4	440.8	4.9	30	Dicer1, Dcr-1 homolog (Drosophila)	DICER1
200675_at	12263.9	7362.2	14130.7	1142.6	29	CD81 antigen (target of antiproliferative antibody 1)	CD81

209041_s_at	876.8	610.3	1024.8	15	29	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	UBE2G2
209060_x_at	1380	753.8	1224.4	112.6	29	nuclear receptor coactivator 3	NCOA3
211279_at	287.2	194.6	367.2	11	29	nuclear respiratory factor 1	NRF1
212680_x_at	2180.1	1447	3705	43.5	29	protein phosphatase 1, regulatory (inhibitor) subunit 14B	PPP1R14B
214338_at	292.1	245.2	539.1	11.6	29	DnaJ (Hsp40) homolog, subfamily B, member 12	DNAJB12
214838_at	911.6	592.2	1570.7	30.9	29	SFT2 domain containing 2	SFT2D2
216350_s_at	654.8	237.3	1216.9	11.5	29	zinc finger protein 10	ZNF10
78330_at	539.8	377.5	856.9	42	29	zinc finger protein 335	ZNF335
211996_s_at	8974.6	6702.7	21416.6	985.7	29	KIAA0220-like protein /// hypothetical gene LOC283846 /// hypothetical protein 348162 /// PI-3-kinase-related kinase SMG-1 pseudogene /// similar to the PI-3-kinase-related kinase SMG-1 family pseudogene 2	LOC23117 /// DKFZp547E087 /// LOC348162 /// LOC440354 /// LOC613037
215554_at	111.1	48.1	454.1	2.4	29	glycosylphosphatidylinositol specific phospholipase D1	GPLD1
208348_s_at	116.4	38	303.5	3.3	29	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	CBLB
222205_x_at	137.1	109.4	502.2	5.7	29	Similar to hypothetical protein FLJ38374	LOC400840
212750_at	930.6	632	6690.7	15.9	29	protein phosphatase 1, regulatory (inhibitor) subunit 16B	PPP1R16B
39729_at	1792.3	1477.1	23054	26.2	29	peroxiredoxin 2	PRDX2
201810_s_at	1070.1	610.6	10902	33.6	29	SH3-domain binding protein 5 (BTK-associated)	SH3BP5
202716_at	2019.7	1174.5	1578.2	117.1	29	protein tyrosine phosphatase, non-receptor type 1	PTPN1
202781_s_at	1392.7	858.7	1351.8	120.4	29	skeletal muscle and kidney enriched inositol phosphatase	SKIP

204817_at	1160.2	785.1	1589.1	61.1	29	extra spindle poles like 1 (S. cerevisiae)	ESPL1
214508_x_at	418.7	356.9	732.4	21.5	29	cAMP responsive element modulator	CREM
215151_at	278.2	98.2	400.7	6.6	29	dedicator of cytokinesis 10	DOCK10
221521_s_at	1660.7	1195.7	2488.9	12.3	29	DNA replication complex GINS protein PSF2	Pfs2
203068_at	278.5	56.5	1212.6	10.2	29	kelch-like 21 (Drosophila)	KLHL21
205590_at	1491.4	641.4	3396.4	11.1	29	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	RASGRP1
216449_x_at	1656.1	608.9	3772	27.5	29	tumor rejection antigen (gp96) 1	TRA1
208068_x_at	663.4	497.8	1784.6	30.3	29	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// chorionic somatomammotropin hormone-like 1 /// growth hormone 1 /// growth hormone 2	CSH1 /// CSH2 /// CSHL1 /// GH1 /// GH2
218888_s_at	386.1	148.1	1168.2	5.5	29	neuropilin (NRP) and tolloid (TLL)-like 2	NETO2
221261_x_at	492.8	164.3	1704.3	9.4	29	melanoma antigen family D, 4 /// melanoma antigen family D, 4	MAGED4
207772_s_at	153.2	86.3	593.2	3.7	29	HMT1 hnRNP methyltransferase-like 4 (S. cerevisiae)	HRMT1L4
215931_s_at	180.6	43.6	533.8	5.3	29	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	ARFGEF2
216184_s_at	163.6	106.5	770.8	5.9	29	regulating synaptic membrane exocytosis 1	RIMS1
201718_s_at	523.7	433.5	1918.3	9.7	29	erythrocyte membrane protein band 4.1-like 2	EPB41L2
220359_s_at	546.9	178.5	15891.5	3.9	29	cyclic AMP-regulated phosphoprotein, 21 kD	ARPP-21
201868_s_at	147.6	120.5	611.9	3.7	29	transducin (beta)-like 1X-linked	TBL1X
202289_s_at	157	84	1169.5	5.2	29	transforming, acidic coiled-coil containing protein 2	TACC2
220059_at	777.8	473.2	9891.4	15.3	29	BCR downstream signaling 1	BRDG1
200704_at	2127.5	1314.5	3636.2	50.4	29	lipopolysaccharide-induced TNF factor	LITAF
201396_s_at	517.4	358.8	590.4	20.8	29	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	SGTA
201625_s_at	730.7	607.5	1053.5	75.3	29	insulin induced gene 1	INSIG1
201730_s_at	3624.8	1911	4999.2	138.9	29	translocated promoter region (to activated MET oncogene)	TPR
207124_s_at	422.6	208.9	510	13.9	29	guanine nucleotide binding protein (G protein), beta 5	GNB5

209052_s_at	1267.4	568.8	2199.3	13.7	29	Wolf-Hirschhorn syndrome candidate 1	WHSC1
212035_s_at	759.8	598.6	1203.5	58.5	29	exocyst complex component 7	EXOC7
215174_at	249	135.5	491.3	8.6	29	flavin containing monooxygenase 6	FMO6
217370_x_at	1147.3	737	1707.2	38.8	29	fusion (involved in t(12;16) in malignant liposarcoma)	FUS
218812_s_at	880.9	570.1	1354.3	76.4	29	chromosome 7 open reading frame 19	C7orf19
219094_at	316.3	236.8	547.6	6.6	29	armadillo repeat containing 8	ARMC8
219174_at	142.9	17.2	203.5	2.2	29	coiled-coil domain containing 2	CCDC2
221745_at	849	567.4	1216.1	16.3	29	WD repeat domain 68	WDR68
215234_at	198.1	112.5	396.3	7.1	29	MRNA,trapped exon e1b7, DCR1-16.0,	---
216573_at	204.4	57.2	559.1	4.7	29	Clone ds1-1 immunoglobulin lambda chain VJ region, (IGL)	---
40837_at	435.6	331	1225.2	34.9	29	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	TLE2
203857_s_at	1302.4	844.3	3509	46.3	29	protein disulfide isomerase family A, member 5	PDIA5
211088_s_at	230	164.8	555.7	7.6	29	polo-like kinase 4 (Drosophila) /// polo-like kinase 4 (Drosophila)	PLK4
211475_s_at	2071.5	1680.1	8077	413	29	BCL2-associated athanogene	BAG1
217127_at	112.2	61.5	291.3	2	29	cystathionase (cystathionine gamma-lyase)	CTH
202286_s_at	153.5	76.9	659.7	7.4	29	tumor-associated calcium signal transducer 2	TACSTD2
207517_at	131.2	61	680.2	4.1	29	laminin, gamma 2	LAMC2
220784_s_at	110.7	31.1	319.1	1.8	29	urotensin 2	UTS2
221152_at	131.1	81.2	448	2.8	29	collagen, type VIII, alpha 1	COL8A1
207894_s_at	269.4	156.9	687.1	21.3	29	T-cell leukemia/lymphoma 6	TCL6
201942_s_at	133.4	82.9	588.8	4.7	29	carboxypeptidase D	CPD
206935_at	54.9	18.9	294.4	0.8	29	protocadherin 8	PCDH8
211341_at	1031	133.9	10201.6	2.1	29	POU domain, class 4, transcription factor 1	POU4F1
201598_s_at	1332.6	1111.7	2082.9	189.5	28	inositol polyphosphate phosphatase-like 1	INPPL1
202769_at	2932.9	1532.5	3398	190.4	28	Cyclin G2	CCNG2
202900_s_at	1820.3	1430.3	2398.2	109.6	28	nucleoporin 88kDa	NUP88
203113_s_at	12072.1	8841.5	11404.7	1180.8	28	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	EEF1D

207499_x_at	922.1	720.5	1197.2	51.5	28	smooth muscle cell associated protein-1	SMAP-1
209535_s_at	889.7	507.2	808.6	65.3	28	---	---
211352_s_at	940.2	324.4	918.2	9.3	28	nuclear receptor coactivator 3	NCOA3
213286_at	422.7	215.1	583.7	12.7	28	zinc finger RNA binding protein	ZFR
214052_x_at	476.4	225.6	618.2	6.3	28	BAT2 domain containing 1	BAT2D1
214336_s_at	1446.5	518.3	1121.1	62.6	28	coatomer protein complex, subunit alpha	COPA
215509_s_at	771.4	220.1	1118.4	11	28	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1
217966_s_at	290.5	157.6	489.7	7.8	28	chromosome 1 open reading frame 24	C1orf24
219207_at	373.8	241.9	568.8	6.8	28	hypothetical protein FLJ21128	FLJ21128
221611_s_at	254.3	148.8	390.6	11.1	28	PHD finger protein 7	PHF7
211274_at	165.9	85.1	342.9	8.3	28	T-box 1	TBX1
208023_at	181.6	76.3	382.3	5.6	28	tumor necrosis factor receptor superfamily, member 4	TNFRSF4
216872_at	120	52.7	514.8	1.8	28	Hr44 antigen	HR44
203836_s_at	444.9	329.7	1706	6.6	28	mitogen-activated protein kinase kinase kinase 5	MAP3K5
214651_s_at	115.1	59.9	7233.4	3	28	homeo box A9	HOXA9
201843_s_at	109.6	78.2	7630.9	4.4	28	EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1
203241_at	1066.4	834.5	1885.9	152.9	28	UV radiation resistance associated gene	UVRAG
204970_s_at	749.8	468.4	1127.1	41.9	28	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	MAFG
214941_s_at	2325.5	1206.9	2919.2	73.8	28	formin binding protein 3	FNBP3
216279_at	188.3	103.8	303	5.3	28	zinc finger protein 272	ZNF272
218810_at	797.5	275.2	968.6	25.1	28	zinc finger CCCH-type containing 12A	ZC3H12A
219717_at	769.6	568.7	1382.9	72.7	28	hypothetical protein FLJ20280	FLJ20280
221664_s_at	763.3	449.2	1121.6	24.1	28	F11 receptor	F11R
221154_at	188.5	47.7	392.8	1.3	28	tripartite motif-containing 49	TRIM49
222320_at	188.7	62.2	779	0.4	28	Cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	CDC73
203876_s_at	221.3	182.3	484.9	18.2	28	matrix metallopeptidase 11 (stromelysin 3)	MMP11
214295_at	178.6	121.5	991	6.2	28	KIAA0485 protein	KIAA0485

202859_x_at	705.3	181.2	4322.1	10.9	28	interleukin 8	IL8
212336_at	118.4	40.8	347.3	3.1	28	erythrocyte membrane protein band 4.1-like 1	EPB41L1
218834_s_at	183.7	97.4	471.7	10.5	28	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) binding protein 1	HSPA5BP1
205612_at	119.4	66.5	613.8	1.8	28	multimerin 1	MMRN1
213400_s_at	404	207.8	1760.6	11.7	28	transducin (beta)-like 1X-linked	TBL1X
208983_s_at	634.7	438	5148	13.9	28	platelet/endothelial cell adhesion molecule (CD31 antigen)	PECAM1
201309_x_at	2136.9	1690.7	3920.1	205.2	27	chromosome 5 open reading frame 13	C5orf13
202154_x_at	3521.2	1931.5	5268.2	196.6	27	tubulin, beta 3	TUBB3
203318_s_at	1287.8	861.9	2184.2	162.8	27	zinc finger protein 148 (pHZ-52)	ZNF148
207556_s_at	1040.9	730.5	1867.1	30.2	27	diacylglycerol kinase, zeta 104kDa	DGKZ
209610_s_at	1038.3	584.6	1530.4	53.6	27	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	SLC1A4
210605_s_at	357.4	171.9	630.5	12.2	27	milk fat globule-EGF factor 8 protein	MFGE8
213182_x_at	210.3	28.2	399	4.5	27	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	CDKN1C
216983_s_at	314.4	198.1	530.3	12.5	27	zinc finger protein 224	ZNF224
217924_at	374.4	211	591.3	11.3	27	chromosome 6 open reading frame 106	C6orf106
218219_s_at	826.9	399	920.1	13.4	27	LanC lantibiotic synthetase component C-like 2 (bacterial)	LANCL2
218981_at	146.5	90.6	269.5	1.2	27	ACN9 homolog (S. cerevisiae)	ACN9
219339_s_at	483.5	242.8	515.2	9.8	27	euchromatic histone-lysine N-methyltransferase 1	EHMT1
221262_s_at	209.5	80.6	360.8	5	27	solute carrier family 2 (facilitated glucose transporter), member 11 /// solute carrier family 2 (facilitated glucose transporter), member 11	SLC2A11
221546_at	307.2	156.8	524.4	10.8	27	PRP18 pre-mRNA processing factor 18 homolog (yeast)	PRPF18
35436_at	470.9	214.4	673.4	19.5	27	golgi autoantigen, golgin subfamily a, 2	GOLGA2
208851_s_at	350.1	209.5	747.3	15.8	27	Thy-1 cell surface antigen	THY1
209201_x_at	27920.9	22826.8	56196.9	1417.6	27	chemokine (C-X-C motif) receptor 4	CXCR4
221829_s_at	2947.8	1924.8	7554.1	350.5	27	transportin 1	TNPO1

222063_s_at	151	55.8	320.1	2.5	27	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	CDS1
216108_at	117.4	38.8	248.7	4.4	27	Transcribed locus, weakly similar to NP_055301.1 neuronal thread protein AD7c-NTP [Homo sapiens]	---
217585_at	133.6	76.5	392.2	4.7	27	nebulette	NEBL
211771_s_at	231.6	49.6	938.8	6.4	27	POU domain, class 2, transcription factor 2 /// POU domain, class 2, transcription factor 2	POU2F2
215609_at	160.3	126.1	450.3	6.3	27	START domain containing 7	STARD7
202953_at	104.2	88	968.1	9.6	27	complement component 1, q subcomponent, beta polypeptide	C1QB
201710_at	2306.4	789.5	2974.5	27.5	27	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	MYBL2
203377_s_at	1193.9	412.3	871.2	27.2	27	cell division cycle 40 homolog (yeast)	CDC40
212085_at	16661.8	13263.8	21255.3	1445.2	27	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	SLC25A6
217094_s_at	478.9	218.5	431.3	12.8	27	itchy homolog E3 ubiquitin protein ligase (mouse)	ITCH
218418_s_at	3248.2	1177.9	4104.1	69.6	27	ankyrin repeat domain 25	ANKRD25
202545_at	554	284.5	2142.8	20.2	27	protein kinase C, delta	PRKCD
203263_s_at	351.6	271.3	737	8.3	27	Cdc42 guanine nucleotide exchange factor (GEF) 9	ARHGEF9
203653_s_at	408.8	335.3	883.7	8.1	27	coilin	COIL
206850_at	540.4	204.2	1160.3	16.3	27	RAS-related on chromosome 22	RRP22
207526_s_at	205	117.9	519.5	4.7	27	interleukin 1 receptor-like 1	IL1RL1
215203_at	847.9	423.2	2505.9	52	27	golgi autoantigen, golgin subfamily a, 4	GOLGA4
217607_x_at	225	134.6	475.7	2	27	eukaryotic translation initiation factor 4 gamma, 2	EIF4G2
220140_s_at	442.2	264.5	1143.6	19.5	27	sorting nexin 11	SNX11
220296_at	283.9	169.2	806	13.1	27	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	GALNT10
205547_s_at	358.7	262.2	1771	11.8	27	transgelin	TAGLN
207479_at	130.3	26.9	503.6	1.7	27	---	---
211538_s_at	335.4	178.3	6151.6	10.9	27	heat shock 70kDa protein 2	HSPA2
217302_at	201.1	124.7	577.8	8.8	27	olfactory receptor, family 2, subfamily F, member 2	OR2F2

220550_at	126.2	51.7	542.1	2.6	27	F-box protein 4	FBXO4
207357_s_at	235	109.4	1081.7	9.9	27	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	GALNT10
212392_s_at	203.4	152.7	545	11.9	27	phosphodiesterase 4D interacting protein (myomegalin)	PDE4DIP
213606_s_at	198.8	76.2	989.3	1.2	27	Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA
202040_s_at	1505.6	1348.4	2800	323.2	27	Jumonji, AT rich interactive domain 1A (RBBP2-like)	JARID1A
202588_at	475.2	260	665.6	33.5	27	adenylate kinase 1	AK1
203272_s_at	767.6	394.4	820.6	38.4	27	tumor suppressor candidate 2	TUSC2
203869_at	227.4	154.5	412.2	7.5	27	ubiquitin specific peptidase 46	USP46
205315_s_at	583.5	457.3	879.7	21.4	27	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	SNTB2
208503_s_at	955.4	562.3	1110.6	62.7	27	GATA zinc finger domain containing 1	GATAD1
208506_at	187.1	113.7	296.6	3.6	27	histone 1, H3f	HIST1H3F
208859_s_at	717.8	264.6	975.1	8.1	27	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	ATRX
208879_x_at	523	396.2	924.3	10.8	27	chromosome 20 open reading frame 14	C20orf14
212794_s_at	6236.8	2719.2	8965.8	303	27	KIAA1033	KIAA1033
213223_at	1355.5	995.3	1388.3	48.2	27	ribosomal protein L28	RPL28
213879_at	680.6	451.6	1000.1	31.2	27	SMT3 suppressor of mif two 3 homolog 2 (yeast)	SUMO2
215001_s_at	6297.3	4027	11499.9	107.4	27	glutamate-ammonia ligase (glutamine synthetase)	GLUL
217208_s_at	515.6	370	839.4	18.8	27	discs, large homolog 1 (Drosophila)	DLG1
217480_x_at	3170.5	1483.4	3437.3	282.6	27	similar to Ig kappa chain	LOC339562
217813_s_at	845.4	613.1	1204.4	48.6	27	spindlin	SPIN
219148_at	688.6	300.2	1139.4	16.5	27	PDZ binding kinase	PBK
220068_at	11799.9	7578.4	22254.1	78.9	27	pre-B lymphocyte gene 3	VPREB3
221051_s_at	249.1	122	462.4	4.6	27	integrin beta 1 binding protein 3	ITGB1BP3
222165_x_at	844.1	506	1300	14.9	27	chromosome 9 open reading frame 16	C9orf16
213751_at	255.7	70.7	596.5	5.5	27	hypothetical protein LOC284352	LOC284352
218012_at	2264.7	844.4	8541.7	53	27	TSPY-like 2	TSPYL2

