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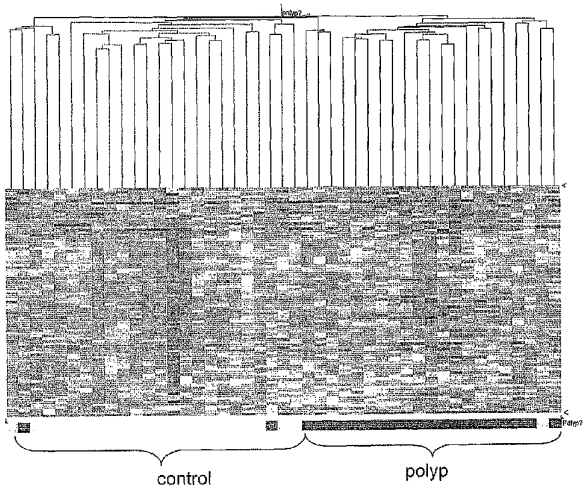
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[Continued on next page]

(54) Title: METHOD AND APPARATUS FOR CORRELATING LEVELS OF BIOMARKER PRODUCTS WITH DISEASE



(57) Abstract: In one aspect the invention is a method of testing for one or more colorectal pathologies or one or more subtypes of colorectal pathology (in one embodiment colorectal cancer) in a test individual by providing data corresponding to a level of products of selected biomarkers and applying the data to a formula to provide an indication of whether the test individual has one or more colorectal pathologies or one or more subtypes of colorectal pathology. In some aspects the method is computer based and a computer applies the data to the formula. In other aspects a computer system is configured with instructions that cause the processor to provide a user with the indication of whether the test individual has colorectal pathology. Also encompassed are kits for measuring data corresponding to the products of selected biomarkers which in some embodiments include a computer readable medium. Also encompassed are kits and methods of monitoring therapeutic efficacy of treatments for one or more colorectal pathologies.

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METHOD AND APPARATUS FOR CORRELATING LEVELS OF BIOMARKER PRODUCTS WITH DISEASE

PRIORITY CLAIM

This application claims the benefit of priority under 35 U.S.C. § 119(e) to U.S. provisional application serial no. 60/729,055, filed October 21, 2005, and to U.S. provisional application serial no. 60/758,418, filed January 12, 2006, both of which are incorporated herein by reference in their entirety.

TECHNICAL FIELD

The disclosure relates to, apparatus and kits and computer based methods for correlating data corresponding to levels of biomarker products with a disease state in a subject.

BACKGROUND

Colorectal cancer is the second-leading cause of cancer-related deaths in the United States (11). Each year, approximately 150,000 people are diagnosed with colorectal cancer and almost 60,000 people die from the disease. Of those diagnosed, nearly half are expected to die within five years, since most cancers are detected when the cancer is less treatable. For those whose cancer is detected at an earlier stage, the five-year survival rate can be greater than 90%. The American Cancer Society recommends that all Americans age 50 and older be screened regularly for colorectal cancer. Unfortunately, only a fraction of this population is screened for

the disease, as currently available screening technologies are considered as either too costly, and/or too invasive or in some cases insufficiently accurate.

Most colorectal cancers begin as small, noncancerous (benign) clumps of cells called polyps. Over time some of these polyps become cancerous. Incidence of polyps increase as individuals get older. It is estimated that 50% of the people over the age of 60 will have at least one polyp.

The significance of identifying one or more colorectal pathologies including polyps is that certain types of polyps are cancerous or indicative of an increased risk to develop cancer. It has been shown that the removal of certain subtypes of polyps reduces the risk of getting colorectal cancer significantly. Therefore, a test to screen for one or more colorectal pathologies including polyps and/or certain subtypes of polyps so as to allow early removal or to prevent unnecessary procedures should markedly reduce the incidence of colorectal cancer (12) and decrease the current costs to the medical system.

Currently utilized screening technologies to identify polyps include 1) a fecal occult blood test (FOBT); 2) a flexible sigmoidoscopy; 3) double contrast barium enema (DCBE); and 4) colonoscopy. Sometimes two or more of these tests are used in combination. The current recommended standards for screening for colorectal cancer in men over the age of 50 and who are considered part of an average risk population include: an FOBT yearly, a sigmoidoscopy every five years, a colonoscopy every ten years and a DCBE every five years. For a high risk population where one or more family members have had colorectal cancer, a colonoscopy is recommended every two years as a follow up to FOBT or sigmoidoscopy.

Each of these tests suffers significant disadvantages. FOBT testing, although a non-invasive procedure, requires significant dietary and other restrictions prior to testing and suffers from a low sensitivity. Sigmoidoscopy and colonoscopy are more sensitive since they involve direct visualization of the lumen, however, sigmoidoscopy only allows partial visualization, and the colonoscopy is known to miss about 12% of advanced adenomas. Both sigmoidoscopy and colonoscopy are highly invasive procedures which cause high levels of discomfort causing many individuals to opt not to undergo these recommended screening procedures. Also sigmoidoscopy and colonoscopy are costly, and may have complications which arise as a result of undergoing the procedure.

Thus, there is a need for an improved test which is minimally invasive so as to permit more widespread testing of the population to indicate the presence of one or more colorectal pathologies, and ensure greater adherence to recommended protocols. To date, despite this need, there have been very few advancements in identifying useful molecular biomarkers to test for colorectal pathology. Recent efforts have focused on DNA based biomarker methods (see for example Shuber et al. U.S. Patent Application Publication No. 2005-0260638A1; or Lofton-Day et al. WO2005/001142).

Identification of biomarkers for use in a non-invasive test for colorectal pathology thus fulfills a longstanding need in the art.

SUMMARY

In contrast to technologies available in the art, the inventions described herein identify biomarkers not previously associated with colorectal pathology whose gene expression levels, measured alone or in combination, and optionally applied to formulas to convert the levels to a measure, give an indication of a likelihood of colorectal pathology.

The present invention discloses novel colorectal pathology-specific biomarkers, such as blood-specific biomarkers, and methods, compositions and kits for use in testing for colorectal pathologies, such as pre-cancerous and cancerous pathologies. This use can be effected in a variety of ways as further described and exemplified herein.

According to one aspect of the present invention there is provided a method of testing for one or more colorectal pathologies in a test subject, the method comprising: (a) providing data representative of a level of one or more products of each of one or more biomarkers in a sample from the test subject; and (b) ascertaining whether the data characterizes either: (i) subjects having the one or more colorectal pathologies, or (ii) subjects not having the one or more colorectal pathologies; thus providing an indication of a probability that the test subject has the one or more colorectal pathologies.

According to another aspect of the present invention there is provided a computer-based method for testing for one or more colorectal pathologies in a test subject, the method comprising: inputting, to a computer, data representing a level of products of each of one or more biomarkers in a sample isolated and/or derived from a test subject, wherein the biomarkers are genes selected from the group consisting of BCNP1, CD163, CDA, MS4A1, BANK1 and

MCG20553; and causing the computer to ascertain whether the data characterizes either: (i) subjects having the one or more colorectal pathologies, or (ii) subjects not having the one or more colorectal pathologies, thus providing an indication of a probability that the test subject has the one or more colorectal pathologies.

According to still another aspect of the present invention there is provided a computer-readable medium comprising instructions for ascertaining whether data characterizes either: (i) subjects having one or more colorectal pathologies, or (ii) subjects not having one or more colorectal pathologies, the data representing a level of one or more products of each of one or more biomarkers in a sample isolated and/or derived from a test subject, wherein the biomarkers are genes selected from the group consisting of BCNP1, CD163, CDA, MS4A1, BANK1, and MCG20553, thus providing an indication of a probability that the test subject has the one or more colorectal pathologies.

According to a yet another aspect of the present invention there is provided a computer system for providing an indication of a probability that a test subject has one or more colorectal pathologies, the computer system comprising a processor; and a memory configured with instructions that cause the processor to provide a user with the indication, wherein the instructions comprise ascertaining whether data characterizes either: (i) subjects having one or more colorectal pathologies, or (ii) subjects not having one or more colorectal pathologies, the data representing a level of one or more products of each of one or more biomarkers in a sample isolated or derived from the test subject, wherein the biomarkers are genes selected from the group consisting of BCNP1, CD163, CDA, MS4A1, BANK1, and MCG20553; thus providing the indication of a probability that the test subject has the one or more colorectal pathologies.

According to further features in preferred embodiments of the invention described below, the products in the sample are RNA.

According to still further features in the described preferred embodiments, the products in the sample are RNA, whereas the data represent a level of cDNA, EST and/or PCR product derived from the RNA.

According to still another aspect of the present invention there is provided a kit comprising packaging and containing one or more primer sets, wherein each set of which is able to generate an amplification product by selective amplification of at least a portion of a polynucleotide complementary to one or more RNA products of a biomarker, wherein the biomarker is a gene

selected from the group consisting of: BCNP1, CD163, CDA, MS4A1, BANK1, and MCG20553; and wherein each set of the primer sets is selective for a different biomarker.

According to further features in preferred embodiments of the invention described below, the complementary polynucleotide is selected from the group consisting of total RNA, mRNA, DNA, cDNA and EST.

According to still further features in the described preferred embodiments, the one or more biomarkers are at least two biomarkers.

According to still further features in the described preferred embodiments, each of the probes is capable of selectively hybridizing to either a sense or an antisense strand of the amplification product.

According to still further features in the described preferred embodiments, the kit further comprises two or more components selected from the group consisting of: a thermostable polymerase, a reverse transcriptase, deoxynucleotide triphosphates, nucleotide triphosphates and enzyme buffer.

According to still further features in the described preferred embodiments, the kit further comprises a computer-readable medium encoded with instructions for ascertaining whether data characterizes either: (i) subjects having one or more colorectal pathologies, or (ii) subjects not having one or more colorectal pathologies, the data representing levels of the amplification product in a sample isolated and/or derived from a test subject, thus providing an indication of a probability that the test subject has the one or more colorectal pathologies.

According to still further features in the described preferred embodiments, ascertaining whether the data characterizes either: (i) subjects having the one or more colorectal pathologies, or (ii) subjects not having the one or more colorectal pathologies, comprises applying to the data a formula based on (i) a dataset representing levels of one or more products of each of the biomarkers in each subject of a reference population having the one or more pathologies, and (ii) a dataset representing levels of one or more products of each of the biomarkers in each subject of a reference population not having the one or more pathologies.

According to still further features in the described preferred embodiments, ascertaining whether the data characterizes either: (i) subjects having the one or more colorectal pathologies, or (ii) subjects not having the one or more colorectal pathologies, comprises ascertaining whether the data correlates more closely with (i) a dataset representing levels of one or more products of

each of the biomarkers in each subject of a reference population of subjects who have the one or more colorectal pathologies, or (ii) a dataset representing levels of one or more products of each of the biomarkers in each subject of a reference population of subjects who do not have the colorectal pathology.

According to still further features in the described preferred embodiments, the formula has a form: $V = C + \Sigma\beta_i X_i$, wherein V is a value indicating a probability that the test subject has the colorectal pathology, X_i is a level of products of an ith biomarker of the biomarkers in the sample, β_i is a coefficient, and C is a constant.

According to still further features in the described preferred embodiments, the formula has a form: $V = C + \Sigma\beta_{ij}(X_i / X_j)$, wherein V is a value indicating a probability that the test subject has the colorectal pathology, X_i is a level of products of an *i*th biomarker of the biomarkers, and X_j is a level of products of a *j*th biomarker of the biomarkers in the sample, where the *i*th biomarker is not the *j*th biomarker, β_{ij} is a coefficient, and C is a constant.

According to still further features in the described preferred embodiments, the formula is derived by a method selected from the group consisting of logistic regression, linear regression, neural networks, and principle component analysis.

According to still further features in the described preferred embodiments, the sample is selected from the group consisting of blood, lymph and lymphoid tissue.

According to still further features in the described preferred embodiments, the sample is selected from the group consisting of a sample of serum-reduced blood, a sample of erythrocyte-reduced blood, a sample of serum-reduced and erythrocyte-reduced blood, a sample of unfractionated cells of lysed blood, and a sample of fractionated blood.

According to a further aspect of the present invention there is provided a composition comprising a collection of two or more isolated polynucleotides, wherein each isolated polynucleotide selectively hybridizes to a biomarker selected from the biomarkers set out in Table 2 and wherein the composition is used to measure the level of expression of at least two of the biomarkers.

According to further features in preferred embodiments of the invention described below, each isolated polynucleotide selectively hybridizes a biomarker selected from the group consisting of membrane-bound transcription factor protease site 1 (MBTPS1); MGC45871; muskelin 1 (MKLN1); nipped-B homolog (NIPBL); acylpeptide hydrolase (APEH); FLJ23091;

MGC40157; and protein phosphatase 1 regulatory subunit 2 (PPP1R2); and wherein the composition is used to measure the level of expression of at least two of the biomarkers.

According to yet a further aspect of the present invention there is provided a composition comprising a collection of two or more isolated polynucleotides, wherein each isolated polynucleotide selectively hybridizes to (a) an RNA product of a biomarker selected from the biomarkers set out in Table 2, and/or (b) a polynucleotide sequence complementary to (a), wherein the composition is used to measure the level of RNA expression of at least two of the biomarkers.

According to further features in preferred embodiments of the invention described below, each isolated polynucleotide selectively hybridizes to (a) an RNA product of a biomarker selected from the group consisting of membrane-bound transcription factor protease site 1 (MBTPS1); MGC45871; muskelin 1 (MKLN1); nipped-B homolog (NIPBL); acylpeptide hydrolase (APEH); FLJ23091; MGC40157; and protein phosphatase 1 regulatory subunit 2 (PPP1R2); and/or (b) a polynucleotide sequence complementary to (a), wherein the composition is used to measure the level of RNA expression of at least two of the biomarkers.

According to still a further aspect of the present invention there is provided a composition comprising a collection of two or more isolated polynucleotides, wherein each isolated polynucleotide selectively hybridizes to (a) an RNA sequences set out in Table 3; and/or (b) a polynucleotide sequences complementary to (a).

According to an additional aspect of the present invention there is provided a composition comprising a collection of two or more sets of biomarker specific primers as set out in Table 4 and/or Table 6.

According to yet an additional aspect of the present invention there is provided a composition comprising two or more polynucleotide probes as set out in Table 4.

According to further features in preferred embodiments of the invention described below, the polynucleotides are useful in quantitative RT-PCR (QRT-PCR).

According to still further features in the described preferred embodiments, the isolated polynucleotides comprise single or double stranded RNA.

According to still further features in the described preferred embodiments, the isolated polynucleotides comprise single or double stranded DNA.

According to still an additional aspect of the present invention there is provided a composition comprising a collection of two or more isolated proteins, wherein each isolated protein binds selectively to a protein product of a biomarker selected from the biomarkers set out in Table 2 and wherein the composition is used to measure the level of expression of at least two of the biomarkers.

According to further features in preferred embodiments of the invention described below, each isolated protein binds selectively to a protein product of a biomarker selected from the group consisting of membrane-bound transcription factor protease site 1 (MBTPS1); MGC45871; muskelin 1 (MKLN1); nipped-B homolog (NIPBL); acylpeptide hydrolase (APEH); FLJ23091; MGC40157; and protein phosphatase 1 regulatory subunit 2 (PPP1R2); and wherein the composition is used to measure the level of expression of at least two of the biomarkers.

According to still further features in the described preferred embodiments, the isolated proteins are selected from the proteins set out in Table 5.

According to still further features in the described preferred embodiments, the isolated proteins are ligands.

According to still further features in the described preferred embodiments, the ligands are antibodies or fragments thereof.

According to still further features in the described preferred embodiments, the antibodies are monoclonal antibodies.

According to yet still an additional aspect of the present invention there is provided a method of diagnosing or detecting one or more colon pathologies in an individual comprising: (a) determining the level of RNA product of one or more biomarker selected from the group consisting of the biomarkers set out in Table 2 in a sample of an individual; and (b) comparing the level of RNA products in the sample with a control, wherein detecting differential expression of the RNA products between the individual and the control is indicative of a one or more colon pathologies in the individual.

According to further features in preferred embodiments of the invention described below, the method of diagnosing or detecting one or more colon pathologiess in an individual comprising: (a) determining the level of RNA product of one or more biomarker selected from the group consisting of the biomarkers set out in Table 2 in a sample of an individual; and (b)

comparing the level of RNA products in the sample with a control further comprises (a) determining the level of RNA product of one or more biomarker selected from the group consisting of membrane-bound transcription factor protease site 1 (MBTPS1); MGC45871; muskelin 1 (MKLN1); nipped-B homolog (NIPBL); acylpeptide hydrolase (APEH); FLJ23091; MGC40157; and protein phosphatase 1 regulatory subunit 2 (PPP1R2); in a sample from an individual; and (b) comparing the level of RNA products in the sample with a control, wherein detecting differential expression of the RNA products between the individual and the control is indicative of a one or more colon pathologies in the individual.

According to still further features in the described preferred embodiments, the sample comprises whole blood.

According to still further features in the described preferred embodiments, the sample comprises a drop of whole blood.

According to still further features in the described preferred embodiments, the sample comprises blood that has been lysed.

According to still further features in the described preferred embodiments, prior to the determining step, the method comprises isolating RNA from the sample.

According to still further features in the described preferred embodiments, the step of determining the level of the RNA products comprises using quantitative RT-PCR (QRT-PCR).

According to still further features in the described preferred embodiments, the QRT-PCR comprises hybridizing primers which hybridize to the one or more RNA products or the complement thereof.

According to still further features in the described preferred embodiments, the primers are 15-25 nucleotides in length.

According to still further features in the described preferred embodiments, the step of determining the level of each of the one or more RNA products comprises hybridizing a first plurality of isolated polynucleotides that correspond to the one or more transcripts, to an array comprising a second plurality of isolated polynucleotides.

According to still further features in the described preferred embodiments, the first plurality of isolated polynucleotides comprises RNA, DNA, cDNA, PCR products or ESTs.

According to still further features in the described preferred embodiments, the array comprises a plurality of isolated polynucleotides comprising RNA, DNA, cDNA, PCR products or ESTs.

According to still further features in the described preferred embodiments, the second plurality of isolated polynucleotides on the array comprises polynucleotides corresponding to one or more of the biomarkers of Table 2.

According to still further features in the described preferred embodiments, the control is derived from an individual that does not have one or more colon pathologies.

According to another aspect of the present invention there is provided a kit for diagnosing or detecting one or more colon pathologies comprising any one of the compositions and instructions for use.

According to yet another aspect of the present invention there is provided a kit for diagnosing or detecting one or more colon pathologies comprising: (a) at least two sets of biomarker specific primers wherein each set of biomarker specific primers produces double stranded DNA complementary to a unique biomarker selected from Table 2; wherein each first primers of the sets contains a sequence which can selectively hybridize to RNA, cDNA or an EST complementary to one of the biomarkers to create an extension product and each the second primers of the sets is capable of selectively hybridizing to the extension product; (b) an enzyme with reverse transcriptase activity; (c) an enzyme with thermostable DNA polymerase activity, and (d) a labeling means; wherein each of the primer sets is used to detect the quantitative expression levels of the biomarker in a test subject.

According to further features in preferred embodiments of the invention described below, the kit for diagnosing or detecting one or more colon pathologies comprising: (a) at least two sets of biomarker specific primers wherein each set of biomarker specific primers produces double stranded DNA complementary to a unique biomarker selected from Table 2; and an enzyme further comprises (a) at least two sets of biomarker specific primers wherein each set of biomarker specific primers produces double stranded DNA complementary to a unique biomarker selected from the group consisting of membrane-bound transcription factor protease site 1 (MBTPS1); MGC45871; muskelin 1 (MKLN1); nipped-B homolog (NIPBL); acylpeptide hydrolase (APEH); FLJ23091; MGC40157; and protein phosphatase 1 regulatory subunit 2 (PPP1R2); wherein each first primers of the sets contains a sequence which can selectively

hybridize to RNA, cDNA or an EST complementary to one of the biomarkers to create an extension product and each the second primers of the sets is capable of selectively hybridizing to the extension product; (b) an enzyme with reverse transcriptase activity; (c) an enzyme with thermostable DNA polymerase activity, and (d) a labeling means; wherein each of the primer sets is used to detect the quantitative expression levels of the biomarker in a test subject.

According to still another aspect of the present invention there is provided a method for diagnosing or detecting one or more colon pathologies in an individual comprising: (a) determining the level of protein product of one or more biomarker selected from the group consisting of the biomarkers set out in Table 2 in a sample from an individual; and (b) comparing the level of protein products in the sample with a control, wherein detecting differential expression of the protein products between the individual and the control is indicative of a one or more colon pathologies in the individual.

According to further features in preferred embodiments of the invention described below, the method for diagnosing or detecting one or more colon pathologies in an individual comprising determining the level of protein product of one or more biomarker selected from the group consisting of the biomarkers set out in Table 2 in a sample from an individual further comprises determining the level of protein product of one or more biomarker selected from the group consisting of membrane-bound transcription factor protease site 1 (MBTPS1); MGC45871; muskelin 1 (MKLN1); nipped-B homolog (NIPBL); acylpeptide hydrolase (APEH); FLJ23091; MGC40157; and protein phosphatase 1 regulatory subunit 2 (PPP1R2); in a sample from an individual; and (b) comparing the level of protein products in the sample with a control, wherein detecting differential expression of the protein products between the individual and the control is indicative of a one or more colon pathologies in the individual.

According to still further features in the described preferred embodiments, the level of protein product is determined using antibodies or fragments thereof.

According to still further features in the described preferred embodiments, the antibodies are selected from the group of antibodies set out in Table 5.

According to still further features in the described preferred embodiments, the antibodies are monoclonal antibodies.

According to a further aspect of the present invention there is provided a composition comprising a collection of two or more isolated polynucleotides, wherein each isolated

polynucleotide selectively hybridizes to a biomarker selected from the biomarkers set out in Table 12 and wherein the composition is used to measure the level of expression in blood of at least two of the biomarkers.

According to yet a further aspect of the present invention there is provided a kit for diagnosing or detecting one or more colon pathologies comprising any one of the compositions comprising a collection of two or more isolated proteins and instructions for use.

The present invention successfully addresses the shortcomings of the presently known configurations, in particular by providing an effective and non-invasive method of testing for colorectal pathologies, such as pre-cancerous and cancerous pathologies, via biomarker analysis in surrogate tissues such as blood.

Other features and advantages of the invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples while indicating preferred embodiments of the invention are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

The invention will now be described in relation to the drawings in which:

FIG. 1 shows an exemplary computer system for practicing certain of the methods described herein.

FIG. 2 is a comparison of gene expression profiles obtained from hybridization of RNA isolated from serum-reduced, erythrocyte-reduced blood from 23 controls having no identified colorectal polyps and 22 subjects with colorectal polyps as described in **Example 2**. Patients with colorectal polyps could have one or more of the subtypes of polyps including Hyperplastic; Tubular Adenoma; Villous Adenoma; Tubulovillous Adenoma; Hyperplasia; High Grade Dysplasia and Colorectal cancer; Gene expression profiles were clustered according to the expression of 86 significantly ($P<0.001$) differentially expressed genes. As noted in grayscale, some of the individuals were misclassified (ie are shown in different grey scale under the appropriate bracket) and are considered outliers. Each column indicates a gene expression profile for a single sample and each row represents the expression level of a single gene in each

of the samples. The color of each band within a row indicates the relative level of gene expression (grayscale represents level of expression, from low to high in expression). The resulting gene list from FIG. 2 is shown in **Table 1**.

FIG. 3 shows blood mRNA levels as tested by QRT-PCR for four upregulated genes (A) and four downregulated genes (B) selected from the genes demonstrating statistically significant differentially expression using microarray analysis as described in **Example 5**. QRT-PCR results were tested as between 50 patients diagnosed as having colorectal pathology (ie one or more subtypes of colorectal polyps) (n=50) as compared with 78 control individuals where the control individuals were diagnosed as not having colorectal pathology (n=78). Comparative (Ct) method based fold change was used. Mann-Whitney test was used for statistical analysis between two groups. Results which demonstrated a f value of less than 0.05 were considered statistically significant suggesting that the gene corresponding to the mRNA level tested is differentially expressed as between the two patient populations (patients with colorectal pathology and patients without colorectal pathology). The lines inside the boxes denote the medians. The boxes mark the interval between the 25^{th} and 75^{th} percentiles. The whiskers denote the interval between the 10^{th} and 90^{th} percentiles. • indicates data points outside the 10^{th} and 90^{th} percentiles.

FIG. 4 depicts an ROC curve for a selected biomarker combination from combinations of pairs of the eight biomarkers tested and shown in **FIG. 3.** Experimental details are as described in **Example 5**. Combinations of a selection of the biomarkers identified in **Table 1** were tested to determine the ability of the combinations to screen test subjects for one or more colorectal pathologies more effectively than can be achieved using the biomarkers of **Table 1** individually. QRT-PCR as described in **Example 3** was performed to measure the level of the RNA products of a select group of individual biomarkers from **Table 1**. Selected combinations of biomarkers were tested by applying logistic regression analysis to the QRT-PCR results of the selected combination and the ROC curve for the resulting logistic regression equation (logit function) determined. Panel (A) - ROC curve (ROC Area 0.72) for logit function for one of the datasets tested (AJ36h). This function returned by Simple Logistic operator in WEKA (ROC Area 0.66).

FIG. 5 depicts the graphical output results of the analysis of all possible combinations of 9 genes selected from the genes depicted in **Table 12** and further described in **Example 8.** Shown is a graphical depiction of ROC area, sensitivity (specificity is set at the 90% threshold) and

specificity (sensitivity is set at the 90% threshold) for each possible combination of 1, 2, 3, 4, 5, 6, 7, 8 or all 9 genes. Further details are described in **Example 8.**

FIG. 6 depicts the graphical output results of the analysis of all possible combinations of 6 genes as further described in **Example 11.** Shown is a graphical depiction of the ROC area, sensitivity (specificity is set at the 90% threshold) and specificity (sensitivity is set at the 90% threshold) for each possible combination of 1, 2, 3, 4, 5 and all 6 of the genes noted in **Example 11.**

BRIEF DESCRIPTION OF THE TABLES

Table 1 (provided herewith on CD-R) shows genes identified as differentially expressed in samples from individuals having or not having one or more of any type of colorectal polyps where the polyps can include be one or more of the following subtypes of polyps: Hyperplastic; Tubular Adenoma; Villous Adenoma; Tubulovillous Adenoma; Hyperplasia; High Grade Dysplasia and Cancer. The table provides the Hugo Gene name (second column), symbol and locus link ID; the human RNA and protein accession number; the p value (which represents the statistical significance of the observed differential expression as determined by measuring RNA encoded by the biomarkers noted) and a measure of the fold change as between the average measured level of individuals having one or more types of colorectal pathology and the average measured level of individuals not having colorectal pathology. Column 1 is AffySpotID, column 2 is GeneSymbol, column 3 is GeneID, Column 4 is pvalue, column 5 is the HumanRNA Accession Number, column 6 is the Human Protein Accession Number, column 7 is the Fold Change, and column 8 is the Gene Description.

Table 2 is a selection of genes listed in **Table 1.** The table provides the gene symbol, locus link ID, and gene description. The table also includes the p value (which represents the statistical significance of the observed differential expression), the Mann-Whitney value (which is another measure to represent the statistical significance of differentiating samples with and without colorectal pathology), the measure of the fold change as between the average measured level of individuals having polyps and the average measured level of individuals not having polyps, and the direction of the differential expression between individuals having colorectal pathology and not having colorectal pathology.

Table 3 provides the human RNA accession number and human protein accession number of various species of the biomarkers identified as differentially expressed in samples from individuals having or not having colorectal polyps. The table provides the gene symbol and a description of the gene.

Table 4 provides a selection of examples of primers and TaqMan® probes useful in the invention for measuring the RNA products of the biomarkers disclosed in **Table 2**.

Table 5 provides reference to antibodies which are commercially available for protein products of the genes identified in **Table 2**.

Table 6 shows primer sequences utilized to perform RT-PCR to measure the differential expression of RNA products of the genes (biomarkers) from **Table 2** as noted in **Example 3** in samples from individuals having or not having one or more polyps. The table also provides the gene symbol and RNA accession number corresponding to the biomarkers tested.

Table 7 provides a summary of the phenotypic information of the patients used as noted in **Example 5** to test selected biomarkers for the ability to test for the presence of colorectal polyps. Parameters including the sample size, gender, age and polyp subtype, (as determined by pathology reports), are listed.

Table 8 lists selected classifiers for use with data corresponding to the eight selected biomarkers MBTPS1, MGC45871, MKLN1, NIPBL APEH, MGC40157, PPP1R2, FLJ23091 which resulted in a ROC area of 0.72 so as to test for the presence of a colorectal polyps as described in **Example 5**. Results of QRT-PCR of the eight selected genes are shown in **FIG. 3**.

Table 9 provides the results of the blind test described in **Example 5** when applying the formula comprised of classifiers noted in **Table 8**.

Table 10 is a list of reporter genes and the properties of the reporter gene products which may be used to identify compounds for use in preventing or treating one or more forms of colorectal pathology.

Table 11 (provided herewith on CD-R) shows genes identified as differentially expressed in samples from individuals having "high risk polyps" as compared with individuals not having high risk polyps (ie having low risk polyps or having no pathology at all) using microarray as described in **Example 2.** The table provides the gene name, gene ID; a representative human RNA accession number, and also provides the p value, the fold change (as between the average of individuals classified as having high risk polyps as compared with the average of individuals

having low risk polyps), along with the coefficient of variation for both the high risk polyp individuals and the low risk polyp individuals (the standard deviation of the normalized intensity divided by the mean normalized intensity). Column 1 is AffySpotID, column 2 is Fold Change, column 3 is p value, Column 4 is CV (Coefficient of Variation) (High RiskPolyp), column 5 is CV(Low Risk Polyp), column 6 is Gene ID, column 7 is the HUGO Gene Symbol, column 8 is the Human RNA Accession Number and column 9 is the Gene Description.

Table 12 shows 48 biomarkers tested for differential expression by QRT-PCR in samples from individuals having colorectal cancer and individuals not having colorectal cancer The 48 biomarkers were tested using QRT-PCR. The table provides the gene symbol, locus link ID, and gene description for each biomarker. The table also includes the p value (which represents the statistical significance of the observed differential expression), the measure of the fold change as between the average measured level of individuals having colorectal cancer and the average measured level of individuals not having colorectal cancer and the direction of the differential expression between individuals having colorectal cancer and not having colorectal cancer.

Table 13 provides the human RNA accession number and human protein accession number of various species of the biomarkers identified as differentially expressed in samples from individuals having or not having colorectal cancer in **Table 12**. The table provides the gene symbol and a description of the gene.

Table 14 provides a selection of examples of primers and TaqMan® probes useful for measuring one or more RNA products of the biomarkers disclosed in **Table 12** as described in **Examples 6, 7, 8** or **9**.

Table 15 provides reference to antibodies which are commercially available to measure protein products of the biomarkers identified in **Table 12**.

Table 16 shows a selection of primers which have been used for the genes described in **Table 12** to quantify one or more RNA products of the biomarkers.

Table 17 shows primers and TaqMan® probes used in **Example 11**.

DETAILED DESCRIPTION

(A) Overview

In one aspect the invention discloses methods of generating formulas/classifiers which can be applied to data corresponding to levels of one or more products of selected biomarker

combinations to classify test subjects as having one or more colorectal pathologies or one or more subtypes of colorectal pathologies. Also disclosed are biomarkers whose product levels are useful for testing subjects for one or more colorectal pathologies or one or more subtypes of colorectal pathologies. Also disclosed are computer-readable media comprising instructions for applying a formula to data representing a level of products of biomarkers so as to test subjects for one or more colorectal pathologies. Also disclosed is a computer system which is configured with instructions to provide the user with an indication of the probability of a test subject having one or more colorectal pathologies by applying a formula to biomarker product data.

The present invention provides biomarker product ligands capable of specific hybridization with RNA biomarker products so as to enable quantitation of the biomarker products. The biomarker product ligands may enable quantitation, either directly and/or indirectly in any one of various ways known to the skilled artisan. The biomarker product ligands capable of specifically hybridizing with biomarker RNA products or polynucleotides derived therefrom may have any one of various compositions. For example, specific ligands of biomarker products, such as biomarker RNA products, may be either polynucleotides (e.g. polynucleotides complementary to at least a portion of the RNA products or polynucleotides derived therefrom) or polypeptides (e.g. antibodies or affinity-selected polypeptides specific for at least a portion of the RNA products or polynucleotides derived therefrom). In one embodiment polynucleotide and/or polypeptide ligands are disclosed which are probes capable of specifically and/or selectively hybridizing with so as to quantitate biomarker RNA products and/or polynucleotides products. Such probes include those useful in techniques such as quantitative real-time PCR (QRT-PCR), and may be used, for example, with SYBR®Green, or using TaqMan® or Molecular Beacon techniques. In one embodiment, the polynucleotides useful as nucleic acid probes which can be spotted onto an array to measure levels of biomarker RNA products, or of polynucleotides derived therefrom, which are isolated or derived from test subjects In another embodiment, arrays for use in measuring the expression of the RNA products are contemplated.

In another embodiment, polynucleotide ligands are disclosed which are biomarker specific primer sets capable of specifically amplifying biomarker RNA products and/or polynucleotides corresponding to biomarker RNA products.

Further disclosed are methods of screening of products of the identified biomarkers to screen for therapeutic targets for treating or preventing one or more colorectal pathologies.

Kits of polynucleotides and/or polypeptide ligands which can be used to detect and monitor differential gene expression of the products of the identified biomarkers and biomarker combinations are also provided as are kits which include a computer readable medium to allow an indication of a probability that a test subject has one or more colorectal pathologies. Methods of generating the formulas for testing for one or more colorectal pathologies are also provided.

Further disclosed is the measurement/monitoring of biomarker product levels to screen for therapeutic targets for treating or preventing one or more colorectal pathologies. Methods of generating the formulas for testing a test subject for a one or more colorectal pathologies are also provided.

Also disclosed are methods of testing combinations of biomarkers by generating classifiers. Classifiers are generated by applying one or more mathematical models to data representative of the level of expression of the RNA and/or protein products of the biomarkers across a reference population encompassing subjects who have one or more colorectal pathologies, or one or more subtypes thereof, and subjects who do not have the one or more colorectal pathologies. Classifiers can be used alone or in combination to create a formula which is useful in testing a subject for the probability of having one or more colon pathologies subtypes. Also disclosed are methods of further selecting classifiers on the basis of area under the curve (AUC), sensitivity and/or specificity. One or more selected classifiers can be used to generate a formula and subsequently classifiers can be selected for inclusion into the formulas. Classifiers are generated by measuring levels of one or more RNA products and/or one or more protein products of the biomarkers in a sample and using the data resulting from said measurement for input into the mathematical model. Note that it is not necessary that the same method used to generate the data for creating the formulas is the method used to generate data from the test subject for inclusion within the formula for diagnostic purposes.

Other aspects of the invention are disclosed herein.

(B) Definitions

The practice of the present invention will employ, unless otherwise indicated, techniques of molecular biology, microbiology and recombinant DNA techniques, which are familiar to one

of the skill in the art. Such techniques are explained fully in the literature. See, e.g., Sambrook, Fritsch & Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Second Edition; Oligonucleotide Synthesis (M.J. Gait, ed., 1984); Nucleic Acid Hybridization (B.D. Harnes & S.J. Higgins, eds., 1984); A Practical Guide to Molecular Cloning (B. Perbal, 1984); and a series, Methods in Enzymology (Academic Press, Inc.); Short Protocols In Molecular Biology, (Ausubel et al., ed., 1995). All patents, patent applications, and publications mentioned herein, both supra and infra, are hereby incorporated by reference in their entireties.

The following definitions are provided for specific terms which are used in the following written description.

As used herein, the "5' end" refers to the end of an mRNA up to the first 1000 nucleotides or 1/3 of the mRNA (where the full length of the mRNA does not include the poly A tail) starting at the first nucleotide of the mRNA. The "5' region" of a gene refers to a polynucleotide (double-stranded or single-stranded) located within or at the 5' end of a gene, and includes, but is not limited to, the 5' untranslated region, if that is present, and the 5' protein coding region of a gene. The 5' region is not shorter than 8 nucleotides in length and not longer than 1000 nucleotides in length. Other possible lengths of the 5' region include but are not limited to 10, 20, 25, 50, 100, 200, 400, and 500 nucleotides.

As used herein, the "3' end" refers to the end of an mRNA up to the last 1000 nucleotides or 1/3 of the mRNA, where the 3' terminal nucleotide is that terminal nucleotide of the coding or untranslated region that adjoins the poly-A tail, if one is present. That is, the 3' end of an mRNA does not include the poly-A tail, if one is present. The "3' region" of a gene refers to a polynucleotide (double-stranded or single-stranded) located within or at the 3' end of a gene, and includes, but is not limited to, the 3' untranslated region, if that is present, and the 3' protein coding region of a gene. The 3' region is not shorter than 8 nucleotides in length and not longer than 1000 nucleotides in length. Other possible lengths of the 3' region include but are not limited to 10, 20, 25, 50, 100, 200, 400, and 500 nucleotides. As used herein, the "internal coding region" of a gene refers to a polynucleotide (double-stranded or single-stranded) located between the 5' region and the 3' region of a gene as defined herein. The "internal coding region" is not shorter than 8 nucleotides in length and not longer than 1000 nucleotides in length. Other possible lengths of the "internal coding region" include but are not limited to 10, 20, 25, 50, 100, 200, 400, and 500 nucleotides. The 5', 3' and internal regions are non-overlapping and may, but

need not be contiguous, and may, but need not, add up to the full length of the corresponding gene.

As used herein, the "amino terminal" region of a polypeptide refers to the polypeptide sequences encoded by polynucleotide sequences (double-stranded or single-stranded) located within or at the 5' end of an mRNA molecule. As used herein, the "amino terminal" region refers to the amino terminal end of a polypeptide up to the first 300 amino acids or 1/3 of the polypeptide, starting at the first amino acid of the polypeptide. The "amino terminal" region of a polypeptide is not shorter than 3 amino acids in length and not longer than 350 amino acids in length. Other possible lengths of the "amino terminal" region of a polypeptide include but are not limited to 5, 10, 20, 25, 50, 100 and 200 amino acids.

As used herein, the "carboxy terminal" region of a polypeptide refers to the polypeptide sequences encoded by polynucleotide sequences (double-stranded or single-stranded) located within or at the 3' end of an mRNA molecule. As used herein, the "carboxy terminal" region refers to the carboxy terminal end of a polypeptide up to 300 amino acids or 1/3 of the polypeptide from the last amino acid of the polypeptide. The "3' end" does not include the polyA tail, if one is present. The "carboxy terminal" region of a polypeptide is not shorter than 3 amino acids in length and not longer than 350 amino acids in length. Other possible lengths of the "carboxy terminal" region of a polypeptide include, but are not limited to, 5, 10, 20, 25, 50, 100 and 200 amino acids.

As used herein, the "internal polypeptide region" of a polypeptide refers to the polypeptide sequences located between the amino terminal region and the carboxy terminal region of a polypeptide, as defined herein. The "internal polypeptide region" of a polypeptide is not shorter than 3 amino acids in length and not longer than 350 amino acids in length. Other possible lengths of the "internal polypeptide region" of a polypeptide include, but are not limited to, 5, 10, 20, 25, 50, 100 and 200 amino acids. The amino terminal, carboxy terminal and internal polypeptide regions of a polypeptide are non-overlapping and may, but need not be contiguous, and may, but need not, add up to the full length of the corresponding polypeptide.

As used herein, the term "amplified", when applied to a nucleic acid sequence, refers to a process whereby one or more copies of a particular nucleic acid sequence is generated from a template nucleic acid, in some embodiments by the method of polymerase chain reaction (Mullis and Faloona, 1987, Methods Enzymol., 155:335). "Polymerase chain reaction" or "PCR" refers

to a method for amplifying a specific template nucleic acid sequence. In some embodiments, the PCR reaction involves a repetitive series of temperature cycles and is typically performed in a volume of 50-100 µl. The number of cycles performed in the PCR reaction can include 15, 20, 25, 30, 35, 40, 45, 50, 55 or 60 cycles. The reaction mix comprises dNTPs (each of the four deoxynucleotides dATP, dCTP, dGTP, and dTTP), primers, buffers, DNA polymerase, and nucleic acid template. The PCR reaction can comprise providing a set of polynucleotide primers wherein a first primer contains a sequence complementary to a region in one strand of the nucleic acid template sequence and primes the synthesis of a complementary strand, and a second primer contains a sequence complementary to a region in a second strand of the target nucleic acid sequence and primes the synthesis of a complementary strand, and amplifying the nucleic acid template sequence employing a nucleic acid polymerase as a template-dependent polymerizing agent under conditions which are permissive for PCR cycling steps of (i) annealing of primers required for amplification to a target nucleic acid sequence contained within the template sequence, (ii) extending the primers wherein the nucleic acid polymerase synthesizes a primer extension product. "A set of polynucleotide primers" or "a set of PCR primers" or "a set of primers" can comprise two, three, four or more primers. In some embodiments, nested PCR can occur using a primer set wherein a first subset of primers is utilized to amplify a single product and then a second subset of primers is utilized which hybridize to the product of the first subset of primers to amplify a smaller version of the. In one embodiment, an exo- Pfu DNA polymerase is used to amplify a nucleic acid template in PCR reaction. Other methods of amplification include, but are not limited to, ligase chain reaction (LCR), polynucleotide-specific based amplification (NSBA), or any other method known in the art.

In one aspect an "array" includes a specific set of probes, such as oligonucleotides and/or cDNA's (e.g. ESTs) corresponding in whole or in part, and/or continuously or discontinuously, to regions of expressed genomic DNA; wherein the probes are localized onto a support. In one embodiment, the probes can correspond to the 5' ends or 3' ends of the internal coding regions of a biomarker RNA product of the invention. Of course, mixtures of a 5' end of one gene may be used as a target or a probe in combination with a 3' end of another gene to achieve the same or similar biomarker RNA product level measurements.

As used herein, an "analog" of a reference proteinaceous agent includes any proteinaceous agent that possesses a similar or identical function as the reference proteinaceous agent but does

not comprise a similar or identical amino acid sequence as reference proteinaceous agent, and/or possess a similar or identical structure as the reference proteinaceous agent. A proteinaceous agent that has a similar amino acid sequence as a second proteinaceous agent is at least one of the following: (a) a proteinaceous agent having an amino acid sequence that is at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or at least 99% identical to the amino acid sequence of the second proteinaceous agent; (b) a proteinaceous agent encoded by a nucleotide sequence that hybridizes under stringent conditions to at least a segment of the nucleotide sequence encoding the second proteinaceous agent, where the segment has a length of at least 5 contiguous amino acid residues, at least 10 contiguous amino acid residues, at least 15 contiguous amino acid residues, at least 20 contiguous amino acid residues, at least 25 contiguous amino acid residues, at least 40 contiguous amino acid residues, at least 50 contiguous amino acid residues, at least 60 contiguous amino residues, at least 70 contiguous amino acid residues, at least 80 contiguous amino acid residues, at least 90 contiguous amino acid residues, at least 100 contiguous amino acid residues, at least 125 contiguous amino acid residues, or at least 150 contiguous amino acid residues; and (c) a proteinaceous agent encoded by a nucleotide sequence that is at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or at least 99% identical to the nucleotide sequence encoding the second proteinaceous agent. A proteinaceous agent with similar structure to a second proteinaceous agent refers to a proteinaceous agent that has a similar secondary, tertiary or quaternary structure as the second proteinaceous agent. The structure of a proteinaceous agent can be determined by methods known to those skilled in the art, including but not limited to, peptide sequencing, X-ray crystallography, nuclear magnetic resonance, circular dichroism, and crystallographic electron microscopy.

To determine the percent identity of two amino acid sequences or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino acid or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the

corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % identity=number of identical overlapping positions/total number of positions.times.100%). In one embodiment, the two sequences are the same length.

The determination of percent identity between two sequences can also be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul, 1990, Proc. Natl. Acad. Sci. U.S.A. 87:2264-2268, modified as in Karlin and Altschul, 1993, Proc. Natl. Acad. Sci. U.S.A. 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al., 1990, J. Mol. Biol. 215:403. BLAST nucleotide searches can be performed with the NBLAST nucleotide program parameters set, e.g., for score=100, wordlength=12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the present invention. BLAST protein searches can be performed with the XBLAST program parameters set, e.g., to score-50, wordlength=3 to obtain amino acid sequences homologous to a protein molecule of the present invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-BLAST can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., of XBLAST and NBLAST) can be used (see, e.g., the NCBI website). Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, 1988, CABIOS 4:11-17. Such an algorithm is incorporated in the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically only exact matches are counted.

As used herein, the term "analog" in the context of a non-proteinaceous molecules refers to a second organic or inorganic molecule which possess a similar or identical function as a first organic or inorganic molecule and is structurally similar to the first organic or inorganic

molecule. The term "analog" includes a molecule whose core structure is the same as, or closely resembles that of the first molecule, but which has a chemical or physical modification. The term "analog" includes copolymers of the first molecule that can be linked to other atoms or molecules. A "biologically active analog" and "analog" are used interchangeably herein to cover an organic or inorganic molecule that exhibits substantially the same agonist or antagonist effect of the first organic or inorganic molecule.

A "nucleotide analog", as used herein, refers to a nucleotide in which the pentose sugar and/or one or more of the phosphate esters is replaced with its respective analog. Exemplary phosphate ester analogs include, but are not limited to, alkylphosphonates, methylphosphonates, phosphoramidates, phosphotriesters, phosphorothioates, phosphorodithioates, phosphoroselenoates, phosphorodiselenoates, phosphoroanilothioates, phosphoroanilidates, phosphoroamidates, boronophosphates, etc., including any associated counterions, if present. Also included within the definition of "nucleotide analog" are nucleobase monomers which can be polymerized into polynucleotide analogs in which the DNA/RNA phosphate ester and/or sugar phosphate ester backbone is replaced with a different type of linkage. Further included within "nucleotide analogs" are nucleotides in which the nucleobase moiety is non-conventional, i.e., differs from one of G, A, T, U or C. Generally a non-conventional nucleobase will have the capacity to form hydrogen bonds with at least one nucleobase moiety present on an adjacent counter-directional polynucleotide strand or provide a non-interacting, non-interfering base.

The term "antibody" also encompasses antigen-binding fragments of an antibody. The term "antigen-binding fragment" of an antibody (or simply "antibody portion," or "fragment"), as used herein, refers to one or more fragments of a full-length antibody that retain the ability to specifically bind to a polypeptide encoded by one of the genes of a biomarker of the invention. Examples of binding fragments encompassed within the term "antigen-binding fragment" of an antibody include (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward *et al.*, (1989) *Nature* 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR). Furthermore, although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be

joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules (known as single chain Fv (scFv); see *e.g.*, Bird *et al.* (1988) *Science* 242:423-426; and Huston *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883). Such single chain antibodies are also intended to be encompassed within the term "antigen-binding fragment" of an antibody. These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are screened for utility in the same manner as are intact antibodies. The antibody is in some embodiments monospecific, *e.g.*, a monoclonal antibody, or antigen-binding fragment thereof. The term "monospecific antibody" refers to an antibody that displays a single binding specificity and affinity for a particular target, *e.g.*, epitope. This term includes a "monoclonal antibody" or "monoclonal antibody composition," which as used herein refer to a preparation of antibodies or fragments thereof of single molecular composition.

As used herein, the terms "attaching" and "spotting" in relation to an array can include a process of depositing or localizing a nucleic acid or proteinaceous agent onto a substrate to form a nucleic acid or protein array. In one embodiment, the substance spotted is attached or localized onto the array via covalent bonds, hydrogen bonds or ionic interactions. .

As used herein, the term "biomarker" refers to a gene whose products can be measured and correlated with disease. A biomarker refers to a gene which encodes one or products (e.g. unspliced RNA, mRNA and/or polypeptide) present at measurably different levels in corresponding samples isolated and/or derived from subjects having the pathology and subjects not having the pathology. A biomarker may be a DNA molecule which is transcribed into RNA product. Alternately, the biomarker may be an RNA molecule which is translated into protein product, or reverse-transcribed into DNA product.

As used herein, a "blood nucleic acid sample" or "blood polynucleotide sample", refers to polynucleotides derived from blood and can include polynucleotides isolated and/or derived from whole blood, serum-reduced whole blood, lysed blood (erthyrocyte depleted blood), centrifuged lysed blood (serum-depleted, erythrocyte depleted blood), serum depleted whole blood or peripheral blood leukocytes (PBLs), globin reduced RNA from blood, or any possible fraction of blood as would be understood by a person skilled in the art. A blood polynucleotide sample can refer to RNA, mRNA or a nucleic acid corresponding to mRNA, for example, cDNA

or EST derived from RNA isolated from said sample. A blood polynucleotide sample can also include a PCR product derived from RNA, mRNA or cDNA.

As used herein, the term "formula" includes one or more classifiers, or combination of classifiers where the term classifier is used to describe the output of a mathematical model.

As used herein the term "colorectal pathology" comprises any of one or more types or subtypes of pathology of the rectum and/or colon. "Colorectal pathologies" include pre-cancerous polyps, cancerous polyps, polyps at risk of becoming cancerous, and polyps of unknown cancer-related status. As would be understood, in some cases a subject according to embodiments of the invention can have at any one time one or more colorectal pathologies, each of which being of the same or a different type or subtype of polyp. Colorectal pathologies may be classified in any one of various ways, for example as is known in the art. In one embodiment "Polyp" or "colorectal polyp" as would be understood in the art, includes an abnormal growth of cells and/or tissue, and/or a growth of cells and/or tissue that may project into the colon or rectum. A polyp can be further defined according to various factors including the morphology of the polyp; the risk of the polyp developing into a cancerous polyp and the like as would be understood by a person ordinarily skilled in the art. In one embodiment, polyps can be classified into various subtypes including: Hyperplastic; Tubular Adenoma; Villous Adenoma; Tubulovillous Adenoma; Hyperplasia; High Grade Dysplasia; and Cancer . For any one individual and or polyp, one or more polyp subtype description could apply. In another embodiment, (7) colorectal cancer can be subclassified into various categories as well. In yet another embodiment, one or more of the listed subtypes can be grouped together according to any one of various parameters in one category. Alternately, one or more of the listed subtypes can be further subclassified according to any one of various parameters. In yet another embodiment, one or more of the listed subtypes can be grouped together according to any one of various parameters in one category. Alternately, one or more of the listed subtypes can be further subclassified according to any one of various parameters. For example, in one embodiment, Tubular Adenoma polyps can be further classified in accordance with the diameter of the Adenoma polyp. For example Adenoma polyps with a diameter greater than 1mm, 2mm, 3mm, 4mm, 5mm, 6mm, 7mm, 8mm, 9mm, 10mm, 11mm, 12mm, 13mm, 14mm or 15mm are possible. In yet another example, colorectal cancer can be further subclassified in accordance with disease progression as would be understood. For example, colorectal cancer can be

subclassified using the Duke or Modified Duke Staging System. The Modified Duke Staging System groups colorectal cancer into four different stages A-D. Stage A indicates the tumor penetrating the mucosa of the colon and/or bowel but no further. Stage B1 indicates the tumor penetrating into, but not through the muscularis propria (the muscular layer) of the colon and/or bowel wall. Stage B2 indicates the tumor has penetrated into and through the muscularis propria of the colon and/or bowel wall. A Stage C1 tumor penetrates into, but not through the muscularis propria of the colon and/or bowel wall; there is pathologic evidence of colorectal cancer in the lymph nodes. Stage C2 tumors penetrates into and through the muscularis propria of the bowel wall; but there is pathologic evidence of colorectal cancer in the lymph nodes. Finally Stage D indicates the tumor has spread beyond the lymph nodes to other organs. In yet another embodiment, colorectal cancer can be subclassified using the TNM staging system. According to the TNM staging system there are four stages, stages I through IV, each reflecting status regarding Tumor, Node, and Metastasis. Tumor is subdivided as follows T1: Tumor invades submucosa, T2: Tumor invades muscularis propria, T3: Tumor invades through the muscularis propria into the subserosa, or into the pericolic or perirectal tissues and T4: Tumor directly invades other organs or structures, and/or perforates. Node is subdivided as follows: N0 indicates no regional lymph node metastasis. N1 indicates metastasis in 1 to 3 regional lymph nodes. N2 indicates metastasis in 4 or more regional lymph nodes. Metastasis is divided as follows: M0 indicates no distant metastasis and M1 indicates distant metastasis present. Thus for Stage I, in accordance with the TNM system, the tumor can either be categorized as T1N0M0 or T2N0M0; the cancer has begun to spread but is still in the inner lining. Stage II is T3N0M0 or T4 N0M0; the cancer has spread to other organs near the colon or rectum but has not yet reached the inner lining. Stage III includes all T's, N1-2 and M0; cancer has spread to lymph nodes but has not been carried to distant parts of the body. Stage IV includes any T, any N and M1; cancer is metastatic and has been carried to other organs, likely the lung or liver.

As used herein, the term "high risk polyps" indicates those subtypes of polyps which are considered at higher risk for developing into cancer or are already cancerous as would be understood by a person skilled in the art, and includes cancer-prone polyps or cancer-disposed polyps and cancerous polyps, whereas a "low risk polyp" includes all other types of polyps. For example, 70 to 90 percent of colorectal cancers arise from adenomatous polyps, and thus are considered high risk polyps. Adenomatous polyps can be further categorized into subtypes

including: Tubular adenoma, which has been suggested to have approximately a 4% potential for malignancy; Tubulovillous adenoma, which has been suggested to have approximately a 16% potential for malignancy and Villous adenoma, which has been suggested to have approximately a 21% potential for malignancy. In addition, high grade dysplasia has increased malignant potential. In one embodiment, polyps which are "high risk polyps" are Tubulovillous Adenoma, Villous Adenoma, High Grade Dysplasia and Tubular Adenoma and also includes polyps which are cancerous including those which are cancerous and localized and those which have already led to dissemination in the peripheral blood. In this embodiment, a "low risk polyp" includes any other polyp morphology. In another embodiment, polyps which are "high risk polyps" are Tubulovillous Adenoma, Villous Adenoma, High Grade Dysplasia and Tubular Adenoma and does not include polyps which are already cancerous. The size of the polyp also correlates with the risk for developing into cancer. For example, polyps greater than 10mm in diameter are considered large polyps and have a greater potential for malignancy. Polyps larger than 2 cm in diameter have a 50 percent chance of becoming malignant. See Zauber (2004) Gastroenterology; 126(5): 1474. In another embodiment "high risk polyps" comprise Tubulovillous Adenoma, Villous Adenoma, High Grade Dysplasia and Tubular Adenoma where the diameter of the Tubular Adenoma polyp is greater than 10mm and the remaining polyp morphologies are considered "low risk polyps".

As used herein, the terms "compound" and "agent" are used interchangeably.

As used herein, the term "control" or "control sample" can include one or more samples isolated and/or derived from a subject or group of subjects who have been diagnosed as having one or more colorectal pathologies, including having one or more polyps or having one or more subtypes of polyps; not having colorectal pathologies; not having polyps; or not having one or more subtypes of polyps. The term control or control sample can also refer to the compilation of data derived from one or more samples of one or more subjects.

A "coding region" in reference to a DNA refers to DNA which encodes RNA.

A "coding region" in reference to RNA refers to RNA which encodes protein.

As used herein, the term "data" in relation to one or more biomarkers, or the term "biomarker data" generally refers to data reflective of the absolute and/or relative abundance (level) of a product of a biomarker in a sample. As used herein, the term "dataset" in relation to one or more biomarkers refers to a set of data representing levels of each of one or more

biomarker products of a panel of biomarkers in a reference population of subjects.. A dataset can be used to generate a formula/classifier of the invention. According to one embodiment the dataset need not comprise data for each biomarker product of the panel for each individual of the reference population. For example, the "dataset" when used in the context of a dataset to be applied to a formula can refer to data representing levels of products of each biomarker for each individual in one or more reference populations, but as would be understood can also refer to data representing levels of products of each biomarker for 99%, 95%, 90%, 85%, 80%, 75%, 70% or less of the individuals in each of said one or more reference populations and can still be useful for purposes of applying to a formula.

As used herein, the term "derivative" in the context of proteinaceous agent (e.g., proteins, polypeptides, peptides, and antibodies) refers to a proteinaceous agent that comprises an amino acid sequence which has been altered by the introduction of amino acid residue substitutions, deletions, and/or additions. The term "derivative" as used herein also refers to a proteinaceous agent which has been modified, i.e., by the covalent attachment of any type of molecule to the proteinaceous agent. For example, but not by way of limitation, an antibody may be modified, e.g., by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. A derivative of a proteinaceous agent may be produced by chemical modifications using techniques known to those of skill in the art, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Further, a derivative of a proteinaceous agent may contain one or more non-classical amino acids. A derivative of a proteinaceous agent possesses a similar or identical function as the proteinaceous agent from which it was derived.

As used herein, the term "derivative" in the context of a non-proteinaceous derivative refers to a second organic or inorganic molecule that is formed based upon the structure of a first organic or inorganic molecule. A derivative of an organic molecule includes, but is not limited to, a molecule modified, e.g., by the addition or deletion of a hydroxyl, methyl, ethyl, carboxyl or amine group. An organic molecule may also be esterified, alkylated and/or phosphorylated.

As used herein the terms "testing", "diagnosis" and "screening", in relation to colorectal pathologies refer to a process of determining a likelihood (probability) of a test subject having one or more colorectal pathologies and includes both traditional medical diagnostic techniques as

well as testing methods as encompassed by one or more aspects of the current invention. Traditional medical diagnostic techniques for testing for colorectal pathology includes physical exam and history, medical evaluation, and appropriate laboratory tests which can include FOBT, sigmoidoscopy and colonoscopy. In one embodiment, "diagnosis of colorectal pathology" refers to a determination as between two options: e.g., (i) that an individual has colorectal pathology or one or more subtypes of colorectal pathology, or one or more polyps and (ii) that an individual does not have the colorectal pathology or the one or more polyps or the one or more subtypes of polyps. In another embodiment diagnosis can include an option that it cannot be determined with sufficient degree of certainty as to whether an individual can be characterized as having colorectal pathology or not. In one context, a "sufficient degree of certainty" takes into account any limitations – such as limitations in the technology, equipment or measuring where as a result of the limitations, the result is within a range which suggests that the test is indeterminate. The range which suggests the test is indeterminate will depend upon the specific limitations of the equipment, reagents and technology used. In another context, "sufficient degree of certainty" depends upon the medical requirements for the sensitivity and/or specificity of the test. More particularly the sufficient degree of certainty includes greater than 50% sensitivity and/or specificity, greater than 60% sensitivity and/or specificity, greater than 70% sensitivity and/or specificity, greater than 80% sensitivity and/or specificity, greater than 90% sensitivity and/or specificity and 100% sensitivity and/or specificity.

As used herein, "normal" refers to an individual or group of individuals who do not have colorectal pathology. In some embodiments, the diagnosis of said individual or group of individuals not having colorectal pathology is determined using conventional diagnostic methods. In some embodiments said individual or group of individuals have not been diagnosed with any other disease. "Normal", according to the invention, also refers to samples isolated from normal individuals and includes blood, total RNA or mRNA isolated from normal individuals. A sample taken from a normal individual can include a sample taken from an individual who does not have colorectal pathology at the time the sample is taken.

As used herein, the term "differential expression" refers to a difference in the level of expression of the products of one or more biomarkers. For instance, the term "differential expression" can refer to the difference in the level of RNA of one or more biomarkers between samples from subjects having and subjects not having one or more colorectal pathologies.

Differences in biomarker RNA product levels can be determined by directly or indirectly measuring the amount or level of Differentially expressed" can also include different levels of protein encoded by the biomarker of the invention between samples or reference populations. "Differential expression can be determined as the ratio of the levels of one or more biomarker products between reference subjects/populations having or not having one or more colorectal pathologies, wherein the ratio is not equal to 1.0. Differential expression between populations can be determined to be statistically significant as a function of p-value. When using p-value to determine statistical significance, a biomarker, the p-value is preferably less than 0.2. In another embodiment the biomarker is identified as being differentially expressed when the p-value is less than 0.15, 0.1, 0.05, 0.01, 0.005, 0.0001 etc. When determining differential expression on the basis of the ratio, a biomarker product is differentially expressed if the ratio of the level of expression in a first sample as compared with a second sample is greater than or less than 1.0. For example, a ratio of greater than 1.0 for example includes a ratio of greater than 1.1, 1.2, 1.5, 1.7, 2, 3, 4, 10, 20 and the like. A ratio of less than 1.0, for example, includes a ratio of less than 0.9, 0.8, 0.6, 0.4, 0.2, 0.1, 0.05 and the like. In another embodiment of the invention a biomarker product is differentially expressed if the ratio of the mean of the level of expression of a first population as compared with the mean level of expression of the second population is greater than or less than 1.0. For example, a ratio of greater than 1.0 includes a ratio of greater than 1.1, 1.2, 1.5, 1.7, 2, 3, 4, 10, 20 and the like and a ratio less than 1.0, for example includes a ration of less than 0.9, 0.8, 0.6, 0.4, 0.2, 0.1, 0.05 and the like. In another embodiment of the invention a biomarker product is differentially expressed if the ratio of its level of expression in a first sample as compared with the mean of the second population is greater than or less than 1.0 and includes for example, a ratio of greater than 1.1, 1.2, 1.5, 1.7, 2, 3, 4, 10, 20, or a ratio less than 1, for example 0.9, 0.8, 0.6, 0.4, 0.2, 0.1, 0.05.

"Differentially increased expression" or "up regulation" refers to biomarker product levels which are at least 10% or more, for example, 20%, 30%, 40%, or 50%, 60%, 70%, 80%, 90% higher or more, and/or 1.1 fold, 1.2 fold, 1.4 fold, 1.6 fold, 1.8 fold higher or more, than a control.

"Differentially decreased expression" or "down regulation" refers to biomarker product levels which are at least 10% or more, for example, 20%, 30%, 40%, or 50%, 60%, 70%, 80%,

90% lower or less, and/or 0.9 fold, 0.8 fold, 0.6 fold, 0.4 fold, 0.2 fold, 0.1 fold or less lower than a control.

For example, up regulated or down regulated genes include genes having an increased or decreased level, respectively, of expression of product (e.g. mRNA or protein) in blood isolated from individuals characterized as having one or more colorectal pathologies as compared with normal individuals. In another example, up regulated or down regulated genes include genes having an increased or decreased level, respectively, of expression of product (e.g. mRNA or protein) in blood isolated from individuals having one type of colorectal pathology or collection of colorectal pathologies as compared with individuals having a different type of colorectal pathology or collection of colorectal pathologies, respectively.

For example, up regulated genes include genes having an increased level of biomarker products in a test sample as compared with a control sample.

As used herein, the term "differential hybridization" refers to a difference in a quantitative level of hybridization of a nucleic acid or derivative thereof isolated and/or derived from a sample from a first individual or individuals with a trait to a complementary nucleic acid target as compared with the hybridization of a nucleic acid or derivative thereof isolated and/or derived from a second individual or individuals not having said trait to a complementary nucleic acid target. A "differential hybridization" means that the ratio of the level of hybridization of the first sample as compared with the second sample is not equal to 1.0. For example, the ratio of the level of hybridization of the first sample to the target as compared to the second sample is greater than 1.1, 1.2, 1.5, 1.7, 2, 3, 4, 10, 20, or less than 1, for example 0.9, 0.8, 0.6, 0.4, 0.2, 0.1, 0.05. A differential hybridization also exists if the hybridization is detectable in one sample but not another sample.

As used herein, the term "drug efficacy" refers to the effectiveness of a drug. "Drug efficacy" is usually measured by the clinical response of the patient who has been or is being treated with a drug. A drug is considered to have a high degree of efficacy, if it achieves desired clinical results, for example, the alteration of gene expression and the gene expression pattern reflective of one or more colorectal pathologies as described herein. The amount of drug absorbed may be used to predict a patient's response. A general rule is that as the dose of a drug is increased, a greater effect is seen in the patient until a maximum desired effect is reached. If

more drug is administered after the maximum point is reached, the side effects will normally increase.

As used herein, the term "effective amount" refers to the amount of a compound which is sufficient to reduce or prevent the progression and/or severity of one or more colorectal pathologies; prevent the development, recurrence of onset of one or more colorectal pathologies; or enhance or improve the prophylactic or therapeutic effect(s) of another therapy.

As used herein, the term "fragment" in the context of a proteinaceous agent refers to a peptide or polypeptide comprising an amino acid sequence of at least 5 contiguous amino acid residues, at least 10 contiguous amino acid residues, at least 15 contiguous amino acid residues, at least 20 contiguous amino acid residues, at least 25 contiguous amino acid residues, at least 40 contiguous amino acid residues, at least 50 contiguous amino acid residues, at least 60 contiguous amino residues, at least 70 contiguous amino acid residues, at least contiguous 80 amino acid residues, at least contiguous 90 amino acid residues, at least contiguous 100 amino acid residues, at least contiguous 125 amino acid residues, at least 150 contiguous amino acid residues, at least contiguous 175 amino acid residues, at least contiguous 200 amino acid residues, or at least contiguous 250 amino acid residues of the amino acid sequence of another polypeptide or a protein. In a specific embodiment, a fragment of a protein or polypeptide retains at least one function of the protein or polypeptide. In another embodiment, a fragment of a protein or polypeptide retains at least two, three, four, or five functions of the protein or polypeptide. In some embodiments, a fragment of an antibody retains the ability to immunospecifically bind to an antigen.

As used herein, the term "fusion protein" refers to a polypeptide that comprises an amino acid sequence of a first protein or polypeptide or functional fragment, analog or derivative thereof, and an amino acid sequence of a heterologous protein, polypeptide, or peptide (i.e., a second protein or polypeptide or fragment, analog or derivative thereof different than the first protein or fragment, analog or derivative thereof). In one embodiment, a fusion protein comprises a prophylactic or therapeutic agent fused to a heterologous protein, polypeptide or peptide. In accordance with this embodiment, the heterologous protein, polypeptide or peptide may or may not be a different type of prophylactic or therapeutic agent.

As used herein, a "gene" of the invention can include a gene expressed in blood, a gene expressed in blood and in a non-blood tissue, a gene differentially expressed in blood, a gene

expressed in a non-blood cell, a gene expressed in a cell which is not of haematopoietic origin, a gene expressed in a specific subtype of cell found in blood including lymphocytes, granulocytes, leukocytes, basophils and the like. A gene can be an immune response gene or a gene not involved in an immune response. In particular an immune response gene is a gene in the major histocompatibility complex that controls a cells response to a foreign antigen. A gene of the invention can also include a gene which is differentially regulated in response to a foreign antigen introduced into peripheral blood.

As used herein, a "gene expression pattern" or "gene expression profile" indicates the pattern of the level of expression of two or more biomarkers of the invention including 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or more or all of the biomarkers of the invention. A gene expression pattern or gene expression profile can be determined from the measurement of expression levels of the products of the biomarkers of the invention using any known technique. For example techniques to measure expression of the RNA products of the biomarkers of the invention include, PCR based methods (including reverse transcription-PCR, PCR, QRT-PCR) and non PCR based method, as well as microarray analysis. To measure levels of protein products of the biomarkers of the invention, techniques include densitometric western blotting and ELISA analysis.

As used herein, the term "hybridizing to" or "hybridization" refers to the sequence specific non-covalent binding interactions with a complementary nucleic acid, for example interactions between a target nucleic acid sequence and a nucleic acid member on an array.

As used herein, the term "immunoglobulin" refers to a protein consisting of one or more polypeptides substantially encoded by immunoglobulin genes. The recognized human immunoglobulin genes include the kappa, lambda, alpha (IgA1 and IgA2), gamma (IgG1, IgG2, IgG3, IgG4), delta, epsilon and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Full-length immunoglobulin "light chains" (about 25 Kd or 214 amino acids) are encoded by a variable region gene at the NH2-terminus (about 110 amino acids) and a kappa or lambda constant region gene at the COOH-terminus. Full-length immunoglobulin "heavy chains" (about 50 Kd or 446 amino acids), are similarly encoded by a variable region gene (about 116 amino acids) and one of the other aforementioned constant region genes, *e.g.*, gamma (encoding about 330 amino acids).

As used herein, the term "in combination" when referring to therapeutic treatments refers to the use of more than one type of therapy (*e.g.*, more than one prophylactic agent and/or therapeutic agent). The use of the term "in combination" does not restrict the order in which therapies (*e.g.*, prophylactic and/or therapeutic agents) are administered to a subject. A first therapy (*e.g.*, a first prophylactic or therapeutic agent) can be administered prior to (*e.g.*, 5 minutes, 15 minutes, 30 minutes, 45 minutes, 1 hour, 2 hours, 4 hours, 6 hours, 12 hours, 24 hours, 48 hours, 72 hours, 96 hours, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 8 weeks, or 12 weeks before), concommitantly with, or subsequent to (*e.g.*, 5 minutes, 15 minutes, 30 minutes, 45 minutes, 1 hour, 2 hours, 4 hours, 6 hours, 12 hours, 24 hours, 48 hours, 72 hours, 96 hours, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 8 weeks, or 12 weeks after) the administration of a second therapy (*e.g.*, a second prophylactic or therapeutic agent) to a subject.

As used herein, "indicative of one or more colorectal pathologies" refers to a determination of a probability that a subject has or will have the one or more colorectal pathologies. In one aspect the application of a formula to data corresponding to biomarker products of a test subject can result in determination of the probability of whether the test subject has one or more colorectal pathologies as compared with not having said one or more colorectal pathologies. In another embodiment, an expression pattern can be indicative of one or more colorectal pathologies including one or more polyps or one or more subtypes of polyps if the expression pattern is found significantly more often in patients with said colorectal pathology than in patients without said colorectal pathology (as determined using routine statistical methods setting confidence levels at a minimum of 70%, 75%, 80%, 85%, 90%, 95% and the like). In some embodiments, an expression pattern which is indicative of disease is found in at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or more in patients who have the disease and is found in less than 10%, less than 8%, less than 5%, less than 2.5%, or less than 1% of patients who do not have the disease. "Indicative of colorectal pathology" can also indicates an expression pattern which more properly categorizes with control expression patterns of individuals with the one or more colorectal pathologies as compared with control expression patterns of individuals without the one or more colorectal pathologies using statistical algorithms for class prediction as would be understood by a person skilled in the art and see for

example commercially available programs such as those provided by Silicon Genetics (e.g. GeneSpring™).

As used herein, "isolated" or "purified" when used in reference to a nucleic acid means that a naturally occurring sequence has been removed from its normal cellular (e.g., chromosomal) environment or is synthesized in a non-natural environment (e.g., artificially synthesized). Thus, an "isolated" or "purified" sequence may be in a cell-free solution or placed in a different cellular environment. The term "purified" does not imply that the sequence is the only nucleotide present, but that it is essentially free (about 90-95% pure) of non-nucleotide material naturally associated with it, and thus is distinguished from isolated chromosomes.

As used herein, the terms "isolated" and "purified" in the context of a proteinaceous agent (e.g., a peptide, polypeptide, protein or antibody) refer to a proteinaceous agent which is substantially free of cellular material and in some embodiments, substantially free of heterologous proteinaceous agents (i.e., contaminating proteins) from the cell or tissue source from which it is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of a proteinaceous agent in which the proteinaceous agent is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, a proteinaceous agent that is substantially free of cellular material includes preparations of a proteinaceous agent having less than about 40%, 30%, 20%, 10%, or 5% (by dry weight) of heterologous proteinaceous agent (e.g., protein, polypeptide, peptide, or antibody; also referred to as a "contaminating protein"). When the proteinaceous agent is recombinantly produced, it is also in some embodiments substantially free of culture medium, i.e., culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When the proteinaceous agent is produced by chemical synthesis, it is in some embodiments substantially free of chemical precursors or other chemicals, i.e., it is separated from chemical precursors or other chemicals which are involved in the synthesis of the proteinaceous agent. Accordingly, such preparations of a proteinaceous agent have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the proteinaceous agent of interest. In some embodiments, proteinaceous agents disclosed herein are isolated.

As used herein, a sample which is "isolated and/or derived" includes a sample which has been removed it from its natural environment in a subject and also includes samples which are

further modified or altered. For example samples can include tissue, lymph, bodily fluid, blood, RNA, protein, mRNA, serum reduced blood, erythrocyte reduced blood, serum reduced and erythrocyte reduced blood, unfractionated cells of a lysed blood, globin reduced mRNA, cDNA, PCR products and the like.

As used herein, the term "level" or "level of expression" when referring to RNA refers to a measurable quantity (either absolute or relative quantity) of a given nucleic acid as determined by hybridization or measurements such as QRT-PCR and includes use of both SYBR® green and TaqMan® technology and which corresponds in direct proportion with the amount of product of the gene in a sample. Level of expression when referring to RNA can also refer to a measurable quantity of a given nucleic acid as determined by PCR wherein the number of cycles of PCR is limited to 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, or 60 cycles. The level of expression when referring to RNA can also refer to a measurable quantity of a given nucleic acid as determined relative to the amount of total RNA, or cDNA used in QRT-PCR wherein the amount of total RNA used is 100ng; 50ng, 25ng; 10ng; 5ng; 1.25ng; 0.05ng; 0.3ng; 0.1ng; 0.09 ng; 0.08ng; 0.07ng; 0.06ng; or 0.05ng. The level of expression of a nucleic acid can be determined by any methods known in the art. For microarray analysis, the level of expression is measured by hybridization analysis using nucleic acids corresponding to RNA isolated from one or more individuals according to methods well known in the art. The label can either be incorporated into the RNA or used in another manner as would be understood so as to monitor hybridization. The label used can be a luminescent label, an enzymatic label, a radioactive label, a chemical label or a physical label. In some embodiments, target and/or probe nucleic acids are labeled with a fluorescent molecule. Preferred fluorescent labels include, but are not limited to: fluorescein, amino coumarin acetic acid, tetramethylrhodamine isothiocyanate (TRITC), Texas Red, Cyanine 3 (Cy3) and Cyanine 5 (Cy5). The level of expression when referring to RNA can also refer to a measurable quantity of a given nucleic acid as determined relative to the amount of total RNA or cDNA used in microarray hybridizations wherein the amount of total RNA is 10 μg, 5 μg, 2.5 μg; 2 μg; 1 μg; 0.5 μg; 0.1 μg; 0.05 μg; 0.01 μg; 0.005 μg; 0.001 μg and the like.

As used herein, a "ligand" is a molecule that binds to another. "Polynucleotide Ligands" are those that specifically and/or selectively hybridize to products of the biomarkers and/or derivatives thereof. Polynucleotide ligands can specifically and/or selectively hybridize to RNA and/or protein products of the biomarkers, allowing measurement of the levels of the biomarker

products. The polynucleotide ligands may be any of various types of molecule, including but not limited to, any of various combinations of oligonucleotides, cDNA, DNA, RNA, PCR products, synthetic DNA, synthetic RNA, and/or modified nucleotides.

A ligand of the invention can also include a "polypeptide ligand" that specifically or selectively binds to the biomarker products, for example, allowing detection or measurement of the level of biomarker products including either RNA products and/or protein products. A polypeptide ligand may include a scaffold peptide, a linear peptide, or a cyclic peptide. In a preferred embodiment, the polypeptide ligand is an antibody. The antibody can be a human antibody, a chimeric antibody, a recombinant antibody, a humanized antibody, a monoclonal antibody, or a polyclonal antibody. The antibody can be an intact immunoglobulin, *e.g.*, an IgA, IgG, IgE, IgD, IgM or subtypes thereof. The antibody can be conjugated to a functional moiety (*e.g.*, a compound which has a biological or chemical function (which may be a second different polypeptide, a therapeutic drug, a cytotoxic agent, a detectable moiety, or a support. A polypeptide ligand e.g. antibody of the invention interacts with a polypeptide, encoded by one of the genes of a biomarker, with high affinity and specificity. For example, the polypeptide ligand binds to a polypeptide, encoded by one of the genes of a biomarker, with an affinity constant of at least 10^7 M^{-1}, preferably, at least 10^8 M^{-1}, 10^9 M^{-1}, or 10^{10} M^{-1}. The polynucleotide ligands and protein ligands may be used, according to standard art knowledge, to practice techniques such as Western blotting, immunoprecipitation, enzyme-linked immunosorbent assay (ELISA), protein microarray analysis and the like to measure the level of disclosed biomarker protein products.

An "mRNA" means an RNA complementary to a gene; an mRNA includes a protein coding region, and also may include 5' end and 3' untranslated regions (UTR).

As used herein, the term "majority" refers to a number representing more than 50% (e.g., 51%, 60%, or 70%, or 80% or 90% or up to 100%) of the total members of a composition. The term "majority", when referring to an array, it means more than 50% (e.g., 51%, 60%, or 70%, or 80% or 90% or up to 100%) of the total nucleic acid members that are stably associated with the solid substrate of the array.

Treatment of one or more colorectal pathologies or one or more subtypes of colorectal pathology is defined herein to provide medical aid to counteract the disease itself, the symptoms and/or the progression of the disease. Treatments also include removing the one or more

colorectal pathologies and include palliative therapy to help relieve symptoms and improve quality of life. Treatments also include reducing or preventing polyp formation, reducing or preventing polyp differentiation or morphology changes, and can also include development, recurrence and onset.

As used herein, "mRNA integrity" refers to the quality of mRNA extracts from either tissue samples or samples. In one embodiment, mRNA extracts with good integrity do not appear to be degraded when examined by methods well known in the art, for example, by RNA agarose gel electrophoresis (e.g., Ausubel et al., John Wiley & Sons, Inc., 1997, *Current Protocols in Molecular Biology*). Preferably, the mRNA samples have good integrity (e.g., less than 10%, in some embodiments less than 5%, and more in some embodiments less than 1% of the mRNA is degraded) to truly represent the gene expression levels of sample from which they are extracted.

As used herein, "nucleic acid(s)" and "nucleic acid molecule(s)" are interchangeable with the term "polynucleotide(s)" and it generally refers to any polyribonucleotide or poly-deoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA or any combination thereof. "Nucleic acids" include, without limitation, single- and double-stranded nucleic acids. As used herein, the term "nucleic acid(s)" also includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "nucleic acids". The term "nucleic acids" as it is used herein embraces such chemically, enzymatically or metabolically modified forms of nucleic acids, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including for example, simple and complex cells. A "nucleic acid" or "nucleic acid sequence" may also include regions of single- or double-stranded RNA or DNA or any combinations thereof and can include expressed sequence tags (ESTs) according to some embodiments of the invention. An EST is a portion of the expressed sequence of a gene (i.e., the "tag" of a sequence), made by reverse transcribing a region of mRNA so as to make cDNA.

As defined herein, a "nucleic acid array" refers a plurality of nucleic acids (or "nucleic acid members") localized on a support where each of the nucleic acid members is localized to a unique pre-selected region of a support. In one embodiment, a nucleic acid member is attached to the surface of the support and the nucleic acid member is DNA. In another embodiment, the nucleic acid member is either cDNA or and oligonucleotide. In another embodiment, the nucleic

acid member localized on the support is cDNA synthesized by polymerase chain reaction (PCR). The term "nucleic acid", as used herein, is interchangeable with the term "polynucleotide". In another preferred embodiment, a "nucleic acid array" refers to a plurality of unique nucleic acids attached to nitrocellulose or other membranes used in Southern and/or Northern blotting techniques.

As used herein "nucleic acid sample for hybridization to an array" is defined as a nucleic acid isolated and/or derived from a sample capable of binding to a nucleic acid bound to an array of complementary sequence through sets of non-covalent bonding interactions including complementary base pairing interactions. The nucleic acid sample for hybridization to an array can either be an isolated nucleic acid sequence corresponding to a gene or portion thereof, total RNA or mRNA isolated from a sample. In one embodiment, the nucleic acid sample for hybridization to an array is a blood nucleic acid sample (including whole blood, lysed blood, serum reduced, erythrocyte reduced blood, or peripheral blood leukocytes (PBLs)). In some embodiments, the nucleic acid sample is single- or double-stranded DNA, RNA, or DNA-RNA hybrids, from human blood and in some embodiments from RNA or mRNA extracts.

As used herein, a "nucleic acid member on an array" or a "nucleic acid member" includes nucleic acid immobilized on an array and capable of binding to a nucleic acid probes or samples of complementary sequence through sets of non-covalent bonding interactions, including complementary base pairing interactions. As used herein, a nucleic acid member or target may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in nucleic acids may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization (i.e., the nucleic acid target still specifically binds to its complementary sequence under standard stringent or selective hybridization conditions). Thus, nucleic acid members may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. In one embodiment, a conventional nucleic acid array of 'target' sequences bound to the array can be representative of the entire human genome, e.g. Affymetrix chip, and the biomarker or isolated biomarker consisting of or comprising one or more of the genes set out in **Table 1, Table 2,** or **Table 11,** or **Table 12** or gene probes (e.g. **Table 4**) is applied to the conventional array. In another embodiment, sequences bound to the array can be the biomarker or isolated biomarker according to the invention and total cellular RNA is applied to the array.

As used herein, the term "oligonucleotide" is defined as a molecule comprised of two or more deoxyribonucleotides and/ or ribonucleotides, and preferably more than three. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide. The oligonucleotides may be from about 8 to about 1,000 nucleotides long. Although oligonucleotides of 8 to 100 nucleotides are useful in the invention, preferred oligonucleotides range from about 8 to about 15 bases in length, from about 8 to about 20 bases in length, from about 8 to about 25 bases in length, from about 8 to about 30 bases in length, from about 8 to about 40 bases in length or from about 8 to about 50 bases in length.

As used herein, "patient" or "individual" or "subject" refers to a mammal and is in some embodiments human.

As used herein the term "peptide" refers to a polypeptide which is 50 amino acids in length or less.

As used herein, the phrase "pharmaceutically acceptable salt(s)" includes, but is not limited to, salts of acidic or basic groups that may be present in compounds identified using the methods of the present invention. Compounds that are basic in nature are capable of forming a wide variety of salts with various inorganic and organic acids. The acids that can be used to prepare pharmaceutically acceptable acid addition salts of such basic compounds are those that form non-toxic acid addition salts, i.e., salts containing pharmacologically acceptable anions, including but not limited to sulfuric, citric, maleic, acetic, oxalic, hydrochloride, hydrobromide, hydroiodide, nitrate, sulfate, bisulfate, phosphate, acid phosphate, isonicotinate, acetate, lactate, salicylate, citrate, acid citrate, tartrate, oleate, tannate, pantothenate, bitartrate, ascorbate, succinate, maleate, gentisinate, fumarate, gluconate, glucaronate, saccharate, formate, benzoate, glutamate, methanesulfonate, ethanesulfonate, benzenesulfonate, p-toluenesulfonate and pamoate (i.e., 1,1'-methylene-bis-(2-hydroxy-3-naphthoate)) salts. Compounds that include an amino moiety may form pharmaceutically acceptable salts with various amino acids, in addition to the acids mentioned above. Compounds that are acidic in nature are capable of forming base salts with various pharmacologically acceptable cations. Examples of such salts include alkali metal or alkaline earth metal salts and, particularly, calcium, magnesium, sodium lithium, zinc, potassium, and iron salts.

As used herein, "polynucleotide" encompasses single and double stranded polynucleotides, such as double-stranded DNA, single-stranded DNA, double-stranded RNA,

single-stranded RNA or DNA-RNA double stranded hybrids, and the like, of more than 8 nucleotides in length. The term "polynucleotide" includes a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides, that comprise purine and pyrimidine bases, or other natural, chemically or biochemically modified, non-natural, or derivatized nucleotide bases. The backbone of the polynucleotide can comprise sugars and phosphate groups, as may typically be found in RNA or DNA, or modified or substituted sugar or phosphate groups. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. The sequence of nucleotides may be interrupted by non-nucleotide components.

As used herein a "polynucleotide ligand that specifically and/or selectively hybridizes to RNA products of the biomarkers" ("biomarker RNA products") and/or to polynucleotides corresponding to biomarker RNA products, allowing measurement of levels of the RNA products are disclosed.

The polynucleotide ligands may be any of various types of molecule, including but not limited to, any of various combinations of oligonucleotides, cDNA, DNA, RNA, PCR products, synthetic DNA, synthetic RNA, and/or modified nucleotides.

As used herein, the term "proteinaceous agent" refers to polypeptides, proteins, peptides, and the like.

As used herein, "polypeptide sequences encoded by or protein products of" refers to the amino acid sequences obtained after translation of the protein coding region of an mRNA transcribed from a gene. As would be understood, one or more mRNA nucleotide sequences for each of the genes (biomarkers) of the invention can be identified using public databases such as the NCBI database found at http://www.ncbi.nlm.nih.gov. For example, representative mRNA species of those biomarkers identified in **Table 2** and **Table 12** are provided by their Human Genbank Accession number (see **Table 3** and **Table 13** respectively) and the corresponding polypeptide sequence is identified by a Protein Accession number (see **Table 3** and **Table 13** respectively). These Genbank Accession numbers provide the sequence of products of the biomarkers. When a protein or fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to a given region or three-dimensional structure on the protein; these regions or structures are referred to as epitopes or antigenic determinants. As used herein, "antigenic fragments" refers

portions of a polypeptide that contains one or more epitopes. Epitopes can be linear, comprising essentially a linear sequence from the antigen, or conformational, comprising sequences which are genetically separated by other sequences but come together structurally at the binding site for the polypeptide ligand. "Antigenic fragments" may be 5000, 1000, 500, 400, 300, 200, 100, 50 or 25 or 20 or 10 or 5 amino acids in length.

As used herein, the terms "prevent", "preventing" and "prevention" refer to the prevention of the development, recurrence or formation or growth or transformation of colorectal pathology including polyps or subtypes of polyps resulting from the administration of one or more compounds identified in accordance the methods of the invention or the administration of a combination of such a compound and another therapy.

The term, "primer", as used herein refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, source of primer and the method used and also the specificity or selectivity of the desired priming (ie so as to act as a point of initation of synthesis which is specific or selective for a given sequence of polynucleotide). For example, for testing applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15-25, but may contain additional nucleotides as well as fewer nucleotides. In addition, in some cases the primer can be selected so as to have a high GC content, can be selected so as to bind to regions which do not contain SNPs, can be selected so as to span an intron/ exon junction of RNA and the like. Other factors involved in determining the appropriate length and/or features of a primer are readily known to one of ordinary skill in the art.

The term "biomarker specific set of primers" or "primer sets" as used herein refers to a set of polynucleotide primers wherein one primer primes the synthesis of a sense strand, and the second primer primes the synthesis of an antisense strand so as to produce double stranded DNA complementary to a portion of one or more RNA products of the biomarker of the

invention. For example, the primers can include a first primer which is a sequence that can selectively hybridize to RNA, cDNA or EST complementary to a region of the biomarker of the invention to create an extension product and a second primer capable of selectively hybridizing to the extension product, which are used to produce double stranded DNA complementary to a region of the biomarker of the invention or products of the biomarker of the invention. The invention includes primers useful for measuring the level of RNA products of a biomarker. **Table 4, Table 6, Table 14, Table 16** and **Table 17** provide representative species of primers of the invention. A biomarker specific set of primers can be selected so that they will selectively amplify only portions of a polynucleotide complementary to one or more RNA products of a biomarker and do not amplify portions of polynucleotides complementary to other biomarkers.

As used herein, the term "probe" means oligonucleotides and analogs thereof and refers to a range of chemical species that recognize polynucleotide target sequences through hydrogen bonding interactions with the nucleotide bases of the target sequences. The probe or the target sequences may be single- or double-stranded RNA or single- or double-stranded DNA or a combination of DNA and RNA bases. A probe is at least 8 nucleotides in length and less than the length of a complete gene. A probe may be 10, 20, 30, 50, 75, 100, 150, 200, 250, 400, 500 and up to 2000 nucleotides in length as long as it is less than the full length of the target gene. In some embodiments, probes can be used as target sequences bound on a microarray. In some embodiments, probes can be used for quantitative real-time PCR (QRT-PCR) and include modifications so as to incorporate a fluorophore, a quencher, a minor groove binding reagent or other substances which allow detection of the probe during PCR amplification. The probe can also be modified so as to have both a detectable tag and a quencher molecule, for example Taqman® and Molecular Beacon® probes. The invention includes probes useful for measuring the expression of RNA products of biomarkers of the invention. For example, **Table 4**, Table 6, and **Table 14** and **Table 17** provides some representative species of a probe of the invention useful for QRT-PCR.

The oligonucleotides and analogs thereof may be RNA or DNA, or analogs of RNA or DNA, commonly referred to as antisense oligomers or antisense oligonucleotides. Such RNA or DNA analogs comprise but are not limited to 2-'O-alkyl sugar modifications, methylphosphonate, phosphorothiate, phosphorodithioate, formacetal, 3'-thioformacetal,

sulfone, sulfamate, and nitroxide backbone modifications, and analogs wherein the base moieties have been modified. In addition, analogs of oligomers may be polymers in which the sugar moiety has been modified or replaced by another suitable moiety, resulting in polymers which include, but are not limited to, morpholino analogs and peptide nucleic acid (PNA) analogs (Egholm, et al. Peptide Nucleic Acids (PNA)--Oligonucleotide Analogues with an Achiral Peptide Backbone, (1992)).

Probes may also be mixtures of any of the oligonucleotide analog types together or in combination with native DNA or RNA and may also include linker species. At the same time, the oligonucleotides and analogs thereof may be used alone or in combination with one or more additional oligonucleotides or analogs thereof.

As used herein, the term "products of the biomarker" or "biomarker products" refers to a species of RNA or a species of protein (wherein a species of RNA or protein can include multiple copies) isolated and/or derived from a sample including a tissue sample, a lymph sample, a lymph tissue sample, or a blood sample, or a fraction of a blood sample which corresponds to the biomarker (i.e., is transcribed from the gene or genetic element or is translated from RNA which is transcribed from the gene or genetic element). See **Table 3** and **Table 13**. The RNA may be pre-mRNA, mRNA, spliced variants of mRNA and the like. The protein may be in its native state or post-translationally processed in any one of various ways.

As used herein, "a plurality of" or "a set of" refers to two or more, for example, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more 10 or more etc.

As used herein, "pre-selected region", "predefined region", or "unique position" refers to a localized area on a substrate which is, was, or is intended to be used for the deposit of a nucleic acid and is otherwise referred to herein in the alternative as a "selected region" or simply a "region." The pre-selected region may have any convenient shape, e.g., circular, rectangular, elliptical, wedge-shaped, etc. In some embodiments, a pre-selected region is smaller than about 1 cm^2, more preferably less than 1 mm^2, still more preferably less than 0.5 mm^2, and in some embodiments less than 0.1 mm^2. A nucleic acid member at a "pre-selected region", "predefined region", or "unique position" is one whose identity (e.g., sequence) can be determined by virtue of its position at the region or unique position.

As used herein, the terms "prophylactic agent" and "prophylactic agents" refer to any compound(s) which can be used to prevent polyp formation, development, recurrence or onset. In certain embodiments, the term "prophylactic agent" refers to a compound identified in the screening assays described herein. In certain other embodiments, the term "prophylactic agent" refers to an agent other than a compound identified in the screening assays described herein which is known to be useful for, or has been or is currently being used to prevent or impede the onset, development and/or progression or transformation of one or more colorectal pathologies including one or more polyps or subtypes of polyps.

As used herein, the phrase "prophylactically effective amount" refers to the amount of a therapy (e.g., a prophylactic agent) which is sufficient to result in the prevention of the development, recurrence or onset or progression or transformation of one or more colorectal pathologies including one or more polyps or subtypes of polyps; the reduction or amelioration of the progression and/or severity of one or more colorectal pathologies including one or more polyps or subtypes of polyps; or the prevention of colorectal pathology including polyps or subtypes of polyps advancing to colorectal cancer.

As used herein, the terms "protein" and "polypeptide" are used interchangeably to refer to a chain of amino acids linked together by peptide bonds. In a specific embodiment, a protein is composed of less than 200, less than 175, less than 150, less than 125, less than 100, less than 50, less than 45, less than 40, less than 35, less than 30, less than 25, less than 20, less than 15, less than 10, or less than 5 amino acids linked together by peptide bonds. In another embodiment, a protein is composed of at least 200, at least 250, at least 300, at least 350, at least 400, at least 450, at least 500 or more amino acids linked together by peptide bonds.

A "protein coding region" refers to the portion of the mRNA encoding a polypeptide.

As used herein the "reference population" or "test population" refers to one or more populations of "control samples" used to develop one or more classifier. In one embodiment a single reference population can be divided into subpopulations. In another embodiment, two or more reference populations can be used. In some instances a classifier can be developed to differentiate between individuals with one or more colorectal pathologies or one or more polyps or one or more subtypes of polyps and individuals without the same colorectal pathology or one or more polyps or one or more subtypes of polyps. In some instances a first reference population would be comprised of individuals with the one or more colorectal pathologies and a

second reference population would be comprised of individuals without the one or more colorectal pathologies. The "reference population" or "test population" can be comprised of control samples from a number of individuals diagnosed with one or more colorectal pathologies including one or more polyps or one or more subtypes of polyps and individuals not having the colorectal pathologies or not having the one or more polyps or not having the one or more subtypes of polyps as determined using conventional diagnostic techniques. Note that in some embodiments the population of individuals having one or more colorectal pathologies can be selected to include individuals having a single subtype of polyp or one or more subtypes of polyps. In other embodiments the individuals who do not have one or more colon pathologies can include individuals who have been diagnosed with other disease or diseases. In another embodiment the individuals who do not have one or more colon pathologies can include individuals who have been diagnosed with other cancers. In one embodiment the "reference population" or "test population" is comprised of a roughly equivalent number of "control samples" from each trait subgroup (e.g., in this instance wherein said trait is a determination of status with regards to the presence of colorectal pathology). In another embodiment, each trait subgroup (e.g. having or not having colorectal pathology) of the "reference population" has a similar distribution with regards to other traits e.g., age, sex, drug status, etc.

As used herein, the term "selectively binds" in the context of proteins encompassed by the invention refers to the specific interaction of any two of a peptide, a protein, a polypeptide an antibody, wherein the interaction preferentially occurs as between any two of a peptide, protein, polypeptide and antibody preferentially as compared with any other peptide, protein, polypeptide and antibody. For example, when the two molecules are protein molecules, a structure on the first molecule recognizes and binds to a structure on the second molecule, rather than to other proteins. "Selective binding", "Selective binding", as the term is used herein, means that a molecule binds its specific binding partner with at least 2-fold greater affinity, and preferably at least 10-fold, 20-fold, 50-fold, 100-fold or higher affinity than it binds a non-specific molecule.

As used herein "selective hybridization" can refer to a hybridization which occurs as between a polynucleotide and an RNA or protein product of the biomarker of the invention wherein the hybridization is such that the polynucleotide binds to the RNA products of the biomarker of the invention preferentially to the RNA products of other genes in the genome in question. In a preferred embodiment a polynucleotide which "selectively hybridizes" is one

which hybridizes with a selectivity of greater than 70%, greater than 80%, greater than 90% and most preferably on 100% (ie cross hybridization with other RNA species preferably occurs at less than 30%, less than 20%, less than 10%). As would be understood to a person skilled in the art, a polynucleotide which "selectively hybridizes" to the RNA products of a biomarker of the invention can be determined by taking into account the length and composition.

As used herein, "specifically hybridizes", "specific hybridization" can refer to hybridization which occurs when two nucleic acid sequences are substantially complementary (at least about 65% complementary over a stretch of at least 14 to 25 nucleotides, preferably at least about 75% complementary, more preferably at least about 90% complementary). See Kanehisa, M., 1984, Nucleic acids Res., 12:203, incorporated herein by reference. As a result, it is expected that a certain degree of mismatch is tolerated. Such mismatch may be small, such as a mono-, di- or tri-nucleotide. Alternatively, a region of mismatch can encompass loops, which are defined as regions in which there exists a mismatch in an uninterrupted series of four or more nucleotides. Numerous factors influence the efficiency and selectivity of hybridization of two nucleic acids, for example, the hybridization of a nucleic acid member on an array to a target nucleic acid sequence. These factors include nucleic acid member length, nucleotide sequence and/or composition, hybridization temperature, buffer composition and potential for steric hindrance in the region to which the nucleic acid member is required to hybridize. A positive correlation exists between the nucleic acid length and both the efficiency and accuracy with which a nucleic acid will anneal to a target sequence. In particular, longer sequences have a higher melting temperature (T_M) than do shorter ones, and are less likely to be repeated within a given target sequence, thereby minimizing non-specific hybridization. Hybridization temperature varies inversely with nucleic acid member annealing efficiency. Similarly the concentration of organic solvents, e.g., formamide, in a hybridization mixture varies inversely with annealing efficiency, while increases in salt concentration in the hybridization mixture facilitate annealing. Under stringent annealing conditions, longer nucleic acids, hybridize more efficiently than do shorter ones, which are sufficient under more permissive conditions.

As used herein, "spotting" or "attaching" refers to a process of depositing a nucleic acid member onto a solid substrate to form a nucleic acid array such that the nucleic acid is stably bound to the solid substrate via covalent bonds, hydrogen bonds or ionic interactions.

As used herein, "stably associated" refers to a nucleic acid that is stably bound to a solid substrate to form an array via covalent bonds, hydrogen bonds or ionic interactions such that the nucleic acid retains its unique pre-selected position relative to all other nucleic acids that are stably associated with an array, or to all other pre-selected regions on the solid substrate under conditions in which an array is typically analyzed (i.e., during one or more steps of hybridization, washes, and/or scanning, etc.).

As used herein, "substrate" or "support" when referring to an array refers to a material capable of supporting or localizing an oligonucleotide or cDNA member. The support may be biological, non-biological, organic, inorganic, or a combination of any of these, existing as particles, strands, precipitates, gels, sheets, tubing, spheres, beads, containers, capillaries, pads, slices, films, plates, slides, chips, etc. Often, the substrate is a silicon or glass surface, (poly)tetrafluoroethylene, (poly)vinylidendifluoride, polystyrene, polycarbonate, a charged membrane, such as nylon 66 or nitrocellulose, or combinations thereof. In one embodiment, the support is glass. In some embodiments, at least one surface of the substrate will be substantially flat. In some embodiments, the support will contain reactive groups, including, but not limited to, carboxyl, amino, hydroxyl, thiol, and the like. In one embodiment, the support is optically transparent.