219264_s_at	432	188.2	1178.5	5.9	27	protein phosphatase 2 (formerly 2A), regulatory subunit B", beta	PPP2R3B
219994_at	886.4	477.3	2329.5	31	27	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	APBB1IP
206142_at	224.2	87	536.9	2.2	27	zinc finger protein 135 (clone pHZ-17)	ZNF135
217332_at	166	71.5	865.4	3.5	27	Hypothetical LOC387937	LOC387937
211751_at	89.3	37.7	420.3	2.9	27	phosphodiesterase 4D interacting protein (myomegalin) /// phosphodiesterase 4D interacting protein (myomegalin)	PDE4DIP
201204_s_at	331.7	173.1	1773.8	14	27	CDNA FLJ41000 fis, clone UTERU2016761, highly similar to Homo sapiens ES/130 mRNA	---
204792_s_at	112	62.2	323.3	4.1	27	WD and tetratricopeptide repeats 2	WDTC2
211463_at	123.6	54.9	349.5	4	27	Zic family member 4	ZIC4
208690_s_at	6571.5	4976.5	24492	198.6	27	PDZ and LIM domain 1 (elfin)	PDLIM1
221037_s_at	61.6	35.4	551.3	0.5	27	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31 /// solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	SLC25A31
206686_at	178	98.2	624.3	13.7	27	pyruvate dehydrogenase kinase, isoenzyme 1	PDK1
201161_s_at	15493.5	6381.9	21619.5	36.5	26	cold shock domain protein A	CSDA
203832_at	3801	1803.9	4672	216.6	26	enolase 1, (alpha) /// small nuclear ribonucleoprotein polypeptide F	ENO1 /// SNRPF
208919_s_at	2456.4	1631.2	2454.9	404.3	26	NAD kinase	NADK
209308_s_at	1454.5	1070.9	1764.3	94.4	26	BCL2/adenovirus E1B 19kDa interacting protein 2	BNIP2
209336_at	509.8	276	745.3	15.7	26	PWP2 periodic tryptophan protein homolog (yeast)	PWP2H
211085_s_at	605.3	105.9	474.3	3.6	26	serine/threonine kinase 4 /// serine/threonine kinase 4	STK4
212078_s_at	932.1	633.4	1296.9	54.9	26	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	MLL
218906_x_at	513.8	291.8	771.3	24.2	26	kinesin light chain 2	KLC2
219833_s_at	519.5	357.9	862.3	8.4	26	EF-hand domain (C-terminal) containing 1	EFHC1

90610_at	3305.2	2444.1	2899	500.2	26	leucine-rich repeats and calponin homology (CH) domain containing 4	LRCH4
204180_s_at	596.7	442.4	1360.7	53.5	26	zinc finger protein 297B	ZNF297B
219213_at	336.6	193.6	1089.7	15.2	26	junctional adhesion molecule 2	JAM2
205106_at	185	127.5	477.4	17.3	26	mature T-cell proliferation 1	MTCP1
215669_at	218.9	124.5	1632.2	7.2	26	major histocompatibility complex, class II, DR beta 4	HLA-DRB4
208511_at	264.1	220	656.1	11.5	26	pituitary tumor-transforming 3	PTTG3
213906_at	210.5	99.7	700.2	5.6	26	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	MYBL1
216070_at	96	60.7	453	1.9	26	ATPase, Na+/K+ transporting, beta 1 polypeptide	ATP1B1
221674_s_at	165.4	84.5	539.1	11.1	26	chordin	CHRD
215901_at	117.6	99	461	3.6	26	zinc finger protein 81 (HFZ20)	ZNF81
217085_at	70.6	36.4	382.5	2.3	26	Solute carrier family 14 (urea transporter), member 2	SLC14A2
205376_at	93.9	65.4	516.9	2.1	26	inositol polyphosphate-4-phosphatase, type II, 105kDa	INPP4B
208096_s_at	76.5	45.3	480.1	3.1	26	collagen, type XXI, alpha 1 /// collagen, type XXI, alpha 1	COL21A1
205933_at	434.8	329.6	2712.4	9.5	26	SET binding protein 1	SETBP1
204446_s_at	2632.3	1297.5	12918.8	3.8	26	arachidonate 5-lipoxygenase	ALOX5
201518_at	1663.8	1366.3	2814.1	80.4	26	chromobox homolog 1 (HP1 beta homolog Drosophila)	CBX1
202407_s_at	689.2	443.7	649.4	8.1	26	PRP31 pre-mRNA processing factor 31 homolog (yeast)	PRPF31
202937_x_at	632.3	314	1072.3	19.1	26	CGI-96 protein	CGI-96
203362_s_at	1114.5	849.3	2198.2	97	26	MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1
208750_s_at	2763.3	1990.4	4772.1	326.7	26	ADP-ribosylation factor 1	ARF1
210458_s_at	140.3	64.3	256.2	1.9	26	TRAF family member-associated NFKB activator	TANK
210633_x_at	3072.4	2422	4202.8	624.1	26	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	KRT10
211804_s_at	761.5	573.6	1161.4	27.6	26	cyclin-dependent kinase 2	CDK2
213548_s_at	604.8	443	972.2	22.9	26	hypothetical protein H41	H41

217157_x_at	1340.3	507.1	1638.1	29.4	26	IGK mRNA for immunoglobulin kappa light chain VLJ region, partial cds, clone:K142	---
219131_at	276.1	193.2	503.7	22.3	26	UbiA prenyltransferase domain containing 1	UBIAD1
219366_at	442.9	229.7	607.7	18.4	26	apoptosis, caspase activation inhibitor	AVEN
219807_x_at	1785.1	1074.6	1756	54.9	26	RAB4B, member RAS oncogene family	RAB4B
221734_at	583.9	329.7	1064.7	32.7	26	hypothetical protein MGC12103	LOC133619
222082_at	382.4	342.7	743.2	13	26	zinc finger and BTB domain containing 7A	ZBTB7A
41386j_at	2681.1	1537.2	3237.1	299.7	26	---	---
203753_at	5156.3	3589.5	11739.6	100.6	26	transcription factor 4	TCF4
206530_at	440.9	314.6	1126.1	26.8	26	RAB30, member RAS oncogene family	RAB30
211514_at	184.3	57.5	481.6	6.7	26	receptor interacting protein kinase 5	RIPK5
216894_x_at	256	28.2	537.5	3.6	26	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	CDKN1C
220898_at	253.3	172.7	581.6	6.1	26	---	---
46142_at	786.4	434.8	1628.2	19.2	26	hypothetical protein FLJ12681	FLJ12681
214443_at	248.3	149.3	1045.7	9.7	26	poliovirus receptor	PVR
220702_at	484.2	331.2	1135.3	11.6	26	---	---
208180_s_at	481.3	295.3	1335.4	3.3	26	histone 1, H4h	HIST1H4H
207228_at	160.2	88	418.2	10.3	26	protein kinase, cAMP-dependent, catalytic, gamma	PRKACG
204257_at	1371.7	1160.5	6143	100.4	26	fatty acid desaturase 3	FADS3
205420_at	90.8	54.9	421.3	2.7	26	peroxisomal biogenesis factor 7	PEX7
213582_at	106.3	74.3	395.4	1.6	26	ATPase, Class VI, type 11A	ATP11A
213222_at	324.3	226.9	1351.7	3.6	26	phospholipase C, beta 1 (phosphoinositide-specific)	PLCB1
220893_at	128.5	44.9	548.2	4.2	26	uncharacterized gastric protein ZA52P	LOC57399
210848_at	153.2	122.9	459.4	5.4	26	---	---
214649_s_at	130.4	97.7	420	3.5	26	myotubularin related protein 2	MTMR2
209825_s_at	519.7	444.7	1963.8	8	26	uridine-cytidine kinase 2	UCK2
200914_x_at	913.4	714.2	983.4	106.9	26	kinectin 1 (kinesin receptor)	KTN1
203787_at	3369.3	2320.4	4268	120.7	26	single-stranded DNA binding protein 2	SSBP2
205932_s_at	529.7	159.8	978.8	11.1	26	msh homeo box homolog 1 (Drosophila)	MSX1
207700_s_at	2273.6	996.8	1781	167.3	26	nuclear receptor coactivator 3	NCOA3
210461_s_at	570.6	262.9	974.7	43.7	26	actin binding LIM protein 1	ABLIM1

213186_at	473.6	342.9	532	9.9	26	zinc finger DAZ interacting protein 3	DZIP3
214738_s_at	607.5	372.4	1062	13.5	26	NIMA (never in mitosis gene a)- related kinase 9	NEK9
218774_at	539.9	338.8	850.7	24.2	26	decapping enzyme, scavenger	DCPS
218908_at	525.1	270.4	786.4	17.6	26	alveolar soft part sarcoma chromosome region, candidate 1	ASPSCR1
211386_at	286.8	178.2	604.1	5	26	hypothetical protein MGC12488	MGC12488
211177_s_at	344.7	152.3	781.9	16.1	26	thioredoxin reductase 2	TXNRD2
215117_at	661.4	193.7	1613.1	2.8	26	recombination activating gene 2	RAG2
206166_s_at	157.6	100.6	383.3	8.1	26	chloride channel, calcium activated, family member 2	CLCA2
211620_x_at	292.2	158.1	710.2	5.8	26	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	RUNX1
214828_s_at	268.6	174.9	680.9	10.9	26	similar to CGI-96	dJ222E13.2
209125_at	133.6	97.9	826.3	5.4	26	keratin 6A /// keratin 6C /// keratin 6E	KRT6A /// KRT6C /// KRT6E
219666_at	924.1	459.5	7946.9	14.9	26	membrane-spanning 4-domains, subfamily A, member 6A	MS4A6A
35974_at	3454.6	2149.4	18984.7	227.5	26	lymphoid-restricted membrane protein	LRMP
208015_at	324.6	243.5	3779.8	5	26	SMAD, mothers against DPP homolog 1 (Drosophila)	SMAD1
202718_at	113.1	58.5	4105.7	4.9	26	insulin-like growth factor binding protein 2, 36kDa	IGFBP2
203401_at	837	652.7	1491.4	29.4	25	phosphoribosyl pyrophosphate synthetase 2	PRPS2
203907_s_at	2033.9	1446.6	3024.1	138	25	IQ motif and Sec7 domain 1	IQSEC1
205017_s_at	339.5	185.8	617.6	12.6	25	muscleblind-like 2 (Drosophila)	MBNL2
208248_x_at	3004.5	1846.7	5417.3	311.7	25	amyloid beta (A4) precursor-like protein 2	APLP2
213007_at	1438.7	874.5	1714.6	104.6	25	hypothetical protein FLJ10719	FLJ10719
216187_x_at	9608.3	6081	10136.8	1384.5	25	Kinesin 2	KNS2
218308_at	2167.3	1016.3	2296.8	32.3	25	transforming, acidic coiled-coil containing protein 3	TACC3
219203_at	407.8	60.7	564.5	13.9	25	chromosome 14 open reading frame 122	C14orf122
222027_at	535.7	147	680	13.7	25	Nuclear casein kinase and cyclin-dependent kinase substrate 1	NUCKS1
206408_at	211	62.4	454.5	6.6	25	leucine rich repeat transmembrane neuronal 2	LRRTM2

213623_at	330.1	213.7	833	8.8	25	kinesin family member 3A	KIF3A
215459_at	317	169.2	668	7.5	25	Tax1 (human T-cell leukemia virus type I) binding protein 3	TAX1BP3
206079_at	343.8	180.7	938.1	11.4	25	choroideremia-like (Rab escort protein 2)	CHML
208465_at	135.9	43.4	1907.9	7.2	25	glutamate receptor, metabotropic 2	GRM2
61732_r_at	83.1	23.6	198.2	0.3	25	coiled-coil domain containing 2	CCDC2
64900_at	95.8	29.2	263.9	3	25	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5 /// hypothetical protein MGC15429	CHST5 /// MGC15429
215653_at	66.6	14.5	411.1	0.3	25	Glypican 5	GPC5
208054_at	83.6	43.8	792.6	2.8	25	hect domain and RLD 4	HERC4
219948_x_at	55.7	18.7	366	1	25	UDP glucuronosyltransferase 2 family, polypeptide A3	UGT2A3
208394_x_at	81.2	54.2	1063.4	2.3	25	endothelial cell-specific molecule 1	ESM1
207555_s_at	356.3	210.5	600.8	14.6	25	thromboxane A2 receptor	TBXA2R
208319_s_at	2462.3	1579.7	4284.6	231.2	25	RNA binding motif (RNP1, RRM) protein 3	RBM3
208415_x_at	2728.8	1776.8	2291.1	315.2	25	inhibitor of growth family, member 1	ING1
209878_s_at	832.2	497.4	1166.4	19.8	25	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	RELA
212475_at	260.3	199.7	517.2	18.7	25	KIAA0241 protein	KIAA0241
212867_at	1495.5	1330.8	1768.6	356.9	25	Nuclear receptor coactivator 2 /// Nuclear receptor coactivator 2	NCOA2
213351_s_at	489.6	270.8	934.5	9.5	25	transmembrane and coiled-coil domain family 1	TMCC1
214447_at	467.1	178.1	514.6	7.8	25	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	ETS1
214861_at	273.2	180.4	482.4	8.3	25	jumonji domain containing 2C	JMJD2C
215415_s_at	378.9	114.3	474.7	7.7	25	lysosomal trafficking regulator	LYST
216172_at	429.1	230.1	708.1	23.5	25	Exosome component 2	EXOSC2
219971_at	237.9	51.2	428	6.2	25	interleukin 21 receptor	IL21R
210057_at	163.6	112.5	892.7	2.5	25	PI-3-kinase-related kinase SMG-1	SMG1
212949_at	375.3	184.4	766.8	20.7	25	barren homolog (Drosophila)	BRRN1
220674_at	323.7	255.8	689.3	6.1	25	hypothetical protein FLJ22814	FLJ22814

63825_at	491.4	340.1	1073.4	14.8	25	---	---
203334_at	444	238.8	946.9	17.3	25	DEAH (Asp-Glu-Ala-His) box polypeptide 8	DHX8
209145_s_at	251.4	105.7	544.1	9.8	25	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	CBFA2T2
216898_s_at	139.4	62.3	546.7	2.9	25	collagen, type IV, alpha 3 (Goodpasture antigen)	COL4A3
219181_at	218.6	128.5	1224.7	4.1	25	lipase, endothelial	LIPG
221606_s_at	156.6	78.7	352	3.4	25	nucleosomal binding protein 1	NSBP1
205577_at	361.7	123.3	1258.9	10.9	25	phosphorylase, glycogen; muscle (McArdle syndrome, glycogen storage disease type V)	PYGM
217505_at	84	10.4	833.9	0.6	25	kelch-like 23 (Drosophila)	KLHL23
208961_s_at	5616	1346.2	20947.3	27.6	25	Kruppel-like factor 6	KLF6
217787_s_at	322.8	234.4	1316.5	6.6	25	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	GALNT2
207575_at	148	70.7	549.6	7	25	golgi autoantigen, golgin subfamily a, 6	GOLGA6 /
206556_at	102.7	72.1	364.7	7.4	25	clusterin-like 1 (retinal)	CLUL1
211646_at	69.8	34.3	452.3	2.7	25	Similar to KIAA1501 protein /// Similar to KIAA1501 protein	LOC388248
213836_s_at	140	94.2	467.8	8.7	25	WD40 repeat protein Interacting with phosphoInositides of 49kDa	WIPI49
216498_at	96.5	66.5	393.4	4.2	25	---	---
219157_at	991.2	639.9	6082.6	20.2	25	kelch-like 2, Mayven (Drosophila)	KLHL2
214282_at	60.3	31.1	462.2	0.3	25	Hermansky-Pudlak syndrome 3	HPS3

Normal" Controls

In one embodiment, a "normal control" used in the methods and kits of the invention 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, CD19, CD10, CD34, CD45, CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 and CD300a or combinations thereof. In embodiments of the invention, 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.

In specific embodiments, it may be necessary to phenotypically differentiate "hematogones" in normal controls from leukemic cells in ALL specimens. Hematogones are benign lymphoid precursors whose morphology and immunophenotype are similar to the blasts found in ALL, but are considered distinctive from cells indicative of MRD or ALL. Hematogone cells are more commonly found in pediatric bone marrow aspirates following therapy.

It is recognized that the accuracy of detecting and diagnosing minimal residual disease in ALL leukemia will vary based on the strength of the correlation between the expression levels of the differentially expressed genes when compared to normal controls. When the values in the expression profiles represent the expression levels of genes whose expression is strongly correlated with the physiologic condition, it may be possible to use a fewer number of values in the expression profile and still obtain an acceptable level of diagnostic or prognostic accuracy.

RNA Expression Profiling

The values in the expression profiles of the invention 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. Patent 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®).

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. *See*, TABLE 1 and TABLE 2. *See* also, 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.

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.

Embodiments of the invention, can include, but are not limited to, the detection of mRNA expression with probes specific for genes shown in TABLE 1 comprising genes overexpressed in B-lineage ALL. Other embodiments of the invention, can include, but are not limited to, the detection of mRNA expression with probes specific for genes shown in TABLE 2 comprising genes underexpressed in B-lineage ALL.