As herein used, the term "standard stringent conditions" means hybridization will occur only if there is at least 95% and preferably, at least 97% identity between the sequences, wherein the region of identity comprises at least 10 nucleotides. In one embodiment, the sequences hybridize under stringent conditions following incubation of the sequences overnight at 42°C, followed by stringent washes (0.2X SSC at 65°C). The degree of stringency of washing can be varied by changing the temperature, pH, ionic strength, divalent cation concentration, volume and duration of the washing. For example, the stringency of hybridization may be varied by conducting the hybridization at varying temperatures below the melting temperatures of the probes. The melting temperature of the probe may be calculated using the following formulas:

For oligonucleotide probes, between 14 and 70 nucleotides in length, the melting temperature (Tm) in degrees Celcius may be calculated using the formula: Tm=81.5+16.6(log [Na+]) + 0.41(fraction G+C)-(600/N) where N is the length of the oligonucleotide.

For example, the hybridization temperature may be decreased in increments of 5 °C from 68°C to 42 °C in a hybridization buffer having a Na^+ concentration of approximately 1M.

Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate stringency" conditions above 50 °C and "low stringency" conditions below 50 °C. A specific example of "moderate stringency" hybridization conditions is when the above hybridization is conducted at 55°C. A specific example of "low stringency" hybridization conditions is when the above hybridization is conducted at 45 °C.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation Tm=81.5+16.6(log [Na +]) + 0.41(fraction G + C)-(0.63% formamide)-(600/N), where N is the length of the probe.

For example, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50 °C. These conditions are considered to be "moderate stringency" conditions above 25% formamide and "low stringency" conditions below 25% formamide. A specific example of "moderate stringency" hybridization conditions is when the above hybridization is conducted at 30% formamide. A specific example of "low stringency" hybridization conditions is when the above hybridization is conducted at 10% formamide.

As used herein, the term "significant match", when referring to nucleic acid sequences, means that two nucleic acid sequences exhibit at least 65% identity, at least 70%, at least 75%, at least 80%, at least 85%, and preferably, at least 90% identity, using comparison methods well known in the art (i.e., Altschul, S.F. et al., 1997, *Nucl. Acids Res.*, 25:3389-3402; Schäffer, A.A. et al., 1999, *Bioinformatics* 15:1000-1011). As used herein, "significant match" encompasses non-contiguous or scattered identical nucleotides so long as the sequences exhibit at least 65%, and preferably, at least 70%, at least 75%, at least 80%, at least 85%, and preferably, at least 90% identity, when maximally aligned using alignment methods routine in the art.

As used herein, the term "synergistic" refers to a combination of a compound identified using one of the methods described herein, and another therapy (e.g., agent), which is more effective than the additive effects of the therapies. In some embodiments, such other therapy has been or is currently being to prevent, treat, or ameliorate one or more colorectal pathologies including one or more polyps or one or more subtypes of polyps. A synergistic effect of a

combination of therapies (e.g., prophylactic or therapeutic agents) permits the use of lower dosages of one or more of the therapies and/or less frequent administration of said therapies to an individual with colorectal pathologies including polyps or subtypes of polyps. The ability to utilize lower dosages of a therapy (e.g., a prophylactic or therapeutic agent) and/or to administer said therapy less frequently reduces the toxicity associated with the administration of said agent to an individual without reducing the efficacy of said therapies in the prevention or treatment of colorectal pathology including polyps or subtypes of polyps. In addition, a synergistic effect can result in improved efficacy of therapies (e.g., agents) in the prevention or treatment of colorectal pathology including polyps or subtypes of polyps. Finally, a synergistic effect of a combination of therapies (e.g., prophylactic or therapeutic agents) may avoid or reduce adverse or unwanted side effects associated with the use of either therapy alone.

As used herein, a "therapeutic agent" or "agent" refers to a compound that increases or decreases the expression of a polynucleotide or polypeptide sequences that are differentially expressed in a sample from an individual having one or more colorectal pathologies including polyps or a subtype of polyps. The invention provides for a "therapeutic agent" that 1) prevents the formation of colorectal pathology 2) reduces, delays, or eliminates advancement or transformation of colorectal pathology and/or 3) restores one or more expression profiles of one or more colorectal pathology indicative nucleic acids or polypeptides of a patient to a profile more similar to that of a normal individual when administered to a patient. In addition, the terms "therapeutic agent" and "therapeutic agents" refer to any compound(s) which can be used in the treatment or prevention of colorectal pathology or polyps or a subtype of polyps. In certain embodiments, the term "therapeutic agent" refers to a compound identified in the screening assays described herein. In other embodiments, the term "therapeutic agent" refers to an agent other than a compound identified in the screening assays described herein which is known to be useful for, or has been or is currently being used to treat or prevent colorectal pathology or polyps or subtypes of polyps.

As used herein, the term "therapeutically effective amount" refers to that amount of a therapy (e.g., a therapeutic agent) sufficient to treat one or more colorectal pathologies including polyps or one or more subtypes of polyps; prevent one or more colorectal pathologies including polyps or one or more subtypes of polyps; prevent colorectal pathologies including polyps or one or more subtypes of polyps from transforming and/or advancing to colorectal cancer, cause

regression of colorectal pathology, polyps or one or more subtypes of polyps, or to enhance or improve the therapeutic effect(s) of another therapy (e.g., therapeutic agent). In a specific embodiment, a therapeutically effective amount refers to the amount of a therapy (e.g., a therapeutic agent) that modulates gene expression of the products of the biomarkers of the inventions. In some embodiments, a therapeutically effective amount of a therapy (e.g., a therapeutic agent) modulates gene expression of the products of the biomarkers of the invention at least 5%, preferably at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 100% relative to a control therapeutic agent such as phosphate buffered saline ("PBS").

As used herein, the terms "treat", "treatment" and "treating" refer to the prevention of one or more colorectal pathologies including polyp formation or the formation of one or more subtypes of polyps, development, recurrence onset or transformation of one or more colorectal pathologies and, the reduction or amelioration of the progression and/or severity of one or more colorectal pathologies including polyps or subtypes thereof resulting from the administration of one or more compounds identified in accordance the methods of the invention, or a combination of one or more compounds identified in accordance with the invention and another therapy.

As used herein, a "tissue nucleic acid sample", refers to nucleic acids isolated and/or derived from tissue, for example polyp tissue, colon tissue, rectum tissue, lymphoid tissue, and the like. In some embodiments, a tissue nucleic acid sample is total RNA, mRNA or is a nucleic acid corresponding to RNA, for example, cDNA. A tissue nucleic acid sample can also include a PCR product derived from total RNA, mRNA or cDNA.

(C) Samples for Use in the Invention

Samples for use in the invention include refers to any one of various type of molecules, cells and/or tissues which can be isolated and/or derived from a test subject and/or control subject, and which contains one or more biomarker products. The sample can be isolated and/or derived from any fluid, cell or tissue. The sample can also be one which is isolated and/or derived from any fluid and/or tissue which predominantly comprises blood cells.

The sample which is isolated and/or derived from an individual can be assayed for gene expression products, particularly genes expression products differentially expressed in individuals with or without one or more colorectal pathologies. In one embodiment, the sample is

a fluid sample, a lymph sample, a lymph tissue sample or a blood sample. In one embodiment the sample is isolated and/or derived from peripheral blood. Alternately, the sample may be isolated and/or derived from alternate sources, including from any one of various types of lymphoid tissue.

Examples of samples isolated and/or derived from blood include samples of whole blood, serum-reduced whole blood, serum-depleted blood, and serum-depleted and erythrocyte depleted blood.

Unless otherwise indicated herein, samples obtained from any individual may be used in accordance with the methods of the invention. Examples of individuals from which such a sample may be obtained and utilized in accordance with the methods of the invention include, but are not limited to, individuals suspected of having one or more colorectal pathologies, individuals diagnosed as having one or more colorectal pathologies; individuals that have not been diagnosed with having one or more colorectal pathologies; individuals who have been confirmed as not having one or more colorectal pathologies.

In a further embodiment, the individual from whom a sample may be obtained is a test subject wherein it is unknown whether the person has one or more colorectal pathologies or not. In another embodiment, the individual from whom a sample may be obtained is a test subject wherein it is unknown whether the person has one or more colorectal pathologies or not.

Blood

In one aspect of the invention, a sample of blood is obtained from an individual according to methods well known in the art. A sample of blood may be obtained from an individual, for example a subject having one or more colorectal pathologies, suspected of having one or more colorectal pathologies or not having one or more colorectal pathologies. In some embodiments, a drop of blood is collected from a simple pin prick made in the skin of an individual. Blood may be drawn from an individual from any part of the body (*e.g.*, a finger, a hand, a wrist, an arm, a leg, a foot, an ankle, a stomach, and a neck) using techniques known to one of skill in the art, in particular methods of phlebotomy known in the art.

The amount of blood collected will vary depending upon the site of collection, the amount required for a method of the invention, and the comfort of the individual. However, an advantage of one embodiment of the present invention is that the amount of blood required to implement the methods of the present invention can be so small that more invasive procedures

are not required to obtain the sample. For example, in some embodiments, all that is required is a drop of blood. This drop of blood can be obtained, for example, from a simple pinprick. In some embodiments, any amount of blood is collected that is sufficient to detect the expression of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or all of the genes in **Table 1** and **Table 2** and **Table 11** and **Table 12**. As such, in some embodiments, the amount of blood that is collected is 1 ml or less, 0.5 ml or less, 0.1 ml or less, or 0.01 ml or less. However, the present invention is not limited to such embodiments. In some embodiments more blood is available and in some embodiments, more blood can be used to effect the methods of the present invention. As such, in various specific embodiments, 0.001 ml, 0.005 ml, 0.01 ml, 0.05 ml, 0.1 ml, 0.15 ml, 0.2 ml, 0.25 ml, 0.5 ml, 0.75 ml, 1 ml, 1.5 ml, 2 ml, 3 ml, 4 ml, 5 ml, 10 ml, 15 ml or more of blood is collected from a subject. In another embodiment, 0.001 ml to 15ml, 0.01 ml to 10 ml, 0.1 ml to 10 ml, 0.1 ml to 5 ml, 1 to 5 ml of blood is collected from an individual. In a further embodiment, 0.001-100ml, preferably 0.01-50ml, more preferably 0.01-25ml and most preferably 0.01-1ml of blood is collected from an individual.

In some embodiments of the present invention, blood is stored within a K3/EDTA tube (e.g., from Becton Dickinson). In another embodiment, one can utilize tubes for storing blood which contain stabilizing agents such as disclosed in U.S. Patent No. 6,617,170 (which is incorporated herein by reference). In another embodiment the PAXgene™ blood RNA system: provided by PreAnalytiX, a Qiagen/BD company, may be used to collect blood. In yet another embodiment, the Tempus™ blood RNA collection tubes, offered by Applied Biosystems may be used. Tempus™ collection tubes provide a closed evacuated plastic tube containing RNA stabilizing reagent for whole blood collection.

The blood collected is in some embodiments utilized immediately or within 1 hour, 2 hours, 3 hours, 4 hours, 5 hours or 6 hours or is optionally stored at temperatures such as 4 °C, or at -20°C prior to use in accordance with the methods of the invention. In some embodiments, a portion of the blood sample is used in accordance with the invention at a first instance of time whereas one or more remaining portions of the blood sample (or fractions thereof) are stored for a period of time for later use. For longer-term storage, storage methods well known in the art, such as storage at cryo temperatures (*e.g.* below -60 °C) can be used. In some embodiments, in addition to storage of the blood or instead of storage of the blood, plasma, serum, isolated

nucleic acid or proteins are stored for a period of time for later use in accordance with methods known in the art.

In one aspect, whole blood is obtained from an individual according to the methods of phlebotomy well known in the art. Whole blood includes blood which can be used as is, and includes blood wherein the serum or plasma has been removed or reduced, and the RNA or mRNA from the remaining blood sample has been isolated in accordance with methods well known in the art (*e.g.*, using, in some embodiments, gentle centrifugation at 300 to 800 xg for 5 to 10 minutes). In a specific embodiment, whole blood (*i.e.*, unfractionated blood) obtained from a subject is mixed with lysing buffer (*e.g.*, Lysis Buffer (1L): 0.6g EDTA; 1.0g $KHCO_2$, 8.2g NH_4Cl adjusted to pH 7.4 (using NaOH)), the sample is centrifuged and the cell pellet retained, and RNA or mRNA extracted in accordance with methods known in the art ("lysed blood") (see for example Sambrook et al.). In one embodiment, it is helpful to use unfractionated whole blood is preferred since it avoids the costly and time-consuming process to separate out the cell types within the blood (Kimoto, 1998, Mol. Gen. Genet 258:233-239; Chelly J et al., 1989, Proc. Nat. Acad. Sci. USA 86:2617-2621; Chelly J et al., 1988, Nature 333:858-860).

In some embodiments of the present invention, whole blood collected from an individual is fractionated (*i.e.*, separated into components) before isolated products of the biomarkers from the sample. In one embodiment, blood is serum depleted (or serum reduced). In another embodiment the blood is plasma depleted (or plasma reduced). In yet other embodiments blood is erythrocyte depleted or reduced. In some embodiments erythrocyte reduction is performed by preferentially lysing the red blood cells. In other embodiments, erythrocyte depletion or reduction is performed by lysing the red blood cells and further fractionating the remaining cells. In yet other embodiments erythrocyte depletion or reduction is performed but the remaining cells are not further fractionated. In other embodiments blood cells are separated from whole blood collected from an individual using other techniques known in the art. For example, blood collected from an individual can be subjected to Ficoll-Hypaque (Pharmacia) gradient centrifugation. Such centrifugation may separate various types of cells from a blood sample. In particular, Ficoll-Hypaque gradient centrifugation is useful to isolate peripheral blood leukocytes (PBLs) which can be used in accordance with the methods of the invention.

By way of example but not limitation, macrophages can be obtained as follows. Mononuclear cells are isolated from peripheral blood of a subject, by syringe removal of blood

followed by Ficoll-Hypaque gradient centrifugation. Tissue culture dishes are pre-coated with the subject's own serum or with AB+ human serum and incubated at 37°C for one hour. Non-adherent cells are removed by pipetting. Cold (4°C) 1mM EDTA in phosphate-buffered saline is added to the adherent cells left in the dish and the dishes are left at room temperature for fifteen minutes. The cells are harvested, washed with RPMI buffer and suspended in RPMI buffer. Increased numbers of macrophages can be obtained by incubating at 37°C with macrophage-colony stimulating factor (M-CSF). Antibodies against macrophage specific surface markers, such as Mac-1, can be labeled by conjugation of an affinity compound to such molecules to facilitate detection and separation of macrophages. Affinity compounds that can be used include but are not limited to biotin, photobiotin, fluorescein isothiocyante (FITC), or phycoerythrin (PE), or other compounds known in the art. Cells retaining labeled antibodies are then separated from cells that do not bind such antibodies by techniques known in the art such as, but not limited to, various cell sorting methods, affinity chromatography, and panning.

Blood cells can be sorted using a using a fluorescence activated cell sorter (FACS). Fluorescence activated cell sorting (FACS) is a known method for separating particles, including cells, based on the fluorescent properties of the particles. See, for example, Kamarch, 1987, Methods Enzymol 151:150-165. Laser excitation of fluorescent moieties in the individual particles results in a small electrical charge allowing electromagnetic separation of positive and negative particles from a mixture. An antibody or ligand used to detect a blood cell antigenic determinant present on the cell surface of particular blood cells is labeled with a fluorochrome, such as FITC or phycoerythrin. The cells are incubated with the fluorescently labeled antibody or ligand for a time period sufficient to allow the labeled antibody or ligand to bind to cells. The cells are processed through the cell sorter, allowing separation of the cells of interest from other cells. FACS sorted particles can be directly deposited into individual wells of microtiter plates to facilitate separation.

Magnetic beads can be also used to separate blood cells in some embodiments of the present invention. For example, blood cells can be sorted using a using a magnetic activated cell sorting (MACS) technique, a method for separating particles based on their ability to bind magnetic beads (0.5-100 m diameter). A variety of useful modifications can be performed on the magnetic microspheres, including covalent addition of an antibody which specifically recognizes a cell-solid phase surface molecule or hapten. A magnetic field is then applied, to physically

manipulate the selected beads. In a specific embodiment, antibodies to a blood cell surface marker are coupled to magnetic beads. The beads are then mixed with the blood cell culture to allow binding. Cells are then passed through a magnetic field to separate out cells having the blood cell surface markers of interest. These cells can then be isolated.

In some embodiments, the surface of a culture dish may be coated with antibodies, and used to separate blood cells by a method called panning. Separate dishes can be coated with antibody specific to particular blood cells. Cells can be added first to a dish coated with blood cell specific antibodies of interest. After thorough rinsing, the cells left bound to the dish will be cells that express the blood cell markers of interest. Examples of cell surface antigenic determinants or markers include, but are not limited to, CD2 for T lymphocytes and natural killer cells, CD3 for T lymphocytes, CD11a for leukocytes, CD28 for T lymphocytes, CD19 for B lymphocytes,CD20 for B lymphocytes, CD21 for B lymphocytes, CD22 for B lymphocytes, CD23 for B lymphocytes, CD29 for leukocytes, CD14 for monocytes, CD41 for platelets, CD61 for platelets, CD66 for granulocytes, CD67 for granulocytes and CD68 for monocytes and macrophages.

Whole blood can be separated into cell types such as leukocytes, platelets, erythrocytes, *etc.* and such cell types can be used in accordance with the methods of the invention. Leukocytes can be further separated into granulocytes and agranulocytes using standard techniques and such cells can be used in accordance with the methods of the invention. Granulocytes can be separated into cell types such as neutrophils, eosinophils, and basophils using standard techniques and such cells can be used in accordance with the methods of the invention. Agranulocytes can be separated into lymphocytes (*e.g.*, T lymphocytes and B lymphocytes) and monocytes using standard techniques and such cells can be used in accordance with the methods of the invention. T lymphocytes can be separated from B lymphocytes and helper T cells separated from cytotoxic T cells using standard techniques and such cells can be used in accordance with the methods of the invention. Separated blood cells (*e.g.*, leukocytes) can be frozen by standard techniques prior to use in the present methods.

(D) RNA Preparation

In one aspect of the invention, RNA is isolated from an individual in order to measure the RNA products of the biomarkers of the invention. RNA is isolated from a sample from individuals diagnosed as having one or more colorectal pathologies including one or more polyps

or one or more subtype of polyps, individuals not having one or more colorectal pathologies, not having one or more polyps or not having a subtype of polyps, or test subjects.

In some embodiments, RNA is isolated from blood which is erythrocyte depleted by the following protocol. Lysis Buffer is added to blood sample in a ratio of 3 parts Lysis Buffer to 1 part blood (Lysis Buffer (1L) 0.6g EDTA; 1.0g $KHCO_2$, 8.2g NH_4Cl adjusted to pH 7.4 (using NaOH)). Sample is mixed and placed on ice for 5-10 minutes until transparent. Lysed sample is centrifuged at 1000 rpm for 10 minutes at 4°C, and supernatant is aspirated. Pellet is resuspended in 5ml Lysis Buffer, and centrifuged again at 1000 rpm for 10 minutes at 4°C. Pelleted cells are homogenized using TRIzol® (GIBCO/BRL) in a ratio of approximately 6ml of TRIzol® for every 10ml of the original blood sample and vortexed well. Samples are left for 5 minutes at room temperature. RNA is extracted using 1.2 ml of chloroform per 1 ml of TRIzol®. Sample is centrifuged at 12,000 x g for 5 minutes at 4°C and upper layer is collected. To upper layer, isopropanol is added in ratio of 0.5 ml per 1 ml of TRIzol®. Sample is left overnight at -20°C or for one hour at -20°C. RNA is pelleted in accordance with known methods, RNA pellet air dried, and pellet resuspended in DEPC treated ddH_2O. RNA samples can also be stored in 75% ethanol where the samples are stable at room temperature for transportation.

In other aspects, RNA is prepared by first collecting blood into a PAXgene™ collection tube and then subsequently isolating the RNA using the PAXgene™ blood RNA isolated system provided by PreAnalytiX, a Qiagen/BD company. In another embodiment, RNA is prepared by first collecting blood into any known stabilizing soluation (e.g. a PAXgene™ collection or a TEMPUS® collection tube and then isolating the RNA using any method known to a person skilled in the art.

In other aspects globin reduced or depleted RNA is prepared. In one embodiment RNA is isolated first and then is subsequently treated to remove globin mRNA using one of any technique known in the art. For example, one can hybridize DNA primers and/or probes specific for globin RNA and utilize RNAse H to selectively degrade globin mRNA. In other embodiments RNA is isolated in a manner which removes the globin RNA during the RNA isolation steps (for example reducing globin RNA by selectively removing globin RNA using globin primers and/or probes attached to paramagnetic particles).

In other aspects of the invention RNA is prepared using one or more known commercial kits for isolating RNA (including isolating total RNA or mRNA and the like) such as oligo dT based purification methods, Qiagen® RNA isolation methods, LeukoLOCKT Total RNA Isolation System, MagMAX-96 Blood Technology from Ambion, Promega® polyA mRNA isolation system and the like.

Purity and integrity of RNA can be assessed by absorbance at 260/280nm and agarose gel electrophoresis followed by inspection under ultraviolet light. In some embodiments RNA integrity is assessed using more sensitive techniques such as the Agilent 2100 Bioanalyzer 6000 RNA Nano Chip.

(E) Biomarkers of the Invention

In one aspect, the invention provides biomarkers and biomarker combinations wherein the measure of the level of expression of the product or products of said biomarkers is indicative of the presence of one or more colorectal pathologies.

Table 1 is a list of biomarkers of one aspect of the invention. Each biomarker is differentially expressed in samples from individuals having or not having polyps using microarray assays. The table provides the Hugo Gene name, symbol and locus link ID; the RNA and protein accession number; and also includes both the p value (which represents the statistical significance of the observed differential expression) and a measure of the fold change as between the average measured level of individuals having polyps and the average measured level of individuals not having polyps.

Table 2 is a selection of those genes listed in **Table 1** and lists the gene symbol and the associated locus link ID for the biomarkers of the invention. The table also provides the fold change and direction of differential gene expression in individuals having polyps as compared to individuals not having polyps. As described, differential expression of the genes between individuals having or not having polyps can be identified using a non-parametic Wilcoxan-Mann-Whitney test or a parametric t test. The results of the tests are also shown in **Table 2**.

Table 11 shows genes identified as differentially expressed in samples from individuals having "high risk polyps" as compared with individuals not having high risk polyps (ie having low risk polyps or having no pathology at all) using microarray as described in **Example 2.** The table provides the gene name, gene ID; a representative human RNA accession number, and also provides the p value, the fold change (as between the average of individuals classified as

having high risk polyps as compared with the average of individuals having low risk polyps), along with the coefficient of variation for both the high risk polyp individuals and the low risk polyp individuals (the standard deviation of the normalized intensity divided by the mean normalized intensity). Column 1 is AffySpotID, column 2 is Fold Change, column 3 is p value, Column 4 is CV (Coefficient of Variation) (High RiskPolyp), column 5 is CV(Low Risk Polyp)., column 6 is Gene ID, column 7 is the HUGO Gene Symbol, column 8 is the Human RNA Accession Number and column 9 is the Gene Description.

Table 12 shows 48 biomarkers tested for differentially expression by QRT-PCR in samples from individuals having colorectal cancer and individuals not having colorectal cancer The 48 biomarkers were tested using QRT-PCR. The table provides the gene symbol, locus link ID, and gene description for each biomarker. The table also includes the p value (which represents the statistical significance of the observed differential expression), the measure of the fold change as between the average measured level of individuals having colorectal cancer and the average measured level of individuals not having colorectal cancer and the direction of the differential expression between individuals having colorectal cancer and not having colorectal cancer.

Other biomarkers of the invention are described within the specification. The invention thus encompasses the use of those methods known to a person skilled in the art to measure the expression of these biomarkers and combinations of biomarkers for each of the purposes outlined above.

As would be understood by a person skilled in the art, the locus link ID can be used to determine the sequence of all the RNA products and all the protein products of the biomarkers of the invention.

(F) Combinations of Biomarkers

In one embodiment, combinations of biomarkers of the present invention includes any combination of the biomarkers listed in **Table 1, Table 2, Table 11,** or **Table 12**. For instance, the number of possible combinations of a subset n of m genes in any of the tables above is described in Feller, *Intro to Probability Theory*, Third Edition, volume 1, 1968, ed. J. Wiley, using the general formula:

$$m!/(n)!\ (m\text{-}n)!$$

For example, where n is 2 and m is 8, the number of combinations of biomarkers is:

$$\frac{8!}{2!\,(8-2)!} = \frac{8x7x6x5x4x3x2x1}{(2x1)\,(6x5x4x3x2x1)} = 40320/1440 = 28$$

unique two-gene combinations. The measurement of the gene expression of each of these two-gene combinations can independently be used to determine whether a patient has one or more colorectal pathologies. In another specific embodiment in which *m* is 8 and *n* is three, there are 8!/3!(8-3)! unique three-gene combinations. Each of these unique three-gene combinations can independently serve as a model for determining whether a patient has one or more colorectal pathologies.

(G) Testing Combinations of Biomarkers by Generating Formulas Resulting from One or More Classifiers

The invention further provides a means of testing combinations of biomarkers from **Table 1, Table 2, Table 11,** or **Table 12** or subsets thereof for their ability to test for one or more colorectal pathologies or one or more subtypes of colorectal pathology. Also provided are methods of evaluating the combinations tested tested for their ability to test an individual for the presence of one or more colorectal pathologies or one or more subtypes of colorectal pathology. In order to test combinations of biomarkers and generate classifiers, a mathematical model of the invention can be used. A mathematical model of the invention can be used to test each selected combination of biomarkers from all combinations of biomarkers or a selected subset thereof.

In some embodiments, it is useful to further select biomarkers to be tested as combinations. in one embodiment, one can select individual biomarkers on the basis of the p value as a measure of the likelihood that the the individual biomarker can distinguish as between the two phenotypic trait subgroups. Thus in one embodiment, biomarkers are chosen to test in combination by input into a model wherein the p value of each biomarker is less than 0.2, 0.1, 0.5; less than 0.1, less than 0.05, less than 0.01, less than 0.005, less than 0.001, less than 0.0005, less than 0.0001, less than 0.00005, less than 0.00001, less than 0.000005, less than 0.000001 etc. We have also surprisingly found that even biomarkers which demonstrate a p value of greater than 0.2 (and thus would normally not be considered to be a useful individual biomarker) do significantly increase the ability of a combination of biomarkers in which they are included to distinguish as between two phenotypic trait subgroups. In otherembodiments, biomarkers for input into the model to test in combination are chosen on the basis of the fold change of

differential expression of the product of the biomarker as between the the two phenotypic trait subgroups. Note that in measuring differential fold change in blood, the fold change differences can be quite small, thus in some embodiments, selection of biomarker subsets for input into classifier is based on a differential fold change where the fold change is greater than 1.01, 1.02, 1.03, 1.04, 1.05, 1.06, 1.07, 1.08, 1.09, 1.1, 1.125, 1.15, 1.175, 1, 1.2, 1.225, 1.25, 1.275, 1.30, greater than 1.3, greater than 1.4, greater than 1.5, greater than 1.6, greater than 1.7, greater than 1.8, greater than 1.9, greater than 2.0, greater than 2.1, greater than 2.2, greater than 2.3, greater than 2.4, greater than 2.5, greater than 2.6, greater than 2.7, greater than 2.8, greater than 2.9, greater than 3.0, greater than 3.1, greater than 3.2. greater than 3.3, greater than 3.4 greater than 3.5, greater than 4.0 and the like. In yet other embodiments in order to select subsets of biomarkers to test in combination, one can also take into account the coefficient of variation as a variability of the data representing the level of expression of the product of the biomarker amongst individuals within a phenotypic trait subgroup. In some embodiments, it is helpful to select biomarkers on thea basis of a combination of factors including p value, fold change, and coefficient of variation as would be understood by a person skilled in the art. In some embodiments, biomarkers are first selected as outlined above on the basis of the p value resulting from the biomarker data and then a subselection of said biomarkers is chosen on the basis of the differential fold change determined from the biomarker data. In other embodiments, biomarkers are first selected on the basis of differential fold change, and then subselection is made on the basis of p value. In some embodiments, the use of one or more of the selection criteria and subsequent ranking permits the selection of the top 2.5%, 5%, 7.5%, 10%, 12.5%, 15%, 17.5%, 20%, 30%, 40%, 50% or more of the ranked biomarkers for input into the model. In some embodiments, the desired number of selected biomarkers can be 4,000; 3,000; 2,000; 1,000; 900; 800; 700; 600; 500; 400; 300; 200; 190; 180; 170; 160; 150; 140; 130; 120; 110; 100; 90; 80; 70; 60; 50; 40; 30; 20; or 10. In other embodiments, the selection criteria noted above can be set on the basis of the desired number of selected biomarkers for use in the model. As would be understood, one can select therefore all of the individually identified biomarkers or subsets of the individually identified biomarkers and test all possible combinations of the selected biomarkers to identify useful combinations of biomarkers. In another embodiment, one can select a subset of biomarkers and then test all possible combinations of 2 biomarkers from that subset, 3 biomarkers from that subset, 4 biomarkers from that subset, 5 biomarkers from that subset, 6

biomarkers from that subset 7 biomarkers from that subset, 8 biomarkers from that subset 9 biomarkers from that subset or 10 biomarkers from that subset in order to identify useful combinations of biomarkers. A selection criteria to determine the number of selected individual biomarkers to test in combination, and to select the number of possible combinations of biomarkers will depend upon the resources available for obtaining the biomarker data and/or the computer resources available for calculating and evaluating classifiers resulting from the model.

The classifier generated by the mathematical model can be subsequently evaluated by determining the ability of the classifier to correctly call each individual for one of the two phenotypic traits of the population used to generate the classifier (ie having or not having one or more colorectal pathologies). In a preferred embodiment, the individuals of the training population used to derive the model are different from the individuals of the training population used to test the model. As would be understood by a person skilled in the art, this allows one to predict the ability of the combinations as to their ability to properly characterize an individual whose phenotypic trait characterization is unknown.

The data which is input into the mathematical model can be any data which is representative of the expression level of the product of the biomarkers being evaluated. Mathematical models useful in accordance with the invention include those using both supervised or unsupervised learning techniques. In a preferred embodiment of the invention, the mathematical model chosen uses supervised learning in conjunction with a "training population" to evaluate each of the possible combination of biomarkers of the invention. In one embodiment of the invention, the mathematical model used is selected from the following: a regression model, a logistic regression model, a neural network, a clustering model, principal component analysis, nearest neighbour classifier analysis, linear discriminant analysis, quadratic discriminant analysis, a support vector machine, a decision tree, a genetic algorithm, classifier optimization using bagging, classifier optimization using boosting, classifier optimization using the Random Subspace Method, a projection pursuit, genetic programming and weighted voting. In a preferred embodiment, a logistic regression model is used. In another preferred embodiment, a neural network model is used.

The results of applying a mathematical model of the invention to the data will generate one or more classifiers using one or more biomarkers. In some embodiments, multiple classifiers are created which are satisfactory for the given purpose (e.g. all have sufficient AUC and/or

sensitivity and/or specificity). In this instance, in some embodiments, a formula is generated which utilizes more than one classifier. For example, a formula can be generated which utilizes classifiers in series (e.g. first obtains results of classifier A, then classifier B e.g. Classifier A differentiates pathology from non pathology; classifier B then determines whether the pathology is colorectal cancer or not colorectal cancer). In another embodiment, a formula can be generated which results from weighting the results of more than one classifier. For example, the results of each classifier can be given a score of 1 and an indication of probability of a test subject having one or more colorectal pathologies is the result of the aggregate score of each of the selected classifiers of a given formula. Other possible combinations and weightings of classifiers would be understood and are encompassed herein.

Classifiers generated can be used to test an unknown or test subject. In one embodiment, the results from equations generated by logistic regression to answer the question does an individual have one or more colorectal pathologies or is an individual "normal". In yet another embodiment of the invention, the answer to the question above may be an answer of non-determinable.

In one embodiment of the invention, each classifier is evaluated for its ability to properly characterize each individual of the training population using those methods known to a person skilled in the art. For example one can evaluate the classifier using cross validation, Leave One out Cross Validation (LOOCV), n-fold cross validation, jackknife analysis using standard statistical methods as disclosed. In another embodiment of the invention, each classifier is evaluated for its ability to properly characterize those individuals of the training population which were not used to generate the classifier.

In one embodiment, the method used to evaluate the classifier for its ability to properly characterize each individual of the training population is a method which evaluates the classifier's sensitivity (TPF, true positive fraction) and 1-specificity (TNF, true negative fraction). In one embodiment, the method used to test the classifier is Receiver Operating Characteristic ("ROC") which provides several parameters to evaluate both the sensitivity and specificity of the result of the equation generated. In one embodiment using the Receiver Operating Characteristic ("ROC") the ROC area (area under the curve) is used to evaluate the equations. A ROC area greater than 0.5, 0.6, 0.7, 0.8, 0.9 is preferred. A perfect ROC area score of 1.0 indicates with both 100% sensitivity and 100% specificity. In some embodiments

classifiers are selected on the basis of the score. For example, where the scoring system used is receiver operating characteristic (ROC) curve score determined by an area under the ROC curve, in some embodiments, those classifiers with scores of greater than 0.95, 0.9, 0.85, 0.8, 0.7, 0.65, 0.6, 0.55 0.5 or 0.45 are chosen. In other embodiments, where specificity is important to the use of the classifier, a sensitivity threshold can be set and classifiers ranked on the basis of the specificity chosen. For example classifiers with a cutoff for specificity of greater than 0.95, 0.9, 0.85, 0.8, 0.7, 0.65, 0.6, 0.55 0.5 or 0.45 can be chosen. Similarly, the specificity threshold can be set and classifiers ranked on the basis of sensitivity greater than 0.95, 0.9, 0.85, 0.8, 0.7, 0.65, 0.6, 0.55 0.5 or 0.45 can be chosen. Thus in some embodiments, only the top 10 ranking classifiers, the top 20 ranking classifiers, or the top 100 ranking classifiers are selected.

As would be understood by a person skilled in the art, the utility of the combinations and classifiers determined by a mathematical model will depend upon the phenotypes of the populations used to generate the data for input into the model. Examples of specific embodiments are described more thoroughly herein.

(H) Populations for Input Into the Mathematical Models

Populations used for input should be chosen so as to result in statistically significant resulting classifier. In some embodiments, the reference or training population includes between 10 and 30 subjects. In another embodiment the reference population contains between 30-50 subjects. In still other embodiments, the reference population includes two or more populations each containing between 50 and 100, 100 and 500, between 500 and 1000, or more than 1000 subjects. The reference population includes two or more subpopulations. In a preferred embodiment, the phenotypic trait characteristics of the subpopulations are similar but for the diagnosis with respect to the presence of one or more colorectal pathologies, for example the distribution within the subpopulations are similar with regards to the age and sex of the subpopulations. It is also preferred that the subpopulations are of roughly equivalent numbers. It is to be understood that the methods herein do not require using data from every member of a population, but instead may rely on data from a subset of a population in question.

For example, for a reference or test population for input into a mathematical model to identify those biomarkers which are useful in identifying an individual as having any polyps or not having any polyps, the reference population is comprised of individuals having polyps (the first subpopulation), and individuals not having polyps (the second subpopulation). For purposes

of characterizing the subpopulations as having or not having polyps, any verified method can be used including digital rectal examiniation, fecal occult blood testing, rigid sigmoidoscopy, flexible sigmoidoscopy, double-contrast barium enema, colonoscopy, and histological examination. Preferably only those individuals whose diagnoses are certain are utilized as part of the reference population.

In another embodiment, to identify those biomarkers which are useful in identifying an individual as having high risk polyps or not, the reference population is comprised of individuals having high risk polyps (the first subpopulation), and individuals not having high risk polyps (the second subpopulation) where high risk polyps are the following: Tubulovillous Adenoma, Villous Adenoma, Cancer High Grade Dysplasia and Tubular Adenoma where the Tubular Adenoma is greater than 10mm. For purposes of characterizing the subpopulations as having or not having high risk polyps, any verified method can be used including digital rectal examiniation, fecal occult blood testing, rigid sigmoidoscopy, flexible sigmoidoscopy, double-contrast barium enema, colonoscopy, and histological examination.

In yet another embodiment, to test biomarkers which are useful in identifying an individual as having early stage of colorectal cancer or not, the reference population can, for example be comprised of individuals having localized colorectal cancer as compared with individuals with other types of colorectal cancer (e.g. late stage).

In another embodiment, to identify those biomarkers which are useful in identifying an individual as having high risk polyps or not, the reference population is comprised of individuals having high risk polyps (the first subpopulation), and individuals not having high risk polyps (the second subpopulation) where high risk polyps are the following: Tubulovillous Adenoma; Villous Adenoma; Cancer; High Grade Dysplasia; and Tubular Adenoma.

(I) Data for Input into the Mathematical Models to Identify Classifiers for Testing for Colorectal Pathology

Data for input into the mathematical models is data representative of the level of the products of the biomarkers of the invention. As such the data is the measure of the level of expression of the products of the biomarkers of the invention including either mRNA and/or protein.

In one embodiment of the invention, the RNA products of the biomarkers of the invention which are measured are the population of RNA products including the mRNA, and all

of the spliced variants of the mRNA. In another embodiment of the invention the products measured are all of the mRNA products expressed in blood. In yet another embodiment of the invention, the products measured include one or more specific spliced variants of the mRNA which are expressed in blood. In yet another embodiment of the invention, the products measured are the RNA products listed in **Table 3** or **Table 13**.

Protein products of the biomarkers of the invention are also included within the scope of the invention. To practice the invention, measurement of the protein products of the biomarkers of the invention can be used for purposes of testing for one or more colorectal pathologies. More particularly, measurement of those populations of protein products of the biomarkers which are differentially expressed in individuals having or not having any polyps are useful for purposes of testing and are encompassed herein.

In one embodiment of the invention the protein products are those translated from the biomarkers listed in **Table 1, Table 2, Table 11,** or **Table 12**. In another embodiment, the protein products are those which are expressed in blood. In yet another embodiment of the invention, the protein products are those corresponding to the proteins listed in **Table 3** or **Table 13**.

In yet another embodiment, data reflective of the level of expression of a combination of protein products and RNA products of the biomarkers are used. As would be understood by a person skilled in the art, other combinations of input data can be utilized to generate classifiers useful in accordance with the invention.

In other embodiments, as would be understood by one of ordinary skill in the art, data reflective of each biomarker in each member of the population is not necessary so long as there are data for sufficient members of each reference population to permit creation of a classifier. For example, data representative of biomarkers in 99%, 95%, 90%, 85%, 80%, or 75% of members of a population may suffice in given circumstances.

(J) Mathematical Models

Formulae for use with the methods described herein may generally have the form:

$$V = C + \Sigma\beta_i f(X_i) + \Sigma\beta_{ij} f(X_i, X_j) + \Sigma\beta_{ijk} f(X_i, X_j, X_k) + \ldots$$

Wherein V is a value indicating the probability that a test subject has one or more colorectal pathologies, X_i is a level of one or more products of an ith biomarker in a sample from the test subject, βi is a coefficient for a term involving only the ith biomarker, β_{ij} is a coefficient for a

term that is a function of the ith and jth biomarkers, β_{ijk} is a coefficient for a term that is a function of the ith, jth and kth biomarkers, and C is a constant. Still other terms may find themselves in this formula, such as terms depending on four or more biomarkers.

By 'indicates' is meant that V might be an actual probability (a number varying between 0 and 1), or V might be a quantity from which a probability can be readily derived.

There are various forms of functions $f(X_i, X_j, \ldots)$ that depend on expression levels of the various biomarkers. For example, the functions may be polynomials in those expression levels, *i.e.*, involve products of the various biomarkers raised to numeric powers. Examples include: $X_iX_j^2$, $X_iX_jX_k$, $(X_iX_j)^{1/2}$, $X_iX_j + X_iX_k$. The functions may additionally or alternatively involve logarithms, exponentials, or still other functions of the expression levels.

In certain embodiments, the $f(X_i, X_j, \ldots)$ depend on ratios of the biomarker expression levels, *i.e.*, $f(X_i, X_j) = X_i/X_j$.

Regression Models

In some embodiments the expression data for some or all of the biomarkers identified in the present invention are used in a regression model, such as but not limited to a logistic regression model or a linear regression model, so as to identify classifiers useful in diagnosing one or more colorectal pathologies. The regression model is used to test various combinations of two or more of the biomarkers identified in **Table 1, Table 2, Table 11,** or **Table 12** to generate classifiers. In the case of regression models, the classifiers which result are in the form of equations which provide a dependent variable Y, which represents the presence or absence of a given phenotype where the data representing the expression of each of the biomarkers in the equation is multiplied by a weighted coefficient as generated by the regression model. The classifiers generated can be used to analyze expression data from a test subject and provide a result indicative of the probability of a test subject having one or more colorectal pathologies. In general, a multiple regression equation of interest can be written

$$Y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_k X_k + \varepsilon$$

where Y, the dependent variable, indicates presence (when Y is positive) or absence (when Y is negative) of the biological feature (e.g., absence or presence of one or more colorectal pathologies) associated with the first subgroup. This model says that the dependent variable Y depends on k explanatory variables (the measured characteristic values for the k select genes (*e.g.*, the biomarkers) from subjects in the first and second subgroups in the reference

population), plus an error term that encompasses various unspecified omitted factors. In the above-identified model, the parameter β_1 gauges the effect of the first explanatory variable X_1 on the dependent variable Y (*e.g.*, a weighting factor), holding the other explanatory variables constant. Similarly, β_2 gives the effect of the explanatory variable X_2 on Y, holding the remaining explanatory variables constant.

A logistic regression model is a non-linear transformation of the linear regression. The logistic regression model is often referred to as the "logit" model and can be expressed as

$$\ln[p/(1-p)] = \alpha + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_k X_k + \varepsilon \quad \text{or}$$

$$[p/(1-p)] = \exp^{\alpha} \exp^{\beta_1 X_1} \exp^{\beta_2 X_2} \times \cdots \times \exp^{\beta_k X_k} \exp^{\varepsilon}$$

where,

α and ϵ are constants

ln is the natural logarithm, $\log_e$, where e=2.71828...,

p is the probability that the event Y occurs, p(Y=1),

p/(1-p) is the "odds ratio",

ln[p/(1-p)] is the log odds ratio, or "logit", and

all other components of the model are the same as the general linear regression equation described above. It will be appreciated by those of skill in the art that the term for α and ϵ can be folded into a single constant. Indeed, in preferred embodiments, a single term is used to represent α and ϵ. The "logistic" distribution is an S-shaped distribution function. The logit distribution constrains the estimated probabilities (p) to lie between 0 and 1.

In some embodiments of the present invention, the logistic regression model is fit by maximum likelihood estimation (MLE). In other words, the coefficients (*e.g.*, α, β_1, β_2, ...) are determined by maximum likelihood. A likelihood is a conditional probability (e.g., P(Y|X), the probability of Y given X). The likelihood function (L) measures the probability of observing the particular set of dependent variable values (Y_1, Y_2, ..., Y_n) that occur in the sample data set. It is written as the probability of the product of the dependent variables:

$$L = \text{Prob}\ (Y_1 * Y_2 *** Y_n)$$

The higher the likelihood function, the higher the probability of observing the Ys in the sample. MLE involves finding the coefficients (α, β_1, β_2, ...) that makes the log of the likelihood function (LL < 0) as large as possible or -2 times the log of the likelihood function (-2LL) as small as possible. In MLE, some initial estimates of the parameters α, β_1, β_2, ... are made. Then

the likelihood of the data given these parameter estimates is computed. The parameter estimates are improved the likelihood of the data is recalculated. This process is repeated until the parameter estimates do not change much (for example, a change of less than .01 or .001 in the probability). Examples of logistic regression and fitting logistic logistic regression models are found in Hastie, *The Elements of Statistical Learning*, Springer, New York, 2001, pp. 95-100 which is incorporated herein in its entirety.

Neural Networks

In another embodiment, the expression measured for each of the biomarkers of the present invention can be used to train a neural network. A neural network is a two-stage regression or classification model. A neural network can be binary or non binary. A neural network has a layered structure that includes a layer of input units (and the bias) connected by a layer of weights to a layer of output units. For regression, the layer of output units typically includes just one output unit. However, neural networks can handle multiple quantitative responses in a seamless fashion. As such a neural network can be applied to allow identification of biomarkers which differentiate as between more than two populations (ie more than two phenotypic traits). In one specific example, a neural network can be trained using expression data from the products of the biomarkers in Table 1, Table 2, Table 11, or Table 12 to identify those combinations of biomarkers which are specific for one or more colorectal pathologies. As a result, the trained neural network can be used to directly identify combinations of biomarkers useful to test for one or more colorectal pathologies. In some embodiments, the back-propagation neural network (see, for example Abdi, 1994, "A neural network primer", J. Biol System. 2, 247-283) containing a single hidden layer of ten neurons (ten hidden units) found in EasyNN-Plus version 4.0g software package (Neural Planner Software Inc.) is used.

Neural networks are described in Duda *et al.*, 2001, *Pattern Classification*, Second Edition, John Wiley & Sons, Inc., New York; and Hastie *et al.*, 2001, *The Elements of Statistical Learning*, Springer-Verlag, New York which is incorporated herein in its entirety.

Singular Value Decomposition (SVD) and Principal Component Analysis (PCA)

Singular value decomposition (SVD) and Principal Component Analysis (PCA) are common techniques for analysis of multivariate data, and we have found that gene expression data is well suited to analysis using SVD/PCA. SVD or equivalently, in this case, PCA, is defined as follows:

Singular value decomposition (SVD) and Principal Component Analysis (PCA) are common techniques for analysis of multivariate data, and we have found gene expression data are well suited to analysis using SVD/PCA. SVD or equivalently, in this case, PCA, is defined as follows:

Let G be an m x n gene expression matrix with rank r, and m $\geq$n, and therefore r $\leq$n where m is a row and n is a column of data of the matrix. In the case of microarray data, gij is the level of one or more products of the ith biomarker in the jth assay. The elements of the ith row of G form the n-dimensional vector bi (where b is a biomarker), which we refer to as the transcriptional response of the ith biomarker. Alternatively, the elements of the jth column of G form the m-dimensional vector aj, which we refer to as the expression profile (or gene expression profile) of the jth assay.

The equation for singular value decomposition of G is the following:

$$G = USV^T$$

where U is an m × n matrix, S is an n × n diagonal matrix, and VT is also an n × n matrix. The columns of U are called the left singular vectors, {uk}, and form an orthonormal basis for the assay expression profiles, so that $u_i \cdot u_j = 1$ for $i = j$, and $u_i \cdot u_j = 0$ otherwise. The rows of V^T contain the elements of the right singular vectors, $\{v_k\}$, and form an orthonormal basis for the gene transcriptional responses. The elements of S are only nonzero on the diagonal, and are called the singular values. Thus, $S = \text{diag}(s_1,\ldots,s_n)$. Furthermore, $s_k > 0$ for $1 \leq k \leq r$, and $s_i = 0$ for $(r+1) \leq k \leq n$. By convention, the ordering of the singular vectors is determined by high-to-low sorting of singular values, with the highest singular value in the upper left index of the S matrix. Note that for a square, symmetric matrix X, singular value decomposition is equivalent to diagonalization, or solution of the eigenvalue problem.

Other Mathematical Models

The pattern classification and statistical techniques described above are merely examples of the types of models that can be used to construct classifiers useful for diagnosing or detecting one or more colorectal pathologies, for example clustering as described on pages 211-256 of Duda and Hart, *Pattern Classification and Scene Analysis*, 1973, John Wiley & Sons, Inc., New York, incorporated herein by reference in its entirety; Principal component analysis, (see for Jolliffe, 1986, *Principal Component* Analysis, Springer, New York, incorporated herein by

reference); nearest neighbour classifier analysis, (see for example Duda, *Pattern Classification*, Second Edition, 2001, John Wiley & Sons, Inc; and Hastie, 2001, *The Elements of Statistical Learning*, Springer, New York); linear discriminant analysis, (see for example Duda, *Pattern Classification*, Second Edition, 2001, John Wiley & Sons, Inc; and Hastie, 2001, *The Elements of Statistical Learning*, Springer, New York; Venables & Ripley, 1997, *Modern Applied Statistics with s-plus*, Springer, New York); Support Vector Machines (see, for example, Cristianini and Shawe-Taylor, 2000, *An Introduction to Support Vector Machines*, Cambridge University Press, Cambridge, Boser *et al.*, 1992, "A training algorithm for optimal margin classifiers, in *Proceedings of the 5th Annual ACM Workshop on Computational Learning Theory,* ACM Press, Pittsburgh, PA, pp. 142-152; Vapnik, 1998, *Statistical Learning Theory*, Wiley, New York, incorporated herein by reference.)

Computer implementation

The methods described herein are preferably performed by a suitably programmed computer. The computer system for use with the methods described herein, as further described herein, is configured to accept and to process data and may be a single-processor or multi-processor computer system. Examples of suitable computer systems include, but are not limited to, any one of various combinations of mainframe computers, minicomputers, personal computers, laptop computers, notebook computers, hand-held computers, personal digital assistants, mobile phones, set-top boxes, microprocessor-based consumer electronics, programmable consumer electronics, and the like. Additionally, the methods of the invention may be practiced on networked computers, CPU-clusters, workstations, and so-called mainframe computers. The computer system may be a locally accessed computer, a remotely accessed computer system (e.g. server), or a combination of both. Depending on the application and purpose, the computer system may have access or be accessible to "the internet" [World Wide Web (WWW)]. It will be appreciated that the computer system may be a stand-alone system or a distributed system comprising multiple devices communicating with each other through a network. Depending on the application and purpose, the computer system may be a static or mobile computer system. One of ordinary skill in the art will possess the necessary knowledge and skills for selecting, obtaining and utilizing a suitable computer system for practicing any aspect of the invention.

It is therefore consistent with the description herein that various methods and formulae are implemented, in the form of computer program instructions, and executed on a computer as also described herein. Suitable programming languages for expressing the program instructions include, but are not limited to, one or more languages selected from the group consisting of: C, C++, an embodiment of FORTRAN such as FORTRAN77 or FORTRAN90, Java, Visual Basic, Perl, Tcl/Tk, JavaScript, and ADA. It is to be understood that various aspects of the methods may be written in different computing languages from one another, where such languages are preferred for particular applications, and the various aspects are caused to communicate with one another by appropriate system-level-tools available on a given computer.

The computer program instructions are stored in a computer memory during execution, and may additionally be stored on any of various forms of computer-readable media known in the art, such as, but not limited to, CD-Rom, CD-R, CD-RW, flash memory, memory cards, memory sticks, DVD-Rom, USB-sticks, optical discs, or high capacity network storage drives. It is thus consistent with ordinary practice of the present invention that the computer program instructions can be delivered to a user on a transferable medium such as a CD-Rom, and also delivered over a computer network, such as by downloading over the Internet through a web-interface.

FIG. 1 shows a schematic of a general-purpose computer system 100 suitable for practicing the methods described herein. The computer system 100, shown as a self-contained unit but not necessarily so limited, comprises at least one data processing unit (CPU) 102, a memory 104, which will typically include both high speed random access memory as well as non-volatile memory (such as one or more magnetic disk drives) but may be simply flash memory, a user interface 108, optionally a disk 110 controlled by a disk controller 112, and at least one optional network or other communication interface card 114 for communicating with other computers as well as other devices. At least the CPU 102, memory 104, user interface 108, disk controller where present, and network interface card, communicate with one another via at least one communication bus 106.

Memory 104 stores procedures and data, typically including: an operating system 140 for providing basic system services; application programs 152 such as user level programs for viewing and manipulating data, evaluating formulae for the purpose of diagnosing a test subject; authoring tools for assisting with the writing of computer programs; a file system 142, a user

interface controller 144 for handling communications with a user via user interface 108, and optionally one or more databases 146 for storing microarray data and other information, optionally a graphics controller 148 for controlling display of data, and optionally a floating point coprocessor 150 dedicated to carrying out mathematical operations. The methods of the present invention may also draw upon functions contained in one or more dynamically linked libraries, not shown in FIG. 1, but stored either in Memory 104, or on disk 110, or accessible via network interface connection 114.

User interface 108 may comprise a display 128, a mouse 126, and a keyboard 130. Although shown as separate components in FIG. 1, one or more of these user interface components can be integrated with one another in embodiments such as handheld computers. Display 128 may be a cathode ray tube (CRT), or flat-screen display such as an LCD based on active matrix or TFT embodiments, or may be an electroluminescent display, based on light emitting organic molecules such as conjugated small molecules or polymers. Other embodiments of a user interface not shown in FIG. 1 include, *e.g.*, several buttons on a keypad, a card-reader, a touch-screen with or without a dedicated touching device, a trackpad, a trackball, or a microphone used in conjunction with voice-recognition software, or any combination thereof, or a security-device such as a fingerprint sensor or a retinal scanner that prohibits an unauthorized user from accessing data and programs stored in system 100.

System 100 may also be connected to an output device such as a printer (not shown), either directly through a dedicated printer cable connected to a serial or USB port, or wirelessly, or via a network connection.

The database 146 may instead, optionally, be stored on disk 110 in circumstances where the amount of data in the database is too great to be efficiently stored in memory 104. The database may also instead, or in part, be stored on one or more remote computers that communicate with computer system 100 through network interface connection 114.

The network interface 134 may be a connection to the internet or to a local area network via a cable and modem, or ethernet, firewire, or USB connectivity, or a digital subscriber line. Preferably the computer network connection is wireless, e.g., utilizing CDMA, GSM, or GPRS, or bluetooth, or standards such as 802.11a, 802.11b, or 802.11g.

It would be understood that various embodiments and configurations and distributions of the components of system 10 across different devices and locations are consistent with practice

of the methods described herein. For example, a user may use a handheld embodiment that accepts data from a test subject, and transmits that data across a network connection to another device or location wherein the data is analyzed according to a formulae described herein. A result of such an analysis can be stored at the other location and/or additionally transmitted back to the handheld embodiment. In such a configuration, the act of accepting data from a test subject can include the act of a user inputting the information. The network connection can include a web-based interface to a remote site at, for example, a healthcare provider. Alternatively, system 10 can be a device such as a handheld device that accepts data from the test subject, analyzes the data, such as by inputting the data into a formula as further described herein, and generating a result that is displayed to the user. The result can then be, optionally, transmitted back to a remote location via a network interface such as a wireless interface. System 100 may further be configured to permit a user to transmit by e-mail results of an analysis directly to some other party, such as a healthcare provider, or a diagnostic facility, or a patient.

(K) Use of the Biomarkers of the Invention for Testing, Screening or Diagnosing a Test Subject

As would be understood by a person skilled in the art, the identification of one or more biomarkers can be used to allow for the testing, screening or diagnosis of one or more colorectal pathologies including polyps or one or more subtypes of polyps within a test subject by measuring the expression of the products of the biomarkers (gene) in the test subject (the "test subject").

In one embodiment, the results from the test subject are compared with the a control wherein the control can be results from one or more individuals having colorectal pathology, having polyps, having one or more subtypes of polyps and/or one or more individuals not having any colorectal pathology, not having any polyps or not having one or more specific subtypes of colorectal polyps.

In another embodiment, one can input data reflective of the expression of the products of the biomarkers of the test subject into a formula of the invention resulting in a determination of whether said test subject has one or more colorectal pathologies. It is not necessary to use the same formula used to test the biomarker combination for its ability to test for colorectal pathologies as to diagnose an individual using the biomarker combination identified. Data

representative of the products of the biomarkers of the invention (including RNA and/or Protein) is input into a formula of the invention so as to determine a probability of a test subject having one or more colorectal pathologies. The data can be generated using any technique known to measure the level of expression of either the RNA and protein products of the biomarkers of the invention.

In one embodiment, use of the formula results in a determination of whether the test subject has polyps or does not have polyps. For example, using logistic regression as the model, Y is used as a predictor of polyps, where when $Y > 0$ a person is diagnosed as having polyps and where $Y < 0$, a person is diagnosed as not having polyps. In yet another embodiment, one can also include a third category of prediction wherein diagnosis is indeterminable. For example, one can determine the standard deviation inherent within the methodology used to measure gene expression of the biomarkers (δ). If $Y < \delta$ but >0 or $Y >- \delta$ but < 0, then the test results are considered indeterminable.

(L) Polynucleotides Used to Measure the Products of the Biomarkers of the Invention

Polynucleotides capable of specifically or selectively binding to the RNA products of the biomarkers of the invention are used to measure the level of expression of the biomarkers. For example: oligonucleotides, cDNA, DNA, RNA, PCR products, synthetic DNA, synthetic RNA, or other combinations of naturally occurring or modified nucleotides which specifically and/or selectively hybridize to one or more of the RNA products of the biomarker of the invention are useful in accordance with the invention.

In a preferred embodiment, the oligonucleotides, cDNA, DNA, RNA, PCR products, synthetic DNA, synthetic RNA, or other combinations of naturally occurring or modified nucleotides oligonucleotides which both specifically and selectively hybridize to one or more of the RNA products of the biomarker of the invention are used.

(M) Techniques to Measure the RNA Products of the Biomarkers of the Invention Array Hybridization

In one embodiment of the invention, the polynucleotide used to measure the RNA products of the biomarkers of the invention can be used as nucleic acid members localized on a support to comprise an array according to one aspect of the invention. The length of a nucleic acid member can range from 8 to 1000 nucleotides in length and are chosen so as to be specific for the RNA products of the biomarkers of the invention. In one embodiment, these members are selective for the RNA products of the biomarkers of the invention. The nucleic acid members may be single

or double stranded, and/or may be oligonucleotides or PCR fragments amplified from cDNA. In some embodiments oligonucleotides are approximately 20-30 nucleotides in length. ESTs are in some embodiments 100 to 600 nucleotides in length. It will be understood to a person skilled in the art that one can utilize portions of the expressed regions of the biomarkers of the invention as a probe on the array. More particularly oligonucleotides complementary to the genes of the invention and or cDNA or ESTs derived from the genes of the invention are useful. For oligonucleotide based arrays, the selection of oligonucleotides corresponding to the gene of interest which are useful as probes is well understood in the art. More particularly it is important to choose regions which will permit hybridization to the target nucleic acids. Factors such as the Tm of the oligonucleotide, the percent GC content, the degree of secondary structure and the length of nucleic acid are important factors. See for example US Patent No. 6,551,784.

As described, microarrays can be used to identify and select genes differentially expressed in individuals having or not having one or more colorectal pathologies, one or more polyps or one or more subtypes of polyps, and can be used to diagnose or detect polyps or one or more subtypes of polyps using the biomarkers of the invention. Genes identified as differentially expressed using microarrays can be seen in **Table 1**, and **Table 11**.

Construction of a nucleic acid array

In the subject methods, an array of nucleic acid members stably associated with the surface of a substantially support is contacted with a sample comprising target nucleic acids under hybridization conditions sufficient to produce a hybridization pattern of complementary nucleic acid members/target complexes in which one or more complementary nucleic acid members at unique positions on the array specifically hybridize to target nucleic acids. The identity of target nucleic acids which hybridize can be determined with reference to location of nucleic acid members on the array.

The nucleic acid members may be produced using established techniques such as polymerase chain reaction (PCR) and reverse transcription (RT). These methods are similar to those currently known in the art (see e.g., *PCR Strategies*, Michael A. Innis (Editor), et al. (1995) and *PCR: Introduction to Biotechniques Series*, C. R. Newton, A. Graham (1997)). Amplified nucleic acids are purified by methods well known in the art (e.g., column purification or alcohol precipitation). A nucleic acid is considered pure when it has been isolated so as to be substantially free of primers and incomplete products produced during the synthesis of the

desired nucleic acid. In some embodiments, a purified nucleic acid will also be substantially free of contaminants which may hinder or otherwise mask the specific binding activity of the molecule.

An array, according to one aspect of the invention, comprises a plurality of nucleic acids attached to one surface of a support at a density exceeding 20 different nucleic acids/cm^2, wherein each of the nucleic acids is attached to the surface of the support in a non-identical pre-selected region (e.g. a microarray). Each associated sample on the array comprises a nucleic acid composition, of known identity, usually of known sequence, as described in greater detail below. Any conceivable substrate may be employed in the invention.

In one embodiment, the nucleic acid attached to the surface of the support is DNA. In a preferred embodiment, the nucleic acid attached to the surface of the support is cDNA or RNA. In another preferred embodiment, the nucleic acid attached to the surface of the support is cDNA synthesized by polymerase chain reaction (PCR). In some embodiments, a nucleic acid member in the array, according to the invention, is at least 10, 25 or 50 nucleotides in length. In one embodiment, a nucleic acid member is at least 150 nucleotides in length. In some embodiments, a nucleic acid member is less than 1000 nucleotides in length. More preferably, a nucleic acid member is less than 500 nucleotides in length.

In the arrays of the invention, the nucleic acid compositions are stably associated with the surface of a support. In one embodiment, the support may be a flexible or rigid support. By "stably associated" is meant that each nucleic acid member maintains a unique position relative to the support under hybridization and washing conditions. As such, the samples are non-covalently or covalently stably associated with the support surface. Examples of non-covalent association include non-specific adsorption, binding based on electrostatic interactions (e.g., ion pair interactions), hydrophobic interactions, hydrogen bonding interactions, specific binding through a specific binding pair member covalently attached to the support surface, and the like. Examples of covalent binding include covalent bonds formed between the nucleic acids and a functional group present on the surface of the rigid support (e.g., --OH), where the functional group may be naturally occurring or present as a member of an introduced linking group, as described in greater detail below

The amount of nucleic acid present in each composition will be sufficient to provide for adequate hybridization and detection of target nucleic acid sequences during the assay in which

the array is employed. Generally, the amount of each nucleic acid member stably associated with the support of the array is at least about 0.001 ng, preferably at least about 0.02 ng and more preferably at least about 0.05 ng, where the amount may be as high as 1000 ng or higher, but will usually not exceed about 20 ng. Where the nucleic acid member is "spotted" onto the support in a spot comprising an overall circular dimension, the diameter of the "spot" will generally range from about 10 to 5,000 μm, usually from about 20 to 2,000 μm and more usually from about 100 to 200 μm.

Control nucleic acid members may be present on the array including nucleic acid members comprising oligonucleotides or nucleic acids corresponding to genomic DNA, housekeeping genes, vector sequences, plant nucleic acid sequence, negative and positive control genes, and the like. Control nucleic acid members are calibrating or control genes whose function is not to tell whether a particular "key" gene of interest is expressed, but rather to provide other useful information, such as background or basal level of expression.

Other control nucleic acids are spotted on the array and used as target expression control nucleic acids and mismatch control nucleotides to monitor non-specific binding or cross-hybridization to a nucleic acid in the sample other than the target to which the probe is directed. Mismatch probes thus indicate whether a hybridization is specific or not. For example, if the target is present, the perfectly matched probes should be consistently brighter than the mismatched probes. In addition, if all control mismatches are present, the mismatch probes are used to detect a mutation.

Use of a Microarray

Nucleic acid arrays according to the invention can be used to assay nucleic acids in a sample comprising one or more target nucleic acid sequences (ie such as RNA products of the biomarkers of the invention). The arrays of the subject invention can be used for testing, screening, and/or diagnosis of one or more colorectal pathologies including polyps or one or more subtypes of polyps, or screening for therapeutic targets and the like.

The arrays are also useful in broad scale expression screening for drug discovery and research, such as the effect of a particular active agent on the expression pattern of biomarkers of the invention, where such information is used to reveal drug efficacy and toxicity, environmental monitoring, disease research and the like.

Arrays can be made using at least one, more preferably a combination of these sequences, as a means of diagnosing colon pathology or one or more subtypes of colon pathology.

The choice of a standard sample would be well understood by a person skilled in the art, and would include a sample complementary to RNA isolated from one or more normal individuals, wherein a normal individual is an individual not having polyps.

Preparation of Nucleic Acid Sample for Hybridization to an Array

The samples for hybridization with the arrays according to the invention are in some embodiments derived from total RNA from blood. In another embodiment, targets for the arrays are derived from mRNA from blood.

The nucleic acid sample is capable of binding to a nucleic acid member of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation.

As used herein, a "nucleic acid derived from an mRNA transcript: or a "nucleic acid corresponding to an mRNA" refers to a nucleic acid for which synthesis of the mRNA transcript or a sub-sequence thereof has ultimately served as a template. Thus, a cDNA reverse transcribed from an mRNA, an RNA transcribed from that cDNA, a DNA amplified from the cDNA, an RNA transcribed from the amplified DNA, etc., are all derived from or correspond to the mRNA transcript and detection of such derived or corresponding products is indicative of or proportional to the presence and/or abundance of the original transcript in a sample. Thus, suitable nucleic acid samples include, but are not limited to, mRNA transcripts of a gene or genes, cDNA reverse transcribed from the mRNA, cRNA transcribed from the cDNA, DNA amplified from a gene or genes, RNA transcribed from amplified DNA, and the like. The nucleic acid samples used herein are in some embodiments derived from blood. Nucleic acids can be single- or double-stranded DNA, RNA, or DNA-RNA hybrids synthesized from human blood using methods known in the art, for example, reverse transcription or PCR.

In the simplest embodiment, such a nucleic acid sample comprises total mRNA or a nucleic acid sample corresponding to mRNA (e.g., cDNA) isolated from blood samples. In another embodiment, total mRNA is isolated from a given sample using, for example, an acid guanidinium-phenol-chloroform extraction method and polyA+ mRNA is isolated by oligo dT column chromatography or by using (dT)n magnetic beads (see, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989), or

Current Protocols in Molecular Biology, F. Ausubel et al., ed. Greene Publishing and Wiley-Interscience, New York (1987). In a preferred embodiment, total RNA is extracted using TRIzol® reagent (GIBCO/BRL, Invitrogen Life Technologies, Cat. No. 15596). Purity and integrity of RNA is assessed by absorbance at 260/280nm and agarose gel electrophoresis followed by inspection under ultraviolet light.

In some embodiments, it is desirable to amplify the nucleic acid sample prior to hybridization, for example, when only limited amounts of sample can be used (e.g. drop of blood). One of skill in the art will appreciate that whatever amplification method is used, if a quantitative result is desired, care must be taken to use a method that maintains or controls for the relative frequencies of the amplified nucleic acids. Methods of "quantitative" amplification are well known to those of skill in the art. For example, quantitative PCR involves simultaneously co-amplifying a known quantity of a control sequence using the same primers. This provides an internal standard that may be used to calibrate the PCR reaction. The high density array may then include probes specific to the internal standard for quantification of the amplified nucleic acid. Detailed protocols for quantitative PCR are provided in *PCR Protocols, A Guide to Methods and Applications*, Innis et al., Academic Press, Inc. N.Y., (1990).

Other suitable amplification methods include, but are not limited to polymerase chain reaction (PCR) (Innis, et al., *PCR Protocols. A Guide to Methods and Application*. Academic Press, Inc. San Diego, (1990)), ligase chain reaction (LCR) (see Wu and Wallace, 1989, *Genomics*, 4:560; Landegren, et al., 1988, *Science*, 241:1077 and Barringer, et al., 1990, *Gene*, 89:117, transcription amplification (Kwoh, et al., 1989, *Proc. Natl. Acad. Sci. USA*, 86: 1173), and self-sustained sequence replication (Guatelli, et al., 1990, *Proc. Nat. Acad. Sci. USA*, 87: 1874).

In a particularly preferred embodiment, the nucleic acid sample mRNA is reverse transcribed with a reverse transcriptase and a primer consisting of oligo dT and a sequence encoding the phage T7 promoter to provide single-stranded DNA template. The second DNA strand is polymerized using a DNA polymerase. After synthesis of double-stranded cDNA, T7 RNA polymerase is added and RNA is transcribed from the cDNA template. Successive rounds of transcription from each single cDNA template results in amplified RNA. Methods of *in vitro* transcription are well known to those of skill in the art (see, e.g., Sambrook, *supra.*) and this particular method is described in detail by Van Gelder, et al., 1990, *Proc. Natl. Acad. Sci. USA*,

87: 1663-1667 who demonstrate that *in vitro* amplification according to this method preserves the relative frequencies of the various RNA transcripts. Moreover, Eberwine et al. *Proc. Natl. Acad. Sci. USA*, 89: 3010-3014 provide a protocol that uses two rounds of amplification via *in vitro* transcription to achieve greater than 10^6 fold amplification of the original starting material thereby permitting expression monitoring even where biological samples are limited.

Labeling of Nucleic Acid Sample or Nucleic Acid Probe

Nucleic acid samples are labelled so as to allow detection of hybridization to an array of the invention. Any analytically detectable marker that is attached to or incorporated into a molecule may be used in the invention. An analytically detectable marker refers to any molecule, moiety or atom which is analytically detected and quantified.

Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include biotin for staining with labeled streptavidin conjugate, magnetic beads (e.g., Dynabeads^{TM}), fluorescent dyes (e.g., fluorescein, texas red, rhodamine, green fluorescent protein, and the like), radiolabels (e.g., ^{3}H, ^{125}I, 35S, ^{14}C, or ^{32}P), enzymes (e.g., horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic (e.g., polystyrene, polypropylene, latex, etc.) beads. Patents teaching the use of such labels include U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241, the entireties of which are incorporated by reference herein.

Means of detecting such labels are well known to those of skill in the art. Thus, for example, radiolabels may be detected using photographic film or scintillation counters, fluorescent markers may be detected using a photodetector to detect emitted light. Enzymatic labels are typically detected by providing the enzyme with a substrate and detecting the reaction product produced by the action of the enzyme on the substrate, and colorimetric labels are detected by simply visualizing the colored label.

The labels may be incorporated by any of a number of means well known to those of skill in the art. However, in one embodiment, the label is simultaneously incorporated during the amplification step in the preparation of the sample nucleic acids. Thus, for example, polymerase chain reaction (PCR) with labeled primers or labeled nucleotides will provide a labeled amplification product. In a preferred embodiment, transcription amplification, as described

above, using a labeled nucleotide (e.g. fluorescein-labeled UTP and/or CTP) incorporates a label into the transcribed nucleic acids.

Alternatively, a label may be added directly to the original nucleic acid sample (e.g., mRNA, polyA mRNA, cDNA, etc.) or to the amplification product after the amplification is completed. Means of attaching labels to nucleic acids are well known to those of skill in the art and include, for example, nick translation or end-labeling (e.g. with a labeled RNA) by kinasing of the nucleic acid and subsequent attachment (ligation) of a nucleic acid linker joining the sample nucleic acid to a label (e.g., a fluorophore).

In another embodiment, the fluorescent modifications are by cyanine dyes e.g. Cy-3/Cy-5 dUTP, Cy-3/Cy-5 dCTP (Amersham Pharmacia) or alexa dyes (Khan,et al., 1998, *Cancer Res.* 58:5009-5013).

In one embodiment, the two Nucleic Acid Sample samples used for comparison are labeled with different fluorescent dyes which produce distinguishable detection signals, for example, nucleic acid samples made from normal intestinal cells are labeled with Cy5 and nucleic acid samples made from intestinal tissue cells are labeled with Cy3. The differently labeled target samples are hybridized to the same microarray simultaneously. In a preferred embodiment, the labeled nucleic acid samples are purified using methods known in the art, e.g., by ethanol purification or column purification.

In another embodiment, the nucleic acid samples will include one or more control molecules which hybridize to control probes on the microarray to normalize signals generated from the microarray. In one embodiment, labeled normalization nucleic acid samples are nucleic acid sequences that are perfectly complementary to control oligonucleotides that are spotted onto the microarray as described above. In another embodiment, labeled normalization nucleic acid samples are nucleic acid sequences that are 99%, 98%, 97%, 96%, 95%, 90%, 85%, 80% or 75% complementary to control oligonucleotides that are spotted onto the microarray as described above. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In one embodiment, signals (e.g., fluorescence intensity) read from all other probes in the array are divided by the signal (e.g., fluorescence intensity) from the control probes, thereby normalizing the measurements.

Preferred normalization nucleic acid samples are selected to reflect the average length of the other nucleic acid samples present in the sample, however, they are selected to cover a range of lengths. The normalization control(s) also can be selected to reflect the (average) base composition of the other probes in the array, however, in one embodiment, only one or a few normalization probes are used and they are selected such that they hybridize well (i.e., have no secondary structure and do not self hybridize) and do not match any nucleic acids on the array.

Normalization probes are localized at any position in the array or at multiple positions throughout the array to control for spatial variation in hybridization efficiency. In one embodiment, normalization controls are located at the corners or edges of the array as well as in the middle.

Hybridization Conditions

Nucleic acid hybridization involves providing a nucleic acid sample under conditions where the sample and the complementary nucleic acid member can form stable hybrid duplexes through complementary base pairing. The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (e.g., low temperature and/or high salt) hybrid duplexes (e.g., DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (e.g., higher temperature or lower salt) successful hybridization requires fewer mismatches.

The invention provides for hybridization conditions comprising the Dig hybridization mix (Boehringer); or formamide-based hybridization solutions, for example as described in Ausubel et al., *supra* and Sambrook et al. *supra.*

Methods of optimizing hybridization conditions are well known to those of skill in the art (see, e.g., *Laboratory Techniques in Biochemistry and Molecular Biology*, Vol. 24: *Hybridization With Nucleic acid Probes*, P. Tijssen, ed. Elsevier, N.Y., (1993)).

Following hybridization, non-hybridized labeled or unlabeled nucleic acid is removed from the support surface, conveniently by washing, thereby generating a pattern of hybridized target nucleic acid on the substrate surface. A variety of wash solutions are known to those of

skill in the art and may be used. The resultant hybridization patterns of labeled, hybridized oligonucleotides and/or nucleic acids may be visualized or detected in a variety of ways, with the particular manner of detection being chosen based on the particular label of the test nucleic acid, where representative detection means include scintillation counting, autoradiography, fluorescence measurement, calorimetric measurement, light emission measurement and the like.

Image Acquisition and Data Analysis

Following hybridization and any washing step(s) and/or subsequent treatments, as described above, the resultant hybridization pattern is detected. In detecting or visualizing the hybridization pattern, the intensity or signal value of the label will be not only be detected but quantified, by which is meant that the signal from each spot of the hybridization will be measured and compared to a unit value corresponding to the signal emitted by a known number of end labeled target nucleic acids to obtain a count or absolute value of the copy number of each end-labeled target that is hybridized to a particular spot on the array in the hybridization pattern.

Methods for analyzing the data collected from hybridization to arrays are well known in the art. For example, where detection of hybridization involves a fluorescent label, data analysis can include the steps of determining fluorescent intensity as a function of substrate position from the data collected, removing outliers, i.e., data deviating from a predetermined statistical distribution, and calculating the relative binding affinity of the test nucleic acids from the remaining data. The resulting data is displayed as an image with the intensity in each region varying according to the binding affinity between associated oligonucleotides and/or nucleic acids and the test nucleic acids.

The following detection protocol is used for the simultaneous analysis of two samples to be compared, where each sample is labeled with a different fluorescent dye.

Each element of the microarray is scanned for the first fluorescent color. The intensity of the fluorescence at each array element is proportional to the expression level of that gene in the sample. The scanning operation is repeated for the second fluorescent label. The ratio of the two fluorescent intensities provides a highly accurate and quantitative measurement of the relative gene expression level in the two samples.

In a preferred embodiment, fluorescence intensities of immobilized nucleic acid sequences were determined from images taken with a custom confocal microscope equipped with laser excitation sources and interference filters appropriate for the Cy3 and Cy5 fluors. Separate scans

were taken for each fluor at a resolution of 225 μm^2 per pixel and 65,536 gray levels. Image segmentation to identify areas of hybridization, normalization of the intensities between the two fluor images, and calculation of the normalized mean fluorescent values at each target are as described (Khan, et al., 1998, *Cancer Res.* 58:5009-5013. Chen, et al., 1997, *Biomed. Optics* 2:364-374). Normalization between the images is used to adjust for the different efficiencies in labeling and detection with the two different fluors. This is achieved by equilibrating to a value of one the signal intensity ratio of a set of internal control genes spotted on the array.

In another preferred embodiment, the array is scanned in the Cy3 and Cy5 channels and stored as separate 16-bit TIFF images. The images are incorporated and analysed using software which includes a gridding process to capture the hybridization intensity data from each spot on the array. The fluorescence intensity and background-subtracted hybridization intensity of each spot is collected and a ratio of measured mean intensities of Cy5 to Cy3 is calculated. A linear regression approach is used for normalization and assumes that a scatter plot of the measured Cy5 versus Cy3 intensities should have a slope of one. The average of the ratios is calculated and used to rescale the data and adjust the slope to one. A ratio of expression not equal to 1 is used as an indication of differential gene expression.

In a particular embodiment, where it is desired to quantify the transcription level (and thereby expression) of one or more nucleic acid sequences in a sample, the nucleic acid sample is one in which the concentration of the mRNA transcript(s) of the gene or genes, or the concentration of the nucleic acids derived from the mRNA transcript(s), is proportional to the transcription level (and therefore expression level) of that gene. Similarly, it is preferred that the hybridization signal intensity be proportional to the amount of hybridized nucleic acid. While it is preferred that the proportionality be relatively strict (e.g., a doubling in transcription rate results in a doubling in mRNA transcript in the sample nucleic acid pool and a doubling in hybridization signal), one of skill will appreciate that the proportionality can be more relaxed and even non-linear and still provide meaningful results. Thus, for example, an assay where a 5 fold difference in concentration of the sample mRNA results in a 3- to 6-fold difference in hybridization intensity is sufficient for most purposes. Where more precise quantification is required, appropriate controls are run to correct for variations introduced in sample preparation and hybridization as described herein. In addition, serial dilutions of "standard" mRNA samples are used to prepare calibration curves according to methods well known to those of skill in the

art. Of course, where simple detection of the presence or absence of a transcript is desired, no elaborate control or calibration is required.

For example, if a nucleic acid member on an array is not labeled after hybridization, this indicates that the gene comprising that nucleic acid member is not expressed in either sample. If a nucleic acid member is labeled with a single color, it indicates that a labeled gene was expressed only in one sample. The labeling of a nucleic acid member comprising an array with both colors indicates that the gene was expressed in both samples. Even genes expressed once per cell are detected (1 part in 100,000 sensitivity). A difference in expression intensity in the two samples being compared is indicative of differential expression, the ratio of the intensity in the two samples being not equal to 1.0, greater than 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 2.0, 3.0, 4.0 and the like or less than 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2 and the like.

PCR

In one aspect of the invention, the level of the expression of the RNA products of the biomarkers of the invention can be measured by amplifying the RNA products of the biomarkers from a sample by first using reverse transcription (RT). Either in combination, or as a second reaction step, the reverse transcribed product can then be amplified with the polymerase chain reaction (PCR). In accordance with one embodiment of the invention, the PCR can be QRT-PCR as would be understood to a person skilled in the art.

Total RNA, or mRNA from a sample is used as a template and a primer specific to the transcribed portion of a biomarker of the invention is used to initiate reverse transcription. Methods of reverse transcribing RNA into cDNA are well known and described in Sambrook et al., 1989, *supra*. Primer design can be accomplished utilizing commercially available software (*e.g.*, Primer Designer 1.0, Scientific Sofware *etc.*). The product of the reverse transcription is subsequently used as a template for PCR.

PCR provides a method for rapidly amplifying a particular nucleic acid sequence by using multiple cycles of DNA replication catalyzed by a thermostable, DNA-dependent DNA polymerase to amplify the target sequence of interest. PCR requires the presence of a nucleic acid to be amplified, two single-stranded oligonucleotide primers flanking the sequence to be amplified, a DNA polymerase, deoxyribonucleoside triphosphates, a buffer and salts.

The method of PCR is well known in the art. PCR, is performed as described in Mullis and Faloona, 1987, Methods Enzymol., 155: 335, which is incorporated herein by reference.

PCR is performed using template DNA (at least 1fg; more usefully, 1-1000 ng) and at least 25 pmol of oligonucleotide primers. A typical reaction mixture includes: 2 ml of DNA, 25 pmol of oligonucleotide primer, 2.5 ml of 10H PCR buffer 1 (Perkin-Elmer, Foster City, CA), 0.4 ml of 1.25 mM dNTP, 0.15 ml (or 2.5 units) of Taq DNA polymerase (Perkin Elmer, Foster City, CA) and deionized water to a total volume of 25 ml. Mineral oil is overlaid and the PCR is performed using a programmable thermal cycler.

The length and temperature of each step of a PCR cycle, as well as the number of cycles, are adjusted according to the stringency requirements in effect. Annealing temperature and timing are determined both by the efficiency with which a primer is expected to anneal to a template and the degree of mismatch that is to be tolerated. The ability to optimize the stringency of primer annealing conditions is well within the knowledge of one of moderate skill in the art. An annealing temperature of between 30 °C and 72 °C is used. Initial denaturation of the template molecules normally occurs at between 92 °C and 99 °C for 4 minutes, followed by 20-40 cycles consisting of denaturation (94-99°C for 15 seconds to 1 minute), annealing (temperature determined as discussed above; 1-2 minutes), and extension (72 °C for 1 minute). The final extension step is generally carried out for 4 minutes at 72 °C, and may be followed by an indefinite (0-24 hour) step at 4 °C.

QRT-PCR (Quantitative real time RT-PCR), can also be performed to provide a quantitative measure of gene expression levels. Similar to reverse transcription PCR, QRT-PCR reverse transcription and PCR can be performed in two steps, or reverse transcription combined with PCR can be performed concurrently. One of these techniques, for which there are commercially available kits such as Taqman (Perkin Elmer, Foster City, CA), is performed with a transcript-specific antisense probe. This probe is specific for the PCR product (*e.g.* a nucleic acid fragment derived from a gene) and is prepared with a quencher and fluorescent reporter probe complexed to the 5' end of the oligonucleotide. Different fluorescent markers are attached to different reporters, allowing for measurement of two products in one reaction. When Taq DNA polymerase is activated, it cleaves off the fluorescent reporters of the probe bound to the template by virtue of its 5'-to-3' exonuclease activity. In the absence of the quenchers, the reporters now fluoresce. The color change in the reporters is proportional to the amount of each specific product and is measured by a fluorometer; therefore, the amount of each color is measured and the PCR product is quantified. The PCR reactions can be performed in 96 well

plates, 384 well plates and the like so that samples derived from many individuals are processed and measured simultaneously. The Taqman system has the additional advantage of not requiring gel electrophoresis and allows for quantification when used with a standard curve.

A second technique useful for detecting PCR products quantitatively without is to use an intercolating dye such as the commercially available QuantiTect SYBR Green PCR (Qiagen, Valencia California). QRT-PCR is performed using SYBR green as a fluorescent label which is incorporated into the PCR product during the PCR stage and produces a flourescense proportional to the amount of PCR product.

Both Taqman and QuantiTect SYBR systems can be used subsequent to reverse transcription of RNA. Reverse transcription can either be performed in the same reaction mixture as the PCR step (one-step protocol) or reverse transcription can be performed first prior to amplification utilizing PCR (two-step protocol).

Additionally, other systems to quantitatively measure mRNA expression products are known including Molecular Beacons® which uses a probe having a fluorescent molecule and a quencher molecule, the probe capable of forming a hairpin structure such that when in the hairpin form, the fluorescence molecule is quenched, and when hybridized the flourescense increases giving a quantitative measurement of gene expression.

Additional techniques to quantitatively measure RNA expression include, but are not limited to, polymerase chain reaction, ligase chain reaction, Qbeta replicase (see, *e.g.*, International Application No. PCT/US87/00880), isothermal amplification method (see, *e.g.*, Walker et al. (1992) PNAS 89:382-396), strand displacement amplification (SDA), repair chain reaction, Asymmetric Quantitative PCR (see, *e.g.*, U.S. Publication No. US20030134307A1) and the multiplex microsphere bead assay described in Fuja et al., 2004, Journal of Biotechnology 108:193-205.

The level of gene expression can be measured by amplifying RNA from a sample using transcription based amplification systems (TAS), including nucleic acid sequence amplification (NASBA) and 3SR. See, *e.g.*, Kwoh et al (1989) PNAS USA 86:1173; International Publication No. WO 88/10315; and U.S. Patent No. 6,329,179. In NASBA, the nucleic acids may be prepared for amplification using conventional phenol/chloroform extraction, heat denaturation, treatment with lysis buffer and minispin columns for isolation of DNA and RNA or guanidinium chloride extraction of RNA. These amplification techniques involve annealing a primer that has

target specific sequences. Following polymerization, DNA/RNA hybrids are digested with RNase H while double stranded DNA molecules are heat denatured again. In either case the single stranded DNA is made fully double stranded by addition of second target specific primer, followed by polymerization. The double-stranded DNA molecules are then multiply transcribed by a polymerase such as T7 or SP6. In an isothermal cyclic reaction, the RNA's are reverse transcribed into double stranded DNA, and transcribed once with a polymerase such as T7 or SP6. The resulting products, whether truncated or complete, indicate target specific sequences.

Several techniques may be used to separate amplification products. For example, amplification products may be separated by agarose, agarose-acrylamide or polyacrylamide gel electrophoresis using conventional methods. See Sambrook et al., 1989. Several techniques for detecting PCR products quantitatively without electrophoresis may also be used according to the invention (see for example *PCR Protocols, A Guide to Methods and Applications*, Innis et al., Academic Press, Inc. N.Y., (1990)). For example, chromatographic techniques may be employed to effect separation. There are many kinds of chromatography which may be used in the present invention: adsorption, partition, ion-exchange and molecular sieve, HPLC, and many specialized techniques for using them including column, paper, thin-layer and gas chromatography (Freifelder, Physical Biochemistry Applications to Biochemistry and Molecular Biology, 2nd ed., Wm. Freeman and Co., New York, N.Y., 1982).

Another example of a separation methodology is done by covalently labeling the oligonucleotide primers used in a PCR reaction with various types of small molecule ligands. In one such separation, a different ligand is present on each oligonucleotide. A molecule, perhaps an antibody or avidin if the ligand is biotin, that specifically binds to one of the ligands is used to coat the surface of a plate such as a 96 well ELISA plate. Upon application of the PCR reactions to the surface of such a prepared plate, the PCR products are bound with specificity to the surface. After washing the plate to remove unbound reagents, a solution containing a second molecule that binds to the first ligand is added. This second molecule is linked to some kind of reporter system. The second molecule only binds to the plate if a PCR product has been produced whereby both oligonucleotide primers are incorporated into the final PCR products. The amount of the PCR product is then detected and quantified in a commercial plate reader much as ELISA reactions are detected and quantified. An ELISA-like system such as the one

described here has been developed by the Raggio Italgene company under the C-Track trade name.

Amplification products must be visualized in order to confirm amplification of the nucleic acid sequences of interest. One typical visualization method involves staining of a gel with ethidium bromide and visualization under UV light. Alternatively, if the amplification products are integrally labeled with radio- or fluorometrically-labeled nucleotides, the amplification products may then be exposed to x-ray film or visualized under the appropriate stimulating spectra, following separation.

In one embodiment, visualization is achieved indirectly. Following separation of amplification products, a labeled, nucleic acid probe is brought into contact with the amplified nucleic acid sequence of interest. The probe in one embodiment is conjugated to a chromophore but may be radiolabeled. In another embodiment, the probe is conjugated to a binding partner, such as an antibody or biotin, where the other member of the binding pair carries a detectable moiety.

In another embodiment, detection is by Southern blotting and hybridization with a labeled probe. The techniques involved in Southern blotting are well known to those of skill in the art and may be found in many standard books on molecular protocols. See Sambrook et al., 1989, *supra*. Briefly, amplification products are separated by gel electrophoresis. The gel is then contacted with a membrane, such as nitrocellulose, permitting transfer of the nucleic acid and non-covalent binding. Subsequently, the membrane is incubated with a chromophore-conjugated probe that is capable of hybridizing with a target amplification product. Detection is by exposure of the membrane to x-ray film or ion-emitting detection devices.

One example of the foregoing is described in U.S. Patent No. 5,279,721, incorporated by reference herein, which discloses an apparatus and method for the automated electrophoresis and transfer of nucleic acids. The apparatus permits electrophoresis and blotting without external manipulation of the gel and is ideally suited to carrying out methods according to the present invention.

One embodiment of the invention includes the primers and probes in **Table 4, 6, 16** or **17** can be used for use in measuring the expression of the biomarkers of the invention.

Nuclease Protection Assays

In another embodiment of the invention, Nuclease protection assays (including both ribonuclease protection assays and S1 nuclease assays) can be used to detect and quantitate the RNA products of the biomarkers of the invention. In nuclease protection assays, an antisense probe (labeled with, *e.g.*, radiolabeled or nonisotopic) hybridizes in solution to an RNA sample. Following hybridization, single-stranded, unhybridized probe and RNA are degraded by nucleases. An acrylamide gel is used to separate the remaining protected fragments. Typically, solution hybridization is more efficient than membrane-based hybridization, and it can accommodate up to 100 μg of sample RNA, compared with the 20-30 μg maximum of blot hybridizations.

The ribonuclease protection assay, which is the most common type of nuclease protection assay, requires the use of RNA probes. Oligonucleotides and other single-stranded DNA probes can only be used in assays containing S1 nuclease. The single-stranded, antisense probe must typically be completely homologous to target RNA to prevent cleavage of the probe:target hybrid by nuclease.

Northern Blots

A standard Northern blot assay can also be used to ascertain an RNA transcript size, identify alternatively spliced RNA transcripts, and the relative amounts of RNA products of the biomarker of the invention, in accordance with conventional Northern hybridization techniques known to those persons of ordinary skill in the art. In Northern blots, RNA samples are first separated by size via electrophoresis in an agarose gel under denaturing conditions. The RNA is then transferred to a membrane, crosslinked and hybridized with a labeled probe. Nonisotopic or high specific activity radiolabeled probes can be used including random-primed, nick-translated, or PCR-generated DNA probes, in vitro transcribed RNA probes, and oligonucleotides. Additionally, sequences with only partial homology (*e.g.*, cDNA from a different species or genomic DNA fragments that might contain an exon) may be used as probes. The labeled probe, *e.g.*, a radiolabelled cDNA, either containing the full-length, single stranded DNA or a fragment of that DNA sequence may be at least 20, at least 30, at least 50, or at least 100 consecutive nucleotides in length. The probe can be labeled by any of the many different methods known to those skilled in this art. The labels most commonly employed for these studies are radioactive elements, enzymes, chemicals that fluoresce when exposed to ultraviolet light, and others. A

number of fluorescent materials are known and can be utilized as labels. These include, but are not limited to, fluorescein, rhodamine, auramine, Texas Red, AMCA blue and Lucifer Yellow. A particular detecting material is anti-rabbit antibody prepared in goats and conjugated with fluorescein through an isothiocyanate. Proteins can also be labeled with a radioactive element or with an enzyme. The radioactive label can be detected by any of the currently available counting procedures. Non-limiting examples of isotopes include ^{3}H, ^{14}C, ^{32}P, ^{35}S, ^{36}Cl, ^{51}Cr, ^{57}Co, ^{58}Co, ^{59}Fe, ^{90}Y, ^{125}I, ^{131}I, and ^{186}Re. Enzyme labels are likewise useful, and can be detected by any of the presently utilized colorimetric, spectrophotometric, fluorospectrophotometric, amperometric or gasometric techniques. The enzyme is conjugated to the selected particle by reaction with bridging molecules such as carbodiimides, diisocyanates, glutaraldehyde and the like. Any enzymes known to one of skill in the art can be utilized. Examples of such enzymes include, but are not limited to, peroxidase, beta-D-galactosidase, urease, glucose oxidase plus peroxidase and alkaline phosphatase. U.S. Patent Nos. 3,654,090, 3,850,752, and 4,016,043 are referred to by way of example for their disclosure of alternate labeling material and methods.

(N) Techniques to Measure the Protein Products of the Biomarkers of the Invention

Antibody Based Methodologies

Standard techniques can also be utilized for determining the amount of the protein or proteins of interest present in a sample. For example, standard techniques can be employed using, *e.g.*, immunoassays such as, for example, Western blot, immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), immunocytochemistry, and the like to determine the amount of the protein or proteins of interest present in a sample. A preferred agent for detecting a protein of interest is an antibody capable of binding to a protein of interest, in one embodiment an antibody with a detectable label.

For such detection methods, protein from the sample to be analyzed can easily be isolated using techniques which are well known to those of skill in the art. Protein isolation methods can, for example, be such as those described in Harlow and Lane (Harlow, E. and Lane, D., *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1988)).

In some embodiments, methods for the detection of the protein or proteins of interest involve their detection via interaction with a protein-specific antibody. For example, antibodies directed a protein of interest can be utilized as described herein. Antibodies can be generated

utilizing standard techniques well known to those of skill in the art. See, *e.g.*, Section 15.13.2 of this application and Section 5.2 of U.S. Publication No. 20040018200 for a more detailed discussion of such antibody generation techniques, which is incorporated herein by reference. Briefly, such antibodies can be polyclonal, or monoclonal. An intact antibody, or an antibody fragment (*e.g.*, Fab or $F(ab')_2$) can, for example, be used. In some embodiments, the antibody is a human or humanized antibody.

Table 5 and **Table 15** are tables showing, in one embodiment of the invention, antibodies which are used to detect the proteins of the biomarkers of the invention.

For example, antibodies, or fragments of antibodies, specific for a protein of interest can be used to quantitatively or qualitatively detect the presence of the protein. This can be accomplished, for example, by immunofluorescence techniques. Antibodies (or fragments thereof) can, additionally, be employed histologically, as in immunofluorescence or immunoelectron microscopy, for *in situ* detection of a protein of interest. *In situ* detection can be accomplished by removing a histological specimen (*e.g.*, a biopsy specimen) from a patient, and applying thereto a labeled antibody thereto that is directed to a protein. The antibody (or fragment) can be applied by overlaying the labeled antibody (or fragment) onto a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of the protein of interest, but also its distribution, its presence in cells (*e.g.*, intestinal cells and lymphocytes) within the sample. A wide variety of well-known histological methods (such as staining procedures) can be utilized in order to achieve such *in situ* detection.

Immunoassays for a protein of interest typically comprise incubating a biological sample of a detectably labeled antibody capable of identifying a protein of interest, and detecting the bound antibody by any of a number of techniques well-known in the art. As discussed in more detail, below, the term "labeled" can refer to direct labeling of the antibody via, *e.g.*, coupling (*i.e.*, physically linking) a detectable substance to the antibody, and can also refer to indirect labeling of the antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody.

For example, the biological sample can be brought in contact with and immobilized onto a solid phase support or carrier such as nitrocellulose, or other support which is capable of immobilizing cells, cell particles or soluble proteins. The support can then be washed with

suitable buffers followed by treatment with the detectably labeled fingerprint gene-specific antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on support can then be detected by conventional means.

By "solid phase support or carrier " in the context of proteinaceous agents is intended any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material can have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody. Thus, the support configuration can be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface can be flat such as a sheet, test strip, etc. Preferred supports include polystyrene beads. Those skilled in the art will know many other suitable carriers for binding antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

One of the ways in which a specific antibody can be detectably labeled is by linking the same to an enzyme and use in an enzyme immunoassay (EIA) (Voller, A., "The Enzyme Linked Immunosorbent Assay (ELISA)", 1978, Diagnostic Horizons 2:1-7, Microbiological Associates Quarterly Publication, Walkersville, MD); Voller, A. et al., 1978, J. Clin. Pathol. 31:507-520; Butler, J.E., 1981, Meth. Enzymol. 73:482-523; Maggio, E. (ed.), 1980, *Enzyme Immunoassay*, CRC Press, Boca Raton, FL; Ishikawa, E. et al., (eds.), 1981, *Enzyme Immunoassay*, Kgaku Shoin, Tokyo). The enzyme which is bound to the antibody will react with an appropriate substrate, in one embodiment a chromogenic substrate, in such a manner as to produce a chemical moiety which can be detected, for example, by spectrophotometric, fluorimetric or by visual means. Enzymes which can be used to detectably label the antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate, dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholinesterase. The detection can be accomplished by colorimetric methods which employ a chromogenic substrate for the enzyme. Detection can also be accomplished by visual

comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared standards.

Detection can also be accomplished using any of a variety of other immunoassays. For example, by radioactively labeling the antibodies or antibody fragments, it is possible to detect a protein of interest through the use of a radioimmunoassay (RIA) (see, for example, Weintraub, B., Principles of Radioimmunoassays, Seventh Training Course on Radioligand Assay Techniques, The Endocrine Society, March, 1986, which is incorporated by reference herein). The radioactive isotope (*e.g.*, ^{125}I, ^{131}I, ^{35}S or ^{3}H) can be detected by such means as the use of a gamma counter or a scintillation counter or by autoradiography.

It is also possible to label the antibody with a fluorescent compound. When the fluorescently labeled antibody is exposed to light of the proper wavelength, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine.

The antibody can also be detectably labeled using fluorescence emitting metals such as ^{152}Eu, or others of the lanthanide series. These metals can be attached to the antibody using such metal chelating groups as diethylenetriaminepentacetic acid (DTPA) or ethylenediamine-tetraacetic acid (EDTA).

The antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-tagged antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound can be used to label the antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in, which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

Protein Arrays

Polypeptides which specifically and/or selectively bind to the protein products of the biomarkers of the invention can be immobilized on a protein array. The protein array can be used as a tool, *e.g.*, to test individual samples (such as isolated cells, tissue, lymph, lymph tissue, blood, synovial fluid, sera, biopsies, and the like) for the presence of the polypeptides protein products of the biomarkers of the invention. The protein array can also include antibodies as well as other ligands, *e.g.*, that bind to the polypeptides encoded by the biomarkers of the invention.