In embodiments of the invention, an expression profile is generated by the detection of nucleic acid corresponding to the expression of mRNA from a specimen. As a first step, a specimen is contacted with a set of probes to CD19 and CD10, wherein a first probe specifically binds to CD19 and a second probe specifically binds to CD10. As

a second step a CD19+/CD10+cell is isolated from said specimen. As a third step, an expression level of at least two gene products encoding CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a is determined in said CD19+/CD10+isolated cell population from step two. As a forth step, an expression profile is generated of the CD19+/CD10+cells of step two. The expression profile of step four, displaying a modulated level of at least one gene product, is indicative of minimal residual disease in acute lymphoblastic leukemia. In embodiments of the invention, modulation of the gene product detected from gene products encoding CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 and CD300a, relative to a normal control, is indicative of minimal residual disease in acute lymphoblastic leukemia.

As is well understood in the art and in yet other embodiments of the invention, various subsets of cells can be isolated for analysis, for example, it may be advantageous to compare CD19+, CD10- cells. In yet other embodiments, other combinations of probes may be included in the first step, for example, CD19, CD10, CD45, and CD34. For example, the subpopulations of cells that can be isolated by contacting a specimen with probes to markers CD19, CD10, CD45, and CD34 can include, but are not limited to: CD19+, CD10+ , CD45+, and CD34+ cells; CD19+, CD10- , CD45+, and CD34+ cells; CD19+, CD10- , CD45-, and CD34+ cells; CD19+, CD10- , CD45+, and CD34-; CD19+, CD10+ , CD45-, and CD34+ cells; CD19+, CD10+ , CD45+, and CD34-; and CD19+, CD10+ , CD45-, and CD34- cells. All of the preceeding subpopulations of cell can be isolated by contacting the specimen with said plurality of probes, but in addition, modulated activity of any one probe of that combination could also be selected thereby increasing the number of subpoplations analysed. The design of assays to optimize detection conditions and determining cell sorting conditions is standard and well within the routine capabilities of those of ordinary skill in the art.

In embodiments of the invention, determining the expression profile of the specimen that is CD10+/CD19+ further comprises probe combinations comprising (a) CD38, CD24, and CD44; (b) CD38, CD58, and CD44; (c) CD38, CD73, and CD15; (d)

CD38, CD200, and CD44; (e) CD66c, CD123, and CD86; (f) CD72, CD13, and CD33; or (g) CD79b, HSPB1, and Bcl-2. In embodiments of the invention said modulated level comprises overexpression of CD44, CD58, CD73, CD200, CD86, HSPB1, BCL2, CD164, CD97, CD99, or CD300a and/or the underexpression of CD38, CD72, or CD79b, relative to a normal control.

In embodiments of the invention, determining the expression level of a gene product in cells expressing each of CD19, CD10, CD34, and CD45, can further comprise probes to detect at least four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, twenty, twenty-one, or twenty-two markers comprising: CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a.

Protein Expression Profile and Antibody Detection

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, *i.e.*, 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.

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.

In embodiments of the invention, 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, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

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, NY), 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, NY); 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).

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. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia Recombinant Phage Antibody System, Catalog No. 27-9400-01; and the Stratagene SurfZAP™ Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in

generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication Nos. WO 92/18619; WO 91/17271; WO 92/20791; WO 92/15679; 93/01288; WO 92/01047; 92/09690; and 90/02809; Fuchs *et al.* (1991) Bio/Technology 9:1370-1372; Hay *et al.* (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse *et al.* (1989) Science 246:1275-1281; Griffiths *et al.* (1993) *EMBO J.* 12:725-734.

Antigen-binding fragments and variants of the monoclonal antibodies disclosed herein are contemplated and within the scope of the present invention. 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. See, for example, Walker and Gaastra, eds. (1983) Techniques in Molecular Biology (MacMillan Publishing Company, New York); Kunkel (1985) Proc. Natl. Acad. Sci. USA 82:488-492; Kunkel *et al.* (1987) Methods Enzymol. 154:367-382; Sambrook *et al.* (1989) Molecular Cloning: A Laboratory Manual (Cold Spring Harbor, New York); U.S. Patent No. 4,873,192; and the references cited therein; herein incorporated by reference. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the polypeptide of interest may be found in the model of Dayhoff *et al.* (1978) in Atlas of Protein Sequence and Structure (Natl. Biomed. Res. Found., Washington, D.C.), herein incorporated by reference. Conservative substitutions, such as exchanging one amino acid with another having similar properties, may be preferred.

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. For purposes of the present invention, percent sequence identity is determined using the Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension

penalty of 2, BLOSUM matrix of 62. The Smith-Waterman homology search algorithm is taught in Smith and Waterman (1981) Adv. Appl. Math. 2:482-489. A variant may, for example, differ from the reference antibody by as few as 1 to 15 amino acid residues, as few as 1 to 10 amino acid residues, such as 6-10, as few as 5, as few as 4, 3, 2, or even 1 amino acid residue.

In embodiments of the invention, 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.

In embodiments of the invention, antibodies specifically bind to and detect markers comprising CD44, BCL2, HSPB1, CD73, CD24, CD123, CD72, CD86, CD200, CD79b, CD164, CD304, CD97, CD102, CD99, CD300a, CD130, PBX1, CTNNA1, ITGB7, CD69, or CD49f.

In embodiments of the invention antibodies specifically bind to and detect markers comprising CD19, CD10, CD34, CD45, CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164,CD304, CD97, CD99, CD102 or CD300a.

Embodiments of the invention include antibodies described in TABLE 3, TABLE 4, and TABLE 5.

Optical Detection Methods:

Detection of antibodies can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance (i.e., 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 ^{125}I, ^{131}I, ^{35}S or ^{3}H. The skilled artisan will understand that additional moieties may be suitable for the method of the invention.

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.

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.

Methods and compositions for detectably labeling nucleic acid probes, such as oligonucleotides, DNA-RNA hybrids, etc. are well known in the art. See, e.g., U.S. Pat. Nos. 6,316,230; 6,297,016; 6,316,610; 6,060,240; 6,150,107; and 6,028,290, each of which is hereby incorporated by reference in their entirety.

The compositions of the invention 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 of the invention. Monoclonal antibodies having the binding characteristics of the antibodies disclosed herein are also encompassed by the present invention. Compositions further comprise antigen-binding variants and fragments of the monoclonal antibodies.

In embodiments of the invention, 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 of the invention 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.

"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.

The methods of the invention 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 ALL. Combinations of fluorophores or other detectable labels can be used by the methods on this invention, thereby greatly increasing the number of distinguishable signals in multicolor protocols.

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.

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, OR) and/or KALUZA™ software (Beckman Coulter, Miami, FL)(Campana, D. (2009) *Hematol Oncol Clin North Am.* 23;1083-98, vii).

In embodiments of the invention, determining an expression profile of a specimen is generated using combinations of probes that bind specifically to CD10, CD19, CD34, and CD45, wherein combinations comprise (a) CD10, CD19, CD34, CD45, CD38, CD24, and CD44; (b) CD10, CD19, CD34, CD45, CD38, CD58, and CD44; (c) CD10, CD19, CD34, CD45, CD38, CD73, and CD15; (d) CD10, CD19, CD34, CD45, CD38, CD200, and CD44; (e) CD10, CD19, CD34, CD45, CD66c,

CD123, and CD86; (f) CD10, CD19, CD34, CD45, CD72, CD13, and CD33; or (g) CD10, CD19, CD34, CD45, CD79b, HSPB1, and Bcl-2.

In other embodiments of the invention, antibodies can be directly conjugated for simultaneous detection. For example, a method of the invention can comprise antibodies directly conjugated to a detectable fluorochrome for simultaneous detection of a plurality of markers wherein: CD34 is conjugated to PerCP, CD19 is conjugated to APC, CD10 is conjugated to PE-Cy5, CD45 is coupled to APC-H7, CD38 is conjugated to FITC, CD24 is conjugated to PE, CD44 is conjugated to Horizon v450, CD58 is conjugated to PE, CD73 is conjugated to PE, CD15 is conjugated to Horizon v450, CD200 is conjugated to PE, CD66c is conjugated to FITC, CD123 is conjugated to PE, CD86 is conjugated to Horizon v450, CD72 is conjugated to FITC, CD13 is conjugated to PE, CD33 is conjugated to v450, CD79b is conjugated to FITC, HSPB1 is conjugated to PE, and Bcl2 is conjugated to Horizon V450. The skilled artisan will understand that any one antibody marker can be coupled to any fluorochrome for use in combination with any other antibody, and that preferred combinations can be used simultaneously with other antibody markers by the selection of different combinations of antibodies labeled with different flurochromes.

TABLE 3 shows exemplary marker combinations for detection of MRD in B-lineage ALL incorporating the top 10 differentially expressed markers including CD24, CD44, CD73, CD200, CD123, CD86, CD72, CD79b, HSPB1, and Bcl2.

TABLE 3: Marker combinations used for MRD studies in B-lineage ALL incorporating the top 10 differentially expressed markers discovered in this study (in *italics*)

FITC	PE	PerCP	APC	PE-Cy7	APC-H7	Horizon
CD38	*CD24*	CD34	CD19	CD10	CD45	*CD44*
CD38	CD58	CD34	CD19	CD10	CD45	*CD44*
CD38	*CD73*	CD34	CD19	CD10	CD45	CD15
CD38	*CD200*	CD34	CD19	CD10	CD45	*CD44*
CD66c	*CD123*	CD34	CD19	CD10	CD45	*CD86*
CD72	CD13	CD34	CD19	CD10	CD45	CD33
CD79b	*HSPB1*	CD34	CD19	CD10	CD45	*Bcl2*

Cell Sorting and Selection of Subpopulations of Cells in a Specimen

Multiparameter flow cytometric cell analysis can be used as part of the methods of this invention. 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.

In embodiments of the invention, 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 of the invention 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.

Multiparameter cell sorting can be used in an embodiment of the invention 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 andCD10the expression of other markers can be interrogated. In another embodiment of the invention, 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.

As is well understood in the art and in yet other embodiments of the invention, various subsets of cells can be isolated for analysis, for example, it may be advantageous to compare CD19+, CD10+ cells and CD19+, CD10- cells. Both subpopulations can be isolated by contacting the specimen with probes to CD19 and CD10, whereas in one condition cells are positively selected (CD19+, CD10+), and in the later, are negatively selected (CD19+, CD10-). Likewise, in yet other embodiments, other combinations of probes may be included in a first step, for example, CD19, CD10, CD45, and CD34, wherein modulated levels of CD45 and CD34 may be reflected in the subsets that are isolated. For example, the subpopulations of cells that could be isolated by contacting a specimen with probes to markers CD19, CD10, CD45, and CD34 could include, but are not limited to: CD19+, CD10+ , CD45+, and CD34+ cells; CD19+, CD10- , CD45+, and CD34+ cells; CD19+, CD10- , CD45-, and CD34+ cells; CD19+, CD10- , CD45+, and CD34-; CD19+, CD10+ , CD45-, and CD34+ cells; CD19+, CD10+ , CD45+, and CD34-; and CD19+, CD10+, CD45-, and CD34- cells. All the preceeding subpopulations of cell could be isolated from by contacting the specimen with said probes, but in addition, using flow cytometry for example, modulated activity could representative of a spectrum of expression to negative to positive, and also be selected. The number of potential subpopulations analyzed could thereby increase the number of subpoplations analysed. The design of assays to optimize detection conditions and determining cell

sorting conditions to isolate specific subpopulations of cells is standard and well within the routine capabilities of those of ordinary skill in the art.

In yet other embodiments of the invention, 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.

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 of the invention 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.

The skilled artisan will recognize that optimization of multiparameter assays designed to detect a plurality of antibody probes simultaneously will be necessary. In embodiments of the invention, 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 of the invention 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

The antibodies used to practice the invention 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 invention (see TABLE 4). The antibodies of the invention 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.

The markers and combinations of markers of the invention include genes or proteins that are selectively expressed, overexpressed or underexpressed in leukemia, and specifically in ALL, 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 of the invention, 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 of invention can comprise probes that can detect markers that include polypeptides and polynucleotides.

The methods of the invention can comprise MRD detection by gene array with preferred combinations of markers. MRD detection can be combined, for example, with at least 3 different marker combinations. Embodiments of the invention, can include, but are not limited to, the detection of mRNA expression with probes specific for genes shown in TABLE 1 comprising genes overexpressed in B-lineage ALL. Other embodiments of the invention, can include, but are not limited to, the detection of mRNA expression with probes specific for genes shown in TABLE 2 comprising genes underexpressed in B-lineage ALL.

Embodiments of the invention can include, but are not limited to, compositions and methods related to the detection of new markers for minimal residual disease (MRD) comprising: CD44, BCL2, HSPB1, CD73, CD24, CD123, CD72, CD86, CD200, CD79b, CD164, CD304, CD97, CD102, CD99, CD300a, CD130, PBX1, CTNNA1, ITGB7, CD69, or CD49f.

In yet other embodiments, diagnosing minimal residual disease in a sample taken from a subject can comprise the detection of combinations of markers including, but not limited to markers CD19, CD10, CD34, and CD45, in combination with markers comprising CD44, BCL2, HSPB1, CD73, CD24, CD123, CD72, CD86, CD200, CD79b, CD164, CD304, CD97, CD102, CD99, CD300a, CD130, PBX1, CTNNA1, ITGB7, CD69, or CD49f.

In yet other embodiments, diagnosing minimal residual disease in a sample taken from a subject can comprise the detection of combinations of markers including, but not limited to: CD19, CD10, CD34, and CD45, in combination with markers comprising CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a.

"CD" or "cluster designation" refers to a system to classify cell markers defining cells based on what molecules are present on their surface. These "cell markers" or "markers" are often used to associate cells with certain immune functions. While using one CD molecule to define populations is uncommon (though a few examples exist), combining markers is often used to identify cell types with very specific characteristics within the immune system. The system was originally intended for the classification of the monoclonal antibodies (mAbs) generated by different laboratories around the world against epitopes on the surface molecules of leukocytes (white blood cells). Since then, the use of the CD nomenclature has expanded to include many other cell types, and more than 320 CD unique clusters and subclusters have been identified. In some instances CD antigens are expressed only at certain stages of development or under certain conditions, for example after cell activation or in certain disease conditions. Unlike the morphological criteria used in classical hematology for the description of specific developmental stages of lymphocytes, the use of monoclonal antibodies, and the "CD"

marker annotation, allows the objective and precise analysis and standardized typing of mature and immature normal and malignant cells of all hematopoietic cell lineages. Antibodies that recognize cell surface markers can also be referred to by the CD designation. The CD designation can help to delineate the biologic traits that distinguish normal immune and hematopoietic cells from their malignant counterparts, which is of fundamental importance in understanding hematological malignancies.

The CD designation of molecules is often used to identify cells and expression patterns detected by various applications including flow cytometry. Very generally, cell populations can be defined using a '+' or a '–' symbol to indicate whether a certain cell fraction expresses or lacks a CD molecule. For example, a "CD34+, CD31–" cell is one that expresses CD34, but not CD31. This exemplary CD combination typically corresponds to a stem cell, opposed to a fully-differentiated endothelial cell. Therefore, generally speaking, use of CD with a number X, as in "CDX," can refer to a protein that in humans is encoded by the CDX gene, for example. Markers can be referred to by their CD designation, but can also be referred to by the gene or encoded protein name. Antibodies recognizing specific proteins can also be referred to by the CD number of the marker that is recognized.

CD34 (cluster designation 34) encompasses the human gene at locus 1q32 corresponding to sequences having GENBANK® Accession Nos: NM_001773, NP_001764.1. The protein is a monomeric cell surface antigen with a molecular mass of approximately 110 kDa that is selectively expressed on human hematopoietic progenitor cells.

CD19 (cluster designation 19) encompasses the human gene at locus 16p11.2 corresponding to sequences having GENBANK® Accession Nos: NM_001178098 and NP_001171569.1. CD19 is a cell surface molecule expressed only by B lymphocytes and follicular dendritic cells of the hematopoietic system. It is the earliest of the B-lineage-restricted antigens to be expressed and is present on most pre-B cells and most non-T-cell acute lymphocytic leukemia cells and B-cell type chronic lymphocytic leukemia cells (Tedder and Isaacs, 1989. *J. Immun.* 143: 712-717).

CD10 (cluster designation 10) encompasses the human gene at locus 3q21-q27 corresponding to sequences GENBANK® Accession Nos: NM_000902 and

NP_000893.2. The protein is also known as "membrane metallo-endopeptidase (MME)" or "common acute lymphocytic leukemia antigen (CALLA)." The common acute lymphocytic leukemia antigen (CALLA) is an important cell surface marker in the diagnosis of human acute lymphocytic leukemia (ALL). It is present on leukemic cells of pre-B phenotype, which represents 85% of cases of ALL. The CALLA gene encodes a 100 kDa type II transmembrane glycoprotein Barker *et al.* (1989) *J. Immun.* 142: 283-287.

CD45 (cluster designation 45), encompasses the human gene at locus 1q31-q32 corresponding to sequences having GENBANK® Accession Nos: NM_002838, NP_002829.2. CD45 is also called B220; CD45R; GP180; LCA; LY5; and T200. It is a membrane-bound protein tyrosine phosphatase expressed in various isoforms, of between 180 and 220 kDa in size. CD45 is expressed on virtually all leukocytes, including myeloid and lymphoid precursors in bone marrow and mature lymphocytes in lymph nodes. CD45 (T200) is expressed on all hematopoietic cells except mature red cells and their immediate progenitors. It is not found, however, on other differentiated tissues; thus, it can be used as an antigenic marker with which to identify undifferentiated hematopoietic tumors.