Methods of producing polypeptide arrays are described, *e.g.*, in De Wildt et al., 2000, Nature Biotech. 18:989-994; Lueking et al., 1999, Anal. Biochem. 270:103-111; Ge, 2000, Nuc. Acids Res. 28:e3; MacBeath and Schreiber, 2000, Science 289:1760-1763; International Publication Nos. WO 01/40803 and WO 99/51773A1; and U.S. Patent No. 6,406,921. Polypeptides for the array can be spotted at high speed, *e.g.*, using commercially available robotic apparatus, *e.g.*, from Genetic MicroSystems and Affymetrix (Santa Clara, California, USA) or BioRobotics (Cambridge, UK). The array substrate can be, for example, nitrocellulose, plastic, glass, *e.g.*, surface-modified glass. The array can also include a porous matrix, *e.g.*, acrylamide, agarose, or another polymer.

For example, the array can be an array of antibodies, *e.g.*, as described in De Wildt, *supra*. Cells that produce the polypeptide ligands can be grown on a filter in an arrayed format. Polypeptide production is induced, and the expressed antibodies are immobilized to the filter at the location of the cell. Information about the extent of binding at each address of the array can be stored as a profile, *e.g.*, in a computer database.

In one embodiment the array is an array of protein products of the 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or all or any combination of the biomarkers of the invention. In one aspect, the invention provides for antibodies that are bound to an array which selectively bind to the protein products of the biomarkers of the invention.

(O) Protein Production

Standard recombinant nucleic acid methods can be used to express a polypeptide or antibody of the invention (*e.g.*, a protein products of a biomarker of the invention). Generally, a nucleic acid sequence encoding the polypeptide is cloned into a nucleic acid expression vector. Of course, if the protein includes multiple polypeptide chains, each chain must be cloned into an expression vector, *e.g.*, the same or different vectors, that are expressed in the same or different

cells. If the protein is sufficiently small, *i.e.*, the protein is a peptide of less than 50 amino acids, the protein can be synthesized using automated organic synthetic methods. Polypeptides comprising the 5' region, 3' region or internal coding region of a biomarker of the invention, are expressed from nucleic acid expression vectors containing only those nucleotide sequences corresponding to the 5' region, 3' region or internal coding region of a biomarker of the invention. Methods for producing antibodies directed to protein products of a biomarker of the invention, or polypeptides encoded by the 5' region, 3' region or internal coding regions of a biomarker of the invention.

The expression vector for expressing the polypeptide can include, in addition to the segment encoding the polypeptide or fragment thereof, regulatory sequences, including for example, a promoter, operably linked to the nucleic acid(s) of interest. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene, La Jolla, California, USA); pTrc99A, pKK223-3, pKK233-3, pDR540, and pRIT5 (Pharmacia, Uppsala, Sweden). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). One preferred class of preferred libraries is the display library, which is described below.

Methods well known to those skilled in the art can be used to construct vectors containing a polynucleotide of the invention and appropriate transcriptional/translational control signals. These methods include *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* recombination/genetic recombination. See, for example, the techniques described in Sambrook & Russell, *Molecular Cloning: A Laboratory Manual*, 3rd Edition, Cold Spring Harbor Laboratory, N.Y. (2001) and Ausubel *et al.*, *Current Protocols in Molecular Biology* (Greene Publishing Associates and Wiley Interscience, N.Y. (1989). Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, mouse metallothionein-I, and various art-known tissue specific promoters. In specific

embodiments, the promoter is an inducible promoter. In other embodiments, the promoter is a constitutive promoter. In yet other embodiments, the promoter is a tissue-specific promoter.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* auxotrophic markers (such as *URA3, LEU2, HIS3,* and *TRPl* genes), and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The polynucleotide of the invention is assembled in appropriate phase with translation initiation and termination sequences, and in some embodiments, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, a nucleic acid of the invention can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression-vectors for bacteria are constructed by inserting a polynucleotide of the invention together with suitable translation initiation and termination signals, optionally in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli, Bacillus subtilis, Salmonella typhimurium* and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus, although others may also be employed as a matter of choice.

As a representative but nonlimiting example, useful expression vectors for bacteria can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega, Madison, Wisconsin, USA).

The present invention provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention also provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with

a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

The present invention further provides host cells containing the vectors of the present invention, wherein the nucleic acid has been introduced into the host cell using known transformation, transfection or infection methods. The host cell can be a eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected, for example, by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. *et al.*, *Basic Methods in Molecular Biology* (1986)). Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention.

Any host/vector system can be used to express one or more of the proteins products of the biomarkers of the invention including those listed in **Table 3** and/or **Table 13**. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook *et al.*, in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is incorporated herein by reference in its entirety. The most preferred host cells are those which do not normally express the particular polypeptide or which expresses the polypeptide at low natural level.

In a specific embodiment, the host cells are engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting, including polyadenylation signals. mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The host of the present invention may also be a yeast or other fungi. In yeast, a number of vectors containing constitutive or inducible promoters may be used. For a review see, Ausubel et al. (eds), *Current Protocols in Molecular Biology*, Vol. 2, Greene Publish. Assoc. & Wiley Interscience, Ch. 13 (1988); Grant et al., 1987, "Expression and Secretion Vectors for Yeast", Methods Enzymol. 153:516-544; Glover, *DNA Cloning*, Vol. II, IRL Press, Wash., D.C., Ch. 3 (1986); Bitter, 1987, "Heterologous Gene Expression in Yeast", Methods Enzymol. 152:673-684; and Strathern et al. (eds), *The Molecular Biology of the Yeast Saccharomyces*, Cold Spring Harbor Press, Vols. I and II (1982).

Potentially suitable yeast strains include *Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli,* enterobacteriaceae such as *Serratia marescans*, bacilli such as *Bacillus subtilis, Salmonella typhimurium*, pseudomonads or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the monkey COS cells such as COS-7 lines of monkey kidney fibroblasts, described by Gluzman, 1981, Cell 23:175 (1981), Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK, C127, 3T3, or Jurkat cells, and other cell lines capable of expressing a compatible vector. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome-binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Recombinant polypeptides produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size

exclusion chromatography steps. In some embodiments, the template nucleic acid also encodes a polypeptide tag, *e.g.*, penta- or hexa-histidine.

Recombinant proteins can be isolated using an techniqe well-known in the art. Scopes (*Protein Purification: Principles and Practice,* Springer-Verlag, New York (1994)), for example, provides a number of general methods for purifying recombinant (and non-recombinant) proteins. The methods include, *e.g.*, ion-exchange chromatography, size-exclusion chromatography, affinity chromatography, selective precipitation, dialysis, and hydrophobic interaction chromatography.

(P) Methods for Identifying Compounds for Use in the Prevention, Treatment, or Amelioration of One or More Colorectal Pathologies

Methods to Identify Compounds that Modulate the Expression or Activity of a Biomarker

The present invention provides methods of identifying compounds that bind to the products of the biomarkers of the invention. The present invention also provides methods for identifying compounds that modulate the expression and/or activity of the products of the biomarkers of the invention. The compounds identified via such methods are useful for the development of one or more animal models to study colorectal pathology including polyps or one or more subtypes of polyps. Further, the compounds identified via such methods are useful as lead compounds in the development of prophylactic and therapeutic compositions for prevention, treatment, and/or amelioration of one or more colorectal pathologies including one or more polyps or one or more subtypes of polyps. Such methods are particularly useful in that the effort and great expense involved in testing potential prophylactics and therapeutics *in vivo* is efficiently focused on those compounds identified via the *in vitro* and *ex vivo* methods described herein.

The present invention provides a method for identifying a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies said method comprising: (a) contacting a cell expressing a protein products of one or more biomarkers of the invention or a fragment thereof, or RNA products of one or more biomarkers of the invention or a fragment thereof with a test compound; and (b) determining the ability of the test compound to bind to the protein products, protein fragment, RNA products, or RNA portion so that if a compound binds to the protein products, protein fragment, RNA products, RNA portions, a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal

pathologies is identified. The cell, for example, can be a prokaryotic cell, yeast cell, viral cell or a cell of mammalian origin. Determining the ability of the test compound to bind to the protein products, protein fragment, RNA products, or RNA portion can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the protein products, protein fragment, RNA products, or RNA portion can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I, ^{35}S, ^{14}C, or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In a specific embodiment, the assay comprises contacting a cell which expresses a protein products of one or more biomarkers of the invention or a fragment thereof, or a RNA products of one or more biomarkers of the invention or a fragment thereof, with a known compound which binds the protein products, protein fragment, RNA products, or RNA portion to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with the protein products, protein fragment, RNA products, or RNA portion, wherein determining the ability of the test compound to interact with the protein products, protein fragment, RNA products, or RNA portion comprises determining the ability of the test compound to preferentially bind to the protein products, protein fragment, RNA products, or RNA portion as compared to the known compound.

Binding of the test compound to the protein products or protein fragment can be determined either directly or indirectly. In a specific embodiment, the assay includes contacting a protein products of one or more biomarkers of the invention or a fragment thereof, or one or more RNA products of one or more biomarkers of the invention or a portion thereof with a known compound which binds the protein products, protein fragment, RNA products, or RNA portion to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with the protein products, protein fragment, RNA products, or RNA portion, wherein determining the ability of the test compound to interact with the protein products, protein fragment, RNA products, or RNA portion comprises determining the ability of the test compound to preferentially bind to the protein products, protein fragment, RNA products, or RNA portion as compared to the known compound.

Techniques well known in the art can be used to determine the binding between a test compound and a protein products of a biomarker of the invention or a fragment thereof, or a RNA products of a biomarker of the invention or a portion thereof.

In some embodiments of the above assay methods of the present invention, it may be desirable to immobilize a RNA products of a biomarker of the invention or a portion thereof, or its target molecule to facilitate separation of complexed from uncomplexed forms of the RNA products or RNA portion, the target molecule or both, as well as to accommodate automation of the assay. In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either a protein products of a biomarker of the invention or a fragment thereof, or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to a protein products of a biomarker of the invention or a fragment thereof can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows one or both of the proteins to be bound to a matrix. For example, glutathione-S-transferase (GST) fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical; St. Louis, MO) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and either the non-adsorbed target protein or a protein products of a biomarker of the invention or a fragment thereof, and the mixture incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components and complex formation is measured either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of binding of a protein products of a biomarker of the invention or a fragment thereof can be determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either a protein products of a biomarker of the invention or a fragment thereof, or a target molecule can be immobilized utilizing conjugation of biotin and streptavidin. A biotinylated protein products of a biomarker of the invention or a target molecule can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the

art (*e.g.*, biotinylation kit, Pierce Chemicals; Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with a protein products of a biomarker of the invention or a fragment thereof can be derivatized to the wells of the plate, and protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with a protein products of a biomarker of the invention, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with a protein products of a biomarker of the invention or a fragment thereof, or target molecule.

The interaction or binding of a protein products of a biomarker of the invention or a fragment thereof to a test compound can also be determined using such proteins or protein fragments as "bait proteins" in a two-hybrid assay or three hybrid assay (*see*, *e.g.*, U.S. Patent No. 5,283,317; Zervos et al. (1993) Cell 72:223-232; Madura et al. (1993) J. Biol. Chem. 268:12046-12054; Bartel et al. (1993) Bio/Techniques 14:920-924; Iwabuchi et al. (1993) Oncogene 8:1693-1696; and International Publication No. WO 94/10300).

The present invention provides a method for identifying a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies, said method comprising: (a) contacting a cell expressing a protein or RNA products of one or more biomarkers of the invention with a test compound; (b) determining the amount of the protein or RNA products present in (a); and (c) comparing the amount in (a) to that present in a corresponding control cell that has not been contacted with the test compound, so that if the amount of the protein or RNA products is altered relative to the amount in the control, a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies is identified. In a specific embodiment, the expression level(s) is altered by 5%, 10%, 15%, 25%, 30%, 40%, 50%, 5 to 25%, 10 to 30%, at least 1 fold, at least 1.5 fold, at least 2 fold, 4 fold, 5 fold, 10 fold, 25 fold, 1 to 10 fold, or 5 to 25 fold relative to the expression level in the control as determined by utilizing an assay described herein (*e.g.*, a microarray or QRT-PCR) or an assay well known to one of skill in the art. In alternate embodiments, such a method comprises determining the amount of the protein or RNA products of at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, 1 to 3, 1 to 5, 1-8, all or any combination of the

biomarkers of the invention present in the cell and comparing the amounts to those present in the control.

The cells utilized in the cell-based assays described herein can be engineered to express a biomarker of the invention utilizing techniques known in the art. *See, e.g.*, Section III entitled "Recombinant Expression Vectors and Host Cells" of U.S. Patent No. 6,245,527, which is incorporated herein by reference. Alternatively, cells that endogenously express a biomarker of the invention can be used. For example, intestinal cells may be used.

In a specific embodiment, intestinal cells are isolated from a "normal" individual, or an individual with one or more colorectal pathologies and are incubated in the presence and absence of a test compound for varying amounts of time (*i.e.*, 30 min, 1 hr, 5 hr, 24 hr, 48 hr and 96 hrs). When screening for prophylactic or therapeutic agents, a clone of the full sequence of a biomarker of the invention or functional portion thereof is used to transfect the cells. The transfected cells are cultured for varying amounts of time (*i.e.*, 1, 2, 3, 5, 7, 10, or 14 days) in the presence or absence of test compound. Following incubation, target nucleic acid samples are prepared from the cells and hybridized to a nucleic acid probe corresponding to a nucleic acid sequence which are differentially expressed in individuals with one or more colorectal pathologies. The nucleic acid probe is labeled, for example, with a radioactive label, according to methods well-known in the art and described herein. Hybridization is carried out by northern blot, for example as described in Ausubel et al., *supra* or Sambrook et al., *supra*). The differential hybridization, as defined herein, of the target to the samples on the array from normal relative to RNA from samples having one or more colorectal pathologies is indicative of the level of expression of RNA corresponding to a differentially expressed specific nucleic acid sequence. A change in the level of expression of the target sequence as a result of the incubation step in the presence of the test compound, is indicative of a compound that increases or decreases the expression of the corresponding polyp biomarker specific nucleic acid sequence.

The present invention also provides a method for identifying a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies, said method comprises: (a) contacting a cell-free extract (*e.g.*, an intestinal cell extract) with a nucleic acid sequence encoding a protein or RNA products of one or more biomarkers of the invention and a test compound; (b) determining the amount of the protein or RNA product present in (a); and (c) comparing the amount(s) in (a) to that present to a corresponding control that has not been

contacted with the test compound, so that if the amount of the protein or RNA product is altered relative to the amount in the control, a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies is identified. In a specific embodiment, the expression level(s) is altered by 5%, 10%, 15%, 25%, 30%, 40%, 50%, 5 to 25%, 10 to 30%, at least 1 fold, at least 1.5 fold, at least 2 fold, 4 fold, 5 fold, 10 fold, 25 fold, 1 to 10 fold, or 5 to 25 fold relative to the expression level in the control sample determined by utilizing an assay described herein (*e.g.*, a microarray or QRT-PCR) or an assay well known to one of skill in the art. In alternate embodiments, such a method comprises determining the amount of a protein or RNA product of at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, 1 to 3, 1 to 5, 1-8, all or any combination of the biomarkers of the invention present in the extract and comparing the amounts to those present in the control.

In certain embodiments, the amount of RNA product of a biomarker of the invention is determined, in other embodiments, the amount of protein products of a biomarker of the invention is determined, while in still other embodiments, the amount of RNA and protein products of a biomarker of the invention is determined. Standard methods and compositions for determining the amount of RNA or protein products of a biomarker of the invention can be utilized. Such methods and compositions are described in detail above.

Kits to Identify Compounds that Modulate the Expression or Activity of a Biomarker

In specific embodiments, in a screening assay described herein, the amount of protein or RNA product of a biomarker of the invention is determined utilizing kits. Such kits comprise materials and reagents required for measuring the expression of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8 protein or RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, all or any combination of the biomarkers of the invention. In specific embodiments, the kits may further comprise one or more additional reagents employed in the various methods, such as: (1) reagents for purifying RNA from blood; (2) primers for generating test nucleic acids; (3) dNTPs and/or rNTPs (either premixed or separate), optionally with one or more uniquely labeled dNTPs and/or rNTPs (*e.g.*, biotinylated or Cy3 or Cy5 tagged dNTPs); (4) post synthesis labeling reagents, such as chemically active derivatives of fluorescent dyes; (5) enzymes, such as reverse transcriptases, DNA polymerases, and the like; (6) various buffer mediums, *e.g.*, hybridization and washing buffers; (7) labeled probe purification reagents and components, like spin columns, etc.; and (8)

protein purification reagents; (9) signal generation and detection reagents, *e.g.*, streptavidin-alkaline phosphatase conjugate, chemifluorescent or chemiluminescent substrate, and the like. In particular embodiments, the kits comprise prelabeled quality controlled protein and or RNA transcript (in some embodiments, mRNA) for use as a control.

In some embodiments, the kits are QRT-PCR kits. In other embodiments, the kits are nucleic acid arrays and protein arrays. Such kits according to the subject invention will at least comprise an array having associated protein or nucleic acid members of the invention and packaging means therefore. Alternatively the protein or nucleic acid members of the invention may be prepackaged onto an array.

In a specific embodiment, kits for measuring a RNA product of a biomarker of the invention comprise materials and reagents that are necessary for measuring the expression of the RNA product. For example, a microarray or QRT-PCR kit may be used and contain only those reagents and materials necessary for measuring the levels of RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, all or any combination of the biomarkers of the invention. Alternatively, in some embodiments, the kits can comprise materials and reagents that are not limited to those required to measure the levels of RNA products of 1, 2, 3, 4, 5, 6, 7, 8 all or any combination of the biomarkers of the invention. For example, a microarray kit may contain reagents and materials necessary for measuring the levels of RNA products 1,2, 3, 4, 5, 6, 7, 8, all or any combination of the biomarkers of the invention, in addition to reagents and materials necessary for measuring the levels of the RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, or more genes other than the biomarkers of the invention. In a specific embodiment, a microarray or QRT-PCR kit contains reagents and materials necessary for measuring the levels of RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, all or any combination of the biomarkers of the invention, and 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300, 350, 400, 450, or more genes that are not biomarkers of the invention, or 1-10, 1-100, 1-150, 1-200, 1-300, 1-400, 1-500, 1-1000, 25-100, 25-200, 25-300, 25-400, 25-500, 25-1000, 100-150, 100-200, 100-300, 100-400, 100-500, 100-1000 or 500-1000 or more genes that are not biomarkers of the invention.

For nucleic acid micoarray kits, the kits generally comprise probes attached or localized to a support surface. The probes may be labeled with a detectable label. In a specific

embodiment, the probes are specific for the 5' region, the 3' region, the internal coding region, an exon(s), an intron(s), an exon junction(s), or an exon-intron junction(s), of 1, 2, 3, 4, 5, 6, 7, 8, all or any combination of the biomarkers of the invention. The microarray kits may comprise instructions for performing the assay and methods for interpreting and analyzing the data resulting from the performance of the assay. The kits may also comprise hybridization reagents and/or reagents necessary for detecting a signal produced when a probe hybridizes to a target nucleic acid sequence. Generally, the materials and reagents for the microarray kits are in one or more containers. Each component of the kit is generally in its own a suitable container.

For QRT-PCR kits, the kits generally comprise pre-selected primers specific for particular RNA products (*e.g.*, an exon(s), an intron(s), an exon junction(s), and an exon-intron junction(s)) of 1, 2, 3, 4, 5, 6, 7, 8, all or any combination of the biomarkers of the invention. The QRT-PCR kits may also comprise enzymes suitable for reverse transcribing and/or amplifying nucleic acids (*e.g.*, polymerases such as Taq, enzymes such as reverse transcriptase etc.), and deoxynucleotides and buffers needed for the reaction mixture for reverse transcription and amplification. The QRT-PCR kits may also comprise biomarker specific sets of primers specific for 1, 2, 3, 4, 5, 6, 7, 8, all or any combination of the biomarkers of the invention. The QRT-PCR kits may also comprise biomarker specific probes which are specific for the sequences amplified from 1, 2, 3, 4, 5, 6, 7, 8, all or any combination of the biomarkers of the invention using the biomarker specific sets of primers. The probes may or may not be labeled with a detectable label (*e.g.*, a fluorescent label). In some embodiments, when contemplating multiplexing it is helpful if the probes are labeled with a different detectable label (e.g. FAM or HEX) Each component of the QRT-PCR kit is generally in its own suitable container. Thus, these kits generally comprise distinct containers suitable for each individual reagent, enzyme, primer and probe. Further, the QRT-PCR kits may comprise instructions for performing the assay and methods for interpreting and analyzing the data resulting from the performance of the assay.

For antibody based kits, the kit can comprise, for example: (1) a first antibody (which may or may not be attached to a support) which binds to protein of interest (*e.g.*, a protein products of 1, 2, 3, 4, 5, 6, 7, 8, all or any combination of the biomarkers of the invention); and, optionally, (2) a second, different antibody which binds to either the protein, or the first antibody and is conjugated to a detectable label (*e.g.*, a fluorescent label, radioactive isotope or enzyme).

The antibody-based kits may also comprise beads for conducting an immunoprecipitation. Each component of the antibody-based kits is generally in its own suitable container. Thus, these kits generally comprise distinct containers suitable for each antibody. Further, the antibody-based kits may comprise instructions for performing the assay and methods for interpreting and analyzing the data resulting from the performance of the assay.

Reporter gene-based assays may also be conducted to identify a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies. In a specific embodiment, the present invention provides a method for identifying a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies, said method comprising: (a) contacting a compound with a cell expressing a reporter gene construct comprising a reporter gene operably linked to a regulatory element of a biomarker of the invention (*e.g.*, a promoter/enhancer element); (b) measuring the expression of said reporter gene; and (c) comparing the amount in (a) to that present in a corresponding control cell that has not been contacted with the test compound, so that if the amount of expressed reporter gene is altered relative to the amount in the control cell, a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies is identified. In accordance with this embodiment, the cell may naturally express the biomarker or be engineered to express the biomarker. In another embodiment, the present invention provides a method for identifying a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies, said method comprising: (a) contacting a compound with a cell-free extract and a reporter gene construct comprising a reporter gene operably linked to a regulatory element of a biomarker of the invention (*e.g.*, a promoter/enhancer element); (b) measuring the expression of said reporter gene; and (c) comparing the amount in (a) to that present in a corresponding control that has not been contacted with the test compound, so that if the amount of expressed reporter gene is altered relative to the amount in the control, a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies is identified.

Any reporter gene well-known to one of skill in the art may be used in reporter gene constructs used in accordance with the methods of the invention. Reporter genes refer to a nucleotide sequence encoding a RNA transcript or protein that is readily detectable either by its presence (by, *e.g.*, RT-PCR, Northern blot, Western Blot, ELISA, *etc.*) or activity. Non-limiting examples of reporter genes are listed in **Table 10**. Reporter genes may be obtained and the

nucleotide sequence of the elements determined by any method well-known to one of skill in the art. The nucleotide sequence of a reporter gene can be obtained, *e.g.*, from the literature or a database such as GenBank. Alternatively, a polynucleotide encoding a reporter gene may be generated from nucleic acid from a suitable source. If a clone containing a nucleic acid encoding a particular reporter gene is not available, but the sequence of the reporter gene is known, a nucleic acid encoding the reporter gene may be chemically synthesized or obtained from a suitable source (*e.g.*, a cDNA library, or a cDNA library generated from, or nucleic acid, preferably poly A+ RNA, isolated from, any tissue or cells expressing the reporter gene) by PCR amplification. Once the nucleotide sequence of a reporter gene is determined, the nucleotide sequence of the reporter gene may be manipulated using methods well-known in the art for the manipulation of nucleotide sequences, *e.g.*, recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., 1990, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY and Ausubel et al., eds., 1998, Current Protocols in Molecular Biology, John Wiley & Sons, NY, which are both incorporated by reference herein in their entireties), to generate reporter genes having a different amino acid sequence, for example to create amino acid substitutions, deletions, and/or insertions.

In accordance with the invention, cells that naturally or normally express one or more, all or any combination of the biomarkers of the invention can be used in the methods described herein. Alternatively, cells can be engineered to express one or more, all or any combination of the biomarkers of the invention, or a reporter gene using techniques well-known in the art and used in the methods described herein. Examples of such techniques include, but are not to, calcium phosphate precipitation (see, *e.g.*, Graham & Van der Eb, 1978, Virol. 52:546), dextran-mediated transfection, calcium phosphate mediated transfection, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the nucleic acid in liposomes, and direct microinjection of the nucleic acid into nuclei.

In a specific embodiment, the cells used in the methods described herein are intestinal cells or cell lines, lymphocytes (T or B lymphocytes), monocytes, neutrophils, macrophages, eosinophils, basophils, erythrocytes or platelets. In a preferred embodiment, the cells used in the methods described herein are intestinal cells. In another preferred embodiment, the cells used in

the methods described herein are lymphocytes. In another embodiment, the cells used in the methods described herein are immortalized cell lines derived from a source, *e.g.*, a tissue.

Any cell-free extract that permits the translation, and optionally but preferably, the transcription, of a nucleic acid can be used in accordance with the methods described herein. The cell-free extract may be isolated from cells of any species origin. For example, the cell-free translation extract may be isolated from human cells, cultured mouse cells, cultured rat cells, Chinese hamster ovary (CHO) cells, Xenopus oocytes, rabbit reticulocytes, wheat germ, or rye embryo (see, *e.g.*, Krieg & Melton, 1984, Nature 308:203 and Dignam et al., 1990 Methods Enzymol. 182:194-203). Alternatively, the cell-free translation extract, *e.g.*, rabbit reticulocyte lysates and wheat germ extract, can be purchased from, *e.g.*, Promega, (Madison, WI). In a preferred embodiment, the cell-free extract is an extract isolated from human cells. In a specific embodiment, the human cells are HeLa cells, lymphocytes, or intestinal cells or cell lines.

In addition to the ability to modulate the expression levels of RNA and/or protein products a biomarker of the invention, it may be desirable, at least in certain instances, that compounds modulate the activity of a protein products of a biomarker of the invention. Thus, the present invention provides methods of identifying compounds to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies, comprising methods for identifying compounds that modulate the activity of a protein products of one or more biomarkers of the invention. Such methods can comprise: (a) contacting a cell expressing a protein products of one or more biomarkers of the invention with a test compound; (b) determining the activity level of the protein products; and (c) comparing the activity level to that in a corresponding control cell that has not been contacted with the test compound, so that if the level of activity in (a) is altered relative to the level of activity in the control cell, a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies is identified. In a specific embodiment, the activity level(s) is altered by 5%, 10%, 15%, 25%, 30%, 40%, 50%, 5 to 25%, 10 to 30%, at least 1 fold, at least 1.5 fold, at least 2 fold, 4 fold, 5 fold, 10 fold, 25 fold, 1 to 10 fold, or 5 to 25 fold relative to the activity level in the control as determined by utilizing an assay described herein (*e.g.*, a microarray or QRT-PCR) or an assay well known to one of skill in the art. In alternate embodiments, such a method comprises determining the activity level of a protein products of at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 12, at least 15, 1 to 5, 1-10, 5-10, 5-15,

or 10-15, or more, or all or any combination of the biomarkers of the invention present in the cell and comparing the activity levels to those present in the control.

The present invention provides methods of identifying compounds to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies, comprising: (a) contacting a cell-free extract with a nucleic acid encoding a protein products of one or more biomarkers of the invention and a test compound; (b) determining the activity level of the protein products; and (c) comparing the activity level to that in a corresponding control that has not been contacted with the test compound, so that if the level of activity in (a) is altered relative to the level of activity in the control, a compound to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies is identified. In a specific embodiment, the activity level(s) is altered by 5%, 10%, 15%, 25%, 30%, 40%, 50%, 5 to 25%, 10 to 30%, at least 1 fold, at least 1.5 fold, at least 2 fold, 4 fold, 5 fold, 10 fold, 25 fold, 1 to 10 fold, or 5 to 25 fold relative to the activity level in the control as determined by utilizing an assay described herein (*e.g.*, a microarray or QRT-PCR) or an assay well known to one of skill in the art. In alternate embodiments, such a method comprises determining the activity level of a protein products of at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, 1 to 3, 1 to 5, 1-8 all or any combination of the biomarkers of the invention present in the sample and comparing the activity levels to those present in the control.

Standard techniques can be utilized to determine the level of activity of a protein products of a biomarker of the invention. Activities of protein productss of biomarkers of the invention that can be determined using techniques well known in the art.

Method to Utilize the Biological Activity of the Compounds

Upon identification of compounds to be tested for an ability to prevent, treat, or ameliorate one or more colorectal pathologies (for convenience referred to herein as a "lead" compound), the compounds can be further investigated. For example, the compounds identified via the present methods can be further tested *in vivo* in accepted animal models of polyp formation. Further, the compounds identified via the methods can be analyzed with respect to their specificity. Techniques for such additional compound investigation are well known to one of skill in the art.

In one embodiment, the effect of a lead compound can be assayed by measuring the cell growth or viability of the target cell. Such assays can be carried out with representative cells of

cell types involved in polyp formation (*e.g.*, intestinal cells; cells isolated from different portions of the gastrointestinal system and the like). Alternatively, instead of culturing cells from a patient, a lead compound may be screened using cells of a cell line.

Many assays well-known in the art can be used to assess the survival and/or growth of a patient cell or cell line following exposure to a lead compound; for example, cell proliferation can be assayed by measuring Bromodeoxyuridine (BrdU) incorporation (see, *e.g.*, Hoshino et al., 1986, Int. J. Cancer 38, 369; Campana et al., 1988, J. Immunol. Meth. 107:79) or (^{3}H)-thymidine incorporation (see, *e.g.*, Chen, J., 1996, Oncogene 13:1395-403; Jeoung, J., 1995, J. Biol. Chem. 270:18367-73), by direct cell count, by detecting changes in transcription, translation or activity of known genes such as proto-oncogenes (*e.g.*, *fos*, *myc*) or cell cycle markers (Rb, cdc2, cyclin A, D1, D2, D3, E, etc). The levels of such protein and RNA (*e.g.*, mRNA) and activity can be determined by any method well known in the art. For example, protein can be quantitated by known immunological based methods such as Western blotting or immunoprecipitation using commercially available antibodies. mRNA can be quantitated using methods that are well known and routine in the art, for example, using northern analysis, RNase protection, the polymerase chain reaction in connection with the reverse transcription. Cell viability can be assessed by using trypan-blue staining or other cell death or viability markers known in the art. In a specific embodiment, the level of cellular ATP is measured to determined cell viability. Differentiation can be assessed, for example, visually based on changes in morphology.

Animal Models

Compounds can be tested in suitable animal model systems prior to use in humans. Such animal model systems include but are not limited to rats, mice, chicken, cows, monkeys, pigs, dogs, rabbits, etc. Any animal system well-known in the art may be used. In certain embodiments, compounds are tested in a mouse model. Compounds can be administered repeatedly.

Accepted animal models can be utilized to determine the efficacy of the compounds identified via the methods described above for the prevention, treatment, and/or amelioration of one or more colorectal pathologies.

Toxicity

The toxicity and/or efficacy of a compound identified in accordance with the invention can be determined by standard pharmaceutical procedures in cell cultures or experimental

animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). Cells and cell lines that can be used to assess the cytotoxicity of a compound identified in accordance with the invention include, but are not limited to, peripheral blood mononuclear cells (PBMCs), Caco-2 cells, and Huh7 cells. The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50}/ED_{50}. A compound identified in accordance with the invention that exhibits large therapeutic indices is preferred. While a compound identified in accordance with the invention that exhibits toxic side effects may be used, care should be taken to design a delivery system that targets such agents to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage of a compound identified in accordance with the invention for use in humans. The dosage of such agents lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any agent used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (*i.e.*, the concentration of the compound that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

Design of Congeners or Analogs

The compounds which display the desired biological activity can be used as lead compounds for the development or design of congeners or analogs having useful pharmacological activity. For example, once a lead compound is identified, molecular modeling techniques can be used to design variants of the compound that can be more effective. Examples of molecular modeling systems are the CHARM and QUANTA programs (Polygen Corporation, Waltham, MA). CHARM performs the energy minimization and molecular dynamics functions. QUANTA performs the construction, graphic modelling and analysis of molecular structure.

QUANTA allows interactive construction, modification, visualization, and analysis of the behavior of molecules with each other.

A number of articles review computer modeling of drugs interactive with specific proteins, such as Rotivinen et al., 1988, Acta Pharmaceutical Fennica 97:159-166; Ripka, 1998, New Scientist 54-57; McKinaly & Rossmann, 1989, Annu. Rev. Pharmacol. Toxiciol. 29:111-122; Perry & Davies, OSAR: Quantitative Structure-Activity Relationships in Drug Design pp. 189-193 (Alan R. Liss, Inc. 1989); Lewis & Dean, 1989, Proc. R. Soc. Lond. 236:125-140 and 141-162; Askew et al., 1989, J. Am. Chem. Soc. 111:1082-1090. Other computer programs that screen and graphically depict chemicals are available from companies such as BioDesign, Inc. (Pasadena, California), Allelix, Inc. (Mississauga, Ontario, Canada), and Hypercube, Inc. (Cambridge, Ontario). Although these are primarily designed for application to drugs specific to particular proteins, they can be adapted to design of drugs specific to any identified region. The analogs and congeners can be tested for binding to the proteins of interest (*i.e.*, the protein products of a biomarker of the invention) using the above-described screens for biologic activity. Alternatively, lead compounds with little or no biologic activity, as ascertained in the screen, can also be used to design analogs and congeners of the compound that have biologic activity.

Compounds

Compounds that can be tested and identified methods described herein can include, but are not limited to, compounds obtained from any commercial source, including Aldrich (1001 West St. Paul Ave., Milwaukee, WI 53233), Sigma Chemical (P.O. Box 14508, St. Louis, MO 63178), Fluka Chemie AG (Industriestrasse 25, CH-9471 Buchs, Switzerland (Fluka Chemical Corp. 980 South 2nd Street, Ronkonkoma, NY 11779)), Eastman Chemical Company, Fine Chemicals (P.O Box 431, Kingsport, TN 37662), Boehringer Mannheim GmbH (Sandhofer Strasse 116, D-68298 Mannheim), Takasago (4 Volvo Drive, Rockleigh, NJ 07647), SST Corporation (635 Brighton Road, Clifton, NJ 07012), Ferro (111 West Irene Road, Zachary, LA 70791), Riedel-deHaen Aktiengesellschaft (P.O. Box D-30918, Seelze, Germany), PPG Industries Inc., Fine Chemicals (One PPG Place, 34th Floor, Pittsburgh, PA 15272). Further any kind of natural products may be screened using the methods of the invention, including microbial, fungal, plant or animal extracts.

Compounds from large libraries of synthetic or natural compounds can be screened. Numerous means are currently used for random and directed synthesis of saccharide, peptide,

and nucleic acid-based compounds. Synthetic compound libraries are commercially available from a number of companies including Maybridge Chemical Co. (Trevillet, Cornwall, UK), Comgenex (Princeton, NJ), Brandon Associates (Merrimack, NH), and Microsource (New Milford, CT). A rare chemical library is available from Aldrich (Milwaukee, WI). Combinatorial libraries are available and are prepared. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available from e.g., Pan Laboratories (Bothell, WA) or MycoSearch (NC), or are readily produceable by methods well known in the art. Additionally, natural and synthetically produced libraries and compounds are readily modified through conventional chemical, physical, and biochemical means.

Furthermore, diversity libraries of test compounds, including small molecule test compounds, may be utilized. Libraries screened using the methods of the present invention can comprise a variety of types of compounds. Examples of libraries that can be screened in accordance with the methods of the invention include, but are not limited to, peptoids; random biooligomers; diversomers such as hydantoins, benzodiazepines and dipeptides; vinylogous polypeptides; nonpeptidal peptidomimetics; oligocarbamates; peptidyl phosphonates; peptide nucleic acid libraries; antibody libraries; carbohydrate libraries; and small molecule libraries (in some embodiments, small organic molecule libraries). In some embodiments, the compounds in the libraries screened are nucleic acid or peptide molecules. In a non-limiting example, peptide molecules can exist in a phage display library. In other embodiments, the types of compounds include, but are not limited to, peptide analogs including peptides comprising non-naturally occurring amino acids, *e.g.*, D-amino acids, phosphorous analogs of amino acids, such as α-amino phosphoric acids and α-amino phosphoric acids, or amino acids having non-peptide linkages, nucleic acid analogs such as phosphorothioates and PNAs, hormones, antigens, synthetic or naturally occurring drugs, opiates, dopamine, serotonin, catecholamines, thrombin, acetylcholine, prostaglandins, organic molecules, pheromones, adenosine, sucrose, glucose, lactose and galactose. Libraries of polypeptides or proteins can also be used in the assays of the invention.

In a specific embodiment, the combinatorial libraries are small organic molecule libraries including, but not limited to, benzodiazepines, isoprenoids, thiazolidinones, metathiazanones, pyrrolidines, morpholino compounds, and benzodiazepines. In another embodiment, the combinatorial libraries comprise peptoids; random bio-oligomers; benzodiazepines; diversomers

such as hydantoins, benzodiazepines and dipeptides;, vinylogous polypeptides; nonpeptidal peptidomimetics; oligocarbamates; peptidyl phosphonates; peptide nucleic acid libraries; antibody libraries; or carbohydrate libraries. Combinatorial libraries are themselves commercially available For example, libraries may be commercially obtained from, *e.g.*, Specs and BioSpecs B.V. (Rijswijk, The Netherlands), Chembridge Corporation (San Diego, CA), Contract Service Company (Dolgoprudny, Moscow Region, Russia), Comgenex USA Inc. (Princeton, NJ), Maybridge Chemicals Ltd. (Cornwall PL34 OHW, United Kingdom), Asinex (Moscow, Russia), ComGenex (Princeton, New Jersey), Ru, Tripos, Inc. (St. Louis, Missouri), ChemStar, Ltd (Moscow, Russia), 3D Pharmaceuticals (Exton, Pennsylvania), and Martek Biosciences (Columbia, Maryland).

In a preferred embodiment, the library is preselected so that the compounds of the library are more amenable for cellular uptake. For example, compounds are selected based on specific parameters such as, but not limited to, size, lipophilicity, hydrophilicity, and hydrogen bonding, which enhance the likelihood of compounds getting into the cells. In another embodiment, the compounds are analyzed by three-dimensional or four-dimensional computer computation programs.

The combinatorial compound library for use in accordance with the methods of the present invention may be synthesized. There is a great interest in synthetic methods directed toward the creation of large collections of small organic compounds, or libraries, which could be screened for pharmacological, biological or other activity. The synthetic methods applied to create vast combinatorial libraries are performed in solution or in the solid phase, *i.e.*, on a support. Solid-phase synthesis makes it easier to conduct multi-step reactions and to drive reactions to completion with high yields because excess reagents can be easily added and washed away after each reaction step. Solid-phase combinatorial synthesis also tends to improve isolation, purification and screening. However, the more traditional solution phase chemistry supports a wider variety of organic reactions than solid-phase chemistry.

Combinatorial compound libraries of the present invention may be synthesized using the apparatus described in U.S. Patent No. 6,190,619 to Kilcoin et al., which is hereby incorporated by reference in its entirety. U.S. Patent No. 6,190,619 discloses a synthesis apparatus capable of holding a plurality of reaction vessels for parallel synthesis of multiple discrete compounds or for combinatorial libraries of compounds.

In one embodiment, the combinatorial compound library can be synthesized in solution. The method disclosed in U.S. Patent No. 6,194,612 to Boger et al., which is hereby incorporated by reference in its entirety, features compounds useful as templates for solution phase synthesis of combinatorial libraries. The template is designed to permit reaction products to be easily purified from unreacted reactants using liquid/liquid or solid/liquid extractions. The compounds produced by combinatorial synthesis using the template will in some embodiments be small organic molecules. Some compounds in the library may mimic the effects of non-peptides or peptides. In contrast to solid phase synthesize of combinatorial compound libraries, liquid phase synthesis does not require the use of specialized protocols for monitoring the individual steps of a multistep solid phase synthesis (Egner et al., 1995, J.Org. Chem. 60:2652; Anderson et al., 1995, J. Org. Chem. 60:2650; Fitch et al., 1994, J. Org. Chem. 59:7955; Look et al., 1994, J. Org. Chem. 49:7588; Metzger et al., 1993, Angew. Chem., Int. Ed. Engl. 32:894; Youngquist et al., 1994, Rapid Commun. Mass Spect. 8:77; Chu et al., 1995, J. Am. Chem. Soc. 117:5419; Brummel et al., 1994, Science 264:399; and Stevanovic et al., 1993, Bioorg. Med. Chem. Lett. 3:431).

Combinatorial compound libraries useful for the methods of the present invention can be synthesized on supports. In one embodiment, a split synthesis method, a protocol of separating and mixing supports during the synthesis, is used to synthesize a library of compounds on supports (see *e.g.* Lam et al., 1997, Chem. Rev. 97:41-448; Ohlmeyer et al., 1993, Proc. Natl. Acad. Sci. USA 90:10922-10926 and references cited therein). Each support in the final library has substantially one type of compound attached to its surface. Other methods for synthesizing combinatorial libraries on supports, wherein one product is attached to each support, will be known to those of skill in the art (*see, e.g.*, Nefzi et al., 1997, Chem. Rev. 97:449-472).

In some embodiments of the present invention, compounds can be attached to supports via linkers. Linkers can be integral and part of the support, or they may be nonintegral that are either synthesized on the support or attached thereto after synthesis. Linkers are useful not only for providing points of compound attachment to the support, but also for allowing different groups of molecules to be cleaved from the support under different conditions, depending on the nature of the linker. For example, linkers can be, *inter alia*, electrophilically cleaved, nucleophilically cleaved, photocleavable, enzymatically cleaved, cleaved by metals, cleaved under reductive conditions or cleaved under oxidative conditions. In a preferred embodiment,

the compounds are cleaved from the support prior to high throughput screening of the compounds.

If the library comprises arrays or microarrays of compounds, wherein each compound has an address or identifier, the compound can be deconvoluted, *e.g.*, by cross-referencing the positive sample to original compound list that was applied to the individual test assays.

If the library is a peptide or nucleic acid library, the sequence of the compound can be determined by direct sequencing of the peptide or nucleic acid. Such methods are well known to one of skill in the art.

A number of physico-chemical techniques can be used for the *de novo* characterization of compounds. Examples of such techniques include, but are not limited to, mass spectrometry, NMR spectroscopy, X-ray crytallography and vibrational spectroscopy.

(Q) Use of Identified Compounds to Prevent, Treat, or Ameliorate One or more Colorectal Pathologies

The present invention provides methods of preventing, treating, or ameliorating one or more colorectal pathologies, said methods comprising administering to a subject in need thereof one or more compounds identified in accordance with the methods of the invention. In a preferred embodiment, the individual is human.

In one embodiment, the invention provides a method of preventing, treating, or ameliorating one or more colorectal pathologies, said method comprising administering to an individual in need thereof a dose of a prophylactically or therapeutically effective amount of one or more compounds identified in accordance with the methods of the invention. In a specific embodiment, a compound identified in accordance with the methods of the invention is not administered to prevent, treat, or ameliorate one or more colorectal pathologies, if such compound has been used previously to prevent, treat, or ameliorate one or more colorectal pathologies. In another embodiment, a compound identified in accordance with the methods of the invention is not administered to prevent, treat, or ameliorate one or more colorectal pathologies, if such compound has suggested to be used to prevent, treat, or ameliorate one or more colorectal pathologies. In another embodiment, a compound identified in accordance with the methods of the invention specifically binds to and/or alters the expression and/or activity level of a protein or RNA products of only one biomarker of the invention. In another embodiment, a compound identified in accordance with the methods of the invention is not

administered to prevent, treat, or ameliorate one or more colorectal pathologies, if such compound binds to and/or alters the expression and/or activity of a protein or RNA products of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or more or all or any combination of the biomarkers of **Tables 2** or **6**. In yet another embodiment, a compound identified in accordance with the methods of the invention binds to and/or alters the expression and/or activity level of a protein or RNA products of at least 2, at least 3, at least 4, at least 5, at least 10, at least 15, or more biomarkers of the invention.

The invention also provides methods of preventing, treating, or ameliorating one or more colorectal pathologies, said methods comprising administering to a subject in need thereof one or more of the compounds identified utilizing the screening methods described herein, and one or more other therapies (*e.g.*, prophylactic or therapeutic agents and surgery). In a specific embodiment, such therapies are currently being used, have been used or are known to be useful in the prevention, treatment, or amelioration of one or more colorectal pathologies (including, but not limited to the prophylactic or therapeutic agents listed herein). The therapies (*e.g.*, prophylactic or therapeutic agents) of the combination therapies of the invention can be administered sequentially or concurrently. In a specific embodiment, the combination therapies of the invention comprise a compound identified in accordance with the invention and at least one other therapy that has the same mechanism of action as said compound. In another specific embodiment, the combination therapies of the invention comprise a compound identified in accordance with the methods of the invention and at least one other therapy (*e.g.*, prophylactic or therapeutic agent) which has a different mechanism of action than said compound. The combination therapies of the present invention improve the prophylactic or therapeutic effect of a compound of the invention by functioning together with the compound to have an additive or synergistic effect. The combination therapies of the present invention reduce the side effects associated with the therapies (*e.g.*, prophylactic or therapeutic agents).

The prophylactic or therapeutic agents of the combination therapies can be administered to a subject in the same pharmaceutical composition. Alternatively, the prophylactic or therapeutic agents of the combination therapies can be administered concurrently to a subject in separate pharmaceutical compositions. The prophylactic or therapeutic agents may be administered to a subject by the same or different routes of administration.

In specific embodiment, a pharmaceutical composition comprising one or more compounds identified in an assay described herein is administered to an individual, in some embodiments a human, to prevent, treat, or ameliorate one or more colorectal pathologies. In accordance with the invention, the pharmaceutical composition may also comprise one or more prophylactic or therapeutic agents. In some embodiments, such agents are currently being used, have been used or are known to be useful in the prevention, treatment, or amelioration of one or more colorectal pathologies.

(R) Compounds of the Invention

Representative, non-limiting examples of compounds that can be used in accordance with the methods of the invention to prevent, treat, and/or ameliorate one or more colorectal pathologies are described in detail below.

First, such compounds can include, for example, antisense, ribozyme, or triple helix compounds that can downregulate the expression or activity of a protein or RNA products of a biomarker of the invention. Such compounds are described in detail in the subsection below.

Second, such compounds can include, for example, antibody compositions that can modulate the expression of a protein or RNA products of a biomarker of the invention, or the activity of a protein products of a biomarker of the invention. In a specific embodiment, the antibody compositions downregulate the expression a protein or RNA products of a biomarker of the invention, or the activity of a protein products of a biomarker of the invention. Such compounds are described in detail in the subsection below.

Third, such compounds can include, for example, protein products of a biomarker of the invention. The invention encompasses the use of peptides or peptide mimetics selected to mimic a protein products of a biomarker of the invention to prevent, treat, or ameliorate one or more colorectal pathologies. Further, such compounds can include, for example, dominant-negative polypeptides that can modulate the expression a protein or RNA products of a biomarker of the invention, or the activity protein products of a biomarker of the invention.

The methods also encompass the use derivatives, analogs and fragments of protein products of a biomarker of the invention to prevent, treat, or ameliorate one or more colorectal pathologies. In particular, the invention encompasses the use of fragments of protein products of a biomarker of the invention comprising one or more domains of such a protein(s) to prevent, treat, or ameliorate one or more colorectal pathologies. In another specific embodiment, the

invention encompasses the use of a protein products of a biomarker of the invention, or an analog, derivative or fragment of such a protein which is expressed as a fusion, or chimeric protein products (comprising the protein, fragment, analog, or derivative joined via a peptide bond to a heterologous protein sequence).

In specific embodiments, an antisense oligonucleotide of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, or more of biomarkers of the invention are administered to prevent, treat, or ameliorate one or more colorectal pathologies. In other embodiments, one or more of protein products of a biomarker of the invention or a fragment, analog, or derivative thereof are administered to prevent, treat, or ameliorate one or more colorectal pathologies. In other embodiment, one or more antibodies that specifically bind to protein products of the invention are administered to prevent, treat, or ameliorate one or more colorectal pathologies. In other embodiments, one or more dominant-negative polypeptides are administered to prevent, treat, or ameliorate one or more colorectal pathologies.

Antisense, Ribozyme, Triple-Helix Compositions

Standard techniques can be utilized to produce antisense, triple helix, or ribozyme molecules reactive to one or more of the genes listed in **Tables 2** or **6**, and transcripts of the genes listed in **Tables 2** or **6**, for use as part of the methods described herein. First, standard techniques can be utilized for the production of antisense nucleic acid molecules, *i.e.*, molecules which are complementary to a sense nucleic acid encoding a polypeptide of interest, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire coding strand, or to only a portion thereof, *e.g.*, all or part of the protein coding region (or open reading frame). An antisense nucleic acid molecule can be antisense to all or part of a non-coding region of the coding strand of a nucleotide sequence encoding a polypeptide of interest. The non-coding regions ("5' and 3' untranslated regions") are the 5' and 3' sequences that flank the coding region and are not translated into amino acids.