CD38 (cluster designation 38) encompasses the human gene at locus 4p15.32 corresponding to sequences having GENBANK® Accession Nos: NM_001775.2, NP_001766.2, as set forth in SEQ ID NO: 1 and SEQ ID NO:2, respectively. CD38 is commonly used as a human leukocyte differentiation marker and is a novel multifunctional ectoenzyme widely expressed in cells and tissues especially in leukocytes. CD38 also functions in cell adhesion, signal transduction and calcium signaling. It has been demonstrated to be involved in the synthesis and hydrolysis of Cyclic ADP-ribose (cADPR) (Takasawa *et al.* (1993). *J. Biol. Chem.* 268: 26052-26054, 1993). Cyclic ADP-ribose is generated in pancreatic islets by glucose stimulation, serving as a second messenger for Ca(2+) mobilization in the endoplasmic reticulum for secretion of insulin (Takasawa *et al.* (1993) *Science* 259: 370-373).

CD24 (cluster designation 24) encompasses the human gene at locus 6q21 corresponding to sequences having GENBANK® Accession Nos: NM_013230, NP_037362.1, as set forth in SEQ ID NO: 3 and SEQ ID NO:4, respectively. CD24 is

also known as "small cell lung carcinoma cluster 4 antigen" Studies with monoclonal antibodies indicate that most other hematopoietic cells, including T cells, monocytes, red blood cells, and platelets, seem not to express the CD24 antigen. CD24 has been implicated in both activation and differentiation of B lymphocytes because its expression pattern changes at critical times during B-cell development. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone ML5 which reacts with a 35-45 kDa two-chain glycoprotein (see TABLE 4, BD Pharmingen™ Cat. NO. 555428)(Schlossman *et al.* ed. (1995) *Leukocyte Typing V: White Cell Differentiation Antigens*. New York: Oxford University Press).

CD44 (cluster designation 44) encompasses the human gene at locus 11p13 corresponding to sequences having GENBANK® Accession Nos: NM_000610, NP_000601.3, as set forth in SEQ ID NO:5 and SEQ ID NO:6, respectively. It is also known as "Indian blood group" antigen. It is a receptor for hyaluronic acid and can also interact with other ligands, such as osteopontin, collagens, and matrix metalloproteinases (MMPs). This integral cell membrane glycoprotein participates in a wide variety of cellular functions including lymphocyte activation, recirculation and homing, hematopoiesis, and tumor metastasis (Aruffo *et al.* (1990) *Cell* 61: 1303-1313). In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone 515 which reacts with a 85 kDa glycoprotein expressed on leukocytes, erythrocytes, epithelial cells and weakly on platelets (see TABLE 4, BD Pharmingen™, Cat. NO. 5500989)(Patel *et al.* "CD44 Workshop Panel Report" In: Kishimoto *et al.* ed. (1997) *Leukocyte Typing Vi: White Cell Differentiation Antigens*. New York: Garland Publishing Inc: 373-375).

CD58 (cluster designation 58) encompasses the human gene at locus 1p13 corresponding to sequences having GENBANK® Accession Nos: NM_001779, NP_001770.1, as set forth in SEQ ID NO:7 and SEQ ID NO:8, respectively. CD58 is also known as "lymphocyte function-associated antigen (LFA3)". The CD58 gene encodes a CD2 receptor. The presence of these both CD2 and CD58 antigens on opposing cells optimizes immune recognition, facilitating contacts between helper T lymphocytes and antigen-presenting cells as well as between cytolytic effectors and target cells (Wang *et al.* (1999) *Cell* 97: 791-803).

CD73 (cluster designation 73) encompasses the human gene at locus 6q14-q21 corresponding to sequences having GENBANK® Accession Nos: NM_002526 and NP_002517.1, as set forth in SEQ ID NO:9 and SEQ ID NO:10, respectively. CD73 is a membrane-bound enzyme also known as "ecto-5-prime-nucleotidase," and is expressed on subsets of B-cells and T-cells as well as other cell types. The enzyme is used as a marker of lymphocyte differentiation. CD73 is thought to function as a cell adhesion molecule and to mediate lymphocyte binding to endothelial cells (Airas, L. *et al.* (1995) *J. Exp. Med.* 182(2): 1603-8) and adhesion between B-cells and follicular dendritic cells (Airas and Jalkanen (1996) *Blood.* 88(5):1755-64). In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone AD2 which reacts with a 70 kDa glycosyl phosphatidylinositol (GPI)-anchored glycoprotein expressed on subsets of T and B lymphocytes, follicular dendritic cells, epithelial cells, and endothelial cells (see TABLE 4, BD Pharmingen™, Cat. NO. 550257)(Schlossman *et al.* ed. (1995) *Leukocyte Typing V: White Cell Differentiation Antigens*. New York: Oxford University Press).

CD15 (cluster designation 15) encompasses the human gene at locus 11q12-qter corresponding to sequences having GENBANK® Accession Nos: NM_002033 and NP_002024.1, as set forth in SEQ ID NO:11 and SEQ ID NO:12, respectively. CD15 expresses a protein also known as "fucosyltransferase 4 (alpha (1,3)," "myeloid-specific fucosyltransferase," "ELAM ligand fucosyltransferase," and "galactoside 3-L-fucosyltransferase." The product of this gene transfers fucose to N-acetyllactosamine polysaccharides to generate fucosylated carbohydrate structures. CD15 catalyzes the synthesis of the non-sialylated antigen, Lewis x (CD15).

CD200 (cluster designation 200) encompasses the human gene located at locus 3q12-q13 corresponding to sequences having GENBANK® Accession Nos: NM_001004196 and NP_001004196.2, as set forth in SEQ ID NO:13 and SEQ ID NO:14, respectively. CD200 was identified as a type II membrane glycoprotein expressed on a number of cell types relevant to the inflammatory and immune cascade, including dendritic cells, endothelial cells, and activated T cells. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone MRC OX-104 which recognizes a 40-45 kDa membrane glycoprotein expressed on

resting and activated T cells and B cells, as well as a subset of CD34+ progenitor cells, but not on NK cells, monocytes, granulocytes, or platelets (see TABLE 4, BD Pharmingen™, Cat. NO. 552475)(Mason *et al.* ed. (2002) *Leukocyte Typing VII.* New York: Oxford University Press).

CD66c (cluster designation 66c) encompasses the human gene at locus 19q13.1-q13.2 corresponding to sequences having GENBANK® Accession Nos: NM_002483 and NP_002474.3, as set forth in SEQ ID NO:15 and SEQ ID NO:16, respectively. CD66c is also known as "carcinoembryonic antigen-related cell adhesion molecule." CD66c is one of the most widely used tumor markers in serum immunoassay determinations of carcinoma.

CD123 (cluster designation 123) encompasses the human gene at loci Xp22.3 and Yp13.3 corresponding to sequences having GENBANK® Accession Nos: NM_002183 and NP_002174.1, as set forth in SEQ ID NO:17 and SEQ ID NO:18, respectively. CD123 is also known as the low affinity receptor for IL-3 encoding an interleukin 3 specific subunit of a heterodimeric cytokine receptor. The receptor is comprised of a ligand specific alpha subunit and a signal transducing beta subunit shared by the receptors for interleukin 3 (IL3), colony stimulating factor 2 (CSF2/GM-CSF), and interleukin 5 (IL5). CD123 is expressed on a subset of peripheral blood dendritic cells, progenitor cells, monocytes, eosinophils, basophils, and hematopoietic cells, such as erythroid cells and B cells. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone 9F5 which reacts to the α-chain of the interleukin-3 receptor (IL-3Rα) expressed on a subset of peripheral blood dendritic cells, on a subset of progenitor cells, monocytes, eosinophils, and basophils (see TABLE 4, BD Pharmingen™, Cat. NO. 303545)(Sun *et al.* (1996) *Blood.* 87: 88-92).

CD86 (cluster designation 86) encompasses the human gene at locus 3q21 corresponding to sequences having GENBANK® Accession Nos: NM_006889 and NP_008820.3, as set forth in SEQ ID NO:19 and SEQ ID NO:20, respectively. CD86 encodes a type I membrane protein that is a member of the immunoglobulin superfamily. This protein is expressed by antigen-presenting cells, and it is the ligand for two proteins at the cell surface of T cells: CD28 antigen and cytotoxic T-lymphocyte-associated protein 4. Binding of this protein with CD28 antigen is a co-stimulatory signal for

activation of the T-cell. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone 2331 (FUN-1) which recognizes a 75 kDa cell surface protein expressed primarily on monocytes and activated B cells (see TABLE 4, BD Pharmingen™, Cat. NO. 555658)(Nozawa *et al.* (1993) *J Path.* 169(3):309-315).

CD72 (cluster designation 72) encompasses the human gene at locus 9p13.3 corresponding to sequences having GENBANK® Accession Nos: NM_001782 and NP_001773.1, as set forth in SEQ ID NO:21 and SEQ ID NO:22, respectively. CD72 is expressed on B cells and is the ligand for CD5. CD5 and/or CD72 engagement delivers critical co-stimulatory signals to B cells. It has been suggested that CD72 is a key molecule in regulating mature B cell differentiation, particularly in preventing the differentiation of naïve B cells into plasma cells (Yamazaki *et al.* (2005) *Eur. J. Immunol.*). In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone JA-117 which reacts with a 39-43 kDa type II integral membrane protein expressed on B cells from early precursor stages through mature B cells, although not on plasma cells (see TABLE 4, BD Pharmingen™, Cat. NO. 555918)(Schlossman *et al.* ed. (1995) *Leukocyte Typing V: White Cell Differentiation Antigens*. New York: Oxford University Press).

CD13 (cluster designation 13) encompasses the human gene at locus 15q25-q26 corresponding to sequences having GENBANK® Accession Nos: NM_001150 and NP_001141.2, as set forth in SEQ ID NO:23 and SEQ ID NO:24, respectively. CD13 encodes a surface antigen glycoprotein of about 150 kDa, also known as "aminopeptidase-N." CD13 is an enzyme thought to be involved in the metabolism of regulatory peptides expressed by diverse cell types, including small intestinal and renal tubular epithelial cells, macrophages, granulocytes, and synaptic membranes from the CNS. Defects in this gene appear to be a cause of various types of leukemia or lymphoma.

CD79b (cluster designation 79b) encompasses the human gene at locus 17q23 corresponding to sequences having GENBANK® Accession Nos: NM_000626 and NP_000617.1, as set forth in SEQ ID NO:25 and SEQ ID NO:26, respectively. CD79b is a B lymphocyte antigen receptor that is a multimeric complex that includes the antigen

specific component, surface immunoglobulin (Ig). Surface Ig non-covalently associates with two other proteins, Ig-alpha and Ig-beta, which are necessary for expression and function of the B-cell antigen receptor. The CD79b gene encodes the Ig-beta protein of the B-cell antigen component. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone AT107-2 which recognizes an immunogen peptide containing 20 amino acid residues derived from murine CD79b (NP_032365.1, NM_008339.2). The antibody is cross reactive with human, rat, pig, and dog CD79b (see TABLE 4, AbDserotec, Cat. NO. MCA2209FT)(Dornan *et al.* (2009) *Blood.* 114:2721-9; Vendel *et al.* (2009) *J. Immunol.* 182: 1509-17) .

CD33 (cluster designation 33) encompasses the human gene at locus 19q13.41 corresponding to sequences having GENBANK® Accession Nos: NM_001082618.1 and NP_001076087.1, as set forth in SEQ ID NO:27 and SEQ ID NO:28, respectively. CD33, or Siglec-3 is a transmembrane receptor expressed on cells of myeloid lineage. It is usually considered myeloid-specific, but it can also be found on some lymphoid cells. CD33 has been implicated in the negative regulation of cell proliferation of normal or leukemic myeloid cells. (Vitale *et al.* (1999) *PNAS.* 96, 15091-15096).

HSPB1 encompasses the human gene at locus 7q11.23 corresponding to sequences having GENBANK® Accession Nos: NM_001540 and NP_001531.1. HSPB1, as set forth in SEQ ID NO:29 and SEQ ID NO:30, respectively, is a gene that encodes the intercellular heat shock 27 kDa protein. Expression of this gene is induced by environmental stress and developmental changes. The encoded protein is involved in stress resistance and actin organization and translocates from the cytoplasm to the nucleus upon stress induction. Synthesis of the small (27-kDa) HSP has been shown to be correlated with the acquisition of thermotolerance. In some embodiments, the variants detected encompass an eptitope recognized by antibody HSP27, clone G3.1 conjugated to biotin that recognizes a 24-27 kDa hsp27 protein (early called 24K) expressed on approximately 50% of breast carcinomas and drug resistant cancer cells (See TABLE 4, Thermo Scientific, Cat. NO.MS-101-BO, -B1, or –B, for biotin labeled). In other embodiments, the variants encompass the eptitope recognized by the antibody HSPB1 derived from G3.1, conjugated to PE (see TABLE 4, Stressgen, Cat. NO. SPA-

800PE)(Edward *et al.* (1980) *Biochem Biophys Research Commun.* 93:804-812; Ciocca *et al.* (1991) *Breast Cancer Research and Treatment.* 20:33-42).

Bcl-2 (B-cell lymphoma 2) encompasses the human gene at locus 18q21.3 corresponding to sequences having GENBANK® Accession Nos: NM_000633 and NM_000657, and NP_000624.2 and NP_000648.2, as set forth in SEQ ID NO:31 and SEQ ID NO:33, and SEQ ID NO:32 and SEQ ID NO:34, respectively. This gene encodes an integral outer mitochondrial membrane protein that blocks the apoptotic death of some cells such as lymphocytes. Bcl-2 derives its name from B-cell lymphoma 2, as it is the second member of a range of proteins initially described in chromosomal translocations involving chromosomes 14 and 18 in follicular lymphomas. Constitutive expression of BCL2, such as in the case of translocation of BCL2 to Ig heavy chain locus, is thought to be the cause of follicular lymphoma. The Bcl-2 gene has been implicated in a number of cancers, including melanoma, breast, prostate, and lung carcinomas. It is also thought to be involved in resistance to conventional cancer treatment. Two transcript variants, produced by alternate splicing, differ in their C-terminal ends. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone 100 which is expressed in lymphocytes and monocytes but not appreciably in granulocytes (see TABLE 4, Invitrogen, Cat. NO. MHBLC014)(Hill *et al.* (1996) *Blood.* 88:1046).

CD164 (cluster designation 164) encompasses the human gene at locus 6q21 corresponding to sequences having GENBANK® Accession Nos: NM_006016 and NP_006007.2, as set forth in SEQ ID NO:35 and SEQ ID NO:36, respectively. CD164 is a type-I integral transmembrane sialomucin that functions as an adhesion receptor. Sialomucins are a heterogeneous group of secreted or membrane-associated mucins that appear to play two key but opposing roles in vivo: first as cytoprotective or anti-adhesive agents, and second as adhesion receptors. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone N6B6 which recognizes a 80-90 kDa mucin-like molecule present on CD34+ progenitor cells during the early stages of B cell, erythroid cell and myelomonocytic cell development. It is also expressed on epithelial cells, peripheral blood monocytes and weakly on lymphocytes

(see TABLE 4, BD Pharmingen™, Cat. NO. 551298)(Watt *et al.* (1998). *Blood* 92 (3):849–66; and Zannettino *et al.* (1998). *Blood.* 92 (8):2613–28).

CD304 (cluster designation 304) encompasses the human gene at locus 10p12 corresponding to sequences having GENBANK® Accession Nos: NM_001024628 and NP_001019799.1, as set forth in SEQ ID NO:37 and SEQ ID NO:38, respectively. CD304 is also known as "NRP1," "Neuropilin-1 (NP-1)," and "BDCA-4, "and encodes a protein with numerous functions. On neurons, it is a receptor for axon growth guidance class-3 semaphorins SEMA3A and plexin-1. On endothelial and some tumor cells it is a VEGF165 receptor, and on plasmacytoid dendritic cells it has a similar role to CD303 but does not decrease interferon production upon activation. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone AD5-17F6 (see TABLE 4, Miltenyi Biotec Cat. NO. 130-090-533)(Dzionek, A., *et al.* (2000) *J. Immunol.* 165:6037-6046.)

CD97 (cluster designation 97) encompasses the human gene at locus 19p13 corresponding to sequences having GENBANK® Accession Nos: NM_078481 and NP_510966.1, as set forth in SEQ ID NO:39 and SEQ ID NO:40, respectively. The encoded product is a glycoprotein present on the surface of most activated leukocytes and spans the membrane seven times, which is a defining feature of G protein-coupled receptors. The protein has an extended extracellular region with several N-terminal epidermal growth factor (EGF)-like domains, which mediate binding to its cellular ligand, decay accelerating factor (DAF, CD55), a regulatory protein of the complement cascade. The presence of structural features characteristic of extracellular matrix proteins and transmembrane proteins suggests that this protein is a receptor involved in both cell adhesion and signaling processes early after leukocyte activation. Alternative splicing has been observed for this gene and three variants have been found. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone VIM3b which recognizes a triplet of membrane proteins of 74, 80 and 89 kDa strongly expressed on phytohemagglutinin (PHA)-activated T and B cells, virtually all monocytes and granulocytes, and several cell lines including HL-60, THP-1, and K562. It is weakly expressed on resting lymphocytes (see TABLE 4, BD

Pharmingen™, Cat. NO. 555774)(Schlossman, *et al.* ed. (1995) *Leukocyte Typing V.* New York: Oxford University Press).

CD99 (cluster designation 99) encompasses the human gene at loci Xp22.32 and Yp11.3 corresponding to sequences having GENBANK® Accession Nos: NM_001122898 and NP_001116370.1, as set forth in SEQ ID NO:41 and SEQ ID NO:42, respectively. CD99 is a cell surface glycoprotein involved in leukocyte migration, T-cell adhesion, ganglioside GM1 and transmembrane protein transport, and T cell death by a caspase-independent pathway. Two transcript variants encoding different isoforms have been found for this gene. This variant 2 lacks an alternate in-frame exon compared to variant 1. The resulting isoform 2 has the same N- and C-termini but is shorter compared to isoform 1. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone TU12 which recognizes a 32 kDa sialoglycoprotein expressed on all leukocyte lineages, although is differentially expressed during T and B-lymphoid and granulocytic development, with higher densities being expressed during early hematopoietic stages (see TABLE 4, BD Pharmingen™, Cat. NO. 555689)(Knapp *et al*, ed. (1989) *Leucocyte Typing IV.* New York: Oxford University Press; 1989).

CD102 (cluster designation 102) encompasses the human gene at locus 17q23-q25 corresponding to sequences having GENBANK® Accession Nos: NM_000873 and NP_000864.2, as set forth in SEQ ID NO:43 and SEQ ID NO:44, respectively. CD102 is also known as intercellular adhesion molecule 2 (ICAM-2). This variant (5) differs in the 5' UTR compared to variant 1. All five variants encode the same protein. The protein encoded by this gene is a member of the intercellular adhesion molecule (ICAM) family. All ICAM proteins are type-I transmembrane glycoproteins, contain 2-9 immunoglobulin-like C2-type domains, and bind to the leukocyte adhesion LFA-1 protein. This protein may play a role in lymphocyte recirculation by blocking LFA-1-dependent cell adhesion. CD102 mediates adhesive interactions important for antigen-specific immune response, NK-cell mediated clearance, lymphocyte recirculation, and other cellular interactions important for immune response and surveillance. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone CBR-IC/2 which recognizes a type-I membrane glycoprotein with an

approximate molecular weight of 55-65kDa expressed on vascular endothelial cells, lymphocytes, monocytes, but not on granuloctyes. (see TABLE 4, BD Pharmingen™, Cat. NO. 558080)(Barclay *et al.* ed. (1997) *The Leukocyte Antigen FactsBook.* San Diego: Academic Press).

CD300a (cluster designation 300a) encompasses the human gene at locus 17q25.2 corresponding to sequences having GENBANK® Accession Nos: NM_007261 and NP_009192.2, as set forth in SEQ ID NO:45 and SEQ ID NO:46, respectively. CD300a also known as "inhibitory receptor protein (IRp60)" is a surface molecule of 60 kDa expressed by all human natural killer (NK) cells. The IRp60 gene, encodes a molecule that is highly O- and N-glycosylated, belonging to the immunoglobulin superfamily (Ig-SF). The ligand of the CD300a is still unknown but IRp60 does not appear to recognize HLA-class I molecules. In some embodiments, the variants detected encompass an eptitope recognized by the antibody derived from clone E59.126 expressed on T lymphocyte subsets, monocytes, and granulocytes (see TABLE 4, Beckman Coulter Cat. NO. A22328).

Intracellular Protein Targets

In some embodiments of the invention, 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.

In embodiments of the invention, 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.

TABLE 4: Antibodies against the new markers

Marker	Antibody	Clone	Conjugate	Source	Catalogue #	Positive Control	Negative Control*
CD44	CD44	515	PE	BD Biosciences	550989	Lymphocytes, monocytes	Jurkat cell line
BCL2	Anti-Human Bcl-2	100	PE	Invitrogen	MHBCL04	Lymphocytes, monocytes	Ramos cell line
HSPB1	HSP27	G3.1	Biotin	Lab Vision Corporation	MS-101	Monocytes	Lymphocytes
HSPB1	HSP27	G3.1	PE	Stressgen	SPA-800PE	Monocytes	Lymphocytes
CD73	CD73	AD2	PE	BD Biosciences	550257	Lymphocyte subset	Monocytes
CD24	CD24	ML5	PE	BD Biosciences	555428	B lymphocytes	T lymphocytes
CD123	CD123	9F5	PE	BD Biosciences	340545	Monocytes	T lymphocytes
CD72	CD72	J4-117	FITC	BD Biosciences	555918	B lymphocytes	T lymphocytes
CD86	CD86	2331	PE	BD Biosciences	555658	Monocytes	Lymphocytes
CD200	CD200	MRC OX-104	PE	BD Biosciences	552475	B lymphocytes	Monocytes
CD79B	CD79b	AT107-2	FITC	Serotec	MCA2209F	B lymphocytes	T lymphocytes
CD164	CD164	N6B6	PE	BD Biosciences	551298	Monocytes	Granulocytes
CD304	CD304	AD5-17F6	PE	Miltenyi Biotec inc	130-090-533	Dendritic cells (doubled with CD123)	Lymphocytes
CD97	CD97	VIM3b	PE	BD Biosciences	555774	Monocytes	Lymphocytes
ITG„7	Anti-Human Integrin „7	FIB504	PE	BD Biosciences	555945	Lymphocyte subset	Lymphocyte subset
CD102	CD102	CBR-IC2/2	PE	BD Biosciences	558080	Monocytes, lymphocytes	Granulocytes
CD99	CD99	TU12	PE	BD Biosciences	555689	T-ALL	Granulocytes

CD300a	Anti-IRp60	E59.126	PE	Beckman Coulter	A22328	Monocytes, lymphocyte subset	Lymphocyte subset
CD130	CD130	AM64	PE	BD Biosciences	555757	Monocytes, lymphocyte subset	B lymphocytes
PBX1	PBX1	4A2	None	Abnova	H00005087-M01	Cell line 697	Lymphocytes
CTNNA1	Anti-Human.	1G5	None	Abcam	Ab17259	Monocytes	Lymphocytes
CD69	CD69	L78	PE	BD Biosciences	341652	Activated lymphocytes	Non-activated lymphocytes
CD49f	CD49f	GoH3	PE	BD Biosciences	555736	Monocytes	Subset of lymphocytes
EPOR	Anti-Human Epo- R	38409	PE	R&D Systems	FAB307P	Subset of erythroblasts	Lymphocytes
CD1c	CD1c	AD5-8E7	PE	Miltenyi Biotec	130-090-508	B lymphocyte subset	Granulocytes
BCL11B	Anti-Human BCL11B	25B6	None	Abcam	Ab18465	Jurkat cell line	NALM6 cell line
CD120a	CD120a	H398	PE	Serotec	MCA1340PE	Monocytes	Lymphocyte subsets
CD37	CD37	BL14	PE	Beckman Coulter	IM0458	B lymphocytes	T lymphocytes
CD62L	CD62L	SK11	PE	BD Biosciences	341012	Monocytes, lymphoid subset	Lymphoid subset
CD132	CD132	AG184	PE	BD Biosciences	555900	Monocytes, lymphocyte subset	Lymphocyte subset
CD83	CD83	HB15a	PE	Beckman Coulter	IM2218	Tonsillar lymphocyte subset	Resting lymphocytes

IL13RA1	Anti-Human IL-13 Receptor .1	GM-1C8	None	Abcam	Ab3772	Monocytes	Lymphocytes
Secondary antibodies/reagent							
Goat F(Ab')2 Anti-Mouse IgG2a			PE	Southern Biotechnology Associates	1082-09		
Goat F(Ab')2 Anti-Mouse IgG1			FITC	Southern Biotechnology Associates	1072-02		
Goat F(Ab')2 Anti-Mouse IgG1			FITC	Southern Biotechnology Associates	1072-02		
Goat F(ab')2 Anti-Rat IgG Fc			PE	Jackson Immuno-Research Laboratories	112-116-071		
Streptavidin			PE	Jackson Immuno-Research Laboratories	016-110-084		

* Dim or no expression

TABLE 5. Standard marker combinations used to monitor MRD in childhood B-lineage ALL

FITC	PE	PerCP	APC
CD58	CD10	CD34	CD19
CD38	CD10	CD34	CD19
CD45	CD10	CD34	CD19
anti-TdT	CD10	CD34	CD19
CD13	CD10	CD34	CD19
anti-TdT*	anti-IgM	CD34	CD19
CD66c	CD10	CD34	CD19
CD33	CD10	CD34	CD19
CD15	CD10	CD34	CD19

*TdT, terminal deoxynucleotidyl transferase

RNA Expression Profiling:

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).

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 of the present

invention. Hybridization of an mRNA with the probe indicates that the marker in question is being expressed.

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 of the present invention.

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 of the invention, marker expression is assessed by quantitative fluorogenic RT-PCR (i.e., 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.

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. Patent 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.

In one embodiment of the invention, 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.

Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, e.g., U.S. Patent 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 herein incorporated by reference.

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 of the invention, RNA can be isolated from a subpopulation of cells with a characteristic expression profile, for example, cells co-expressing markers CD19 andCD10.

In embodiments of the invention, 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.

In embodiments of the invention, an mRNA probe set can include probes corresponding to those in TABLE 1 and TABLE 2. Embodiments of the invention, include but are not limited to the detection of markers and combinations of markers in TABLE 1 comprising genes overexpressed in B-lineage ALL. Embodiments of the invention, include but are not limited to the detection of markers and combinations of markers in TABLE 2 comprising genes underexpressed in B-lineage ALL.

Embodiments of the invention can include, but are not limited to, compositions and methods related to the detection of new markers for the detection of minimal residual disease (MRD) comprising: CD44, BCL2, HSPB1, CD73, CD24, CD123, CD72, CD86, CD200, CD79b, CD164, CD304, CD97, CD102, CD99, CD300a, CD130, PBX1, CTNNA1, ITGB7, CD69, or CD49f.

In embodiments of the invention, an expression profile is generated by the detection of nucleic acid corresponds to the expression of mRNA. Embodiments of the method comprise a method of diagnosing minimal residual disease in a subject by obtaining a specimen from the subject. The specimen is contacted with a plurality of probes, wherein each of the probes specifically binds to a distinct marker, wherein a first probe specifically binds to CD19 and a second probe specifically binds to CD10. A CD19+/ CD10+ cell is isolated from the specimen. An expression level of at least one, two, three, four, five, six or more gene products expressed in said CD19+, CD10+ cell is determined, wherein the at least one, two, three, four, five, six or more gene products encode CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a. An expression profile is then generated by combining the expression values of the gene products. In such methods, the expression of CD19 andCD10 and a modulated level of at least one gene products encoding CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164,CD304, CD97, CD99, CD102, or CD300a relative to a normal control is indicative of minimal residual disease in acute lymphoblastic leukemia.

Other embodiments of the method comprise contacting a specimen with a plurality of probes to detect expression levels of markers comprising CD19 andCD10 and at least four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen,

fifteen, sixteen, seventeen, eighteen, nineteen, twenty, twenty-one, or twenty-two markers comprising: CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a.

In embodiments of the invention, determining the expression profile of a specimen that is CD10+/ CD19+further comprises probe combinations comprising (a) CD38, CD24, and CD44; (b) CD38, CD58, and CD44; (c) CD38, CD73, and CD15; (d) CD38, CD200, and CD44; (e) CD66c, CD123, and CD86; (f) CD72, CD13, and CD33; or (g) CD79b, HSPB1, and Bcl-2.

In yet other embodiments of the invention, a kit for detecting minimal residual disease in a subject is disclosed. The kit can comprise a plurality of antibodies, antibody fragments, or molecular probes wherein each antibody, antibody fragment, or molecular probe is reactive to each of markers CD10, CD19, CD34, and CD45, and at least one additional of antibody, antibody fragment, or molecular probe that specifically binds to at least one additional marker comprising CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a. The kit can include at least one antibody, antibody fragment, or molecular probe that is detectably labeled. Embodiments of the invention include detectable labels, which can be, but are not limited to a radiolabel, a fluorophore, a peptide, an enzyme, a quantum dot, or a combination thereof.

In embodiments of the invention, a kit can comprise combinations of probes comprising (a) CD10, CD19, CD34, CD45, CD38, CD24, and CD44; (b) CD10, CD19, CD34, CD45, CD38, CD58, and CD44; (c) CD10, CD19, CD34, CD45, CD38, CD73, and CD15; (d) CD10, CD19, CD34, CD45, CD38, CD200, and CD44; (e) CD10, CD19, CD34, CD45, CD66c, CD123, and CD86; (f) CD10, CD19, CD34, CD45, CD72, CD13, and CD33; or (g) CD10, CD19, CD34, CD45, CD79b, HSPB1, and Bcl-2.

Data and Expression Profile Analysis

Any method known in the art for comparing two or more data sets to detect similarity and/or variance between them may be used to compare a subject expression profile to a normal expression profile. To determine whether two or more expression

profiles show statistically significant similarity and/or variance, statistical tests may be performed to determine whether any differences between the expression profiles are likely to have been achieved by a random event. Methods for comparing gene expression profiles to determine whether they share statistically significant similarity or variance are known in the art and also reviewed in Holloway *et al.* (2002) *Nature Genetics Suppl.* 32:481-89, Churchill (2002) *Nature Genetics Suppl.* 32:490-95, Quackenbush (2002) *Nature Genetics Suppl.* 32: 496-501; Slonim (2002) *Nature Genetics Suppl.* 32:502-08; and Chuaqui *et al.* (2002) *Nature Genetics Suppl.* 32:509-514; each of which is herein incorporated by reference in its entirety.

An expression profile is "distinguishable" or "statistically distinguishable" from a normal control expression profile according to the invention if the two expression profiles do not share statistically significant similarity.

Kits for Detection of Minimal Residual Disease

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

As used herein, "kit" refers to a set of reagents for the purpose of performing the method embodiments of the invention, 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 of the invention. The kit may be promoted, distributed, or sold as a unit for performing the methods of the present invention. Additionally, the kits may contain a package insert describing the kit and methods for its use.

In embodiments of the invention, 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.

The kit can comprise a plurality of antibodies, antibody fragments, or molecular probes wherein each antibody, antibody fragment, or molecular probe is specific for CD10, CD19, CD34, CD45, CD38, CD58, CD15, CD66c, CD13, CD33, CD44, BCL2, HSPB1, CD73, CD24, CD123, CD72, CD86, CD200, CD79b, CD164, CD304, CD97, CD102, CD99, CD300a, CD130, PBX1, CTNNA1, ITGB7, CD69, or CD49f.

The kit can comprise a plurality of antibodies, antibody fragments, or molecular probes wherein each antibody, antibody fragment, or molecular probe is reactive to each of markers CD10, CD19, CD34, and CD45, and at least one additional antibody, antibody fragment, or molecular probe that specifically binds to at least one additional marker comprising CD44, BCL2, HSPB1, CD73, CD24, CD123, CD72, CD86, CD200, CD79b, CD164, CD304, CD97, CD102, CD99, CD300a, CD130, PBX1, CTNNA1, ITGB7, CD69, or CD49f.

The kit can comprise a plurality of antibodies, antibody fragments, or molecular probes wherein each antibody, antibody fragment, or molecular probe is reactive to each of markers CD10, CD19, CD34, and CD45, and at least one additional antibody, antibody fragment, or molecular probe that specifically binds to at least one additional marker comprising CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164,CD304, CD97, CD99, CD102 or CD300a. The kit can include at least one antibody, antibody fragment, or molecular probe that is detectably labeled. Embodiments of the invention include detectable labels, which can be, but are not limited to a radiolabel, a fluorophore, a peptide, an enzyme, a quantum dot, or a combination thereof.

In embodiments of the invention, a kit can comprise combinations of probes comprising (a) CD10, CD19, CD34, CD45, CD38, CD24, and CD44; (b) CD10, CD19, CD34, CD45, CD38, CD58, and CD44; (c) CD10, CD19, CD34, CD45, CD38, CD73, and CD15; (d) CD10, CD19, CD34, CD45, CD38, CD200, and CD44; (e) CD10, CD19,

CD34, CD45, CD66c, CD123, and CD86; (f) CD10, CD19, CD34, CD45, CD72, CD13, and CD33; or (g) CD10, CD19, CD34, CD45, CD79b, HSPB1, and Bcl-2.

In yet another embodiment, a kit can comprises an array having a substrate with a plurality of addresses, where each address has a capture probe that can specifically bind a nucleic acid molecule comprising CD38, CD58, CD66c, CD79b, CD164, CD44, BCL2, HSPB1, CD72, CD73, CD24, CD123, CD86, CD200, CD304, CD97, CD99, CD102 or CD300a.

The methods of the invention can comprise MRD detection by gene array with preferred combinations of probes to specific markers. MRD detection can be combined, for example, with at least 3 different probes. Embodiments of the invention, can include, but are not limited to, the detection of mRNA expression with probes specific for genes shown in TABLE 1 comprising genes overexpressed in B-lineage ALL. Other embodiments of the invention, can include, but are not limited to, the detection of mRNA expression with probes specific for genes shown in TABLE 2 comprising genes underexpressed in B-lineage ALL.

One of skill in the art will further appreciate that any or all steps in the screening and diagnostic methods of the invention could be implemented by personnel or, alternatively, performed in an automated fashion. For example, the methods can be performed in an automated, semi-automated, or manual fashion, and as one-step or multi-step processes. Furthermore, the methods disclosed herein can also be combined with other methods known or later developed to permit a more accurate identification of patients having an increased likelihood of having minimal residual disease or a more reliable diagnosis of ALL.

The article “a” and “an” are used herein to refer to one or more than one (i.e., to at least one) of the grammatical object of the article. By way of example, “an element” means one or more element.

Throughout the specification the word "comprising," or variations such as “comprises” or “comprising,” will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

Embodiments of the present invention are further defined in the following Examples. It should be understood that these Examples are given by way of illustration only. From the above discussion and these Examples, one skilled in the art can ascertain the essential characteristics of this invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the embodiments of the invention to adapt it to various usages and conditions. Thus, various modifications of the embodiments of the invention, in addition to those shown and described herein, will be apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims.

EXPERIMENTAL

Patients

Bone marrow samples were collected at presentation from 470 patients aged <1 to 18 years with newly diagnosed B-lineage ALL; 270 samples were included in genome-wide gene expression studies, and 200 were tested to validate the gene expression findings by flow cytometry. Bone marrow samples were obtained during therapy in 51 patients and samples obtained at relapse in 9. The diagnosis of B-lineage ALL was unequivocal and based on morphology, cytochemistry and cell marker expression. To determine gene expression and immunophenotype of normal lymphoid progenitors, bone marrow samples were collected from 22 healthy donors aged 2-25 yrs (median, 10 yrs) during the harvest of bone marrow for stem cell transplantation, and bone marrow samples obtained from 27 patients with B-lineage ALL, 7 with T-lineage ALL and 5 with acute myeloid leukemia (AML) during therapy.