An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides or more in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art.

For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxy-hydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylamino-methyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyl-uracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest).

Antisense nucleic acid molecules administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA encoding the polypeptide of interest to thereby inhibit expression, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue, *e.g.*, a joint (*e.g.*, a knee, hip, elbow, and knuckle), site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell, *e.g.*, a T cell or intestinal cell, surface, *e.g.*, by

linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using vectors, *e.g.*, gene therapy vectors, described below. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

An antisense nucleic acid molecule of interest can be an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α-units, the strands run parallel to each other (Gaultier et al., 1987, Nucleic Acids Res. 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al., 1987, Nucleic Acids Res. 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region, and can also be generated using standard techniques. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach, 1988, Nature 334:585-591)) can be used to catalytically cleave mRNA transcripts to thereby inhibit translation of the protein encoded by the mRNA. A ribozyme having specificity for a nucleic acid molecule encoding a polypeptide of interest can be designed based upon the nucleotide sequence of a cDNA disclosed herein. For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a Cech et al. U.S. Patent No. 4,987,071; and Cech et al. U.S. Patent No. 5,116,742. Alternatively, an mRNA encoding a polypeptide of interest can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. *See, e.g.*, Bartel and Szostak, 1993, Science 261:1411-1418.

Triple helical structures can also be generated using well known techniques. For example, expression of a polypeptide of interest can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the gene encoding the polypeptide (*e.g.*, the promoter and/or enhancer) to form triple helical structures that prevent transcription of the gene in target cells. *See generally* Helene, 1991, Anticancer Drug Des. 6(6):569-84; Helene, 1992, Ann. N.Y. Acad. Sci. 660:27-36; and Maher, 1992, Bioassays 14(12):807-15.

In various embodiments, nucleic acid compositions can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (*see* Hyrup et al., 1996, Bioorganic & Medicinal Chemistry 4(1): 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al.,1996, *supra*; Perry-O'Keefe et al., 1996, Proc. Natl. Acad. Sci. USA 93: 14670-675.

PNAs can, for example, be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated which may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNAse H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup, 1996, *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup, 1996, *supra,* and Finn et al., 1996, Nucleic Acids Res. 24(17):3357-63. For example, a DNA chain can be synthesized on a support using standard phosphoramidite coupling chemistry and modified nucleoside analogs. Compounds such as 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite can be used as a link between the PNA and the 5' end of DNA (Mag et al., 1989, Nucleic Acids Res. 17:5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al., 1996, Nucleic Acids Res. 24(17):3357-63). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment (Peterser et al., 1975, Bioorganic Med. Chem. Lett. 5:1119-11124).

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the

cell membrane (*see, e.g.*, Letsinger et al., 1989, Proc. Natl. Acad. Sci. USA 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. USA 84:648-652; International Publication No. W0 88/09810) or the blood-brain barrier (*see, e.g.*, International Publication No. W0 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (*see, e.g.*, Krol et al., 1988, Bio/Techniques 6:958-976) or intercalating agents (*see, e.g.*, Zon, 1988, Pharm. Res. 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

Antibody Compositions

In one embodiment, antibodies that specifically bind to one or more protein products of one or more biomarkers of the invention are administered to an individual, in some embodiments a human, to prevent, treat, or ameliorate one or more colorectal pathologies. In another embodiment, any combination of antibodies that specifically bind to one or more protein products of one or more biomarkers of the invention are administered to a subject, in some embodiments a human, to prevent, treat, or ameliorate one or more colorectal pathologies. In a specific embodiment, one or more antibodies that specifically bind to one or more protein products of one or more biomarkers of the invention are administered to a subject, in some embodiments a human, in combination with other types of therapies to prevent, treat, or ameliorate one or more colorectal pathologies.

One or more antibodies that specifically bind to one or more protein products of one or more biomarkers of the invention can be administered to a subject, in some embodiments a human, using various delivery systems are known to those of skill in the art. For example, such antibodies can be administered by encapsulation in liposomes, microparticles or microcapsules. See, *e.g.*, U.S. Patent No. 5,762,904, U.S. Patent No. 6,004,534, and International Publication No. WO 99/52563. In addition, such antibodies can be administered using recombinant cells capable of expressing the antibodies, or retroviral, other viral vectors or non-viral vectors capable of expressing the antibodies.

Antibodies that specifically bind one or more protein products of one or more biomarkers of the invention can be obtained from any known source. For example, **Table 5** provides a list of commercially available antibodies specific for one or more of the protein products of the biomarkers of the invention. Alternatively, antibodies that specifically bind to one or more

protein products of one or more biomarkers of the invention can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or in some embodiments, by recombinant expression techniques.

Antibodies include, but are not limited to, polyclonal antibodies, monoclonal antibodies, bispecific antibodies, multispecific antibodies, human antibodies, humanized antibodies, camelised antibodies, chimeric antibodies, single-chain Fvs (scFv) (see *e.g.*, Bird *et al.* (1988) *Science* 242:423-426; and Huston *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883), single chain antibodies, single domain antibodies, Fab fragments, F(ab') fragments, disulfide-linked Fvs (sdFv), and anti-idiotypic (anti-Id) antibodies (including, *e.g.*, anti-Id antibodies to antibodies of the invention), and epitope-binding fragments of any of the above. The term "antibody", as used herein, refers to immunoglobulin molecules and immunologically active fragments of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site. Immunoglobulin molecules can be of any type (*e.g.*, IgG, IgE, IgM, IgD, IgA and IgY), class (*e.g.*, IgG_1, IgG_2, IgG_3, IgG_4, IgA_1 and IgA_2) or subclass. Examples of immunologically active fragments of immunoglobulin molecules include F(ab) fragments (a monovalent fragment consisting of the VL, VH, CL and CH1 domains) and F(ab')2 fragments (a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region) which can be generated by treating the antibody with an enzyme such as pepsin or papain. Immunologically active fragments also include, but are not limited to, Fd fragments (consisting of the VH and CH1 domains), Fv fragments (consisting of the VL and VH domains of a single arm of an antibody), dAb fragments (consisting of a VH domain; Ward *et al.*, (1989) *Nature* 341:544-546), and isolated complementarity determining regions (CDRs). Antibodies that specifically bind to an antigen can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or in some embodiments, by recombinant expression techniques.

Polyclonal antibodies that specifically bind to an antigen can be produced by various procedures well-known in the art. For example, a human antigen can be administered to various host animals including, but not limited to, rabbits, mice, rats, etc. to induce the production of sera containing polyclonal antibodies specific for the human antigen. Various adjuvants may be used to increase the immunological response, depending on the host species, and include but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide,

surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and corynebacterium parvum. Such adjuvants are also well known in the art.

The term "monospecific antibody" refers to an antibody that displays a single binding specificity and affinity for a particular target, *e.g.*, epitope. This term includes monoclonal antibodies. Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies, or a combination thereof. See, *e.g.*, U.S. Pat. Nos. RE 32,011, 4,902,614, 4,543,439, 4,411,993 and 4,196,265; Kennett et al (eds.), *Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses*, Plenum Press (1980); and Harlow and Lane (eds.), *Antibodies. A Laboratory Manual*, Cold Spring Harbor Laboratory Press (1988), which are incorporated herein by reference. For example, monoclonal antibodies can be produced using hybridoma techniques including those known in the art and taught, for example, in Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: *Monoclonal Antibodies and T-Cell Hybridomas* 563-681 (Elsevier, N.Y., 1981) (said references incorporated by reference in their entireties). Other techniques that enable the production of antibodies through recombinant techniques (*e.g.*, techniques described by William D. Huse et al., 1989, Science, 246: 1275-1281; L. Sastry et al., 1989, Proc. Natl. Acad. Sci. USA, 86: 5728-5732; and Michelle Alting-Mees et al., Strategies in Molecular Biology, 3: 1-9 (1990) involving a commercial system available from Stratacyte, La Jolla, Calif.) may also be utilized to construct monoclonal antibodies. The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art. Briefly, mice can be immunized with a protein products of a biomarker of the invention, and once an immune response is detected, *e.g.*, antibodies specific for the protein are detected in the mouse serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells, for example cells from cell line SP20 available from the ATCC. Hybridomas are selected

and cloned by limited dilution. Additionally, a RIMMS (repetitive immunization multiple sites) technique can be used to immunize an animal (Kilptrack et al., 1997, Hybridoma 16:381-9, incorporated by reference in its entirety). The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding a polypeptide of the invention. Ascites fluid, which generally contains high levels of antibodies, can be generated by immunizing mice with positive hybridoma clones.

Accordingly, the present invention provides methods of generating antibodies by culturing a hybridoma cell secreting an antibody of the invention wherein, in some embodiments, the hybridoma is generated by fusing splenocytes isolated from a mouse immunized with a protein products of a biomarker of the invention, with myeloma cells and then screening the hybridomas resulting from the fusion for hybridoma clones that secrete an antibody able to bind to the protein or protein fragment.

Antibody fragments which recognize specific epitopes of a protein products of a biomarker of the invention may be generated by any technique known to those of skill in the art. For example, Fab and F(ab')2 fragments of the invention may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). F(ab')2 fragments contain the variable region, the light chain constant region and the CH1 domain of the heavy chain. Further, the antibodies of the present invention can also be generated using various phage display methods known in the art.

In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In particular, DNA sequences encoding VH and VL domains are amplified from animal cDNA libraries (*e.g.*, human or murine cDNA libraries of affected tissues). The DNA encoding the VH and VL domains are recombined together with an scFv linker by PCR and cloned into a phagemid vector. The vector is electroporated in *E. coli* and the *E. coli* is infected with helper phage. Phage used in these methods are typically filamentous phage including fd and M13 and the VH and VL domains are usually recombinantly fused to either the phage gene III or gene VIII. Phage expressing an antigen binding domain that binds to a particular antigen can be selected or identified with antigen, *e.g.*, using labeled antigen or antigen bound or captured to a solid surface or bead. Examples of phage display methods that can be used to make the antibodies of the present

invention include those disclosed in Brinkman et al., 1995, J. Immunol. Methods 182:41-50; Ames et al., 1995, J. Immunol. Methods 184:177-186; Kettleborough et al. , 1994, Eur. J. Immunol. 24:952-958; Persic et al., 1997, Gene 187:9-18; Burton et al., 1994, Advances in Immunology 57:191-280; PCT Application No. PCT/GB91/O1 134; International Publication Nos. WO 90/02809, WO 91/10737, WO 92/01047, WO 92/18619, WO 93/1 1236, WO 95/15982, WO 95/20401, and WO97/13844; and U.S. Patent Nos. 5,698,426, 5,223,409, 5,403,484, 5,580,717, 5,427,908, 5,750,753, 5,821,047, 5,571,698, 5,427,908, 5,516,637, 5,780,225, 5,658,727, 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, *e.g.*, as described below. Techniques to recombinantly produce Fab, Fab' and F(ab')2 fragments can also be employed using methods known in the art such as those disclosed in International Publication No. WO 92/22324; Mullinax et al., 1992, BioTechniques 12(6):864-869; Sawai et al., 1995, AJRI 34:26-34; and Better et al., 1988, Science 240:1041-1043 (said references incorporated by reference in their entireties).

To generate whole antibodies, PCR primers including VH or VL nucleotide sequences, a restriction site, and a flanking sequence to protect the restriction site can be used to amplify the VH or VL sequences in scFv clones. Utilizing cloning techniques known to those of skill in the art, the PCR amplified VH domains can be cloned into vectors expressing a VH constant region, *e.g.*, the human gamma 4 constant region, and the PCR amplified VL domains can be cloned into vectors expressing a VL constant region, *e.g.*, human kappa or lamba constant regions. In some embodiments, the vectors for expressing the VH or VL domains comprise an EF-1a promoter, a secretion signal, a cloning site for the variable domain, constant domains, and a selection marker such as neomycin. The VH and VL domains may also cloned into one vector expressing the necessary constant regions. The heavy chain conversion vectors and light chain conversion vectors are then co-transfected into cell lines to generate stable or transient cell lines that express full-length antibodies, *e.g.*, IgG, using techniques known to those of skill in the art.

For some uses, including *in vivo* use of antibodies in humans and *in vitro* detection assays, it may be preferable to use human or chimeric antibodies. Completely human antibodies are particularly desirable for therapeutic treatment of human subjects. Human antibodies can be made by a variety of methods known in the art including phage display methods described above using antibody libraries derived from human immunoglobulin sequences. See also U.S. Patent Nos. 4,444,887 and 4,716,111; and International Publication Nos. WO 98/46645, WO 98/50433, WO 98/24893, WO98/16654, WO 96/34096, WO 96/33735, and WO 91/10741; each of which is incorporated herein by reference in its entirety.

Antibodies can also be produced by a transgenic animal. In particular, human antibodies can be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. For example, the human heavy and light chain immunoglobulin gene complexes may be introduced randomly or by homologous recombination into mouse embryonic stem cells. Alternatively, the human variable region, constant region, and diversity region may be introduced into mouse embryonic stem cells in addition to the human heavy and light chain genes. The mouse heavy and light chain immunoglobulin genes may be rendered non-functional separately or simultaneously with the introduction of human immunoglobulin loci by homologous recombination. In particular, homozygous deletion of the J_H region prevents endogenous antibody production. The modified embryonic stem cells are expanded and microinjected into blastocysts to produce chimeric mice. The chimeric mice are then be bred to produce homozygous offspring which express human antibodies. The transgenic mice are immunized in the normal fashion with a selected antigen, *e.g.*, all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained from the immunized, transgenic mice using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA, IgM and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995, Int. Rev. Immunol. 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, *see, e.g.*, International Publication Nos. WO 98/24893, WO 96/34096, and WO 96/33735; and U.S. Patent Nos. 5,413,923, 5,625,126, 5,633,425, 5,569,825,

5,661,016, 5,545,806, 5,814,318, and 5,939,598, which are incorporated by reference herein in their entirety. In addition, companies such as Abgenix, Inc. (Freemont, CA) and Genpharm (San Jose, CA) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

U.S. Patent No. 5,849,992, for example, describes a method of expressing an antibody in the mammary gland of a transgenic mammal. A transgene is constructed that includes a milk-specific promoter and nucleic acids encoding the antibody of interest and a signal sequence for secretion. The milk produced by females of such transgenic mammals includes, secreted-therein, the antibody of interest. The antibody can be purified from the milk, or for some applications, used directly.

A chimeric antibody is a molecule in which different portions of the antibody are derived from different immunoglobulin molecules. Methods for producing chimeric antibodies are known in the art. See *e.g.*, Morrison, 1985, Science 229:1202; Oi et al., 1986, BioTechniques 4:214; Gillies et al., 1989, J. Immunol. Methods 125:191-202; and U.S. Patent Nos. 5,807,715, 4,816,567, 4,816,397, and 6,331,415, which are incorporated herein by reference in their entirety.

A humanized antibody is an antibody or its variant or fragment thereof which is capable of binding to a predetermined antigen and which comprises a framework region having substantially the amino acid sequence of a human immunoglobulin and a CDR having substantially the amino acid sequence of a non-human immunoglobulin. A humanized antibody comprises substantially all of at least one, and typically two, variable domains (Fab, Fab', F(ab').sub.2, Fabc, Fv) in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin (*i.e.*, donor antibody) and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. In some embodiments, a humanized antibody also comprises at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Ordinarily, the antibody will contain both the light chain as well as at least the variable domain of a heavy chain. The antibody also may include the CH1, hinge, CH2, CH3, and CH4 regions of the heavy chain. The humanized antibody can be selected from any class of immunoglobulins, including IgM, IgG, IgD, IgA and IgE, and any isotype, including IgG_1, IgG_2, IgG_3 and IgG_4. Usually the constant domain is a complement fixing constant domain where it is desired that the humanized antibody

exhibit cytotoxic activity, and the class is typically IgG_1. Where such cytotoxic activity is not desirable, the constant domain may be of the IgG_2 class. The humanized antibody may comprise sequences from more than one class or isotype, and selecting particular constant domains to optimize desired effector functions is within the ordinary skill in the art. The framework and CDR regions of a humanized antibody need not correspond precisely to the parental sequences, *e.g.*, the donor CDR or the consensus framework may be mutagenized by substitution, insertion or deletion of at least one residue so that the CDR or framework residue at that site does not correspond to either the consensus or the import antibody. Such mutations, however, will not be extensive. Usually, at least 75% of the humanized antibody residues will correspond to those of the parental FR and CDR sequences, more often 90%, and most often greater than 95%. Humanized antibody can be produced using variety of techniques known in the art, including but not limited to, CDR-grafting (European Patent No. EP 239,400; International Publication No. WO 91/09967; and U.S. Patent Nos. 5,225,539, 5,530,101, and 5,585,089), veneering or resurfacing (European Patent Nos. EP 592,106 and EP 519,596; Padlan, 1991, Molecular Immunology 28(4/5):489-498; Studnicka et al., 1994, Protein Engineering 7(6):805-814; and Roguska et al. , 1994, PNAS 91:969-973), chain shuffling (U.S. Patent No. 5,565,332), and techniques disclosed in, *e.g* ., U.S. Pat. No. 6,407,213, U.S. Pat. No. 5,766,886, WO 9317105, Tan et al., 2002, J. Immunol. 169:1119-25, Caldas et al., 2000, Protein Eng. 13(5):353 - 60, Morea et al., 2000, Methods 20(3):267-79, Baca et al., 1997, J. Biol. Chem. 272(16):10678-84, Roguska et al., 1996, Protein Eng. 9(10):895-904, Couto et al., 1995, Cancer Res. 55 (23 Supp):5973s - 5977s, Couto et al., 1995, Cancer Res. 55(8):1717-22, Sandhu JS, 1994, Gene 150(2):409-10, and Pedersen et al., 1994, J. Mol. Biol. 235(3):959-73. Often, framework residues in the framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, preferably improve, antigen binding. These framework substitutions are identified by methods well known in the art, *e.g.*, by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual framework residues at particular positions. (See, *e.g.*, Queen et al., U.S. Patent No. 5,585,089; and Riechmann et al., 1988, Nature 332:323, which are incorporated herein by reference in their entireties.)

Single domain antibodies, for example, antibodies lacking the light chains, can be produced by methods well-known in the art. See Riechmann et al., 1999, J. Immuno. 231:25-38;

Nuttall et al., 2000, Curr. Pharm. Biotechnol. 1(3):253-263; Muylderman, 2001, J. Biotechnol. 74(4):277302; U.S. Patent No. 6,005,079; and International Publication Nos. WO 94/04678, WO 94/25591, and WO 01/44301, each of which is incorporated herein by reference in its entirety.

Further, the antibodies that specifically bind to an antigen can, in turn, be utilized to generate anti-idiotype antibodies that "mimic" an antigen using techniques well known to those skilled in the art. (See, *e.g.*, Greenspan & Bona, 1989, FASEB J. 7(5):437-444; and Nissinoff, 1991, J. Immunol. 147(8):2429-2438). Such antibodies can be used, alone or in combination with other therapies, in the prevention, treatment, or amelioration of one or more colorectal pathologies.

The invention encompasses polynucleotides comprising a nucleotide sequence encoding an antibody or fragment thereof that specifically binds to an antigen. The invention also encompasses polynucleotides that hybridize under high stringency, intermediate or lower stringency hybridization conditions to polynucleotides that encode an antibody of the invention.

The polynucleotides may be obtained, and the nucleotide sequence of the polynucleotides determined, by any method known in the art. The nucleotide sequences encoding known antibodies can be determined using methods well known in the art, *i.e.*, nucleotide codons known to encode particular amino acids are assembled in such a way to generate a nucleic acid that encodes the antibody. Such a polynucleotide encoding the antibody may be assembled from chemically synthesized oligonucleotides (*e.g.*, as described in Kutmeier et al., 1994, BioTechniques 17:242), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding the antibody, fragments, or variants thereof, annealing and ligating of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

Alternatively, a polynucleotide encoding an antibody may be generated from nucleic acid from a suitable source. If a clone containing a nucleic acid encoding a particular antibody is not available, but the sequence of the antibody molecule is known, a nucleic acid encoding the immunoglobulin may be chemically synthesized or obtained from a suitable source (*e.g.*, an antibody cDNA library or a cDNA library generated from, or nucleic acid, in some embodiments poly A+ RNA, isolated from, any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody of the invention) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe

specific for the particular gene sequence to identify, *e.g.*, a cDNA clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by PCR may then be cloned into replicable cloning vectors using any method well known in the art.

Once the nucleotide sequence of the antibody is determined, the nucleotide sequence of the antibody may be manipulated using methods well known in the art for the manipulation of nucleotide sequences, *e.g.*, recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., 1990, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY and Ausubel et al., eds., 1998, Current Protocols in Molecular Biology, John Wiley & Sons, NY, which are both incorporated by reference herein in their entireties), to generate antibodies having a different amino acid sequence, for example to create amino acid substitutions, deletions, and/or insertions.

Once a polynucleotide encoding an antibody molecule, heavy or light chain of an antibody, or fragment thereof (in some embodiments, but not necessarily, containing the heavy or light chain variable domain) of the invention has been obtained, the vector for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well-known in the art.

In one preferred embodiment, monoclonal antibodies are produced in mammalian cells. Preferred mammalian host cells for expressing the clone antibodies or antigen-binding fragments thereof include Chinese Hamster Ovary (CHO cells) (including dhfr- CHO cells, described in Urlaub and Chasin (1980, Proc. Natl. Acad. Sci. USA 77:4216-4220), used with a DHFR selectable marker, *e.g.*, as described in Kaufman and Sharp (1982, Mol. Biol. 159:601-621), lymphocytic cell lines, *e.g.*, NS0 myeloma cells and SP2 cells, COS cells, and a cell from a transgenic animal, *e.g.*, a transgenic mammal. For example, the cell is a mammary epithelial cell.

In addition to the nucleic acid sequence encoding the diversified immunoglobulin domain, the recombinant expression vectors may carry additional sequences, such as sequences that regulate replication of the vector in host cells (*e.g.*, origins of replication) and selectable marker genes. The selectable marker gene facilitates selection of host cells into which the vector has been introduced (see *e.g.*, U.S. Patents Nos. 4,399,216, 4,634,665 and 5,179,017). For example, typically the selectable marker gene confers resistance to drugs, such as G418,

hygromycin or methotrexate, on a host cell into which the vector has been introduced. Preferred selectable marker genes include the dihydrofolate reductase (DHFR) gene (for use in *dhfr*⁻ host cells with methotrexate selection/amplification) and the *neo* gene (for G418 selection).

In an exemplary system for recombinant expression of an antibody, or antigen-binding portion thereof, of the invention, a recombinant expression vector encoding both the antibody heavy chain and the antibody light chain is introduced into *dhfr*⁻ CHO cells by calcium phosphate-mediated transfection. Within the recombinant expression vector, the antibody heavy and light chain genes are each operatively linked to enhancer/promoter regulatory elements (*e.g.*, derived from SV40, CMV, adenovirus and the like, such as a CMV enhancer/AdMLP promoter regulatory element or an SV40 enhancer/AdMLP promoter regulatory element) to drive high levels of transcription of the genes. The recombinant expression vector also carries a DHFR gene, which allows for selection of CHO cells that have been transfected with the vector using methotrexate selection/amplification. The selected transformant host cells are cultured to allow for expression of the antibody heavy and light chains and intact antibody is recovered from the culture medium. Standard molecular biology techniques are used to prepare the recombinant expression vector, transfect the host cells, select for transformants, culture the host cells and recover the antibody from the culture medium. For example, some antibodies can be isolated by affinity chromatography with a Protein A or Protein G.

For antibodies that include an Fc domain, the antibody production system preferably synthesizes antibodies in which the Fc region is glycosylated. For example, the Fc domain of IgG molecules is glycosylated at asparagine 297 in the CH2 domain. This asparagine is the site for modification with biantennary-type oligosaccharides. It has been demonstrated that this glycosylation is required for effector functions mediated by Fcg receptors and complement C1q (Burton and Woof, 1992, Adv. Immunol. 51 :1-84 ; Jefferis et al., 1998, Immunol. Rev. 163:59-76). In a preferred embodiment, the Fc domain is produced in a mammalian expression system that appropriately glycosylates the residue corresponding to asparagine 297. The Fc domain can also include other eukaryotic post-translational modifications.

Once an antibody molecule has been produced by recombinant expression, it may be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (*e.g.*, ion exchange, affinity, particularly by affinity for the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential

solubility, or by any other standard technique for the purification of proteins. Further, the antibodies or fragments thereof may be fused to heterologous polypeptide sequences known in the art to facilitate purification.

Gene Therapy Techniques

Gene therapy refers to therapy performed by the administration to a subject of an expressed or expressible nucleic acid. Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

In specific embodiments, one or more antisense oligonucleotides for one or more biomarkers of the invention are administered to prevent, treat, or ameliorate one or more colorectal pathologies, by way of gene therapy. In other embodiments, one or more nucleic acid molecules comprising nucleotides encoding one or more antibodies that specifically bind to one or more protein products of one or more biomarkers of the invention are administered to prevent, treat, or ameliorate one or more colorectal pathologies, by way of gene therapy. In other embodiments, one or more nucleic acid molecules comprising nucleotides encoding protein products of one or more biomarkers of the invention or analogs, derivatives or fragments thereof, are administered to prevent, treat, or ameliorate one or more colorectal pathologies, by way of gene therapy. In yet other embodiments, one or more nucleic acid molecules comprising nucleotides encoding one or more dominant-negative polypeptides of one or more protein products of one or more biomarker of the invention are administered to prevent, treat, or ameliorate one or more colorectal pathologies, by way of gene therapy.

For general reviews of the methods of gene therapy, see Goldspiel et al., 1993, Clinical Pharmacy 12:488-505; Wu and Wu, 1991, Biotherapy 3:87-95; Tolstoshev, 1993, Ann. Rev. Pharmacol. Toxicol. 32:573-596; Mulligan, 1993, Science 260:926-932; and Morgan and Anderson, 1993, Ann. Rev. Biochem. 62:191-217; May, 1993, TIBTECH 11(5):155-215. Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds.), 1993, Current Protocols in Molecular Biology, John Wiley & Sons, NY; and Kriegler, 1990, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY.

In one aspect, a composition of the invention comprises nucleic acid sequences encoding one or more antibodies that specifically bind to one or more protein products of one or more biomarkers of the invention, said nucleic acid sequences being part of expression vectors that

express one or more antibodies in a suitable host. In particular, such nucleic acid sequences have promoters operably linked to the antibodies, said promoter being inducible or constitutive, and, optionally, tissue-specific.

In another aspect, a composition of the invention comprises nucleic acid sequences encoding dominant-negative polypeptides of one or protein products of one or more biomarkers of the invention, said nucleic acid sequences being part of expression vectors that express dominant-negative polypeptides in a suitable host. In particular, such nucleic acid sequences have promoters operably linked to the dominant-negative polypeptides, said promoter being inducible or constitutive, and, optionally, tissue-specific. In another particular embodiment, nucleic acid molecules are used in which the dominant-negative coding sequences and any other desired sequences are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intrachromosomal expression of the dominant-negative nucleic acids (Koller and Smithies, 1989, Proc. Natl. Acad. Sci. USA 86:8932-8935; Zijlstra et al., 1989, Nature 342:435-438).

Delivery of the nucleic acids into a patient may be either direct, in which case the patient is directly exposed to the nucleic acid or nucleic acid-carrying vectors, or indirect, in which case, cells are first transformed with the nucleic acids *in vitro*, then transplanted into the patient. These two approaches are known, respectively, as *in vivo* or *ex vivo* gene therapy.

In a specific embodiment, the nucleic acid sequence is directly administered *in vivo*, where it is expressed to produce the encoded product. This can be accomplished by any of numerous methods known in the art, *e.g.*, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that they become intracellular, *e.g.*, by infection using defective or attenuated retrovirals or other viral vectors (see U.S. Patent No. 4,980,286), or by direct injection of naked DNA, or by use of microparticle bombardment (*e.g.*, a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, encapsulation in liposomes, microparticles, or microcapsules, or by administering them in linkage to a peptide which is known to enter the nucleus, by administering it in linkage to a ligand subject to receptor-mediated endocytosis (see, *e.g.*, Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432) (which can be used to target cell types specifically expressing the receptors), etc. In another embodiment, nucleic acid-ligand complexes can be formed in which the ligand comprises a fusogenic viral peptide to disrupt endosomes, allowing the nucleic acid to avoid

lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted *in vivo* for cell specific uptake and expression, by targeting a specific receptor (see, *e.g.*, International Publication Nos. WO 92/06180 dated April 16, 1992 (Wu et al.); WO 92/22635 dated December 23, 1992 (Wilson et al.); WO92/20316 dated November 26, 1992 (Findeis et al.); WO 93/14188 dated July 22, 1993 (Clarke et al.), WO 93/20221 dated October 14, 1993 (Young)). Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, 1989, Proc. Natl. Acad. Sci. USA 86:8932-8935; Zijlstra et al., 1989, Nature 342:435-438).

For example, a retroviral vector can be used. These retroviral vectors have been modified to delete retroviral sequences that are not necessary for packaging of the viral genome and integration into host cell DNA. The nucleic acid sequences encoding the antibodies of interest, or proteins of interest or fragments thereof to be used in gene therapy are cloned into one or more vectors, which facilitates delivery of the gene into a patient. More detail about retroviral vectors can be found in Boesen et al., 1994, Biotherapy 6:291-302, which describes the use of a retroviral vector to deliver the mdr1 gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes et al., 1994, J. Clin. Invest. 93:644-651; Kiem et al., 1994, Blood 83:1467-1473; Salmons and Gunzberg, 1993, Human Gene Therapy 4:129-141; and Grossman and Wilson, 1993, Curr. Opin. in Genetics and Devel. 3:110-114.

Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, 1993, Current Opinion in Genetics and Development 3:499-503 present a review of adenovirus-based gene therapy. Bout et al., 1994, Human Gene Therapy 5:3-10 demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., 1991, Science 252:431-434; Rosenfeld et al., 1992, Cell 68:143-155; Mastrangeli et al., 1993, J. Clin. Invest. 91:225-234; PCT Publication WO94/12649; and Wang, et al., 1995, Gene Therapy 2:775-783. In a preferred embodiment, adenovirus vectors are used.

Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., 1993, Proc. Soc. Exp. Biol. Med. 204:289-300; U.S. Patent No. 5,436,146).

Another approach to gene therapy involves transferring a gene to cells in tissue culture by such methods as electroporation, lipofection, calcium phosphate mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection to isolate those cells that have taken up and are expressing the transferred gene. Those cells are then delivered to a patient.

In this embodiment, the nucleic acid is introduced into a cell prior to administration *in vivo* of the resulting recombinant cell. Such introduction can be carried out by any method known in the art, including but not limited to transfection, electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes into cells (see, *e.g.*, Loeffler and Behr, 1993, Meth. Enzymol. 217:599-618; Cohen et al., 1993, Meth. Enzymol. 217:618-644; Cline, 1985, Pharmac. Ther. 29:69-92) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is expressible by the cell and preferably heritable and expressible by its cell progeny.

The resulting recombinant cells can be delivered to a patient by various methods known in the art. Recombinant blood cells (*e.g.*, hematopoietic stem or progenitor cells) and/or intestinal cells are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be determined by one skilled in the art.

Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to epithelial cells, endothelial cells, keratinocytes, intestinal cells, fibroblasts, muscle cells, hepatocytes; blood cells such as T lymphocytes, B lymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, granulocytes; various stem or progenitor cells, in particular hematopoietic stem or progenitor cells, *e.g.*, as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

In one embodiment in which recombinant cells are used in gene therapy, nucleic acid sequences encoding antibodies of interest, or proteins of interest or fragments thereof are introduced into the cells such that they are expressible by the cells or their progeny, and the recombinant cells are then administered *in vivo* for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and maintained *in vitro* can potentially be used in accordance with this embodiment of the present invention (see, *e.g.*, International Publication No. WO 94/08598, dated April 28, 1994; Stemple and Anderson, 1992, Cell 71:973-985; Rheinwald, 1980, Meth. Cell Bio. 21A:229; and Pittelkow and Scott, 1986, Mayo Clinic Proc. 61:771).

Promoters that may be used to control the expression of nucleic acid sequences encoding antibodies of interest, proteins of interest or fragments thereof may be constitutive, inducible or tissue- specific. Non-limiting examples include the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al., 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. USA 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, Nature 296:39-42); prokaryotic expression vectors such as the β-lactamase promoter (Villa-Kamaroff et al., 1978, Proc. Natl. Acad. Sci. USA 75:3727-3731), or the *tac* promoter (DeBoer et al., 1983, Proc. Natl. Acad. Sci. USA 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; plant expression vectors comprising the nopaline synthetase promoter region (Herrera-Estrella et al., Nature 303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner et al., 1981, Nucl. Acids Res. 9:2871), and the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella et al., 1984, Nature 310:115-120); promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter, and the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift et al., 1984, Cell 38:639-646; Ornitz et al., 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl et al., 1984, Cell 38:647-658;

Adames et al., 1985, Nature 318:533-538; Alexander et al., 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986, Cell 45:485-495), albumin gene control region which is active in liver (Pinkert et al., 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., 1985, Mol. Cell. Biol. 5:1639-1648; Hammer et al., 1987, Science 235:53-58; alpha 1-antitrypsin gene control region which is active in the liver (Kelsey et al., 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogram et al., 1985, Nature 315:338-340; Kollias et al., 1986, Cell 46:89-94; myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead et al., 1987, Cell 48:703-712); myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason et al., 1986, Science 234:1372-1378).

In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription.

(S) Pharmaceutical Compositions

Biologically active compounds identified using the methods of the invention or a pharmaceutically acceptable salt thereof can be administered to a patient, in some embodiments a mammal, including a human, having one or more colorectal pathologies. In a specific embodiment, a compound or pharmaceutically acceptable salt thereof is administered to a patient, in some embodiments a mammal, including a human, having one or more colorectal pathologies. In another embodiment, a compound or a pharmaceutically acceptable salt thereof is administered to a patient, in some embodiments a mammal, including a human, as a preventative measure against one or more colorectal pathologies. In accordance with these embodiments, the patient may be a child, an adult or elderly, wherein a "child" is a subject between the ages of 24 months of age and 18 years of age, an "adult" is a subject 18 years of age or older, and "elderly" is a subject 65 years of age or older.

When administered to a patient, the compound or a pharmaceutically acceptable salt thereof is administered as component of a composition that optionally comprises a

pharmaceutically acceptable vehicle. The composition can be administered orally, or by any other convenient route, for example, by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (*e.g.*, oral mucosa, rectal, and intestinal mucosa, *etc.*) and may be administered together with another biologically active agent. Administration can be systemic or local. Various delivery systems are known, *e.g.*, encapsulation in liposomes, microparticles, microcapsules, capsules, *etc.*, and can be used to administer the compound and pharmaceutically acceptable salts thereof.

Methods of administration include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, oral, sublingual, intranasal, intracerebral, intravaginal, transdermal, rectally, by inhalation, or topically, particularly to the ears, nose, eyes, or skin. The mode of administration is left to the discretion of the practitioner. In most instances, administration will result in the release of the compound or a pharmaceutically acceptable salt thereof into the bloodstream.

In specific embodiments, it may be desirable to administer the compound or a pharmaceutically acceptable salt thereof locally. This may be achieved, for example, and not by way of limitation, by local infusion during surgery, topical application, *e.g.*, in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. In a specific embodiment, a compound is administered locally to one or more sections of the gastrointestinal system.

In certain embodiments, it may be desirable to introduce the compound or a pharmaceutically acceptable salt thereof into the gastrointestinal system by any suitable route, including intraventricular, intrathecal and epidural injection. Intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir.

Pulmonary administration can also be employed, *e.g.*, by use of an inhaler or nebulizer, and formulation with an aerosolizing agent, or via perfusion in a fluorocarbon or synthetic pulmonary surfactant. In certain embodiments, the compound and pharmaceutically acceptable salts thereof can be formulated as a suppository, with traditional binders and vehicles such as triglycerides.

In another embodiment, the compound and pharmaceutically acceptable salts thereof can be delivered in a vesicle, in particular a liposome (see Langer, 1990, Science 249:1527-1533; Treat et al., in Liposomes in the Therapy of Infectious Disease and Cancer, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353-365 (1989); Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*).

In yet another embodiment, the compound and pharmaceutically acceptable salts thereof can be delivered in a controlled release system (see, *e.g.*, Goodson, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115-138 (1984)). Other controlled-release systems discussed in the review by Langer, 1990, Science 249:1527-1533 may be used. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, 1987, CRC Crit. Ref. Biomed. Eng. 14:201; Buchwald et al., 1980, Surgery 88:507; Saudek et al., 1989, N. Engl. J. Med. 321:574). In another embodiment, polymeric materials can be used (see Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida (1974); Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, 1983, J. Macromol. Sci. Rev. Macromol. Chem. 23:61; see also Levy et al., 1985, Science 228:190; During et al., 1989, Ann. Neurol. 25:351; Howard et al., 1989, J. Neurosurg. 71:105). In yet another embodiment, a controlled-release system can be placed in proximity of a target RNA of the compound or a pharmaceutically acceptable salt thereof, thus requiring only a fraction of the systemic dose.

The compounds described herein can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the active compound and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

The invention includes methods for preparing pharmaceutical compositions for modulating the expression or activity of a polypeptide or nucleic acid of interest. Such methods comprise formulating a pharmaceutically acceptable carrier with an agent that modulates

expression or activity of a polypeptide or nucleic acid of interest. Such compositions can further include additional active agents. Thus, the invention further includes methods for preparing a pharmaceutical composition by formulating a pharmaceutically acceptable carrier with an agent that modulates expression or activity of a polypeptide or nucleic acid of interest and one or more additional active compounds.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Intravenous administration is preferred. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF; Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyetheylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for

example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a polypeptide or antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed.

Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from a pressurized container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the individual to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

For antibodies, the preferred dosage is 0.1 mg/kg to 100 mg/kg of body weight (more preferably, 0.1 to 20 mg/kg, 0.1-10 mg/kg). Generally, partially human antibodies and fully

human antibodies have a longer half-life within the human body than other antibodies. Accordingly, lower dosages and less frequent administration is often possible. Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration (*e.g.*, into the gastrointestinal system). A method for lipidation of antibodies is described by Cruikshank et al. (1997, J. Acquired Immune Deficiency Syndromes and Human Retrovirology 14:193).

In a specific embodiment, an effective amount of protein or polypeptide (*i.e.*, an effective dosage) ranges from about 0.001 to 30 mg/kg body weight, preferably about 0.01 to 25 mg/kg body weight, more preferably about 0.1 to 20 mg/kg body weight, and even more preferably about 0.1 to 1.0 mg/kg, 1 to 10 mg/kg, 2 to 9 mg/kg, 3 to 8 mg/kg, 4 to 7 mg/kg, or 5 to 6 mg/kg body weight.

The skilled artisan will appreciate that certain factors may influence the dosage required to effectively treat an individual, including but not limited to the severity of the disease or disorder, previous treatments, the general health and/or age of the individual, and other diseases present. Moreover, treatment of a individual with a therapeutically effective amount of a protein, polypeptide, or antibody can include a single treatment or, preferably, can include a series of treatments.

In addition to those compounds described above, the present invention encompasses the use of small molecules that modulate expression or activity of a nucleic acid or polypeptide of interest. Non-limiting examples of small molecules include peptides, peptidomimetics, amino acids, amino acid analogs, polynucleotides, polynucleotide analogs, nucleotides, nucleotide analogs, organic or inorganic compounds (*i.e.*, including heteroorganic and organometallic compounds) having a molecular weight less than about 10,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 5,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 1,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 500 grams per mole, and salts, esters, and other pharmaceutically acceptable forms of such compounds.

It is understood that appropriate doses of small molecule agents depends upon a number of factors within the ken of the ordinarily skilled physician, veterinarian, or researcher. The dose(s) of the small molecule will vary, for example, depending upon the identity, size, and condition of the individual or sample being treated, further depending upon the route by which

the composition is to be administered, if applicable, and the effect which the practitioner desires the small molecule to have upon the nucleic acid or polypeptide of the invention. Exemplary doses include milligram or microgram amounts of the small molecule per kilogram of individual or sample weight (*e.g.*, about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram). It is furthermore understood that appropriate doses of a small molecule depend upon the potency of the small molecule with respect to the expression or activity to be modulated. Such appropriate doses may be determined using the assays described herein. When one or more of these small molecules is to be administered to an individual (*e.g.*, a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher may, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

(T) Kits

The present invention provides kits for measuring the expression of the protein and RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 12, at least 15, or all or any combination of the biomarkers of the invention. Such kits comprise materials and reagents required for measuring the expression of such protein and RNA products. In specific embodiments, the kits may further comprise one or more additional reagents employed in the various methods, such as: (1) reagents for purifying RNA from blood; (2) biomarker specific primer sets for generating test nucleic acids; (3) dNTPs and/or rNTPs (either premixed or separate), optionally with one or more uniquely labeled dNTPs and/or rNTPs (*e.g.*, biotinylated or Cy3 or Cy5 tagged dNTPs); (4) post synthesis labeling reagents, such as chemically active derivatives of fluorescent dyes; (5) enzymes, such as reverse transcriptases, DNA polymerases, and the like; (6) various buffer mediums, *e.g.*, hybridization,

washing and/or enzymatic buffers; (7) labeled probe purification reagents and components, like spin columns, etc.; and (8) protein purification reagents; (9) signal generation and detection reagents, *e.g.*, streptavidin-alkaline phosphatase conjugate, chemifluorescent or chemi-luminescent substrate, and the like. In particular embodiments, the kits comprise prelabeled quality controlled protein and or RNA isolated from a sample (*e.g.*, blood) or synthesized for use as a control. In some embodiments kits can include a computer-readable medium which has a formula which uses data representing a level of products of at least one biomarker and generating an indication of the probability that a test subject has one or more colorectal pathologies including one or more polyps or one or more subtypes of polyps. The formula of the computer-readable medium can be generated by using the methods outlined in section (G).

In some embodiments, the kits are PCR kits or Real time PCR kits and/or QRT-PCR kits. In other embodiments, the kits are nucleic acid arrays and protein arrays. Such kits according to the subject invention will at least comprise an array having associated protein or nucleic acid members of the invention and packaging means therefore. Alternatively the protein or nucleic acid members of the invention may be prepackaged onto an array.

In one embodiment, the QRT-PCR kit includes the following: (a) two or more biomarker specific primer sets, each set used to amplify a biomarker within the combination of biomarkers of the invention; (b) buffers and enzymes including a reverse transcripase; (c) one or more thermos table polymerases; and (d) Sybr® Green. In another embodiment, the kit of the invention can include (a) a reference control RNA and/or(b) a spiked control RNA. In another embodiment, the kit also includes a computer readable medium which has a formula which uses data representing a level of products of at least one biomarker and generating an indication of the probability that a test subject has one or more colorectal pathologies including one or more polyps or one or more subtypes of polyps. The formula of the computer-readable medium can be generated by using the methods outlined in section (G).

The invention provides kits that are useful for testing, detecting, screening, diagnosing, monitoring and prognosing one or more colorectal pathologies including one or more polyps or one or more subtypes of polyps. For example, in a particular embodiment of the invention a kit is comprised a forward and reverse primer wherein the forward and reverse primer are designed to quantitate expression of all of the species of mRNA corresponding to a single distinct biomarker, where each of the distinct biomarkers is selected from the group identified in **Tables**

1, 2 , 11, or **12.** In certain embodiments, at least one of the primers of a primer set is designed to span an exon junction of a species of mRNA.

The invention includes kits that are useful for testing, detecting, screening, diagnosing, monitoring and prognosing one or more colorectal pathologies including one or more types or subtypes of polyps based upon the expression levels of protein or RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, or all or any combination of the biomarkers of the invention in a sample.

The invention includes kits useful for monitoring the efficacy of one or more therapies that an individual is undergoing based upon the expression of a protein or RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, or all or any combination of the biomarkers of the invention in a sample.

The invention includes kits using for determining whether an individual will be responsive to a therapy based upon the expression of a protein or RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, or all or any combination of the biomarkers of the invention in a sample.

The invention includes kits for measuring the expression of a RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, or all or any combination of the biomarkers of the invention in a sample. In a specific embodiment, such kits comprise materials and reagents that are necessary for measuring the expression of a RNA products of a biomarker of the invention. For example, a microarray or QRT-PCR kit may be produced for detecting one or more colon pathologies including polyps or one or more subtypes of polyps and contain only those reagents and materials necessary for measuring the levels of RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, or all or any combination of the biomarkers of the invention. Alternatively, in some embodiments, the kits can comprise materials and reagents that are not limited to those required to measure the levels of RNA products of 1,2, 3, 4, 5, 6, 7, 8 or all or any combination of the biomarkers of the invention. For example, a microarray kit may contain reagents and materials necessary for measuring the levels of RNA products not necessarily associated with or indicative of one or more colorectal pathologies , in addition to reagents and materials necessary for measuring the levels of the RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, or all or any combination of the biomarkers of the invention. In a specific

embodiment, a microarray or QRT-PCR kit contains reagents and materials necessary for measuring the levels of RNA products of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, or all or any combination of the biomarkers of the invention, and 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300, 350, 400, 450, or more genes other than the biomarkers of the invention, or 1-10, 1-100, 1-150, 1-200, 1-300, 1-400, 1-500, 1-1000, 25-100, 25-200, 25-300, 25-400, 25-500, 25-1000, 100-150, 100-200, 100-300, 100-400, 100-500, 100-1000, 500-1000 other genes than the biomarkers of the invention.

For nucleic acid micoarray kits, the kits generally comprise probes attached or localized to a support surface. The probes may be labeled with a detectable label. In a specific embodiment, the probes are specific for an exon(s), an intron(s), an exon junction(s), or an exon-intron junction(s)), of RNA products of 1, 2, 3, 4, 5, 6, 7, 8, all or any combination of the biomarkers of the invention. The microarray kits may comprise instructions for performing the assay and methods for interpreting and analyzing the data resulting from the performance of the assay. In a specific embodiment, the kits comprise instructions for detecting or diagnosing one or more colorectal pathologies including one or more polyps or one or more subtypes of polyps. The kits may also comprise hybridization reagents and/or reagents necessary for detecting a signal produced when a probe hybridizes to a target nucleic acid sequence. Generally, the materials and reagents for the microarray kits are in one or more containers. Each component of the kit is generally in its own a suitable container. In another embodiment, the kit also includes a computer readable medium which has a formula which uses data representing a level of products of at least one biomarker and generating an indication of the probability that a test subject has one or more colorectal pathologies or a subtype of colorectal pathology including a polyp or one or more subtypes of polyps. The formula of the computer-readable medium can be generated by using the methods outlined in section (G).

For QRT-PCR kits, the kits generally comprise pre-selected primers specific for particular RNA products (*e.g.*, an exon(s), an intron(s), an exon junction(s), and an exon-intron junction(s)) of 1, 2, 3, 4, 5, 6, 7, 8, or all or any combination of the biomarkers of the invention. The QRT-PCR kits may also comprise enzymes suitable for reverse transcribing and/or amplifying nucleic acids (*e.g.*, polymerases such as Taq), and deoxynucleotides and buffers needed for the reaction mixture for reverse transcription and amplification. The QRT-PCR kits

may also comprise probes specific for RNA products of 1,2, 3, 4, 5, 6, 7, 8, or all or any combination of the biomarkers of the invention. The probes may or may not be labeled with a detectable label (*e.g.*, a fluorescent label). Each component of the QRT-PCR kit is generally in its own suitable container. In another embodiment, the kit also includes a computer readable medium which has a formula which uses data representing a level of products of at least one biomarker and generating an indication of the probability that a test subject has one or more colorectal pathologies or a subtype of colorectal pathology including a polyp or one or more subtypes of polyps. The formula of the computer-readable medium can be generated by using the methods outlined in section (G).

Thus, these kits generally comprise distinct containers suitable for each individual reagent, enzyme, primer and probe. Further, the QRT-PCR kits may comprise instructions for performing the assay and methods for interpreting and analyzing the data resulting from the performance of the assay. In a specific embodiment, the kits contain instructions for diagnosing or detecting one or more colorectal pathologies including one or more polyps or one or more subtypes of polyps.

In a specific embodiment, the kit is a QRT-PCR kit. Such a kit may comprise a 96 well plate and reagents and materials necessary for SYBR Green detection. The kit may comprise reagents and materials so that beta-actin can be used to normalize the results. The kit may also comprise controls such as water, phospate buffered saline, and phage MS2 RNA. Further, the kit may comprise instructions for performing the assay and methods for interpreting and analyzing the date resulting from the performance of the assay. In a specific embodiment, the instructions state that the level of a RNA products of 1, 2, 3, 4, 5, 6, 7, 8, all or any combination of the biomarkers of the invention should be examined at two concentrations that differ by, *e.g.*, 5 fold to 10-fold.