Sample Preparation

Leukemic and normal mononuclear cells were collected after centrifugation on a density gradient (AccuPrep, Nycomed, Oslo, Norway) and washed three times in phosphate-buffered saline (PBS). Leukemic cells used in gene expression studies were cryopreserved. Normal bone marrow CD19+ cells used for gene expression analysis were first enriched using a MACS separation system (Miltenyi Biotec, Auburn, CA)

from fresh samples, yielding >98% CD19+ cell purity. Cells were then stained with anti-CD19 conjugated to phycoerythrin (PE) and anti-CD10 conjugated to fluorescein isothiocyanate (FITC; both from Becton Dickinson, San Jose, CA) and CD19+CD10+ cells were sorted using a MoFlo high-speed fluorescence-activated cell sorter (CYTOMATION®, Fort Collins, CO). All samples were processed or cryopreserved within 5 hours of collection.

Flow cytometric analysis and MRD studies

Flow cytometry using the antibodies listed in TABLES 3-5 were used to verify the differential expression of gene products in ALL cells. In most tests, the antibodies were used in combination with anti-CD19 conjugated to allophycocyanin (APC), anti-CD10 conjugated to either FITC or PE, and anti-CD34 conjugated to peridinin chlorophyll protein (PerCP). Isotype-matched nonreactive antibodies were used as controls. For cell staining, 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% paraformaldehyde. For intracellular markers, cells were permeabilized and fixed before exposure to antibodies using a permeablization reagent 8E. Measurements of antibody labeling were performed by multiparameter flow cytometry, using a FACSCALIBER® flow cytometer (Becton Dickinson, San Jose, CA).

Studies of MRD by flow cytometry were performed using combinations of monoclonal antibodies that identified leukemia -associated immunophenotypes determined at diagnosis. Cell staining was essentially performed as described above, using a combination of 4 markers simultaneously (see TABLE 4) and, where indicated, with 6-marker combinations (SEE TABLE 3). Data acquisition and analysis was done as previously described, using BD FACSCALIBER™ LSRII flow cytometers (Becton Dickinson), BD CELLQUEST Pro™, BD FACSDiVA™ software (both from Becton Dickinson), FlowJo software (Tree Star, Ashland, OR) and/or Kaluza™ software (Beckman Coulter, Miami, FL). Determination of MRD by PCR amplification of immunoglobulin and T-cell receptor genes was done as previously described (Stow. P.

(2010) *Blood.*115:4657-4663). The results of MRD studies by the two methods were recorded independently.

Example 1. Identification of genes differentially expressed in leukemic and normal immature B cells

Gene expression arrays studies

A first-generation gene array study was previously performed (Chen *et al.* (2001) *Blood.* 97:2115-2120) and as previously described (Ross *et al.* (2003) *Blood.* 102:2951-2959). In Chen *et al.*, diagnostic ALL samples from 4 patients were compared to $CD19^+$ $CD10^+$ bone marrow immature B cells taken from 2 healthy donors. The array contained probes for approximately 4000 genes.

In an embodiment of the invention, a gene expression array probing over 23,000 genes was used to screen a larger set of samples, including 270 cases of B-lineage ALL. The B-lineage ALLs encompassed the spectrum of genetic abnormalities occurring in ALL and were included to specifically identify other prognostic markers. Briefly, total RNA was isolated from freshly thawed B-lineage ALL cells and flow sorted normal CD19+CD10+ cells using the TRIZOL® reagent (Invitrogen, Carlsbad, CA). After generating cDNA, biotin-labeled cRNA was prepared according to the protocols of Affymetrix (Santa Clara, CA). The solutions were hybridized to HG-U133A oligonucleotide microarrays (Affymetrix). After staining with phycoerythrin-conjugated streptavidin, the arrays were read with a laser confocal scanner (Agilent, Palo Alto, CA). Signal values were computed from the image files using Affymetrix GENECHIP® Operating Software. Intensity values for a total of 22,283 probe sets on the U133A microarray were obtained (See Affymetrix Data Sheet (Part No. 701484 Rev. 4 (2003-2004), Santa Clara, CA, USA, GENECHIP® Human Genome U133A 2.0 Array, Part Nos. #900471, 468, 469)

Expression data was generated using genome-wide expression data detected from 270 B-lineage ALL samples and CD19+CD10+ lymphoid progenitors obtained from the bone marrow of 4 healthy donors. Of the 23, 000 genes compared, a total of 133 probe sets (corresponding to 112 genes, TABLE 1) had signals higher than 2-fold of the highest value obtained among normal CD19+CD10+ cells in 75% or more of ALL cases studied.

Conversely, 192 probe sets (corresponding to 165, TABLE 2) had signals at least 50% lower than the lowest signal among the normal CD19+CD10+ cells in 75% or more of ALL cases. When the criteria for inclusion was extended to genes that were differentially expressed in at least 25% of ALL cases, 1405 probe sets were over-expressed and 1474 were under-expressed. The results are summarized in TABLES 1 and 2.

Among the genes that were differentially expressed, some had been previously identified as abnormally expressed in ALL cells. For example, CD58 was over-expressed in 81.9% of cases (See also Chen J.S., *et al.* (2001) *Blood.* 97:2115-2120), and WT1 in 32.6% of cases (See also Ogawa *et al.* (2002) *Blood.* 101:1698-1704) whereas PAX5 was under-expressed in 86.7% and CD38 in 73.7% of cases (See also Coustan-Smith *et al.* (2002) *Blood.* 100:52-58). Among the 23 ALL specimens with MLL gene rearrangements, 100% over-expressed galectin-1 and 91.3% under-expressed CD10, characteristic features of this subset of ALL (See also Juszczynski *et al.* (2010) *Clin Cancer Res.* 16:2122-2130; Pui *et al.* (1994) *J.Clin.Oncol.*12:909-915); most of these cases also over-expressed a cohort of genes (*e.g.*, FLT3, LMO2, ADAM10, MEIS1) previously reported to be associated with MLL-rearranged leukemia (see also Ferrando *et al.* (2003) *Blood.* 102:262-268).

All 26 cases with TCF3-PBX1 over-expressed PBX1 (See also Kamps *et al.* (1991). *Genes Dev.* 5:358-368), and, among the 62 cases with ETV6-RUNX1, 46.8% over-expressed CD13 and 29.0% CD33 (Baruchel *et al.* (1997) *Br J Haematol.* 99:101-106).

Example 2. Validation of gene expression array results by flow cytometry

Among the genes differentially expressed by gene array analysis, there were some already widely used for MRD studies by flow cytometry, *i.e.*, CD58, CD38, CD13, and CD34, suggesting the possibility that other useful markers could be present among the remaining genes (Basso *et al.* (2009) *J Clin Oncol.* 27:5168-5174; Lucio *et al.* (2001) *Leukemia.* 15:1185- 1192; Chen *et al.* (2001) *Blood.* 97:2115-2120; Coustan-Smith *et al.* (2002) *Blood.* 100:52-58).

To prioritize genes for validation by flow cytometry, an initial inclusion criteria was applied: a) differential expression in at least 25% of cases of ALL, or 40% of cases

of a genetic subtype of ALL; b) over-expression in leukemic cells by at least 3-fold of the maximum value in normal cells, or under-expression by 3-fold of the minimum value in normal cells; and c) commercial availability of specific antibodies conjugated to fluorochromes suitable for flow cytometry. Guided by these criteria, 30 genes (25 overexpressed in ALL and 5 underexpressed) were selected (TABLE 6) and compared to determine whether the differential expression measured by microarray analysis at the mRNA level corresponded to differential expression of the encoded proteins.

After confirming the specificity of the antibodies with known positive and negative target cells (TABLE 6), the antibodies were tested for reactivity using ALL samples obtained at diagnosis (n = 200) and leukemia-free bone marrow samples (n = 61). Importantly, comparisons included not only bone marrow specimens from healthy donors (n = 22) but also bone marrow from children with ALL (MRD-negative according to PCR amplification of antigen-receptor genes) and AML (MRD negative by flow cytometry) during chemotherapy (n = 39), some with a high proportion of hematogones. When the overall expression in the ALL versus normal CD19+ CD10+ B-cell progenitor groups were compared the difference in overall expression was statistically significant ($P < 0.05$) for 13 of the 30 markers tested. Additionally, 11 of the 25 proteins encoded by the over-expressed genes were expressed at a significantly higher level in B-lineage ALL cells, while 2 of the 5 proteins encoded by under-expressed genes had a significantly lower expression (Fig. 1).

TABLE 6. Expression level in ALL cells and normal $CD19^+CD10^+$ cells of the genes selected for study

Probeset	Gene symbol/CD number	Range expression in normal $CD19^+$ $CD10^+$ (n = 4)[1]		Range expression in ALL (n = 270)[1]		% ALL cases with higher/lower expression
		Min	Max	Min	Max	
Overexpressed in ALL						
203685_at	BCL2	149.1	229	150.1	5203.8	90%
201841_s_at	HSPB1	15.6	302	36.4	8938.9	87%
207643_s_at	TNFRSF1A/ CD120a	94.4	234.7	28	3029.5	84%
209933_s_at	CD300A	59.1	126.1	29.3	1481.7	81%
202910_s_at	CD97	149.2	303.4	31.5	6537	80%
212298_at	NRP1/CD304	5.6	10.6	3.3	2155.1	80%
204563_at	SELL/CD62L	288.1	415.7	205	16680.8	79%
210916_s_at	CD44	40.8	109.2	18.8	4864.2	78%
215177_s_at	ITGA6/CD49f	31.5	145.9	14.6	12400.9	75%
209583_s_at	CD200	313.2	423.9	42.3	3955.4	72%
203939_at	NT5E/CD73	54.3	121.1	5	5133.9	67%
213620_s_at	ICAM2/CD102	871.1	983	233.8	7321.1	65%
210895_s_at	CD86	31.9	106.9	13.6	1392.7	60%
204116_at	IL2RG/CD132	604	1213.2	574.9	8123.4	56%
201028_s_at	CD99	1148.8	2047.8	325.4	19384.2	50%
201887_at	IL13RA1	81.2	159.2	30.4	2829.5	41% (59% of *BCR-ABL1*)
208654_s_at	CD164	754.9	1274.4	667.6	15234.8	39% (71%of hyperdiploid; 59% of *BCR-ABL1*)
209963_s_at	EPOR	49.4	127.9	17.8	1950.4	36%
212151_at	PBX1	30.4	114.4	16.5	10825.3	36% (100% of *TCF3-PBX1)*
205987_at	CD1C	16	249.7	9.7	7020.6	27% (71% of hyperdiploid)
204863_s_at	IL6ST/CD130	119.4	160.9	8.5	837.1	27%
205718_at	ITGB7	12.1	208.5	10.9	3223.5	25% (50% of *BCR-ABL1*)
206148_at	IL3RA/CD123	53.6	260.6	18.7	3497.2	22% (71% of hyperdiploid)

208651_x_at	CD24	3125.7	4310.4	258.6	14231.4	17% (54% of *TCF3-PBX1*)
209617_s_at	CTNNA1	23.3	68.7	6	424.5	9% (40.3% of *ETV6-RUNX1*)
Underexpressed in ALL						
205297_s_at	CD79B	11257.6	17637	19.1	8701	96%
204440_at	CD83	1759.5	4557.9	47.8	9729.2	91%
209795_at	CD69	6458.6	7502.8	31.6	16301.1	77%
204192_at	CD37	5624.7	13251.7	225.6	10302.9	67% (81% of *ETV6-RUNX1*)
215925_s_at	CD72	1888.1	4238.1	9.1	4968.5	57%

[1]Data expressed as units calculated by MAS5.0 to a median target intensity of 500.

Figure 1 shows the differential expression of markers in ALL cells compared to CD19+ CD10+ B cell progenitors. Shown are mean fluorescence intensity (MFI) values obtained in CD19+ leukemic lymphoblasts from bone marrow samples of patients with newly diagnosed ALL ("L") and bone marrow CD19+CD10+ cells from healthy donors or from patients with leukemia in remission and no evidence of MRD ("N"). Each symbol indicates results of one sample; horizontal bars correspond to median values within each group

For the remaining 17 markers, the difference in overall expression between ALL cells and normal B-cell progenitors was not statistically significant (Fig. 2). Figure 2 shows markers that were not expressed at levels significantly different ($P > 0.05$) in ALL cells and CD19+CD10+ B-cell progenitors as determined by flow cytometry. Shown are mean fluorescence intensity (MFI) values obtained in CD19+ leukemic lymphoblasts from bone marrow samples of patients with newly diagnosed ALL ("L") and bone marrow CD19+CD10+ cells from healthy donors or from patients with leukemia in remission and no evidence of MRD ("N"). Each symbol indicates results of one sample; horizontal bars correspond to median values within each group.

However, some these later markers were found to be overexpressed when the mean fluorescent intensity MFI values were compared to normal controls. For example, in some cases the MFI values of a marker in ALL specimens was higher than the highest mean fluorescence intensity (MFI) value recorded among normal B-cell progenitors. In other ALL specimens, markers were found to be underexpressed in ALL cells. For markers that were under-expressed in ALL cells, for example, specimens had at least 50% lower MFI values compared to the lowest MFI measured in normal B-cell progenitors. Using MFI levels as a criteria for differential expression, a substantial proportion of ALL cases expressed markers whose MFI values that were higher or lower than that of normal B cell progenitors. Overall, 22 of the 30 markers were found differentially expressed in 5%-81.4% (median, 35%) of cases These results are summarized in TABLE 6.

For example, CD44 was differentially expressed in 81.4% cases studied, BCL2 was over-expressed in 76.6%, HSPB1 (heat shock protein 27) in 63.4% and CD73 in 54.5%. Notably, CD44 and CD24 were over-expressed in some cases and under-expressed in others. Importantly, some of the markers, such as CD97, CD99 and CD102 appeared to be over-expressed in a much larger proportion of cases when the

comparisons included only resting bone marrow samples. However, when regenerating specimens rich in hematogones were included, it became clear that expression in leukemic cells for many of these cases was not outside the range of normality. Of the 30 markers studied, only 8 (EPOR, CD1c, CD120a, CD37, CD62L, CD132, CD83 and IL13RA1) showed no clear differential expression by the above criteria and were excluded from further studies.

Example 3: Validation of the new markers for MRD detection

To determine the reliability of the new markers to identify leukemic cells in clinical samples, 128 bone marrow samples were collected during treatment (46 during or at the end of remission induction therapy and 82 during post-remission therapy) from 51 patients with B-lineage ALL in whom expression of the markers on the leukemic cells had been measured at diagnosis. The markers included in these studies were the top 16 differentially expressed markers listed in TABLE 7, for a total of 258 tests.

Newly identified markers (TABLE 3, 4) were compared to standard marker combinations presently used in for MRD detection (TABLE 5). Using a threshold of 0.01% ALL cells to define MRD positivity, no discordant results were observed except for one comparison in which MRD was negative with the standard markers and 0.012% with the new markers. Overall, there was an excellent correlation in MRD estimates between new and standard markers ($r = 0.9816$, $P < 0.0001$ by Spearman's regression analysis of the MRD-positive tests; Fig. 3).

Figure 3 graphically illustrates the relationship between results of MRD monitoring using flow cytometry targeting the new markers and those of PCR amplification of antigen-receptor genes. Each symbol on the graph represents results obtained by 4-color flow cytometry including antibodies against CD19, CD10, CD34 and one of the new markers; $r = 0.8178$, $P < 0.0001$ by Spearman's regression analysis of the positive MRD results. The dashed line is the line of identity.

In a subset of 52 samples from 18 patients studied with some of the markers (CD44, BCL2, HSPB1, CD73, CD24, CD123, CD86, CD200, CD304, CD97, CD99,

TABLE 7. Expression of the new markers in ALL cells relative to their expression in bone marrow $CD19^+$ $CD10^+$ cells from healthy individuals as determined by flow cytometry

Marker	Number of ALL cases studied	Number of cases with overexpression (%)[1]	Number of cases with underexpression (%)[2]
CD44	86	46 (53.5%)	24 (27.9%)
BCL2	77	59 (76.6%)	-
HSPB1	93	59 (63.4%)	-
CD73	77	42 (54.5%)	-
CD24	139	16 (11.5%)	55 (39.6%)
CD123	142	72 (50.7%)	-
CD72	45	-	22 (48.9%)
CD86	135	63 (46.7%)	-
CD200	95	41 (43.2%)	-
CD79b	74	-	31 (41.9%)
CD164	75	31 (41.3%)	-
CD304	129	37 (28.7%)	-
CD97	81	22 (27.2%)	-
CD102	76	15 (19.7%)	2 (2.6%)
CD99	77	17 (22.1%)	-
CD300A	92	18 (19.6%)	-
CD130	71	12 (16.9%)	-
PBX1	64	4 (11.8%)	-
CTNNA1	44	4 (9.1%)	-
ITGB7	90	7 (7.8%)	-
CD69	33	2 (6.1%)	-
CD49f	38	2 (5.3%)	-
EPOR	45	2 (4.4%)	-
CD1C	86	3 (3.5%)	-
CD120a	35	1 (<2.9%)	-
CD37	46	1 (<2.2%)	-
CD62L	34	0	-
CD132	33	0	-
CD83	33	0	-
IL13RA1	10	0	-

[1] 1 Number of ALL cases that expressed the indicated marker at levels higher than the highest mean fluorescence intensity (MFI) value recorded among normal B-cell progenitors, and had an MFI higher than 10.

2 Number of ALL cases that expressed the indicated marker at levels lower than the lowest MFI measured in normal B-cell progenitors, excluded cases in which a marker had an MFI lower than 10 on normal B-cell progenitors.

CD102 and CD300a), MRD estimates by PCR amplification of clonally rearranged immunoglobulin and T-cell receptor genes were also available. Using the threshold of 0.01% ALL cells to define MRD positivity, MRD was negative (<0.01%) by flow cytometry and PCR analysis in 35 of the 52 samples studied. By contrast, MRD was ≥ 0.01% according to both methods in 15 samples. Two additional samples had MRD ≥0.01% by flow cytometry while PCR showed detectable signals but below the 0.01% threshold: 0.007% and 0.003%. Among the 101 tests performed, MRD was <0.01% by flow cytometry in 63 and ≥0.01% in 38, with a good correlation in the MRD positive estimates by the two techniques ($r = 0.8178$, $P < 0.0001$). Two samples had MRD ≥0.01% by flow cytometry (1 tested with two markers) and also had positive PCR but below the 0.01% threshold.

To determine stability of the new markers during the course of the disease, a prerequisite for reliable MRD tracking (Gaipa *et al.* (2005) *Leukemia.* 19:49-56) the level of expression was compared to that recorded during MRD monitoring in 10 patients who had persistent MRD during remission induction therapy (day 19 and 42 from diagnosis). Fig. 4 illustrates the results obtained in 4 representative cases showing the expression of the new markers before, during and at the end of remission induction therapy.

The long-term stability of the markers was assessed by comparing the immunophenotype of paired samples collected at diagnosis and relapse from nine patients whose leukemic cells at diagnosis expressed some of the newly identified markers identified. In Fig. 4 symbols indicate mean fluorescence intensity (MFI) of each marker as measured on ALL cells at diagnosis and on residual leukemic lymphoblasts detected on days 19 and 42 of remission induction therapy. At all time points, all markers were expressed at levels that exceeded those measured in normal CD19+CD10+ cells. Although levels of expression fluctuated during therapy, they consistently remained outside the range of normality in all cases studied.

As shown in TABLE 8, abnormal marker expression at diagnosis reverted to expression within the normal range at relapse in 7 of 55 (12.7%) of comparisons. In the remaining cases, marker expression remained abnormal. Importantly, in all 9 patients studied at least one marker remained abnormally expressed at relapse. In 58 additional comparisons where the markers at diagnosis were within the normal range, there were 10 instances (17.2%) in which expression became abnormal at relapse. These results suggest

that false-negative results due to phenotypic shifts affecting these markers would be unlikely.

TABLE 8. Expression of new markers in paired samples of B-lineage ALL collected at diagnosis (D) and at relapse (R)[1]

Marker	Patient 1		Patient 2		Patient 3		Patient 4		Patient 5		Patient 6		Patient 7		Patient 8		Patient 9	
	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R
CD44	-	-	233	235	372	-[2]	325	-[2]	-	-	-	-	3	4	208	93	292	307
BCL2	254	249	240	262	-	-	286	326	144	137	332	562	150	151	87	137	273	188
HSPB1	18	47	44	94	-	74[3]	169	143	141	165	64	351	23	267	15	158	80	36
CD73	30	39	37	64	56	149	29	105	-	-	95	30	33	-[2]	168	33	103	63
CD24	-	-	338	504	-	333[3]	204	146	104	2	-	277[3]	-	-	-	-	-	77[3]
CD123	-	-	62	31	-	-	45	133	-	-	-	-	-	-	-	-	-	25[3]
CD72	6	7	NT	NT	NT	NT	-	-	-	-	5	3	8	13	6	6	4	4
CD86	-	-	26	23	-	-	33	-[2]	-	-	-	-	-	-	-	-	-	-
CD200	86	65	107	88	-	-	80	201	260	154	-	-	102	126	-	72[3]	83	-2
CD164	-	-	18	49	-	-	-	-	-	-	-	-	-	29[3]	NT	NT	NT	NT
CD97	-	-	119	53	-	-	84	200	-	-	-	54[3]	-	-	-	-	-	-
CD102	-	-	-	-	-	-	96	92	-	-	-	-	-	100[3]	-	-	-	136[3]
CD99	-	-	-	-	-	-	-	329[3]	184	-[2]	124	-[2]	-	-	-	-	122	488

NT, not tested

1 Values indicate MFI as determined by flow cytometry. Dash indicates MFI within the normal range

2 Significant change in expression: from abnormal expression at diagnosis to expression within the normal range at relapse

3 Significant change in expression: from expression within the normal range at diagnosis to abnormal expression at relapse

Example 4. Association of the new markers with genetic subtypes of ALL

The new markers used in embodiments of the invention were associated with known genetic subtypes of ALL, including hyperdiploidy (51-65 chromosomes), ETV6-RUNX1, TCF3-PBX1, BCR-ABL1, or MLL gene rearrangements. Figure 5 shows the results of this analysis as a heat map including markers that were differentially expressed in at least 20% of cases. The heatmap graphically displays the percentage of cases among the main genetic subtypes of childhood ALL in which the markers studied were differentially expressed by flow cytometry. Percentages refer to cases in which each marker was over-expressed in ALL cases as compared to CD19+CD10+ cells from non-leukemic bone marrow samples; markers under-expressed in ALL cells are indicated by "u".

Expression of some markers was clearly related to ALL genetic subtype. For example, among hyperdiploid (51-65 chromosomes) ALL cases, there was a significantly higher prevalence of CD123 ($P < 0.0001$ by Fisher's exact test), CD86 ($P < 0.0001$), CD200 ($P = 0.0003$) and CD97 ($P < 0.0001$) over-expression as compared to the other cases without this genetic abnormality. Among cases with ETV6-RUNX1, there was a higher prevalence of CD200 over-expression ($P < 0.0001$), and of CD44 ($P < 0.0001$), CD72 ($P = 0.0073$) and CD79b ($P = 0.0109$) under-expression. Finally, abnormal expression of CD164 was most prevalent among cases lacking all the genetic abnormalities analyzed ($P = 0.002$).

Example 5: Comparisons between new markers and established leukemia-associated immunophenotypes

In a proportion of patients with ALL, MRD cannot currently be monitored because of the lack of suitable immunophenotypes differentiating ALL from normal controls. (Campana (2009) *Hematol.Oncol Clin North Am.* 23:1083-98, vii; Bruggemann *et al.* (2010) *Leukemia.* 24:521-535) In other patients, leukemic cells express only one set of markers, and have an increased risk of false-negative MRD results due to immunophenotypic shifts (Coustan-Smith *et al.* (1998) *Lancet.* 351:550-554). The availability of the additional markers of embodiments of the invention enables MRD studies in patients whose ALL cells currently lack suitable leukemia-associated immunophenotypes and minimize the risk of false-negative results.

Using a method of the invention, expression profiling was used to evaluate 171 ALL diagnostic samples including: 11 subjects lacking detectable leukemia-associated immunophenotypes with the standard panel of antibodies; and another 37 subjects having only one immunophenotypic abnormality detectable with the standard panel.

In contrast to the standard method, the method of the present invention detected a phenotypic abnormality indicative of MRD in all of the 11 cases previously lacking a leukemia-associated immunophenotype. Moreover, the method of the present invention identified additional abnormalities in 36 of the 37 cases with one standard abnormality. Thus, the new markers substantially improved the potential for flow cytometric monitoring of MRD in 47 of 48 cases that could not be adequately studied previously. The number of new markers differentially expressed ranged from two to twelve (median, six). In 45 of the 47 cases, one or more markers were expressed at levels that exceeded by at least two-fold the normal range, allowing a particularly clear identification of ALL cells.

The availability of additional markers of leukemia improved the resolution of leukemic and normal cells during flow cytometric analysis. This was clearly demonstrated in experiments in which mixtures of leukemia and normal cells were analyzed using either one standard phenotypic abnormality (*e.g.*, under-expression of CD38), or additional abnormalities revealed by the new markers. An example of such an experiment is shown in Fig. 6.

Fig. 6 shows an example of the comparison of flow cytometric data from 5 non-leukemic bone marrow samples cells (gray dots) and one diagnostic ALL sample (black dots) that were merged and analyzed as radial plots using the KALUZA™ software after selecting all CD19+ CD10+ CD34+ cells. Mixtures containing 0.01% ALL cells (top row) and 0.001% ALL cells (bottom row) are shown. Under-expression of CD38 alone, a standard MRD marker, could not discriminate well between ALL cells and normal CD19+ CD10+ CD34+ cells (left panels) in this case; the discrimination was improved by analyzing expression of CD97 (middle panels), and further improved by the inclusion of CD86 and the use of a 3-dimensional space (right panels). Using embodiments of the invention improve the discrimination between normal and leukemic $CD19^{+}$, $CD10^{+}$,

$CD34^+$ cells thereby allowing the unequivocal detection of ALL cells at a level of 0.001%.

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

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

THAT WHICH IS CLAIMED:

1. A method of diagnosing minimal residual disease in a subject comprising:

(a) obtaining a specimen from a subject;

(b) contacting the specimen with a plurality of probes, wherein each of said probes specifically binds to a distinct marker, wherein a first probe specifically binds to CD19, a second probe specifically binds to CD10, a third probe specifically binds to CD34, a fourth probe specifically binds to CD45, and at least two additional probes that specifically binds to any two of CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102, or CD300a;

(c) detecting a complex formed between each of said probes in step (b) with said markers, wherein a value is generated corresponding to an expression level of each of said marker;

(d) generating an expression profile by combining the values generated in step (c);

wherein the expression of CD19, a modulated level of CD10, CD34 and CD45,and a modulated level of at least one of CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164,CD304, CD97, CD99, CD102, or CD300a relative to a normal control is indicative of minimal residual disease in acute lymphoblastic leukemia.

2. The method of claim 1, said plurality of probes comprises at least three additional probes which specifically binds to a distinct marker comprising CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164,CD304, CD97, CD99, CD102 or CD300a.

3. The method of claim 1 or 2, wherein a modulated level comprises the underexpression or the overexpression of at least one of CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a relative to a normal control.

4. The method of claim 3, wherein said modulated level comprises the overexpression of CD44, CD58, CD73, CD200, CD86, HSPB1, BCL2, CD164, CD97, CD99, or CD300a and/or the underexpression of CD38, CD72, or CD79b, relative to a normal control.

5. The method of claim 2, wherein said plurality of probes specifically bind distinct markers comprising:

(a) CD10, CD19, CD34, CD45, CD38, CD24, and CD44;

(b) CD10, CD19, CD34, CD45, CD38, CD58, and CD44;

(c) CD10, CD19, CD34, CD45, CD38, CD73, and CD15;

(d) CD10, CD19, CD34, CD45, CD38, CD200, and CD44;

(e) CD10, CD19, CD34, CD45, CD66c, CD123, and CD86;

(f) CD10, CD19, CD34, CD45, CD72, CD13, and CD33; or,

(g) CD10, CD19, CD34, CD45, CD79b, HSPB1, and Bcl-2.

6. The method of claim 5, wherein said modulated level comprises the overexpression of CD44, CD58, CD73, CD200, CD86, HSPB1, BCL2, CD164, CD97, CD99, or CD300a and the underexpression of CD38, CD72, or CD79b, relative to a normal control.

7. The method of any of claims 1-5, wherein cells in the specimen are permeabilized prior to the contacting the specimen with the probe which specifically binds to the distinct marker comprising CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a.

8. The method of any one of claims 1-7, wherein minimal residual disease in acute lymphoblastic leukemia is detected when there is 1 leukemic cell among 100,000 normal cells.

9. The method of any one of claims 1-8, wherein the specimen is from a blood sample or a bone marrow sample.

10. The method of any one of claims 1-8, wherein at least one probe is an antibody.

11. The method of any one of claim 1-8, wherein the at least one antibody is conjugated with a detectable moiety.

12. The method of claim 11, wherein the detectable moiety is a fluorophore, a chromophore, a radionuclide, or an enzyme.

13. The method of claim 12, wherein at least one antibody is conjugated to a fluorophore comprising phycoerythrin (PE), fluorescein isothiocyanate (FITC), PerCP, APC, PE-Cy7, APC-H7, or Horizon v450.

14. The method of claim 13, wherein the antibody is a $F(ab')_2$, Fab', Fv, Fd', or Fd fragment.

15. The method of any one of claims 1-14, wherein detecting utilizes an optical detection technique.

16. The method of any one of claims 1-15, wherein said detecting utilizes flow cytometry.

17. The method of any one of claims 1-15, wherein said detecting utilizes microscopy.

18. A method of diagnosing minimal residual disease in a subject, the method comprising:

(a) obtaining a specimen from a subject;

(b) contacting the specimen with a plurality of probes, wherein each of said probes specifically binds to a distinct marker, wherein a first probe specifically binds to CD19 and a second probe specifically binds to CD10;

(c) isolating a CD19+/CD10+ cell from said specimen;

(d) determining an expression level of at least two gene products expressed in said CD19+/CD10+ cell from step (c), wherein the at least two gene products encode CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a;

(e) generating an expression profile by combining the values generated in step (d);

wherein the expression of CD19 andCD10and a modulated level of at least one gene products encoding CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164,CD304, CD97, CD99, CD102, or CD300a relative to a normal control is indicative of minimal residual disease in acute lymphoblastic leukemia.

19. The method of claim 18, wherein step (d) comprises determining the expression level of at least three gene products expressed in said CD19+/CD10+cell.

20. The method of any one of claims 18-19, wherein the expression level corresponds to the expression of mRNA.

21. The method of any one of claims 18-20, wherein said modulated level comprises the overexpression of CD44, CD58, CD73, CD200, CD86, HSPB1, BCL2, CD164, CD97, CD99, or CD300a and the underexpression of CD38, CD72 or CD79b, relative to a normal control.

22. The method of claim 19, wherein the at least three gene products expressed in said CD19+/CD10+ cell from step (c) comprise polynucleotides encoding:

(a) CD38, CD24, and CD44;

(b) CD38, CD58, and, CD44;

(c) CD38, CD73, and, CD15;

(d) CD38, CD200, and, CD44;

(e) CD66c, CD123, and, CD86;

(f) CD72, CD13, and, CD33; or,

(g) CD79b, HSPB1, and, Bcl-2.

23. A kit for detecting minimal residual disease in a subject comprising a plurality of probes wherein

(a) each of said probes specifically binds to a distinct marker; and,

(b) said distinct markers comprise CD10, CD19, CD34, and CD45, and at least two of CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102 or CD300a.

24. The kit of claim 23, wherein said probe comprises an antibody, an antibody fragment, or a nucleic acid probe.

25. The kit of any one of claims 23-24, wherein one or more of said antibodies, antibody fragments, or molecular probes, is detectably labeled.

26. The kit of any one of claims 23-24, wherein said probe is a radiolabel, a fluorophore, a peptide, an enzyme, a quantum dot, or a combination thereof.

27. The kit of any one of claims 23-24, wherein each of said probes in said plurality of probes is reactive to a distinct marker comprising:

(a) CD10, CD19, CD34, CD45, CD38, CD24, and CD44;

(b) CD10, CD19, CD34, CD45, CD38, CD58, and, CD44;

(c) CD10, CD19, CD34, CD45, CD38, CD73, and, CD15;

(d) CD10, CD19, CD34, CD45, CD38, CD200, and, CD44;

(e) CD10, CD19, CD34, CD45, CD66c, CD123, and, CD86;

(f) CD10, CD19, CD34, CD45, CD72, CD13, and, CD33; or

(g) CD10, CD19, CD34, CD45, CD79b, HSPB1, and, Bcl-2.

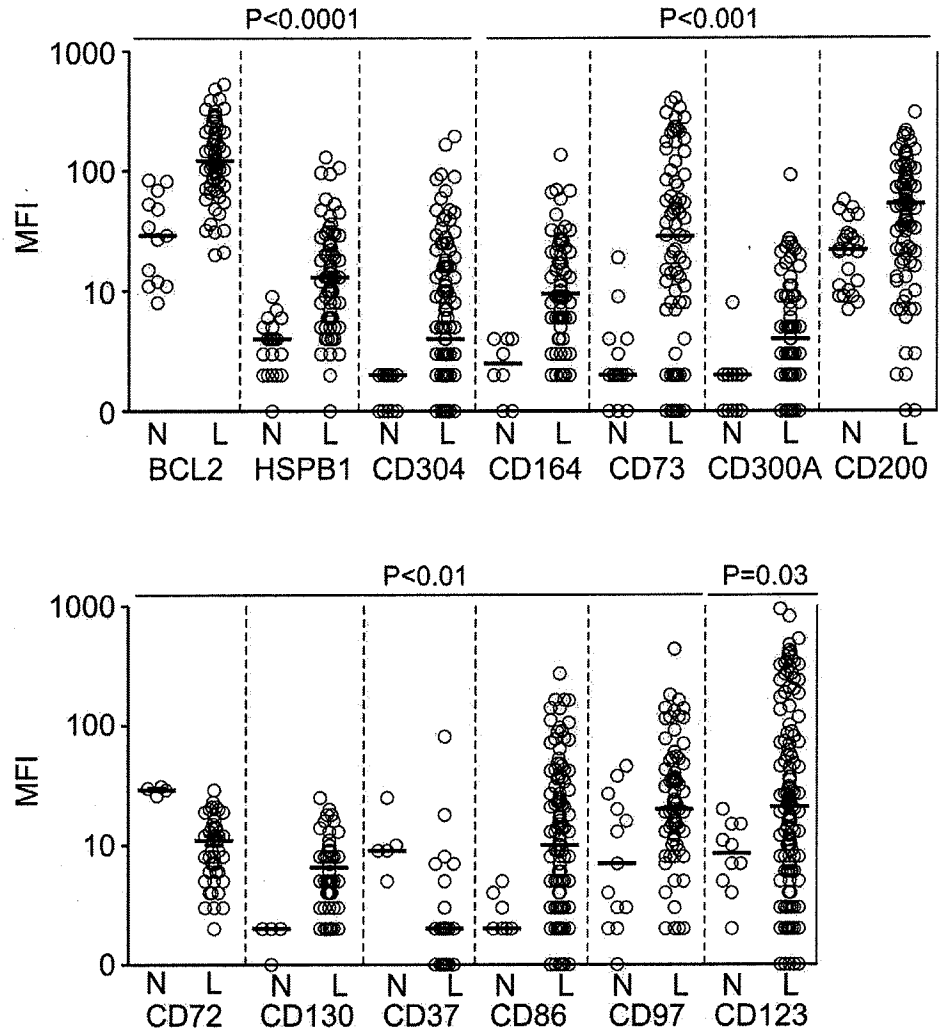

P<0.0001
P<0.001
1000
100
10
0
MFI
N L N L N L N L N L N L N L
BCL2 HSPB1 CD304 CD164 CD73 CD300A CD200
P<0.01
P=0.03
1000
100
10
0
MFI
N L N L N L N L N L N L
CD72 CD130 CD37 CD86 CD97 CD123