For antibody based kits, the kit can comprise, for example: (1) a first antibody (which may or may not be attached to a support) which binds to protein of interest (*e.g.*, a protein products of 1, 2, 3, 4, 5, 6, 7, 8, all or any combination of the biomarkers of the invention); and, optionally, (2) a second, different antibody which binds to either the protein, or the first antibody and is conjugated to a detectable label (*e.g.*, a fluorescent label, radioactive isotope or enzyme). The antibody-based kits may also comprise beads for conducting an immunoprecipitation. Each component of the antibody-based kits is generally in its own suitable container. Thus, these kits

generally comprise distinct containers suitable for each antibody. Further, the antibody-based kits may comprise instructions for performing the assay and methods for interpreting and analyzing the data resulting from the performance of the assay. In a specific embodiment, the kits contain instructions for diagnosing or detecting one or more colorectal pathologies including one or more polyps or one or more subtypes of polyps. In another embodiment, the kit contains instructions for applying the data to a formula in the form of a computer readable medium which contains said instructions. Said computer readable medium can also contain instructions for interpreting the analyzing the data resulting from the performance of the assay.

(U) SNPs

A Single Nucleotide Polymorphism (SNP) is a single nucleotide variation at a specific location in the genome of different individuals. SNPs are found in both coding and non-coding regions of genomic DNA. In spite of the paucity of scorable phenotypes, SNPs are found in large numbers throughout the human genome (Cooper et al., Hum Genet 69:201-205, 1985). SNPs are stable genetic variations frequently found in genes, and contribute to the wide range of phenotypic variations found in organisms. Single nucleotide polymorphisms (SNPs) can be of predictive value in identifying many genetic diseases, as well as phenotypic characteristics. It is known for example that certain SNPs result in disease-causing mutations such as the SNP correlated with heritable breast cancer (Cannon-Albright and Skolnick, Semin. Oncol. 23:1-5, 1996).

A SNP may be identified in the DNA of an organism by a number of methods well known to those of skill in the art, including but not limited to identifying the SNP by DNA sequencing, by amplifying a PCR product and sequencing the PCR product, by Oligonucleotide Ligation Assay (OLA), by Doublecode OLA, by Single Base Extension Assay, by allele specific primer extension, or by mismatch hybridization.

The instant invention offers a more focused and efficient method of screening SNPs to identify those SNPs which are specifically associated with one or more colorectal pathologies by having identified a selection of genes which are differentially expressed in blood from individuals having one or more colorectal pathologies as compared with individuals not having said one or more colorectal pathologies. In one aspect of the invention, a selection of SNPs to be screened are those SNPs found in the genes listed in **Tables 2** and **6**. In another aspect of the

invention, novel SNPs can be identified in the disease-associated biomarkers using those methods listed above.

In particular, this invention focuses on methods for identifying those SNPs which are associated with one or more colorectal pathologies by screening only those SNPs in the biomarkers identified herein. Those SNPs which are identified using the methods disclosed herein will be convenient diagnostic markers.

More specifically a SNP is considered to be a polyp associated SNP, if those individuals having one or more colorectal pathologies have a different polymorphism at the SNP locus than those individuals not having the one or more colorectal pathologies. Further, a particular SNP is considered to be diagnostic for one or more colorectal pathologies if a particular polymorphism of the SNP is found to present at a statistically significant higher frequency in those individuals having one or more colorectal pathologies than in those individuals not having the one or more colorectal pathologies. Indices of statistical significance include $p < 0.05$, $p < .001$, $p < .01$, and $p < .10$. This invention includes methods of determining the diagnostic value of SNPs with respect to diagnosing or detecting one or more colorectal pathologies.

As would be understood, a preferred sample is blood, but these methods encompass any samples from which DNA can be obtained including epithelial cells, buccal cells, hair, saliva, tissue cells and the like. There are a variety of available methods for obtaining and storing tissue and/or blood samples. These alternatives allow tissue and blood samples to be stored and transported in a form suitable for the recovery of genomic DNA from the samples for genotype analysis. DNA samples can be collected and stored on a variety of solid mediums, including Whatmann paper, Guthrie cards, tubes, swabs, filter paper, slides, or other containers. When whole blood is collected on filter paper, for example, it can be dried and stored at room temperature.

The blood sample may be any one of various types of blood samples, including, for example, a sample of serum-depleted blood, a sample of erythrocyte-depleted blood, a sample of serum-depleted and erythrocyte-depleted blood, a sample of lysed blood, a blood sample which has not been fractionated into cell types and a sample of unfractionated cells of a lysed blood sample. Examples of blood samples are described in **Example 1** of the Examples section below.

In another aspect of the invention, polyp associated SNPs can be identified from RNA transcripts of the polyp biomarker genes, listed in **Tables 2** and **6**, instead of from genomic

DNA. In one embodiment, RNA is isolated from a sample such as blood, from individuals with and without the given disease or disorder, and transcripts encoded by these polyp biomarker genes are reversed transcribed into cDNA. The cDNA is amplified and analyzed to determine the presence of SNPs in the polyp biomarker genes. A polyp associated SNP, can be identified by then comparing the distribution of each of the SNPs identified in the polyp associated biomarker gene(s) differentially expressed in those individuals having one or more colorectal pathologies and individuals who do not have one or more colorectal pathologies. In a further variation of this embodiment, instead analyzing cDNA for the presence of SNPs, the RNA transcripts of the disease specific biomarker genes, or their amplified products, are analyzed for the presence of SNPs.

Analysis of genomic DNA comprising the polyp biomarker genes has the potential to identify SNPs in the coding region as well as in regulatory regions, the latter which may contribute to the change in expression levels of the gene. Analysis of cDNA encoded SNPs has the potential to identify only SNPs in the coding region of the polyp biomarker genes, which may be instrumental in deciphering protein based mechanisms of polyp formation. Methods of analyzing cDNA encoded SNPs can be carried out by analyzing the cDNA generated in the reverse transcription PCR reactions described herein that are used to identify the level of the biomarker in samples from patients and non patients.

A polyp associated SNP may be identified in the DNA of the polyp biomarker genes by a number of methods well known to those of skill in the art (see for example U.S. Pat. Nos. 6,221,592 and 5,679,524), including but not limited to identifying the SNP by PCR or DNA amplification, Oligonucleotide Ligation Assay (OLA) (Landegren et al., Science 241:1077, 1988), Doublecode OLA, mismatch hybridization, mass spectrometry, Single Base Extension Assay, (US6,638,722), RFLP detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy, Lancet ii: 910-912, 1978), hybridization with allele-specific oligonucleotide probes (Wallace et al., Nucl Acids Res 6:3543-3557, 1978), including immobilized oligonucleotides (Saiki et al., Proc Natl Acad Sci USA 86:6230-6234, 1989) or oligonucleotide arrays (Maskos and Southern, Nucl Acids Res 21:2269-2270, 1993), allele-specific PCR (Newton et al., Nucl Acids Res 17:2503-16, 1989), mismatch-repair detection (MRD) (Faham and Cox, Genome Res 5:474-482,1995), binding of MutS protein (Wagner et al., Nucl Acids Res 23:3944-3948, 1995), single-strand-conformation-polymorphism detection

(Orita et al., Genomics 5:874-879, 1983), RNAase cleavage at mismatched base-pairs (Myers et al., Science 230:1242, 1985), chemical (Cotton et al., Proc Natl Acad Sci USA 85:4397-4401, 1988) or enzymatic (Youil et al., Proc Natl Acad Sci USA 92:87-91, 1995) cleavage of heteroduplex DNA, methods based on allele specific primer extension (Syvanen et al., Genomics 8:684-692, 1990), genetic bit analysis (GBA) (Nikiforov et al., Nuci Acids Res 22:4167-4175, 1994), and radioactive and/or fluorescent DNA sequencing using standard procedures well known in the art.

The instant methods of screening a subset of SNPs to identify polyp associated SNPs in polyp biomarker genes also encompass non-PCR methods of DNA. These methods include ligase chain reaction ("LCR"), disclosed in European Patent Application No. 320,308, Qbeta Replicase, described in PCT Patent Application No. PCT/US87/00880, isothermal amplification methods, Walker et al. (Nucleic Acids Res 20(7):1691-6, 1992), Strand Displacement Amplification (SDA) described in U.S. Pat. Nos. 5,712,124, 5,648,211 and 5,455,166, Cyclic Probe Reaction, Transcription-Based Amplification, including nucleic acid sequence based amplification (NASBA) and 3SR, Kwoh et al., Proc Natl Acad Sci USA, 86:1173-77, 1989; PCT Patent Application WO 88/10315 et al., 1989, other amplification methods, as described in British Patent Application No. GB 2,202,328, and in PCT Patent Application No. PCT/US89/01025, Davey et al., European Patent Application No. 329,822, Miller et al., PCT Patent Application WO 89/06700, "race and "one-sided PCR TM." described in Frohman, In: PCR Protocols: A Guide To Methods And Applications, Academic Press, N.Y., 1990, methods based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide, described in Wu et al., Genomics 4:560-569, 1989.

While it is generally contemplated that the polymerase employed will be thermostable, non-thermostable polymerases may also be employed in the context of the present disclosure. Exemplary polymerases and nucleic acid modifying enzymes that may be used in the context of the disclosure include the thermostable DNA Polymerases of OmniBase Sequencing Enzyme, Pfu DNA Polymerase,Taq DNA Polymerase, Taq DNA Polymerase, Sequencing Grade, TaqBead Hot Start Polymerase, AmpliTaq Gold, Vent DNA Polymerase, Tub DNA Polymerase, TaqPlus DNA Polymerase, Tfl DNA Polymerase, Tli DNA Polymerase, Tth DNA Polymerase; the DNA Polymerases of DNA Polymerase I, Klenow Fragment, Exonuclease Minus, DNA Polymerase I, DNA Polymerase I Large (Klenow) Fragment, Terminal Deoxynucleotidyl

Transferase, T7 DNA Polymerase, T4 DNA Polymerase; the Reverse trancriptases of AMV Reverse Transcriptase and M-MLV Reverse Transcriptase; T4 DNA ligase and T4 polynucleotide kinase.

Recognition moieties incorporated into primers, incorporated into the amplified product during amplification, or attached to probes are useful in the identification of the amplified molecules. A number of different labels may be used for this purpose such as, for example: fluorophores, chromophores, radio-isotopes, enzymatic tags, antibodies, chemiluminescence, electroluminescence, affinity labels, etc. One of skill in the art will recognize that these and other fluorophores not mentioned herein can also be used with success in this disclosure. Examples of affinity labels include but are not limited to the following: an antibody, an antibody fragment, a receptor protein, a hormone, biotin, DNP, or any polypeptide/protein molecule that binds to an affinity label and may be used for separation of the amplified gene. Examples of enzyme tags include enzymes such as urease, alkaline phosphatase, or peroxidase. Additionally, colorimetric indicator substrates can be employed to provide a detection means visible to the human eye or spectrophotometrically, to identify specific hybridization with complementary nucleic acid-containing samples. All these examples are generally known in the art and the skilled artisan will recognize that the present disclosure is not limited to the examples described above. The following fluorophores are specifically contemplated to be useful in the present disclosure: Alexa 350, Alexa 430, AMCA, BODIPY 630/650, BODIPY 650/665, BODIPY-FL, BODIPY-R6G, BODIPY-TMR, BODIPY-TRX, Cascade Blue, Cy2, Cy3, Cy5, 6-FAM, Fluorescein, HEX, 6-JOE, Oregon Green 488, Oregon Green 500, Oregon Green 514, Pacific Blue, REG, Rhodamine Green, Rhodamine Red, ROX, TAMRA, TET, Tetramethylrhodamine, and Texas Red.

In the context of the present disclosure, it is specifically contemplated that the DNA amplification products of the disclosed methods may be analyzed using DNA chips or microarrays in order to detect SNPs. The amplified DNA products may then be passed over a DNA chip or microarray encompassing oligonucleotide or polynucleotide probes. The ability or inability of the amplified DNA to hybridize to the microarray or DNA chip will facilitate the characterization of the SNPs present in the biomiarker genes encoding the transcripts present in the sample.

The following non-limiting examples are illustrative of the present invention:

EXAMPLES

EXAMPLE 1

RNA isolation from unfractionated whole bood

(a) Centrifuged Lysed blood (Serum Reduced, Erythrocyte Reduced Blood Sample)

Ten ml of peripheral whole blood was collected in EDTA Vacutainer tubes (Becton Dickinson, Franklin Lakes, N.J.) and stored on ice until processing (within 6 hours). Upon centrifugation, blood samples separated into plasma (including the buffy coat) and red blood cell layers. The plasma was removed and a hypotonic buffer (1.6 mM EDTA, 10 mM KHCO3, 153 mM NH4Cl, pH 7.4) was added to lyse the red blood cells at a 3:1 volume ratio. The mixture was centrifuged to yield a cell pellet, which was dissolved and homogenized into 1.0 ml of TRIzol® Reagent (Invitrogen Corp., Carlsbad, CA) and 0.2 ml of chloroform according to the manufacture's instructions. After centrifugation, isopropanol was added to the aqueous phase at a 1:1 ratio and allowed to precipitate at –20°C. Subsequent centrifugation yielded an RNA pellet that was resuspended in water for experimental use. RNA quality was assessed on Agilent 2100 Bioanalyzer RNA 6000 Nano Chips as specified by the manufacturer, and RNA quantity was determined by absorbance at 260 nm in a Beckman-Coulter DU640 Spectrophotometer.

(b) Lysed blood

10 ml whole blood is obtained in a Vacutainer or any smaller volume container desired. Lysis Buffer is added directly to the blood sample (where the blood sample does not have the serum removed) in a ratio of 3 parts Lysis Buffer to 1 part blood (Lysis Buffer (1L) 0.6g EDTA; 1.0g KHCO2, 8.2g NH4Cl adjusted to pH 7.4 (using NaOH)). Sample is mixed and placed on ice for 5-10 minutes until transparent. Lysed sample is centrifuged at 1000 rpm for 10 minutes at 4°C, and supernatant is aspirated. Pellet is resuspended in 5ml Lysis Buffer, and centrifuged again at 1000 rpm for 10 minutes at 4°C. Pelleted cells are homogenized using TRIzol (GIBCO/BRL) in a ratio of approximately 6ml of TRIzol for every 10ml of the original blood sample and vortexed well. Samples are left for 5 minutes at room temperature. RNA is extracted using 1.2 ml of chloroform per 1 ml of TRIzol. Sample is centrifuged at 12,000 x g for 5 minutes at 4°C and upper layer is collected. To upper layer, isopropanol is added in ratio of 0.5 ml per 1 ml of TRIzol. Sample is left overnight at -20°C or for one hour at -20°C. RNA is pelleted in accordance with known methods, RNA pellet air dried, and pellet resuspended in DEPC treated ddH_2O. RNA samples can also be stored in 75% ethanol where the samples are stable at room temperature for transportation.

(c) From serum reduced whole blood

10 ml whole blood is obtained in a Vacutainer and spun at 2,000 rpm (800g) for 5 min at 4°C and the plasma layer removed. The remaining blood sample is homogenized using TRIzol (GIBCO/BRL) in a ratio of approximately 6ml of TRIzol for every 10ml of the original blood sample and vortexed well. Samples are left for 5 minutes at room temperature. RNA is extracted using 1.2 ml of chloroform per 1 ml of TRIzol. Sample is centrifuged at 12,000 x g for 5 minutes at 4°C and upper layer is collected. To upper layer, isopropanol is added in ratio of 0.5 ml per 1 ml of TRIzol. Sample is left overnight at -20°C or for one hour at -20°C. RNA is pelleted in accordance with known methods, RNA pellet air dried, and pellet resuspended in DEPC treated ddH_2O. RNA samples can also be stored in 75% ethanol where the samples are stable at room temperature for transportation.

d) From whole blood

10 ml whole blood is obtained in a Vacutainer and the sample is homogenized using TRIzol (GIBCO/BRL) in a ratio of approximately 6ml of TRIzol for every 10ml of the blood sample and vortexed well. Samples are left for 5 minutes at room temperature. RNA is extracted using 1.2 ml of chloroform per 1 ml of TRIzol. Sample is centrifuged at 12,000 x g for 5 minutes at 4°C and upper layer is collected. To upper layer, isopropanol is added in ratio of 0.5 ml per 1 ml of TRIzol. Sample is left overnight at -20°C or for one hour at -20°C. RNA is pelleted in accordance with known methods, RNA pellet air dried, and pellet resuspended in DEPC treated ddH_2O. RNA samples can also be stored in 75% ethanol where the samples are stable at room temperature for transportation.

(e) From whole blood using PAXgene™

2.5 ml whole blood is collected into PAXgene™ Blood RNA Tubes and processed in accordance with the instructions of the PAXgene™ Blood RNA Kit protocol. In brief after storing the blood in the PAXgene™ tube for at least 2 hours, the blood sample is centriguted and the supernatant discarded. To the remaining sample, 360 µl of the supplied Buffer BR1 is added and the sample is pipetted into the spin column and centrifuged an then washed with numerous wash steps and finally eluted and stored.

(f) From whole blood using PAXgene™ and subsequent globin reduction

RNA isolated from PAXGene™ as noted in (d) above is subsequently treated to selectively remove globin mRNA as is described in Affymetrix® technical note entitled "Globin

Reduction Protocol". Oligonucleotides specific for the alpha 1, alpha 2 and beta globin species are incubated with an oligonucleotide hybridization buffer and RNAse H used to specifically target degredation of the globin mRNA and the cRNA clean up column from Affymetrix used to remove the globin mRNA.

EXAMPLE 2

Target nucleic acid preparation and hybridization

(a) Genes which are differentially expressed with the presence of One or more colorectal pathologies

Total RNA (5 μg) was labeled and hybridized onto Affymetrix U133Plus 2.0 GeneChips (Affymetrix; Santa Clara, CA) along with other similarly prepared samples from individuals having or not having polyps and hybridized according to the manufacturer's instructions. Briefly, the five μg total RNA was used for cDNA synthesis with GeneChip T7-Oligo(dT) primer provided in the promoter primer kit (Affymetrix, P/N 900375). cDNA was cleaned up with cDNA Cleanup Spin Column and then subjected to synthesis of Biotin-Labeled cRNA with Enzo®BioArray™High Yield™ RNA Transcript Labeling Kit. The labeled cRNA was further purified using the IVT cTNA Cleanup Spin Column and quantified using spectrophotometer with absorbance at 260 nm. 20 μg cRNA was then added into the hybridization cocktail and the cocktail was applied to the probe array cartridge. After approximately 16 hours hybridization, the array was washed with Affymetrix fluidics station 400. The array was then scanned with Affymetrix®GeneChip®Scanner.

Hybridization signals were scaled in the Affymetrix GCOS software (version 1.1.1), using a scaling factor determined by adjusting the global trimmed mean signal intensity value to 500 for each array, and imported into GeneSpring version 7.2 (Silicon Genetics; Redwood City, CA). Signal intensities were then centered to the 50th percentile of each chip, and for each individual gene, to the median intensity of the whole sample set. Only genes called present or marginal by the GCOS software in at least 80% of each group of samples were used for further analysis. Differentially expressed genes were identified using 1) the non-parametric Wilcoxon-Mann-Whitney non-parametric test (P<0.05), 2) parametric t test (P <0.05), and/or the 3) unsupervised analysis method (14). In the un-supervised analysis, the signal-intensity filtered genes were used to select genes with at least 2-fold change (up or down) in expression level, away from the mean, in at least 15% of the samples. Hierarchical cluster analysis was performed

on each comparison to assess correlation analysis using Spearman correlation among samples for each identified gene set as the similarity measure with average centroid linkage in GeneSpring v6.0. Results from numerous experiments were analyzed and a compiled list of results provided in **Table 1.**

(b) Genes which are differentially expressed with the presence of High Risk Polyps

Total RNA was isolated from centrifuged lysed blood (ie serum reduced, erythrocyte reduced blood) as described in **Example 1** from patients diagnosed with having high risk polyps. 1 μg of Oligo-dT primers were annealed to 10 μg of total RNA for each individual tested in a total volume of 10 μl, by heating to 70°C for 10 min, and cooled on ice. Individuals were diagnosed as having one or more of the high risk polyp subtypes (colorectal pathology during a colonoscopy identified the polyp identified as one or more of the following types: Tubulovillous Adenoma; Villous Adenoma; Cancer; High Grade Dysplasia; and Tubular Adenoma wherein the diameter of the Tubular Adenoma is greater than 10mm). Procedures were otherwise carried out as described in **Example 2(a)** above.

Results from numerous experiments were analyzed and a compiled list of results provided in **Table 11.**

EXAMPLE 3

Quantitative real time PCR (QRT-PCR)

QRT-PCR was performed on a selection of the genes in **Table 1** which are disclosed in **Table 2.** QRT-PCR was done using either the SYBR® Green Kit from Qiagen (Product Number 204143) and/or using Applied Biosystems PCR reagent kits (Cat 4334973). Amplicons were detected in real time using a Prism 7500 instrument (Applied Biosystems).

Reverse transcription was first performed using the High-Capacity cDNA Archive Kit from Applied Biosystems (Product number 4322171) and following the protocol utilized therein.

More specifically purified RNA as described previously herein was incubated with reverse transcriptase buffer, dNTPs, random primers and reverse transcriptase and incubated for 25°C for 10 minutes and subsequently for 37 °C for two hours and the resulting mixture utilized as the starting product for quantitative PCR.

cDNA resulting from reverse transcription was incubated with the QuantiTect SYBR® Green PCR Master Mix as provided and no adjustments were made for magnesium concentration. Uracil-N-Glycosylase was not added. 5μM of both forward primer and reverse

primer specific to the genes of the invention were added and the reaction was incubated and monitored in accordance with the standard protocol utilizing the ABI PRISM 7700/ABI GeneAmp 5700/iCycler/DNA Engine Opticon. Primers utilized are shown in **Table 6.** Other examples of primers which can be used are disclosed in **Table 4**. Forward and reverse primers for the candidate biomarkers were designed using "PrimerQuest". A tool which is available from Integrated DNA Technologies, Coralville, IA. **Table 6** lists the primer sets for eight of the genes of **Table 2**, namely, MBTPS1 (membrane-bound transcription factor protease site 1), MGC45871, MKLN1 (muskelin 1), NIPBL (Nipped-B homolog (Drosophila)), APEH (acylpeptide hydrolase), FLJ23091, MGC40157, and PPP1R2 (protein phosphatase 1, regulatory (inhibitor) subunit 2). Serial dilution measurements for the target genes and a housekeeping gene (beta-actin, ACTB) were assayed, to ensure that the values were within linear range and the amplification efficiency was approximately equal for the target and ACTB. ACTB was selected as a housekeeping gene because no statistical significant differences were observed between control and disease group in this study (data not shown). The melting temperature [Tm] in thermal dissociation, and examination on agarose gels provided confirmation of specific PCR amplification and the lack of primer-dimer formation in each reaction well.

For individual target gene analysis, changes in Ct value between each gene and the ACTB house-keeping was calculated as ΔCt= Ct (target gene) - Ct (house-keeping gene).

EXAMPLE 4

TaqMan® QRT PCR can also be performed using the QuantiTect™ Probe RT-PCR system from Qiagen (Product Number 204343) in conjunction with a TaqMan® dual labelled probe and primers corresponding to the gene of interest. The TaqMan® probe and primers can be ordered from Applied Biosystems Assays-On-Demand™.

The dual labelled probe contains both a fluorophore and a quencher molecule. The proximity of the fluorescent reporter with the quencher prevents the reporter from fluorescing, but during the PCR extension step, the 5' – 3' exonuclease activity of the Taq DNA polymerase releases the fluorophore which allows it to fluoresce. As such, the amount of fluorescence correlates with the amount of PCR product generated. Examples of TaqMan® probes which can be utilized with the genes disclosed in **Table 2** are shown in **Table 6** and/or **4.**

EXAMPLE 5

Identification of combinations of biomarkers using logistic regression

A selection of eight genes from **Table 2** were chosen as follows: MBTPS1, MGC45871, MKLN1, NIPBL APEH, MGC40157, PPP1R2, FLJ23091. Combinations of pairs of the selected eight genes were tested to determine the ability of each combination of pairs to screen for one or more colorectal pathologies. Blood samples were drawn into into lavender-top BD Vacutainer tube prior to anaesthesia and prior to any surgery. RNA from whole blood was prepared by first removing the serum and subsequently treating the remaining sample with hypotonic Lysis Buffer (Lysis Buffer (1L) 0.6g EDTA; 1.0g $KHCO_2$, 8.2g NH_4Cl adjusted to pH 7.4 (using NaOH))in a ratio of 3 parts Lysis Buffer to 1 part blood so as to preferentially lyse the red blood cells. The samples were centrifuged and RNA extracted from the unfractionated cells of the sample.

Real-time quantitative PCR was conducted on 68 patients diagnosed as having colorectal pathology (ie one or more subtypes of polyps) (n=68) and 110 control individuals where the control individuals were diagnosed as not having one or more colorectal pathologies (n=110). QRT-PCR was performed using a two step procedure whereby cDNA was first prepared before performing PCR using ABI reagents. In this example, a matrix containing the ΔCt of "ratios" of the eight biomarkers was used to create a reference training data set (AJ36h). The ratios used to generate the matrix of ΔCts was further constrained by requiring each ratio to be comprised of one upregulated gene and a second downregulated gene where the ΔCt was generated by subtracting the Ct of the downregulated gene from the Ct of the upregulated gene. MBTPS1, MGC45871, MKLN1, NIPBL were identified as upregulated genes (ie when comparing polyps vs non polyp individuals) (**FIG. 3**). APEH, MGC40157, PPP1R2, FLJ23091 were identified as down regulated genes (**FIG. 3**). The advantages of gene-pair ratio method include a) reducing inter-individual variability, b) permitting analysis of individual samples without references so as to ensure technical differences between plates are minimized, c) can use any reliable method (microarray, real-time PCR, etc), d) independent of the platform utilized for data acquisition, e) no housekeeping gene required (relatively independent of the input of sample amount), f) translating the strengths of micorarray expression profiling into simple clinical tests, g) highly precise in disease discrimination.

A reference (training) data set (AJ36h) was constructed containing ΔCt values for each possible ratio as described and constrained as noted above for the above eight genes assayed against a total of 178 subjects including 110 subject without pathology (Female/male: 55/54 with

one missing information, age average 57 year ranging 23 to 83 years of age) and 68 subjects with diagnosed colorectal pathology (Female/male: 22/45 with one missing information, age average 57 ranging from 38 to 82 years). The types of pathology identified include 21 (31%) tubular adenomas, 18 (27%) hyperplastic and 7 (10%) high risk pathology (villous morphology) and 22 (32%) other minor polyp (see **Table 7**).

Logistic regression (15-18) was used to analyze the dependence of the binary variable Y (0=control (has no pathology), 1=disease (has pathology) on all possible combinations of the ΔCt values from the reference data training set AJ36h. If P = probability that a patient sample is diagnosed as "diseased", then a function X = Logit (p) can be defined as follows:

$$X = \text{Logit}(P) = \ln(P/(1-P)) = b_0 + b_1 \Delta Ct_1 + b_2 \Delta Ct_2 + \ldots + b_n \Delta Ct_n \qquad \text{(Eq 1)}$$

If X ≥threshold then Y=1 (diagnosis = "diseased"), and if X < threshold then Y=0 (diagnosis = "control"). The (empirical) coefficients {bi} that define the relationship between X and the experimental measurements {ΔCti, where i represents a sample} were obtained by a maximum-likelihood (ML) fitting method. Identical {bi} values were obtained using several different commercial software programs: MedCalc (MedCalc Software, Mariakerke, Belgium) and XL-Stat (Addinsoft Software, Paris, France). ROC curve analysis was then used to evaluate the discriminatory power of each combination of ratios wherein all combinations of ratios as described above were tested (19-21). Each combinations of ratios resulted in an equation in the form of Equation 1. The top 10 best equations that gave an ROC = 0.72 were used in a formula where each equation was given equal ranking to perform the subsequent blind test prediction.

Cross Validation

Cross-validation was performed on dataset AJ36h (the 178-sample training set) using WEKA (www.cs.waikato.ac.nz/~ml/weka/index.html) (22). Two different cross-validation schemes were used. The WEKA MetaAnalysis function was used to construct 100 bootstrap replicates of dataset AJ36h. Each of the new datasets was analyzed with the SimpleLogistic classifier. Each of the resultant 100 logistic equations was then analyzed by 10-fold cross-validation. The results for all equations were averaged ("bootstrap aggregating").

Prospective (Blind) Test

A blind set of 80 clinical samples were tested. The test set consisted of 40 controls and 40 subjects with one or more colorectal pathologies (having one or more polyps of any type). None of the test subjects used in the blind test were used to generate a classifier for each possible

combination of the ratio of biomarkers "ratios" where each ratio is selected as a combination of an upregulated gene (when comparing colorectal pathology to no colorectal pathology) and a down regulated gene (when comparing colorectal pathology to no colorectal pathology). MBTPS1, MGC45871, MKLN1, NIPBL were identified as upregulated genes (ie when comparing polyps vs non polyp individuals (**FIG. 3**). APEH, MGC40157, PPP1R2, FLJ23091 were identified as down regulated genes (**FIG. 3**).

Medical information on subjects in this blind set, including age, gender, and pathologist's report, is summarized in **Table 7**. Samples were run on a single 96-well plate for Q RT-PCR with each of the eight genes measured in triplicate.

The measured values for each blind sample were evaluated using the following algorithm, which consists of an initial calculation, a binary logic gate, and a "committee machine" vote. *Initial Calculation:* The logit function X_i is computed for each of the equations (I = 1 to N) that gave ROC Area = 0.72 against the reference data set AJ36h. *Logic Gate*: If $X_i <$ threshold of j (where j stands for an equation number), then the blind sample is given score $S_i = -1$ for Eqn #j. If $X_i \geq$threshold of j, then it is given score $S_i = +1$ for Eqn #j. *Vote by Committee Machine (23):* A vote is taken over the scores from the 10 logit equations used for diagnosis. By definition, Vote = $\sum S_i$. If Vote ≤ 0 then the sample is called "no pathology", while if Vote > 0 then the sample is called "diseased or with pathology".

The best equation gives an ROC area 0.72 as shown in **FIG. 4**. Ten top equations that gave ROC=0.72 were used for the blind test prediction. **Table 8** lists the parameters for the 10 equations.

Cross-validation was done with the SimpleLogistic function in WEKA. 100 bootstrap replicates of dataset AJ36h were constructed and analyzed each with the WEKA SimpleLogistic function. The resultant set of 100 logistic equations was subjected to 10-fold cross-validation. The results for all equations were then averaged which gave an ROC Area = 0.66, overall accuracy 65%, sensitivity (TPF) 41%, specificity (TNF) 83%.

Prediction of Blind Samples

A blind test was conducted on an additional set of 80 samples (40 samples without pathology and 40samples with colorectal pathology). A committee vote was taken over the ten (10) best logit equations from Reference Dataset AJ36h, to predict a state of either "colorectal pathology present" or "colorectal pathology absent (control)". For the set of blind samples the

sensitivity (true positive fraction, TPF) is 43 % (17/40), and the specificity (true negative fraction, TNF) is 80 % (32/40), with an overall accuracy of 61 % (49/80, **Table 9**).

While the present invention has been described with reference to what are presently considered to be the preferred examples, it is to be understood that the invention is not limited to the disclosed examples. To the contrary, the invention is intended to cover various modifications and equivalent arrangements included within the spirit and scope of the appended claims.

All publications, patents and patent applications are herein incorporated by reference in their entirety to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated by reference in its entirety.

EXAMPLE 6

Testing of combinations of biomarkers using logistic regression and application of said combinations to screen for one or more types of colorectal pathology or one or more pathologies.

A selection of seven genes were chosen including: LIM domain containing preferred translocation partner in lipoma (LPP) Gene ID 4026; cytidine deaminase (CDA) Gene ID 978; sarcoma antigen NY-SAR-48 (MCG20553) Gene ID 93323; serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPINE 2) Gene ID 5270; B-cell novel protein 1 (BCNP1) Gene ID 199786; hypothetical protein MGC45871 (MGC45871) Gene ID 359845; membrane-bound transcription factor protease, site 1 (MBTPS1) Gene ID 8720. Genes were chosen from either **Table 1** or other similar experiments.

Clinical Question - Polyp v. No Pathology

A reference (training) data set was constructed containing ΔCt values for the above seven genes assayed against a total of 185 subjects having any type of polyp and 239 subjects not having polyps.

Logistic regression was used to analyze the dependence of the binary variable Y (0=control, 1=disease) on the ΔCt values from the reference data set. If P = probability that a patient sample is identified as "diseased", then a function X = Logit (p) can be defined as follows:

$$X = \text{Logit}(P) = \ln(P/(1-P)) = b_0 + b_1 \Delta Ct_1 + b_2 \Delta Ct_2 + \ldots + b_n \Delta Ct_n \qquad \text{(Eq 1)}$$

If X ≥threshold then Y=1 (diagnosis = "has polyps"), and if X < threshold then Y=0 (diagnosis = does not have polyps). The (empirical) coefficients {bi} that define the relationship between X and the experimental measurements {ΔCti, where i represents a sample} were obtained by a maximum-likelihood (ML) fitting method. Identical {bi} values were obtained using several different commercial software programs: MedCalc (MedCalc Software, Mariakerke, Belgium) and XL-Stat (Addinsoft Software, Paris, France). ROC curve analysis was then used to evaluate the discriminatory power of the combinations. The best equation used the following genes (LPP; CDA; MBTPS1; SERPINE2; BCNP1) and shown as follows:

X = Logit (*P*) = ln (*P*/(1-*P*)) = -4.9104-0.4278 ΔCtMGC20553 -0.6164ΔCtCDA +0.8230 ΔCtMBTPS1+0.3961ΔCtSERPINE2 + 0.1641 ΔCtBCNP1 gave an ROC = 0.73 with a sensitivity of 80% and a specificity of 50%.

Clinical Question - High Risk Pathology v. Other

Using the same selection of seven biomarkers, but this time tested against a reference (training) data set with ΔCt values for the above seven genes assayed against a total of 129 subjects having "high risk" polyp and 295 subjects either having a polyp not classified as high risk or having no pathology, where subjects where classified as having "high risk polyps" if they had one of the following categories of polyps: Tubulovillous Adenoma; Villous Adenoma; High Grade Dysplasia and Tubular Adenoma where the diameter of the Tubular Adenoma polyp is greater than 10mm and cancer

Logistic regression was used to analyze the dependence of the binary variable Y (0=control, 1=disease) on the ΔCt values from the reference data set. If *P* = probability that a patient sample is identified as "diseased", then a function X = Logit (p) can be defined as follows:

$$X = \text{Logit}(P) = \ln\left(P/(1-P)\right) = b_0 + b_1 \Delta Ct_1 + b_2 \Delta Ct_2 + \ldots + b_n \Delta Ct_n \qquad \text{(Eq 1)}$$

If X ≥threshold then Y=1 (diagnosis = "has high risk polyps"), and if X < threshold then Y=0 (diagnosis = does not have high risk polyps). The (empirical) coefficients {bi} that define the relationship between X and the experimental measurements {ΔCti, where i represents a sample} were obtained by a maximum-likelihood (ML) fitting method. Identical {bi} values were obtained using several different commercial software programs: MedCalc (MedCalc

Software, Mariakerke, Belgium) and XL-Stat (Addinsoft Software, Paris, France). ROC curve analysis was then used to evaluate the discriminatory power of the combinations. The best equation used the following genes (CDA; MGC20553; MBTPS1; SERPINE2; BCNP1;) and shown as follows:

$$X = \text{Logit}(P) = \ln(P/(1-P)) = -5.2981 - 0.5433\Delta\text{CtCDA} - 0.4958\Delta\text{CtMGC20553} + 0.8551\Delta\text{CtMBTPS1} + 0.3554\Delta\text{CtBCNP1} + 0.2438\Delta\text{Ct SERPINE2}$$

gave an ROC = 0.74 with a sensitivity of 83% and a specificity of 46%.

Clinical Question– Cancer v. Other

Finally the same seven genes were tested in combinations using a reference (training) data set containing ΔCt values for the above seven genes assayed against a total of 80 subjects having cancerous polyps and 344 subjects having other types of polyps or having no pathology.

Logistic regression was used to analyze the dependence of the binary variable Y (0=control, 1=disease) on the ΔCt values from the reference data set. If P = probability that a patient sample is identified as "diseased", then a function X = Logit (p) can be defined as follows:

$$X = \text{Logit}(P) = \ln(P/(1-P)) = b_0 + b_1 \Delta Ct_1 + b_2 \Delta Ct_2 + \ldots + b_n \Delta Ct_n \qquad \text{(Eq 1)}$$

If X ≥threshold then Y=1 (diagnosis = "has cancerous polyps"), and if X < threshold then Y=0 (diagnosis = does not have cancerous polyps). The (empirical) coefficients {bi} that define the relationship between X and the experimental measurements {ΔCti, where i represents a sample} were obtained by a maximum-likelihood (ML) fitting method. Identical {bi} values were obtained using several different commercial software programs: MedCalc (MedCalc Software, Mariakerke, Belgium) and XL-Stat (Addinsoft Software, Paris, France). ROC curve analysis was then used to evaluate the discriminatory power of the combinations. The best equation used the following genes (MGC20553, CDA, MBTPS1, SERPINE2, MGC45871; BCNP1) and shown as follows:

$$X = \text{Logit}(P) = \ln(P/(1-P)) = -12.9149 - 0.5378\Delta\text{CtCDA} - 0.5398\Delta\text{CtMGC20553} + 1.0386\Delta\text{CtMBTPS1} + +0.7405\Delta\text{CtBCNP1} + 0.4002\ \Delta\text{CtMGC45871} + 0.2074\Delta\text{CtSERPINE2}$$

gave an ROC = 0.83 with a sensitivity of 90% and a specificity of 55%.

Clinical Question - High Risk Pathology v. Other

A reference (training) data set was constructed containing ΔCt values for the above seven genes assayed against a total of 252 subjects having high risk polyps and 272 subjects having other types of polyps or having no pathology where by high risk polyps is meant Tubulovillous Adenoma, Villous Adenoma, High Grade Dysplasia and Tubular Adenoma – regardless of diameter of polyp.

Logistic regression was used to analyze the dependence of the binary variable Y (0=control, 1=disease) on the ΔCt values from the reference data set. If P = probability that a patient sample is identified as "diseased", then a function X = Logit (p) can be defined as follows:

$$X = \text{Logit}(P) = \ln(P/(1-P)) = b_0 + b_1 \Delta Ct_1 + b_2 \Delta Ct_2 + \ldots + b_n \Delta Ct_n \qquad \text{(Eq 1)}$$

If X ≥threshold then Y=1 (diagnosis = "has high risk polyps"), and if X < threshold then Y=0 (diagnosis = does not have high risk polyps). The (empirical) coefficients {bi} that define the relationship between X and the experimental measurements {ΔCti, where i represents a sample} were obtained by a maximum-likelihood (ML) fitting method. Identical {bi} values were obtained using several different commercial software programs: MedCalc (MedCalc Software, Mariakerke, Belgium) and XL-Stat (Addinsoft Software, Paris, France). ROC curve analysis was then used to evaluate the discriminatory power of the combinations. The best equation used the following genes (MGC20553; CDA; MBTPS1; SERPINE2; BCNP1;) and shown as follows:

$$X = \text{Logit}(P) = \ln(P/(1-P)) = -3.5819 - 0.7625\Delta\text{CtCDA} - 0.6117\Delta\text{CtMGC20553} + 1.15\Delta\text{CtMBTPS1} + 0.2174\Delta\text{CtBCNP1} + 0.2439\Delta\text{Ct SERPINE2}$$

gave an ROC = 0.76 with a sensitivity of 82% and a specificity of 52%.

EXAMPLE 7

Biomarkers to screen for presence of colorectal cancer. Deriving classifiers to be used with combinations of biomarkers and application of said classifiers to determine presence of colorectal cancer

QRT-PCR was performed on a selection of the genes identified from one or more microarray analyses (data not shown) as being able to differentiate as between individuals having colorectal cancer and individuals not having colorectal cancer. Some of genes selected for QRT-PCR were selected from microarray data performed on samples collected from three regions of

China for over 593 samples including 61 samples from individuals having been diagnosed with colorectal cancer and 532 from individuals not having colorectal cancer (data not shown). Other genes were selected from other similar microarray experiments with individuals from North America and/or Asia. Among the individuals not having colorectal cancer was a mixture of individuals having breast cancer, kidney cancer, prostate cancer, bladder cancer, and individuals having other subtypes of colorectal pathology which were not colorectal cancer.

QRT-PCR was done on each individual gene across a population of individuals having colorectal cancer and a population of individuals not having colorectal cancer. QRT-PCR experiments were done using either the SYBR® Green Kit from Qiagen (Product Number 204143) and/or using Applied Biosystems PCR reagent kits (Cat 4334973) and/or using TaqMan Assay using the QuantiTect® Probe PCR Kit (Qiagen, Cat. # 204345). TaqMan® probes were developed for each gene of interest and labelled with FAM and the Black Hole Quencher® from Biosearch Technologies. Beta-actin was used as a housekeeping gene in the duplexed assays and labelled using HEX and Black Hole Quencher®. Amplicons were detected in real time using a Prism 7500 instrument (Applied Biosystems). Results of the QRT-PCR for each gene across the population tested are shown in **Table 12.**

Rather than testing all possible combinations of the biomarkers noted in Table 12, in other embodiments, all possible combinations of biomarkers with a p value of less than 0.05 can be chosen and all or a portion of combinations of biomarkers tested. Discussed below is representative classifiers identified for selected combinations tested.

Classifiers were derived for all two gene combinations of the biomarkers identified in **Table 12** using QRT-PCR for 28 of the genes identified in **Table 12** across 58 individuals having colorectal cancer and 57 individuals not having colorectal cancer. The 28 genes utilized are represented by the following gene symbols and are described in more detail herein: **OSBPL10, LOC283130, BANK1, COBLL1, MGC24039, C9orf85, BLNK, BCNP1, PDE3B, AKAP13, WDFY1, CDA, AGTRAP, ACTR2, UTS2, MS4A1, SPAP1, ANK3, KIAA1559, GBP5, MGC20553, CEACAM1, HIST1H4H, PRG1, BRD2, LTBP3, MAP4K3, and NIPA2** Primers utilized for the real time RT-PCR are further described in Table **16.** Classifiers derived for selection combinations of two genes are shown as follows:

Table A: Table showing Resulting Classifiers for a Selection of Two Gene Combinations Wherein the Combinations are in the Form of Ratios and the Biomarkers Are Selected from the

28 Genes Selected from **Table 12.** Shown is the resulting ROC area of the Classifiers, the Sensitivity (at the noted cutoff Sens) and Specificity (at the noted cutoff Spec) are shown. The constant, and the coefficient for the selected two gene ratio are noted.

Table A

	ROCarea	*Sensitivity at 90% Specificity*	*Specificity at 90% Sensitivity*	*Constant*	*Coeffic for Ratio*
BANK1/CDA	0.8621	46.55	68.42	-3.7808	1.256
BCNP1/CDA	0.8451	43.10	57.89	-2.7251	1.2554
CDA/MS4A	0.8430	43.10	63.16	-1.3171	-1.0944
C9orf85/CDA	0.8382	44.83	52.63	-16.482	2.2374
CDA/OSBPL10	0.8367	56.90	47.37	-5.9699	-1.2875
CDA/SPAP1	0.8364	48.28	59.65	-3.3047	-0.9384
BLNK/CDA	0.8361	50.00	68.42	-4.8603	1.2367
CDA/LOC283130	0.8339	67.24	52.63	-3.9388	-1.6368
CDA/COBLL1	0.8321	53.45	56.14	-6.9371	-1.3126
BANK1/PRG1	0.8306	55.17	54.39	-8.6282	1.2825
BANK1/CEACAM1	0.8291	56.9	56.14	-1.7783	1.1225
BCNP1/PRG1	0.8224	60.34	45.61	-7.4478	1.2631
BANK1/MGC20553	0.8197	44.83	59.65	2.2412	0.9436
BANK1/NIPA2	0.8176	58.62	50.88	-2.2946	1.6015
ACTR2/BANK1	0.8155	41.38	54.39	-9.1667	-1.4596
CDA/HIST1H4H	0.8134	51.72	47.37	1.6688	-1.5062
AKAP13/GBP5	0.7012	22.41	22.81	-0.7784	0.6743
BCNP1/CEACAM1	0.8131	44.83	52.63	-0.8916	1.1843
CEACAM1/SPAP1	0.8128	34.48	56.14	-1.8563	-0.88
CDA/MAP4K3	0.8128	39.66	45.61	-9.7566	-1.7304
BCNP1/GBP5	0.8107	36.21	57.89	-4.611	1.1411

As noted for each two gene combination the ROC area is provided in addition to the specificity (when sensitivity is set at 90%) and sensitivity (when specificity is set at 90%). The

cutoff utilized to generate the sensitivity and specificity as noted are provided in the two righthand most columns. The classifier for each of the two gene combinations can be generically described as follows:

$$X \text{ (having colorectal cancer)} = \text{Logit}(P) = \ln(P/(1-P)) = b_0 + b_1(\Delta Ct_1 - \Delta Ct_2)$$

Where b_0 is identified as the coefficient and b_1 is noted as the coefficient for the ratio.

EXAMPLE 8

Classifiers were also derived for all possible combinations of a selection of nine of the biomarkers identified in **Table 12.** Data for use in generating the classifiers for the combinations were obtained using real time RT-PCR for each of the nine genes tested across the same 58 individuals having colorectal cancer and 57 individuals not having colorectal cancer described in **Example 7.** The 9 genes utilized are represented by the following gene symbols and are described in more detail herein: **CDA, MGC20553, MS4A1, BCNP1, BANK1, GBP5, OSBPL10, SPAP1, LOC283130.** Primers utilized for the real time RT-PCR are further described in Table **16.** A selection of the resulting classifiers are described below in **Table B** below:

Table B

#	ROC area	Constant	CDA	MGC20553	MS4A1	BCNP1	BANK1	GBP5	OSBPL10	SPAP1	LOC283130
1	0.8364	-14.48				1.61					
1	0.8197	-10.07			1.25						
1	0.8091	-10.56								1.02	
2	0.8681	-21.35				1.39			0.77		
2	0.8648	-7.58	-0.93				1.41				
2	0.8594	-21.80					1.27		0.81		
3	0.8839	-12.85	-1.26			1.20			0.93		
3	0.8811	-13.04	-1.25				1.06		0.97		
3	0.8757	-10.48	-1.20			1.11					0.94
4	0.8963	-9.09	-1.47			1.34		-0.72	0.93		
4	0.8917	-7.25	-1.29	-0.51		1.17			1.02		
4	0.8902	-5.32	-1.59			1.11		-0.88			1.14

5	0.8987	-10.60	-1.42			0.99	0.43	-0.71	0.92		
5	0.8984	-8.84	-1.63			1.16		-0.80	0.75		0.52
5	0.8969	-9.34	-1.65				0.94	-0.72	0.69		0.75
6	0.9035	-10.25	-1.57			0.82	0.43	-0.78	0.73		0.52
6	0.9005	-10.91	-1.42		-0.32	1.13	0.62	-0.72	0.91		
6	0.9005	-10.64	-1.41			1.19	0.57	-0.71	0.88	-0.26	
7	0.9053	-10.60	-1.57		-0.31	0.96	0.61	-0.79	0.73		0.51
7	0.9020	-10.31	-1.55			0.98	0.53	-0.77	0.71	-0.20	0.49
7	0.9014	-11.32	-1.59	0.14		0.82	0.46	-0.87	0.71		0.52
8	0.9056	-10.57	-1.57		-0.27	0.99	0.62	-0.79	0.72	-0.06	0.50
8	0.9044	-11.30	-1.59	0.09	-0.29	0.95	0.62	-0.85	0.71		0.51
8	0.9026	-11.17	-1.57	0.11		0.96	0.55	-0.85	0.70	-0.18	0.49
9	0.9041	-11.26	-1.58	0.09	-0.25	0.98	0.63	-0.85	0.71	-0.06	0.50

The classifiers shown above can be generically described in the following equation.

X (possibility of having colorectal cancer) = Logit (P) = ln ($P/(1-P)$) = $b_0 + b_1 \Delta Ct_1 + b_2 \Delta Ct_2 + \ldots + b_n \Delta Ct_n$

Noted above are selected classifiers for combinations of 1, 2, 3, 4, 5, 6, 7, 8 or all 9 of the selected genes. The area under the curve is noted (ROC Area). Also provided is the constant b_0 and the coefficient for each biomarker (e.g. b_n) required for the selected classifier to be applied to the delta Ct of the noted gene for a test sample. As would be understood, where no coefficient is noted, that biomarker is not required for the classifier. Additional sensitivity and specificity determinations can be ma de for each classifier, and will vary depending upon the threshold set.

The results of all of the combinations of the 9 genes is graphically represented in **FIG. 5.**

EXAMPLE 9

All possible combinations of biomarkers identified in **Table 12** are tested by applying logistic regression to data corresponding to level of product of the biomarkers noted. QRT-PCR is conducted on each of the genes noted in **Table 12** for a population of individuals who have

been diagnosed as having colorectal cancer or not having colorectal cancer. A matrix containing the ΔCt for RNA corresponding to each gene for each individual of the two populations is created and classifiers derived for each possible combination of biomarkers of those listed in **Table 12** (whether individually statistically significant or not) using techniques as described herein. For each classifier the ROC curve is plotted and the area under the curve determined. Classifiers are chosen depending on the specific sensitivity and specificity requirements of the specific intended use of the biomarkers (for example, if may be desirable to have a high sensitivity and fewer false negatives so as to miss less colorectal cancers); (alternatively high specificity resulting in lower false positives is also desirable as it can decrease costs of additional unnecessary medical interventions). A blind test is conducted on one or more of the resulting classifiers so as to demonstrate the utility of the classifier to test for colorectal cancer in a test individual. One or more the classifiers is applied to test an individual to determine the likelihood of said test subject having colorectal cancer.