FIGURE 1

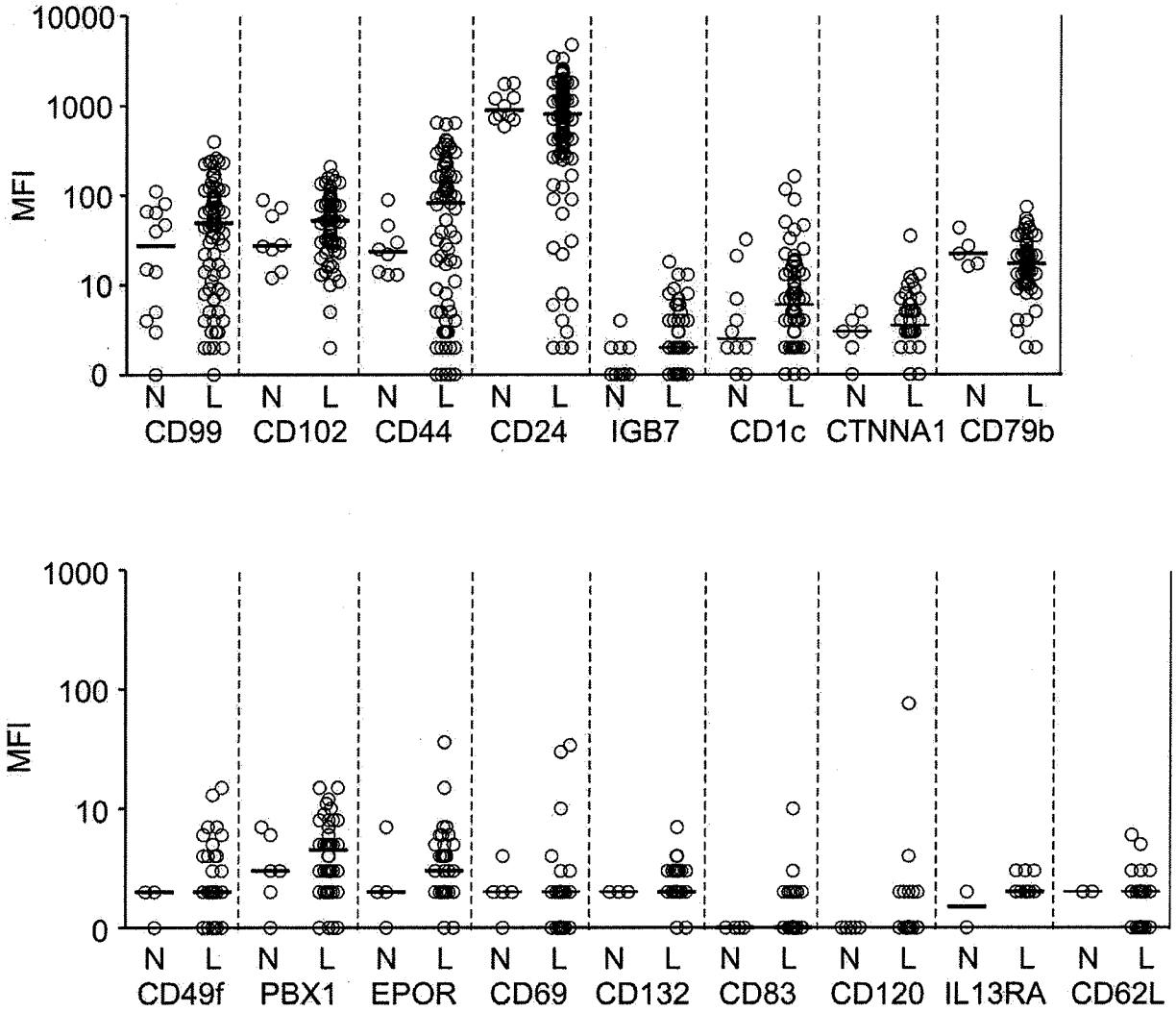

MFI
10000
1000
100
10
0
N L N L N L N L N L N L N L N L
CD99 CD102 CD44 CD24 IGB7 CD1c CTNNA1 CD79b
MFI
1000
100
10
0
N L N L N L N L N L N L N L N L N L
CD49f PBX1 EPOR CD69 CD132 CD83 CD120 IL13RA CD62L

FIGURE 2

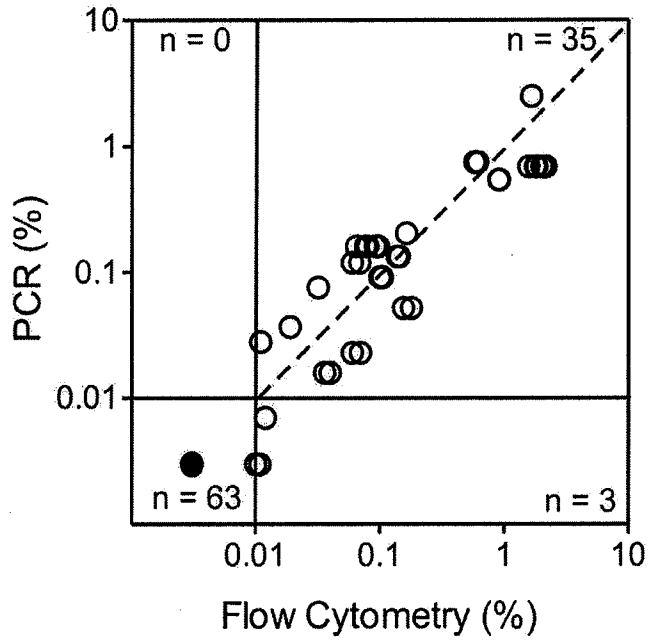


FIGURE 3

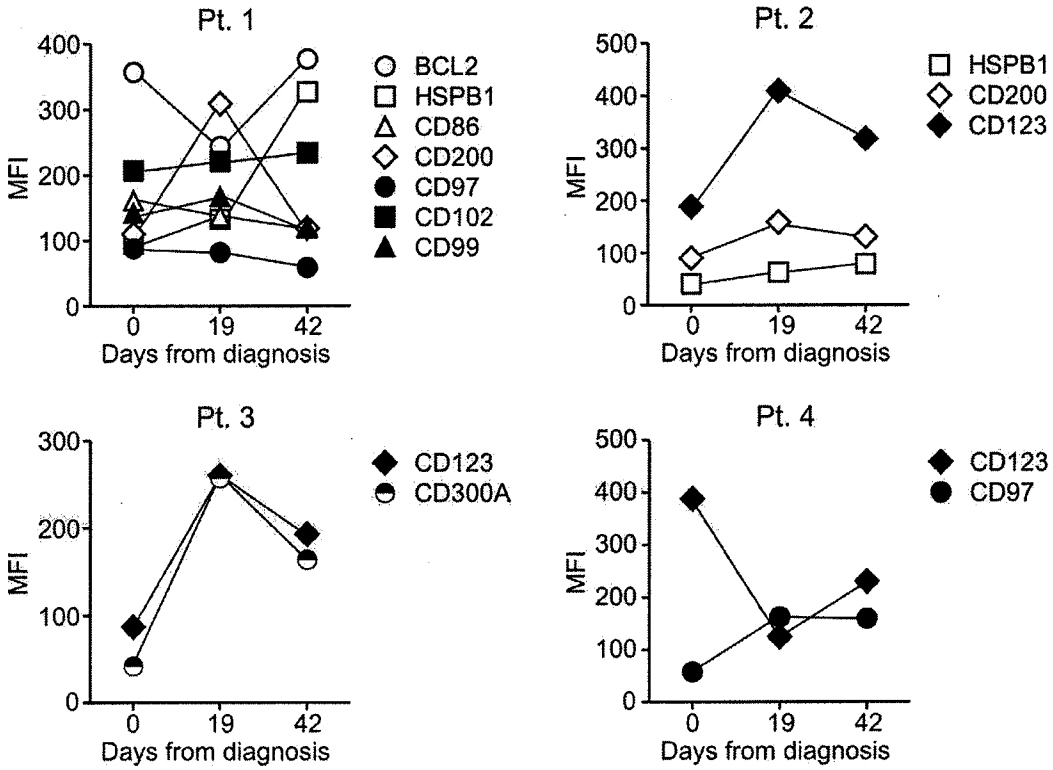

Pt. 1
MFI
400
300
200
100
0
0
19
42
Days from diagnosis
BCL2
HSPB1
CD86
CD200
CD97
CD102
CD99
Pt. 2
MFI
500
400
300
200
100
0
0
19
42
Days from diagnosis
HSPB1
CD200
CD123
Pt. 3
MFI
300
200
100
0
0
19
42
Days from diagnosis
CD123
CD300A
Pt. 4
MFI
500
400
300
200
100
0
0
19
42
Days from diagnosis
CD123
CD97

FIGURE 4

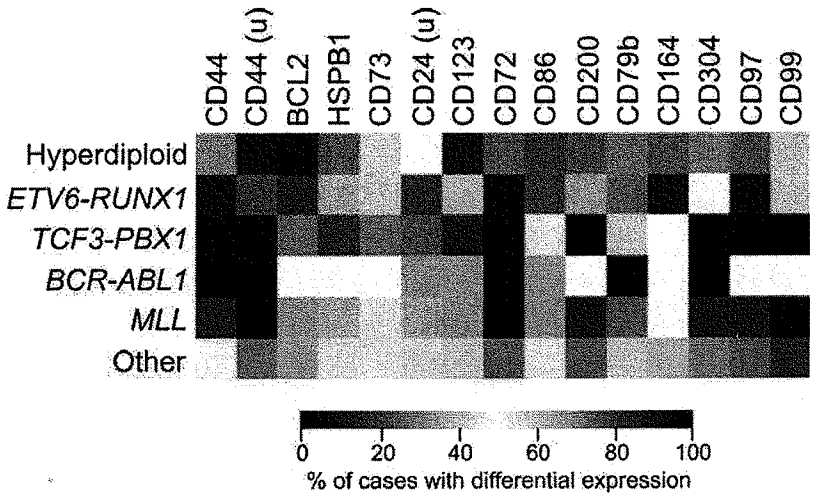

CD44
CD44 (u)
BCL2
HSPB1
CD73
CD24 (u)
CD123
CD72
CD86
CD200
CD79b
CD164
CD304
CD97
CD99
Hyperdiploid
ETV6-RUNX1
TCF3-PBX1
BCR-ABL1
MLL
Other
0
20
40
60
80
100
% of cases with differential expression

FIGURE 5

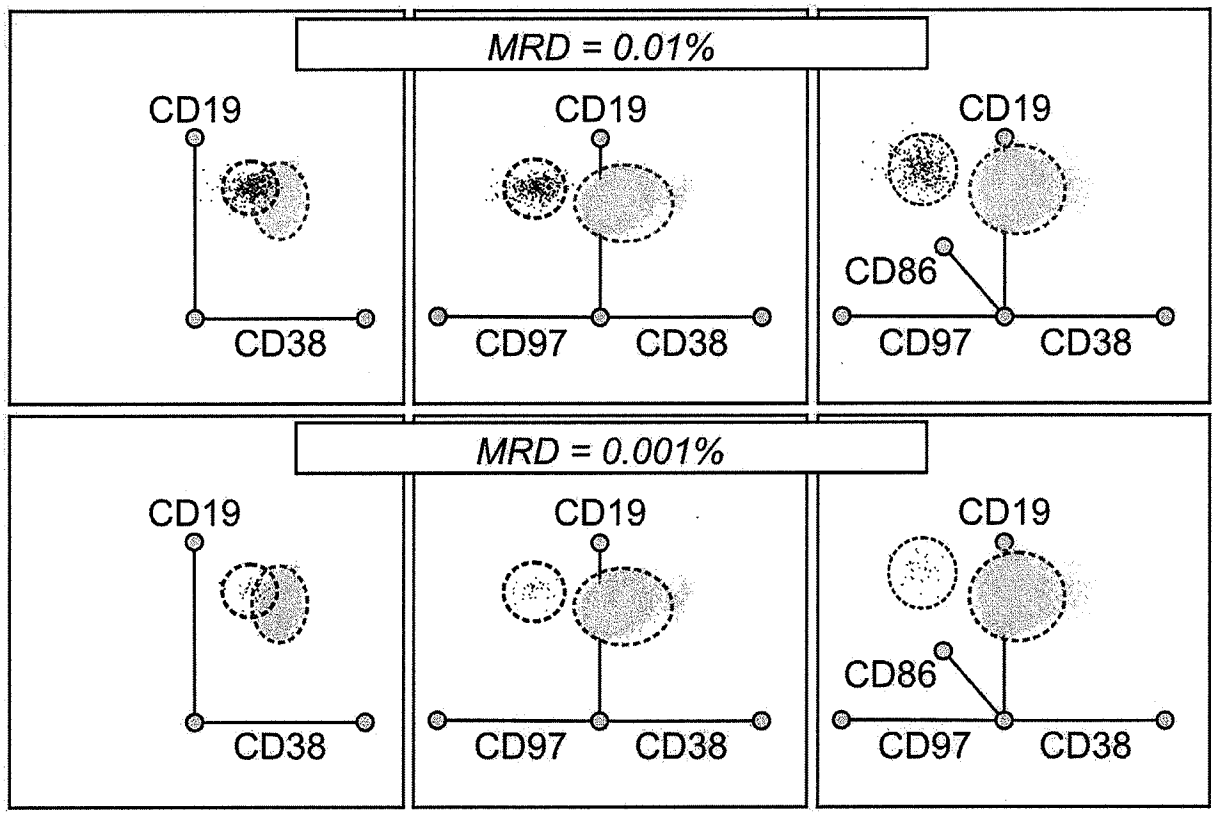

MRD = 0.01%
CD19
CD38
CD19
CD97
CD38
CD19
CD86
CD97
CD38
MRD = 0.001%
CD19
CD38
CD19
CD97
CD38
CD19
CD86
CD97
CD38

FIGURE 6

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2012/028993

A. CLASSIFICATION OF SUBJECT MATTER
INV. G01N33/574 G01N33/50
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, BIOSIS, CHEM ABS Data, EMBASE, INSPEC, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 2 259 065 A1 (UNIV ERASMUS MEDICAL CT [NL]) 8 December 2010 (2010-12-08) paragraph [0046] - paragraph [0049] table 7 claims 1-13 ----- -/--	1-27

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
3 August 2012	14/08/2012

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Bayer, Martin

4

Form PCT/ISA/210 (second sheet) (April 2005)

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2012/028993

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	COUSTAN-SMITH E ET AL: "Immunologic minimal residual disease detection in acute lymphoblastic leukemia: A comparative approach to molecular testing", BEST PRACTICE & RESEARCH CLINICAL HAEMATOLOGY, BAILLIÈRE TINDALL, AMSTERDAM, NL, vol. 23, no. 3, 1 September 2010 (2010-09-01), pages 347-358, XP027521898, ISSN: 1521-6926 [retrieved on 2010-10-28] the whole document	1-27
X	WO 2007/008759 A2 (HEMATOLOGICS INC [US]; LOKEN MICHAEL R [US]; ZEHENTNER-WILKINSON BARBA) 18 January 2007 (2007-01-18) claims 1-42 page 29 - page 31	1-27
X	SHEHATA MEDHAT ET AL: "Partial Characterization and In Vitro Expansion of Putative CLL Precursor/Stem Cells Which Are Dependent on Bone Marrow Microenvironment for Survival", BLOOD, vol. 116, no. 21, November 2010 (2010-11), page 1009, XP002681139, & 52ND ANNUAL MEETING OF THE AMERICAN-SOCIETY-OF-HEMATOLOGY (ASH); ORLANDO, FL, USA; DECEMBER 04 -07, 2010 the whole document	1-27
A	KATO ET AL: "Antibody arrays for quantitative immunophenotyping", BIOMATERIALS, ELSEVIER SCIENCE PUBLISHERS BV., BARKING, GB, vol. 28, no. 6, 28 November 2006 (2006-11-28), pages 1289-1297, XP005788963, ISSN: 0142-9612, DOI: 10.1016/J.BIOMATERIALS.2006.11.007 the whole document	1-27

4

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2012/028993

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:

   a. (means)

   [ ] on paper

   [X] in electronic form

   b. (time)

   [X] in the international application as filed

   [ ] together with the international application in electronic form

   [ ] subsequently to this Authority for the purpose of search

2. [ ] In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2012/028993

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

1-27(partially)

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-27(partially)

The first invention relates to methods and kits for diagnosing minimal residual disease associated with acute lymphoblastic leukemia (ALL) comprising determining a plurality of markers with a plurality of probes specifically binding the distinct markers CD19, CD10, CD34, CD45, CD38, CD24.

2-231. claims: 1-27(partially)

The inventions relate to methods and kits for diagnosing minimal residual disease associated with acute lymphoblastic leukemia (ALL) comprising determining a plurality of markers with a plurality of probes specifically binding the distinct markers CD19, CD10, CD34, CD45 and at least two out of the panel CD38, CD24, CD44, CD58, CD73, CD15, CD200, CD66c, CD123, CD86, CD72, CD13, CD33, CD79b, HSPB1, BCL2, CD164, CD304, CD97, CD99, CD102, or CD300a.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2012/028993

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP 2259065 A1	08-12-2010	AU 2010254680 A1	12-01-2012
		CA 2764670 A1	09-12-2010
		EP 2259065 A1	08-12-2010
		EP 2438446 A1	11-04-2012
		US 2012165213 A1	28-06-2012
		WO 2010140885 A1	09-12-2010
WO 2007008759 A2	18-01-2007	US 2007020670 A1	25-01-2007
		WO 2007008759 A2	18-01-2007