EXAMPLE 10

Blind Testing of one of the Combinations of the Genes in Table 12 using the Derived Classifier.

A five gene combination encompassing B-cell scaffold protein with ankyrin repeats (BANK1), B-cell novel protein 1 (BCNP1), cytidine deaminase (CDA) membrane-spanning 4-domains, subfamily A, member 1 (MS4A1) and FERM domain containing 3 (MGC20553 aka FRMD3) was selected to pursue further blind sample testing.

The reference (training) data set was constructed containing ΔCt values for the above five genes assayed against a total of 57 subjects having colorectal cancer and 58 subjects not having colorectal cancer as described in more detail in Example 7.

Logistic regression was used to analyze the dependence of the binary variable Y (0=control, 1=disease) on the ΔCt values from the reference data set. If P = probability that a patient sample is identified as "having colorectal cancer), then a function X = Logit (p) can be defined as follows:

$$X = \text{Logit}(P) = \ln(P/(1-P)) = b_0 + b_1 \Delta Ct_1 + b_2 \Delta Ct_2 + \ldots + b_n \Delta Ct_n \qquad \text{(Eq 1)}$$

If X ≥threshold then Y=1 (diagnosis = "has colorectal cancer"), and if X < threshold then Y=0 (diagnosis = does not have colorectal cancer). The (empirical) coefficients {bi} that define the relationship between X and the experimental measurements {ΔCti, where i represents a

sample} were obtained by a maximum-likelihood (ML) fitting method. Identical {bi} values were obtained using several different commercial software programs: MedCalc (MedCalc Software, Mariakerke, Belgium) and XL-Stat (Addinsoft Software, Paris, France). ROC curve analysis was then used to evaluate the discriminatory power of the combinations. The classifier derived using the selected genes(BANK1, BCNP1, CDA, MS4A1, and MGC20553) and shown as follows:

X = Logit (*P*) = ln (*P*/(1-*P*)) = -5.1338 -0.8399 (ΔCt CDA) -0.3314 (ΔCtMGC20553) - 0.3245 (ΔCtMS4A1) + 1.0903 (ΔCtBCNP1) + 0.7842 (ΔCtBANK1) gave an area under the curve of 0.883 ± 0.032. One can adjust the sensitivity or specificity by adjusting the testing cut off point as follows:

Cut-off	Sens. (95% C.I.)	Spec. (95% C.I.)
-0.53	89.7 (78.8- 96.1)	78.9 (66.1- 88.6)
-0.31	86.2 (74.6- 93.8)	80.7 (68.1- 89.9)
-0.04	81.0 (68.6- 90.1)	82.5 (70.1- 91.2)
0.47	72.4 (59.1- 83.3)	87.7 (76.3- 94.9)
0.59	67.2 (53.7- 79.0)	89.5 (78.5- 96.0)
1.46	43.1 (30.2- 56.8)	94.7 (85.4- 98.8)

Using a cutoff of -1.1 gives a sensitivity of 98.3% and a specificity 50.9%.

A first blind test was performed using a scoring population comprised of 15 individuals not having colorectal cancer and 6 individuals having colorectal cancer. This blind test utilized individuals selected from a single site in Penang. The first blind test resulted in a sensitivity of 100% and a specificity of 43%. A second blind test was performed using a second scoring population (non overlapping with the first scoring population) of 31 non colorectal patients and 23 colorectal patients. Patient samples were collected from three different sites in Asia. The test resulted in a sensitivity of 100% (all samples with colorectal cancer properly identified) and a specificity of 47% (almost half of the samples without colorectal cancer properly identified). A final blind test was performed utilizing samples obtained from two clinics in North America including 15 colorectal cancer patients and 16 non colorectal cancer patients resulting in a sensitivity of 88% and a specificity of 33%.

EXAMPLE 11

Selection of 6 Biomarkers (BCNP1, CD163, CDA, MS4A1, BANK1, MCG20553) to derive classifiers which are particularly useful in screening for the presence of colorectal cancer

and application of the classifiers with the combinations selected to determine presence of colorectal cancer

QRT-PCR was performed on the selection of genes BCNP1, CD163, CDA, MS4A1, BANK1, MCG20553 identified from one or more microarray analyses (selected from **Table 12** and **Table 11).** QRT-PCR data was most recently collected on RNA samples from centrifuged lysed blood from 109 samples, 60 individuals having colorectal cancer and 59 individuals not having colorectal cancer. QRT-PCR was performed using a duplexed TaqMan Assay using the QuantiTect® Probe PCR Kit (Qiagen, Cat. # 204345). TaqMan® probes were developed for each gene of interest and labelled with FAM and the Black Hole Quencher® from Biosearch Technologies. Beta-actin was used as a housekeeping gene in the duplexed assays and labelled using HEX and Black Hole Quencher®. ΔCts (Ct gene of interest – Ct Beta-actin) were calculated.

Results of the average QRT-PCR results for each gene across the population tested are shown in **Table C** below. The average ΔCt (Ct gene-Ct Beta-actin) of each gene in both the control population and the population having colorectal cancer (CRC) are shown, as is the standard deviation (SD) as amongst the data from the population. The p value for each gene individually is shown. The change in ΔCt as between the ΔCt of the Control samples for each gene and the ΔCt for the CRC samples for each gene are shown as ΔΔCt and the standard deviation are shown. Also shown is the fold change for each individual marker.

Table C

Control		BANK1	BCNP1	CDA	MGC20553	MS4A1	CD163
	Avg ΔCt of Control (non CRC)	7.5998	6.5558	3.4814	9.7375	3.9940	5.2012
	SD	0.767	0.907	0.491	1.036	0.974	0.381
Colorectal Cancer (CRC)		BANK1	BCNP1	CDA	MGC20553	MS4A1	CD163
	CRC Avg	8.3398	7.6368	3.2070	9.3773	5.1298	5.3896
	Standard Deviation	0.708	0.893	0.539	0.867	1.041	0.482
	p-value	2.6E-07	1.6E-09	4.4E-03	4.2E-02	1.1E-08	2.0E-02

(CRC v. Control)

	BANK1	BCNP1	CDA	MGC20553	MS4A1	CD163
ΔΔCt(ΔCtCont-ΔCtCRC)	-0.7400	-1.0810	0.2743	0.3602	-1.1359	-0.1884
Standard Deviation	1.044	1.273	0.729	1.351	1.425	0.614

	BANK1	BCNP1	CDA	MGC20553	MS4A1	CD163
Regulation (direction of regulation comparing CRC v. Control)	Down regulated	Down Regulated	Up regulated	Up regulated	Down regulated	Down regulated
Fold change (CRC v. Control)	1.67	2.12	1.21	1.28	2.20	1.14
Standard Deviation (Fold change)	2.06	2.42	1.66	2.55	2.69	1.53

A matrix of the individual QRT-PCR data corresponding to each of the six biomarkers across a population comprising 60 individuals having colorectal cancer and 59 individuals not having colorectal cancer was generated using the same methods noted above. The matrix of data was used to generate classifiers for all possible combinations of the six biomarkers by applying logistic regression to the data of each possible combination. A listing of all of the combinations and the biomarkers which make up each combination are noted in **Table D** below. The ROC curve for each resulting classifier was measured to determine the ability of each derived classifier to properly identify a test patient as having colorectal cancer. The given sensitivity (at a pre-defined specificity) and the specificity (at a pre-defined sensitivity) can be determined from the ROC curve. The resulting classifiers from this analysis is shown in **Table E** and the results of these classifiers are shown graphically in **FIG. 5**.

Table D Each combination is noted as a unique combination number ranging from 1 to 63. Presence of the number 1 in a column below a noted Gene indicates the presence of that gene within the generated classifier.

Table D

Combination #	BANK1 Gene01	BCNP1 Gene02	CDA Gene03	MS4A1 Gene04	MGC20553 Gene05	CD163 Gene06
1	1					
2		1				
3	1	1				
4			1			
5	1		1			
6		1	1			
7	1	1	1			
8				1		
9	1			1		
10		1		1		
11	1	1		1		
12			1	1		
13	1		1	1		
14		1	1	1		
15	1	1	1	1		
16					1	
17	1				1	
18		1			1	
19	1	1			1	
20			1		1	
21	1		1		1	
22		1	1		1	
23	1	1	1		1	
24				1	1	
25	1			1	1	
26		1		1	1	
27	1	1		1	1	
28			1	1	1	
29	1		1	1	1	
30		1	1	1	1	
31	1	1	1	1	1	
32						1
33	1					1
34		1				1
35	1	1				1
36			1			1
37	1		1			1
38		1	1			1
39	1	1	1			1
40				1		1
41	1			1		1

42		1		1		1
43	1	1		1		1
44			1	1		1
45	1		1	1		1
46		1	1	1		1
47	1	1	1	1		1
48					1	1
49	1				1	1
50		1			1	1
51	1	1			1	1
52			1		1	1
53	1		1		1	1
54		1	1		1	1
55	1	1	1		1	1
56				1	1	1
57	1			1	1	1
58		1		1	1	1
59	1	1		1	1	1
60			1	1	1	1
61	1		1	1	1	1
62		1	1	1	1	1
63	1	1	1	1	1	1

In preferred embodiments, data representing levels of products of any combination of two of the six biomarkers in a sample isolated or derived from a test subject are input to a formula as further described herein, for the purpose of providing a probability that the test subject has one or more colorectal pathologies. In certain other embodiments, data representing levels of products of any combination of three, four, or five of the six biomarkers are input to a formula as further described herein. It is also consistent with the methods described herein that data representing levels of products of all six of the six biomarkers are input to a formula to provide a probability that a test subject has one or more colorectal pathologies.

Table E Classifiers resulting from each possible combination of the six biomarkers are noted. The Combination number corresponds to the combinations as noted in **Table D**. The number of genes contributing to the combination is noted, and the coefficient for that biomarker are noted within the row. Where 0 is noted as a coefficient, this biomarker does not contribute to the resulting classifier. The area under the curve (ROC area) is noted as is the sensitivity at 90% specificity and the specificity at 90% sensitivity.

Table E

Comb #	# of genes	ROCarea	Sensitivity @ 90% spec	Specificity @ 90% sens	Constant	BANK1	BCNP1	CDA	MGC20553	MS4A1	CD163
2	1	0.8065	48.33	50.85	-9.4336	0	1.3378	0	0	0	0
16	1	0.8062	33.33	40.68	-5.1508	0	0	0	0	1.1456	0
1	1	0.7664	25.00	40.68	-10.646	1.3395	0	0	0	0	0
8	1	0.6531	11.67	18.64	3.9001	0	0	0	-0.40595	0	0
4	1	0.6421	26.67	15.25	3.5585	0	0	-1.0592	0	0	0
32	1	0.6232	18.33	18.64	-5.4467	0	0	0	0	0	1.0322
48	2	0.8285	36.67	61.02	-10.284	0	0	0	0	1.1534	0.96391
34	2	0.8184	48.33	54.24	-14.22	0	1.3294	0	0	0	0.91273
6	2	0.8155	33.33	52.54	-6.6582	0	1.2559	-0.65891	0	0	0
18	2	0.8130	48.33	50.85	-8.6118	0	1	0	0	0.3475	0
20	2	0.8102	35.00	42.37	-2.2241	0	0	-0.78667	0	1.0765	0
3	2	0.8093	48.33	47.46	-10.046	0.18289	1.2184	0	0	0	0
10	2	0.8068	51.67	52.54	-11.01	0	1.3885	0	0.12681	0	0
24	2	0.8065	31.67	42.37	-4.3207	0	0	0	-7.84E-02	1.1282	0
17	2	0.8048	28.33	42.37	-3.938	-0.24835	0	0	0	1.3149	0
33	2	0.7921	36.67	49.15	-16.106	1.3541	0	0	0	0	1.0097
5	2	0.7754	30.00	54.24	-7.6711	1.2227	0	-0.61344	0	0	0
9	2	0.7718	35.00	52.54	-8.8519	1.2937	0	0	-0.14952	0	0
36	2	0.7113	20.00	27.12	-2.8691	0	0	-1.391	0	0	1.4243
40	2	0.6983	15.00	25.42	-1.5982	0	0	0	-0.47483	0	1.1646
12	2	0.6961	18.33	18.64	7.3191	0	0	-1.0488	-0.39666	0	0
52	3	0.8319	26.67	61.02	-8.1557	0	0	-1.0734	0	1.0665	1.3105
49	3	0.8299	38.33	64.41	-9.4457	-0.16237	0	0	0	1.2638	0.95548
38	3	0.8291	51.67	52.54	-11.787	0	1.2127	-0.90702	0	0	1.1775
50	3	0.8288	43.33	55.93	-13.395	0	0.96662	0	0	0.38068	0.91813

56	3	0.8285	40.00	59.32	-8.8677	0	0	0	-0.16768	1.1205	1.0282
35	3	0.8226	50.00	52.54	-15.171	0.2494	1.1715	0	0	0	0.92838
22	3	0.8192	38.33	50.85	-5.7441	0	0.90176	-0.66762	0	0.35836	0
21	3	0.8192	25.00	42.37	1.8168	-0.71915	0	-0.9327	0	1.5568	0
42	3	0.8178	48.33	52.54	-14.643	0	1.3458	0	4.17E-02	0	0.89513
14	3	0.8158	38.33	52.54	-8.2509	0	1.3096	-0.66151	0.1273	0	0
7	3	0.8155	33.33	52.54	-6.6677	-2.33E-03	1.2544	-0.65841	0	0	0
19	3	0.8147	45.00	52.54	-7.7027	-0.18144	0.99459	0	0	0.47486	0
28	3	0.8124	38.33	42.37	-1.6155	0	0	-0.78053	-5.87E-02	1.0615	0
26	3	0.8116	48.33	52.54	-9.8432	0	1.0675	0	9.36E-02	0.31563	0
11	3	0.8085	51.67	47.46	-11.398	0.15545	1.2828	0	0.11619	0	0
25	3	0.8068	28.33	47.46	-3.1168	-0.24726	0	0	-7.82E-02	1.2971	0
37	3	0.8020	25.00	57.63	-13.206	1.1841	0	-0.93208	0	0	1.3051
41	3	0.8017	38.33	55.93	-13.824	1.2908	0	0	-0.23193	0	1.0935
13	3	0.7788	20.00	52.54	-5.7872	1.1714	0	-0.61629	-0.15341	0	0
44	3	0.7500	23.33	49.15	0.93831	0	0	-1.3775	-0.46832	0	1.5416
53	4	0.8421	28.33	62.71	-4.0963	-0.72824	0	-1.2159	0	1.5557	1.3112
54	4	0.8359	43.33	54.24	-10.864	0	0.79246	-0.93889	0	0.43542	1.215
60	4	0.8345	26.67	61.02	-6.7979	0	0	-1.0645	-0.16209	1.0289	1.3733
57	4	0.8322	41.67	64.41	-8.0548	-0.15788	0	0	-0.16741	1.2282	1.0198
39	4	0.8294	51.67	52.54	-11.969	-4.28E-02	1.1857	-0.89948	0	0	1.179
58	4	0.8288	43.33	55.93	-13.371	0	0.96496	0	-2.24E-03	0.38154	0.91909
51	4	0.8285	41.67	55.93	-12.968	-7.93E-02	0.9637	0	0	0.43635	0.91323
46	4	0.8285	51.67	50.85	-12.048	0	1.2235	-	2.49E-02	0	1.1669

								0.90636			
23	4	0.8237	41.67	44.07	-1.9249	-0.65485	0.87804	-0.81254	0	0.81182	0
43	4	0.8212	50.00	52.54	-15.382	0.2432	1.1845	0	2.32E-02	0	0.91822
30	4	0.8195	43.33	47.46	-6.9954	0	0.97268	-0.669	9.40E-02	0.32588	0
29	4	0.8192	28.33	47.46	2.3538	-0.71624	0	-0.92591	-5.37E-02	1.5416	0
15	4	0.8164	38.33	52.54	-8.1437	-3.34E-02	1.3322	-0.66871	0.12965	0	0
27	4	0.8124	45.00	54.24	-8.9424	-0.1764	1.0611	0	9.25E-02	0.43969	0
45	4	0.8014	30.00	67.80	-10.66	1.1055	0	-0.93995	-0.24668	0	1.3918
55	5	0.8410	30.00	57.63	-6.9559	-0.67682	0.76786	-1.0879	0	0.9056	1.2208
61	5	0.8393	28.33	64.41	-2.722	-0.73359	0	-1.2079	-0.16199	1.523	1.3754
62	5	0.8379	43.33	55.93	-10.555	0	0.76996	-0.94059	-2.76E-02	0.44682	1.228
59	5	0.8285	41.67	55.93	-12.939	-7.94E-02	0.96171	0	-2.68E-03	0.43746	0.91437
47	5	0.8277	51.67	50.85	-12.173	3.61E-02	1.1995	-0.90005	2.22E-02	0	1.1693
31	5	0.8212	41.67	40.68	-3.1633	-0.65384	0.94851	-0.81521	9.32E-02	0.77795	0
63	6	0.8407	31.67	61.02	-6.5754	-0.67929	0.74043	-1.0901	-3.29E-02	0.92168	1.2365

Primers and probes which were utilized for the QRT-PCR) are further described in Table 17.

EXAMPLE 12

Testing a Test Subject for One or More Colorectal Pathologies Using The 6 Biomarkers (BCNP1, CD163, CDA, MS4A1, BANK1, MCG20553).

A reference population of 200 individuals is used to generate a formula which will be used to test the test subject. 100 of said individuals are confirmed to have colorectal cancer by colonoscopy. The remaining 100 individuals are screened for colorectal cancer by colonoscopy and are confirmed to be negative for colorectal cancer. Blood Samples are obtained for each of the 200 individuals and total RNA isolated from each isolated blood sample. RNA from each sample is reverse transcribed using an oligo dT primer and cDNA corresponding to the total mRNA is obtained. QRT-PCR is performed on each of the six genes in each of the samples derived from the blood sample and a ΔCt generated for each gene in reference to a Beta-actin control. A data matrix is generated of all of the data across the population. A classifier is developed using each of the following methods (a) logistic regression, (b) linear regression (c) neural networks and (d) principle component analysis. A formula consisting of each of the classifiers, wherein each classifier itself is given a weighting of equal value is generated (ie the results of each classifier when applied to a test subject will give an indication of whether the test subject has a colorectal pathology, and then the results of each classifier are tallied such that if, for example, 3 of the 4 classifiers indicate the test subject has colorectal pathology, the results of the formula indicate the test subject has colorectal pathology).

A blood sample is isolated from a test subject. Total RNA from the blood sample is isolated and cDNA derived using an oligo dT primer. QRT-PCR is performed in each of the six genes in the sample and a ΔCt generated for each gene in reference to a Beta-actin control. The data from the test subject's sample is input into the formula consisting of the four classifiers and a result of each classifier determined, along with the results of the sum of the four classifiers to provide an indication of whether said test subject has colorectal pathology, and in particular colorectal cancer.

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All patents, patent applications, and published references cited herein are hereby incorporated by reference in their entirety.

One skilled in the art will readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those objects, ends and advantages inherent herein. The present examples, along with the methods, procedures,

treatments, molecules, and specific compounds described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention as defined by the scope of the claims.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

TABLES

Table 1 is found in the instant specification after Table 17, and before the sequence listing and claims.

TABLE 2

Gene Symbol	AffySpot	p-value(MW)	p-value (t-test)	Fold change	Direction	Gene Description
APEH	201284_s_at		6.0e-03	0.91	downregulated	N-acylaminoacyl-pept
C1orf22	220342_x_at	<0.001	3.15049390173162e-03	1.07	upregulated	chromosome 1 open re
ESR1	215551_at	0.058	0.03	0.87	downregulated	estrogen receptor 1
ETS1	214447_at	0.132	0.15	0.93	downregulated	v-ets erythroblastos
FLJ14624	225666_at		0.01	0.76	downregulated	hypothetical protein
FLJ20701			0.01	0.76	downregulated	hypothetical protein
FLJ23091	221958_s_at		0.05	0.83	downregulated	putative NFkB activa
G2	234784_at	0.182	0.18	0.78	downregulated	G2 protein
ICOS	210439_at		0.07	0.88	downregulated	inducible T-cell co-
ITCH	235057_at	<0.001	1.73049856446377e-06	1.13	upregulated	itchy homolog E3 ubi
MBTPS1	217543_s_at		8.0e-03	1.21	upregulated	membrane-bound trans
MGC40157	225065_x_at	0.301	0.04	1.19	downregulated	hypothetical protein
MGC45871	226905_at		0.11	1.35	upregulated	hypothetical protein
MKLN1	242984_at	0.003	0.04	1.06	upregulated	muskelin 1, intracel
MMP9	203936_s_at	0.006	7.80154116715436e-03	1.24	upregulated	matrix metalloprotei
NIPBL	1560474_at	0.005	0.01	1.07	upregulated	Nipped-B homolog (Dr
RPS24	1555878_at		0.05	0.88	downregulated	ribosomal protein S2
SMARCA1	203874_s_at	0.077	0.06	0.82	downregulated	SWI/SNF related, mat

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TABLE 3

Gene Symbol	RNA Accession No.	Protein Accession No.	Description
FLJ14624	NM_032813	NP_116202	Homo sapiens hypothetical protein FLJ14624 (FLJ14624), mRNA
FLJ14624	NM_032813	NP_116202	Homo sapiens hypothetical protein FLJ14624 (FLJ14624), mRNA
ETS1	NM_005238	NP_005229	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), mRNA
RPS24	NM_033022	NP_148982	Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA
RPS24	NM_001026	NP_001017	Homo sapiens ribosomal protein S24 (RPS24), transcript variant 2, mRNA
FLJ20701	NM_017933	NP_060403	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
MKLN1	NM_013255	NP_037387	Homo sapiens muskelin 1, intracellular mediator containing kelch motifs (MKLN1), mRNA
NIPBL	NM_133433	NP_597677	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant A, mRNA
NIPBL	NM_015384	NP_056199	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant B, mRNA
FLJ20701	NM_017933	NP_060403	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
RPS24	NM_033022	NP_148982	Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA
RPS24	NM_001026	NP_001017	Homo sapiens ribosomal protein S24 (RPS24), transcript variant 2, mRNA
APEH	NM_001640	NP_001631	Homo sapiens N-acylaminoacyl-peptide hydrolase (APEH), mRNA
MBTPS1	NM_003791	NP_003782	Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcrip
MBTPS1	NM_201268	NP_957720	Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcrip
SMARCA1	NM_003069	NP_003060	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromat
SMARCA1	NM_139035	NP_620604	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromat
SMARCA1	NM_003069	NP_003060	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromat
SMARCA1	NM_139035	NP_620604	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromat
MMP9	NM_004994	NP_004985	Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type I
MKLN1	NM_013255	NP_037387	Homo sapiens muskelin 1, intracellular mediator containing kelch motifs (MKLN1), mRNA
ESR1	NM_000125	NP_000116	Homo sapiens estrogen receptor 1 (ESR1), mRNA
NIPBL	NM_133433	NP_597677	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant A, mRNA
NIPBL	NM_015384	NP_056199	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant B, mRNA
ITCH	NM_031483	NP_113671	Homo sapiens itchy homolog E3 ubiquitin protein ligase (mouse) (ITCH), mRNA
ITCH	NM_031483	NP_113671	Homo sapiens itchy homolog E3 ubiquitin protein ligase (mouse) (ITCH), mRNA
ICOS	NM_012092	NP_036224	Homo sapiens inducible T-cell co-stimulator (ICOS), mRNA
ESR1	NM_000125	NP_000116	Homo sapiens estrogen receptor 1 (ESR1), mRNA
ESR1	NM_000125	NP_000116	Homo sapiens estrogen receptor 1 (ESR1), mRNA
ESR1	NM_000125	NP_000116	Homo sapiens estrogen receptor 1 (ESR1), mRNA
ESR1	NM_000125	NP_000116	Homo sapiens estrogen receptor 1 (ESR1), mRNA
NIPBL	NM_133433	NP_597677	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant A, mRNA

NIPBL	NM_015384	NP_056199	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant B, mRNA
NIPBL	NM_133433	NP_597677	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant A, mRNA
NIPBL	NM_015384	NP_056199	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant B, mRNA
NIPBL	NM_133433	NP_597677	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant A, mRNA
NIPBL	NM_015384	NP_056199	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant B, mRNA
ETS1 mRNA	NM_005238	NP_005229	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1),
SMARCA1	NM_003069	NP_003060	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromat
SMARCA1	NM_139035	NP_620604	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromat
ESR1	NM_000125	NP_000116	Homo sapiens estrogen receptor 1 (ESR1), mRNA
ESR1	NM_000125	NP_000116	Homo sapiens estrogen receptor 1 (ESR1), mRNA
ITCH	NM_031483	NP_113671	Homo sapiens itchy homolog E3 ubiquitin protein ligase (mouse) (ITCH), mRNA
ESR1	NM_000125	NP_000116	Homo sapiens estrogen receptor 1 (ESR1), mRNA
ESR1	NM_000125	NP_000116	Homo sapiens estrogen receptor 1 (ESR1), mRNA
MBTPS1	NM_003791	NP_003782	Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcrip
MBTPS1	NM_201268	NP_957720	Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcrip
FLJ20701	NM_017933	NP_060403	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
C1orf22	NM_025191	NP_079467	Homo sapiens chromosome 1 open reading frame 22 (C1orf22), mRNA
C1orf22	NM_025191	NP_079467	Homo sapiens chromosome 1 open reading frame 22 (C1orf22), mRNA
FLJ23091	NM_024911	NP_079187	Homo sapiens putative NFkB activating protein 373 (FLJ23091), transcript variant 1, m
FLJ23091	NM_001002292	NP_001002292	Homo sapiens putative NFkB activating protein 373 (FLJ23091), transcript variant 2, m
C1orf22	NM_025191	NP_079467	Homo sapiens chromosome 1 open reading frame 22 (C1orf22), mRNA
ETS1 mRNA	NM_005238	NP_005229	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1),
MGC40157	NM_152350	NP_689563	Homo sapiens hypothetical protein MGC40157 (MGC40157), mRNA
MKLN1 mRNA	NM_013255	NP_037387	Homo sapiens muskelin 1, intracellular mediator containing kelch motifs (MKLN1),
FLJ14624	NM_032813	NP_116202	Homo sapiens hypothetical protein FLJ14624 (FLJ14624), mRNA
MGC45871	NM_182705	NP_874364	Homo sapiens hypothetical protein MGC45871 (MGC45871), mRNA
MGC45871	NM_182705	NP_874364	Homo sapiens hypothetical protein MGC45871 (MGC45871), mRNA
FLJ23091	NM_024911	NP_079187	Homo sapiens putative NFkB activating protein 373 (FLJ23091), transcript variant 1, m
FLJ23091	NM_001002292	NP_001002292	Homo sapiens putative NFkB activating protein 373 (FLJ23091), transcript variant 2, m
FLJ23091	NM_024911	NP_079187	Homo sapiens putative NFkB activating protein 373 (FLJ23091), transcript variant 1, m
FLJ23091	NM_001002292	NP_001002292	Homo sapiens putative NFkB activating protein 373 (FLJ23091), transcript variant 2, m
MKLN1 mRNA	NM_013255	NP_037387	Homo sapiens muskelin 1, intracellular mediator containing kelch motifs (MKLN1),
ESR1	NM_000125	NP_000116	Homo sapiens estrogen receptor 1 (ESR1), mRNA
ITCH	NM_031483	NP_113671	Homo sapiens itchy homolog E3 ubiquitin protein ligase (mouse) (ITCH), mRNA

MKLN1 mRNA	NM_013255	NP_037387	Homo sapiens muskelin 1, intracellular mediator containing kelch motifs (MKLN1),
FLJ20701	NM_017933	NP_060403	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
FLJ20701	NM_017933	NP_060403	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
ITCH	NM_031483	NP_113671	Homo sapiens itchy homolog E3 ubiquitin protein ligase (mouse) (ITCH), mRNA
NIPBL	NM_133433	NP_597677	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant A, mRNA
NIPBL	NM_015384	NP_056199	Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant B, mRNA
MKLN1 mRNA	NM_013255	NP_037387	Homo sapiens muskelin 1, intracellular mediator containing kelch motifs (MKLN1),
MKLN1 mRNA	NM_013255	NP_037387	Homo sapiens muskelin 1, intracellular mediator containing kelch motifs (MKLN1),

TABLE 4

Gene Symbol	SensePrimer	SEQ ID NO	AntisensePrimer	SEQ ID NO	TaqManProbe	SEQ ID NO
APEH	GCCCTGTATTATGTGGACCT	54	AGATGGGTACTGCAGGTAGA	55	CCGGCTGAGCCCAGACCAAT	56
APEH	CACTCGGAGACACACTTGTT	57	CTTGGTCTGGCTTCTTCAG	58	CATCGCTGGCACTGACGTCCA	59
APEH	ACTCGGAGACACACTTGTTG	60	CTTGGTCTGGCTTCTTCAG	61	CATCGCTGGCACTGACGTCCA	62
APEH	AGTGGTGGTAGATGTTGTGC	63	AGACCACTCTCTGGCTGTC	64	TGCAGCCTTCTGCCTTTGGGA	65
APEH	CACTTGTTGTATGTGGCAGA	66	GCCTGGCTATCTCATCATC	67		
C1orf22	TAGGGAGGAGAAACAGAAGC	68	GGCCTCTAACTCGACCTCTA	69	TGGAACATGCTTACCCTGCTGATGA	70
C1orf22	TGTGGTGGATAAGAGCTGTC	71	CCCATCTTCTTCAGGATTTC	72	TGGCCATGAAATCTCTGGCTCTCA	73
C1orf22	GAGGAGAGTTTCAGGAGTGG	74	CTCCCATCTTTGAGGTGAAT	75	TGGCCATGAAATCTCTGGCTCTCA	76
C1orf22	TTGCTTGGAGATGACAGTTT	77	AGCATTGGTTTGTGGATATG	78		
ESR1	GGCACATCTTCTGTCTTCTG	79	CTGTGAAGAGCTACGGGAAT	80	TGGAATCCCTTTGGCTGTTCCC	81
ESR1	TGGCACATCTTCTGTCTTCT	82	CTGTGAAGAGCTACGGGAAT	83	TGGAATCCCTTTGGCTGTTCCC	84
ESR1	CCCTACTACCTGGAGAACGA	85	ATTGGTACTGGCCAATCTTT	86	CTGCCACCCTGGCGTCGATT	87
ESR1	CACCATTCCCAAGTTAATCC	88	GAAATGCAGTTGGAAACAGA	89	TGGGACCAAAGTTCATTTGCTCCA	90
ESR1	TGCCCTACTACCTGGAGAAC	91	ATTGGTACTGGCCAATCTTT	92	AGCCCAGCGGCTACACGGTG	93
ESR1	GTGCCCTACTACCTGGAGAA	94	ATTGGTACTGGCCAATCTTT	95	AGCCCAGCGGCTACACGGTG	96
ESR1	TGTGCAATGACTATGCTTCA	97	TTATCAATGGTGCACTGGTT	98		
ESR1	TGTGCAATGACTATGCTTCA	99	TTTATCAATGGTGCACTGGT	100		
ETS1	TGGGTGGTTTATACACTGGA	101	ATAAGGGTTTCACCCAGCTA	102	CCAGATTTGCCCATCCTTCCTCTG	103
ETS1	GAGCTCCTCTCCCTCAAGTA	104	GGTGACGACTTCTTGTTTGA	105	CCTCGGTCATTCTCCGAGACCC	106
ETS1	GGATGTCAGGTGAGACTGTG	107	GCCTTCAAGTCATTCCTCTC	108	CCCTGGCATCACCTGTGCCA	109
ETS1	TCAAACAAGAAGTCGTCACC	110	GCGATCACAACTATCGTAGC	111	CCCGAGTTTACCACGACTGGTCCTC	112
ETS1	CCGCTATACCTCGGATTACT	113	GCGTCTGATAGGACTCTGTG	114	CCCAGTGTGTTCCACCATCGGA	115
FLJ14624	ACAGCTGCCATCAGAAACTA	116	GCTTCCTGTAGCTCATTCCT	117	CCGGGAAGCTGTAAGATTAAATCCCAA	118
FLJ14624	TGATAAAGGCAACCAGACAG	119	AGCTTCCTGTAGCTCATTCC	120	TGCCATCAGAAACTACCGGGAAGC	121
FLJ14624	GGATTTCTCGTTATCCCATT	122	TCTTGGTATGTTTGCTCAGG	123	AGGACACGCTCCGCGACCAC	124
FLJ14624	CAAATACAGCCAGACTTTGC	125	TTTAATTGCTGTCCGGTAAC	126	TGCTGCTTCAAACCGTTTCAGGC	127
FLJ14624	CAAATACAGCCAGACTTTGC	128	GTTTAATTGCTGTCCGGTAA	129	TGCTGCTTCAAACCGTTTCAGGC	130
FLJ14624	CTTGGTGATAGGCAAATTCA	131	AGCAGGGTCATTCTGAAGAG	132	CCCGTTCCTGAGCATGCCGA	133

FLJ14624	TTTGGCTGTGCTCTTATCATC	134	CAGCAGACCGTAATTCTCCT	135	TGTTTCTTGGCCAAGTCTAGATGTCCC	136
FLJ20701	ATTGGAGGACAAGAGCAGAT	137	CCATCGCTCTCTAGATTGG	138	TTCTTAGGTGCCGCAGTGCCC	139
FLJ20701	CCTTCAGGAAGACTTTCCAC	140	CTCAAGTTCATTCAGCCATC	141	ACGGGCGGATCCCACAGCAAC	142
FLJ20701	TGATCAGCAAGTGAACACAC	143	CTCGGTGATAGCAAATCAGA	144	TGCATCCTTGATGGCAAGCTTCA	145
FLJ20701	GTGATCAGCAAGTGAACACA	146	CTCGGTGATAGCAAATCAGA	147	TGCATCCTTGATGGCAAGCTTCA	148
FLJ20701	TTAATGGTCCTGTCTGATGC	149	GGGTCTCTAGACAAGCCAAG	150		
FLJ20701	AGATTTGCAGACACAGAAGC	151	TTCTAACATCAGGTGGTTGC	152		
FLJ23091	TACAACTCACGAATCCCTTCT	153	ACAGGAAGTAGAGGCAGAGG	154		
FLJ23091	CAACTCACGAATCCCTTCTAC	155	ACAGGAAGTAGAGGCAGAGG	156		
FLJ23091	ACAACTCACGAATCCCTTCTA	157	ACAGGAAGTAGAGGCAGAGG	158		
FLJ23091	AACTCACGAATCCCTTCTACA	159	ACAGGAAGTAGAGGCAGAGG	160		
FLJ23091	GGGATTTCCATGACCTTTAT	161	ATCCAGAAGGACAGAAGCAT	162	TGCCCTGTCGGATGTCACCA	163
FLJ23091	ATTGAAGAGGCAATTCCAAG	164	TTTAGCTTGAAGGCAATGTC	165	CCACATGGAGATGAGTCCTTGGTTCC	166
ICOS	CATGTGTAATGCTGGATGTG	167	AAACAACTCAGGGAACACCT	168	TGGACAACCTGACTGGCTTTGCA	169
ICOS	CAGGCCTCTGGTATTTCTTT	170	ATTTGTACACCTCCGTTGTG	171	TTGGCAGAACCATTGATTTCTCCTGTT	172
ICOS	AAACATGAAGTCAGGCCTCT	173	GTACACCTCCGTTGTGAAAT	174	TTGGCAGAACCATTGATTTCTCCTGTT	175
ICOS	GTCAGGCCTCTGGTATTTCT	176	ATTTGTACACCTCCGTTGTG	177	TTGGCAGAACCATTGATTTCTCCTGTT	178
ICOS	GAAGTCAGGCCTCTGGTATT	179	ATTTGTACACCTCCGTTGTG	180	TTGGCAGAACCATTGATTTCTCCTGTT	181
ITCH	CAGATCCAAGGATGAAACAA	182	ACCACCATTTGAGAGTGATG	183	CACCAGCTCCTGCATCTTCAGGG	184
ITCH	TCAATCCAGATCACCTGAAA	185	AATCCTTGAGTCCAACTGGT	186	CCCATGGAACAGAGCCATGGC	187
ITCH	AAGCTGTTGTTTGCCATAGA	188	CAGAGAAGGACAAACATTGC	189	TGCCCATTCATGGTGCAAGTTCTC	190
ITCH	AAGCTGTTGTTTGCCATAGA	191	GCAGAGAAGGACAAACATTG	192	TGCCCATTCATGGTGCAAGTTCTC	193
ITCH	GCTGTTGTTTGCCATAGAAG	194	CAGAGAAGGACAAACATTGC	195	TGCCCATTCATGGTGCAAGTTCTC	196
ITCH	GCTGTTGTTTGCCATAGAAG	197	GCAGAGAAGGACAAACATTG	198	TGCCCATTCATGGTGCAAGTTCTC	199
MBTPS1	CAATGACGGACCTCTTTATG	200	GGTAGCTCCCAGGTAGTCAT	201	TGCCGCCTACTCCAATCACATCC	202
MBTPS1	TCTGTGGGAAGAAACATCTG	203	TGATGAGAATTCCACCTTCA	204		
MBTPS1	AATCCATCCAGTGACTACCC	205	ACTTGAGGGAACGAAAGACT	206	AACATCAAACGGGTCACGCCC	207
MBTPS1	CAGCCAAAGCTAGAAATTCA	208	TAGGGTAGTCACTGGATGGA	209	TTCACTGCTCTTCAGGGCACTTGAA	210
MBTPS1	GCAATGACGGACCTCTTTAT	211	GGTAGCTCCCAGGTAGTCAT	212	TGCCGCCTACTCCAATCACATCC	213
MGC40157	AGAATCAGCATCATGTTTGG	214	ATAACCTTCTCTTGGGCTGA	215	CCTCATGGCAGGCTCCTGGC	216
MGC40157	TCAGCCCAAGAGAAGGTTAT	217	TGAGCATGTCCTCTGATACA	218	TCCCAAGGACCAGTAGCTGCCA	219
MGC40157	GACTACAGCTCACAGCACAC	220	AAAGCTACAACTTGGCCTGT	221	TGCCCAGGCTGGTCTCAGGC	222
MGC40157	TCAGCCCAAGAGAAGGTTAT	223	AGGCAAGCATGTTTCTACAC	224	TCCCAAGGACCAGTAGCTGCCA	225
MGC40157	ACTACAGCTCACAGCACACC	226	AAAGCTACAACTTGGCCTGT	227	TGCCCAGGCTGGTCTCAGGC	228

MGC40157	TCAGCCCAAGAGAAGGTTAT	229	CATAAGGCAAGCATGTTTCT	230	TCCCAAGGACCAGTAGCTGCCA	231
MGC40157	AGGCTCATGGATCACTCTTT	232	GGTACGCAATCCAGTTCTCT	233	CCGGCCTTCGCAGACTCCAG	234
MCG45871	GACCTCTCTGATGAATGCTG	235	AATGACGTGAAGGGTAAGGT	236	ACCGGCTCTCTCCCGCTGTCCT	237
MCG45872	GACCTCTCTGATGAATGCTG	238	GAATGACGTGAAGGGTAAGG	239	ACCGGCTCTCTCCCGCTGTCCT	240
MCG45873	GACCTCTCTGATGAATGCTG	241	GAATGACGTGAAGGGTAAGGT	242	ACCGGCTCTCTCCCGCTGTCCT	243
MCG45874	GACCTCTCTGATGAATGCTG	244	GGAATGACGTGAAGGGTAAG	245	ACCGGCTCTCTCCCGCTGTCCT	246
MCG45875	CCTCTCTGATGAATGCTGAC	247	GAATGACGTGAAGGGTAAGG	248	ACCGGCTCTCTCCCGCTGTCCT	249
MCG45876	ACCTCTCTGATGAATGCTGA	250	GAATGACGTGAAGGGTAAGG	251	ACCGGCTCTCTCCCGCTGTCCT	252
MKLN1	CCAGTGAACCACACAATTCAGT	253	ATGCAGTGTCCTATTCGAGA	254	TGGATGTCCTCAGGCCCAGCA	255
MKLN1	GGATCACACCTATGCTCAAA	256	CCATTTCTGTGTCCAGTGAC	257	TGACAGCATGACTCCTCCTAAAGGCA	258
MKLN1	ATTTGAGAGAGGAGGCTGAG	259	AATGAAATGCCTGTCAGTTG	260	CCACTGGACAACCACACAAACCATTTCTC	261
MKLN1	GACTTGTAATGGCAGCGTAG	262	CTCGAAGAAGTTTCCAGGTT	263	TGACAGCAGAGCCAGTGAACCACA	264
MKLN1	ACTTGTAATGGCAGCGTAGA	265	CTCGAAGAAGTTTCCAGGTT	266	TGACAGCAGAGCCAGTGAACCACA	267
MMP9	ACTTTGACAGCGACAAGAAGT	268	GCGGTACATAGGGTACATGA	269	CGCCGCCACGAGGAACAAAC	270
MMP9	AACTTTGACAGCGACAAGAA	271	GAAGCGGTACATAGGGTACAT	272	CGCCGCCACGAGGAACAAAC	273
MMP9	CAGTACCACGGCCAACTAC	274	TGGAAGATGAATGGAAACTG	275	CCCATCAGCATTGCCGTCCC	276
MMP9	CCACTACTGTGCCTTTGAGT	277	GTACTTCCCATCCTTGAACA	278	TTCCCAATCTCCGCGATGGC	279
MMP9	CCACTACTGTGCCTTTGAGT	280	CTTCCCATCCTTGAACAAA	281	TTCCCAATCTCCGCGATGGC	282
NIPBL	CACGAATAGCAGAAGAGGTG	283	GTATGTCACCTTCTGGGTCA	284	CAGCTTGTCCATAGCCTCAACCAGG	285
NIPBL	CCCATCCTTCAAGTTACACA	286	ATTAGCTGAATTGCCAGACA	287	TCCACAGATGCAACAAGCATCGG	288
NIPBL	GGGATTGCTAGTCTCACAGA	289	TCTTCTGCTATTCGTGCATT	290	TCCTGAACCAGCTGCCTCTTCCA	291
NIPBL	CCCATCCTTCAAGTTACACA	292	AGACAACGGACCAGAAACTT	293	TCCACAGATGCAACAAGCATCGG	294
NIPBL	GCACAGGCTAAGTAGTGACG	295	AGGTGGTCTTGAGCCTTTAG	296	TTTCCCTTGAGATCTCCACAGCCA	297
NIPBL	CACGAATAGCAGAAGAGGTG	298	GTATGTCACCTTCTGGGTCA	299	CAGCTTGTCCATAGCCTCAACCAGG	300
NIPBL	CCCATCCTTCAAGTTACACA	301	ATTAGCTGAATTGCCAGACA	302	TCCACAGATGCAACAAGCATCGG	303
NIPBL	GGGATTGCTAGTCTCACAGA	304	TCTTCTGCTATTCGTGCATT	305	TCCTGAACCAGCTGCCTCTTCCA	306
NIPBL	CCCATCCTTCAAGTTACACA	307	AGACAACGGACCAGAAACTT	308	TCCACAGATGCAACAAGCATCGG	309
NIPBL	GCACAGGCTAAGTAGTGACG	310	AGGTGGTCTTGAGCCTTTAG	311	TTTCCCTTGAGATCTCCACAGCCA	312
RPS24	CACCGTAACTATCCGCACTA	313	CGGTGTGGTCTTGTACATTT	314	AGGCACTGTCGCCTTCCCGG	315
RPS24	AAGAAAGCAACGAAAGGAAC	316	TCATTGCAGCACCTTTACTC	317	TGCCAGCACCAACATTGGCC	318
RPS24	AGACATGGCCTGTATGAGAA	319	ATCCAATCTCCAGCTCACTT	320	TGCCAGCACCAACATTGGCC	321
RPS24	AAGACATGGCCTGTATGAGA	322	ATCCAATCTCCAGCTCACTT	323	TGCCAGCACCAACATTGGCC	324
RPS24	GACATGGCCTGTATGAGAAG	325	ATCCAATCTCCAGCTCACTT	326	TGCCAGCACCAACATTGGCC	327
RPS24	AAGGAACGCAAGAACAGAAT	328	ATTGCAGCACCTTTACTCCT	329	TGCCAGCACCAACATTGGCC	330

SMARCA1	TACCTGGTCATTGATGAAGC	331	CAAAGGTGTTCCAGTTAGGA	332	CGTGAGTTCAAGTCGACTAACCGCTTG	333
SMARCA1	TACCTGGTCATTGATGAAGC	334	TTATTCTGCAAAGGTGTTCC	335	TTCAAGTCGACTAACCGCTTGCTCC	336
SMARCA1	TGGACCCAGAATATGAAGAG	337	ATGTTCAGTGGAGATGTTGG	338	TCTCTTTGCTCGGTCGGCTTTCA	339
SMARCA1	CTTTGCTTGGTTACCTGAAA	340	AAACAAATGACACGGAGAGA	341	CCGAAATATTCCTGGACCTCACATGG	342
SMARCA1	GGAAATGGACCCAGAATATG	343	GTTGGAGATTTCTGTGCTGA	344	TCTCTTTGCTCGGTCGGCTTTCA	345
SMARCA1	AAGGAAATGGACCCAGAATA	346	CTGAAGGCTGAATGAAATGT	347	TCTCTTTGCTCGGTCGGCTTTCA	348
SMARCA1	AGTGGGATGTTTGCGTTACT	349	CACGAACAATCTCTGAAAGC	350	TCATCAATGACCAGGTATCGCCAGTG	351

TABLE 5

Gene Symbol	Description	Commercially Available Antibody Reference	Scientific Reference
APEH	N-acylaminoacyl-peptide hydrolase		
C1orf22	chromosome 1 open reading frame 22		
ESR1	estrogen receptor 1	Ab2746 (Abcam)	Shevde NK & Pike JW Estrogen modulates the recruitment of myelopoietic cell progenitors in rat through a stromal cell-independent mechanism involving apoptosis. *Blood* **87**:2683-92 (1996). Yang NN *et al.* Identification of an estrogen response element activated by metabolites of 17beta-estradiol and raloxifene. *Science* **273**:1222-5 (1996).
ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	Ab10936 (Abcam)	Pande P *et al.* Ets-1: a plausible marker of invasive potential and lymph node metastasis in human oral squamous cell carcinomas. *J Pathol* **189**:40-5 (1999). Nakayama T *et al.* Expression of the Ets-1 proto-oncogene in human gastric carcinoma: correlation with tumor invasion. *Am J Pathol* **149**:1931-9 (1996). Bories JC *et al.* Increased T-cell apoptosis and terminal B-cell differentiation induced by inactivation of the Ets-1 proto-oncogene. *Nature* **377**:635-8 (1995). Wernert N *et al.* Stromal expression of c-Ets1 transcription factor correlates with tumor invasion. *Cancer Res* **54**:5683-8 (1994).
FLJ14624			
FLJ20701	putative NFkB activating protein 373		
FLJ23091	inducible T-cell co-stimulator		
G2	G2 protein		
ICOS	inducible T-cell co-stimulator	Ab3744 (Abcam)	

ITCH	itchy homolog E3 ubiquitin protein ligase (mouse)		
MBTPS1	membrane-bound transcription factor protease, site 1		
MGC40157	hypothetical protein MGC40157		
MGC45871	hypothetical protein MGC45871		
MKLN1	muskelin 1, intracellular mediator containing kelch motifs		
MMP9	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	Ab5707	
NIPBL	Nipped-B homolog (Drosophila)		
RPS24	ribosomal protein S24		
SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	Ab21924 (Abcam)	Lazzaro MA & Picketts DJ Cloning and characterization of the murine Imitation Switch (ISWI) genes: differential expression patterns suggest distinct developmental roles for Snf2h and Snf2l. *J Neurochem* 77:1145-56 (2001).

TABLE 6

		5' Primer		3' Primer		Product Length
Symbol	Ref. ID	Primer Sequence	Position	Primer Sequence	Position	
APEH	NM_001640	AAGGATGTCCAGTTTGCAGTGG	2081	TGGCAGGAAATGAAGCCACCAT	2184	104
FLJ23091	NM_024911	ACAGGCATCTATGGGATGTGGA	1694	AGATCGCCATTGGACTGGTCTT	1794	101
MBTPS1	NM_003791	TCGGTACTCCAAGGTTCTGGA	3220	TGTTTCCAAAGGTTACTGGGCG	3348	129
MGC40157	NM_152350	ACCCGAGAGAACTGGATTGCGT	359	GCTCCAATACTCAGCTGCCAAA	469	111
MGC45871	NM_182705	CCACCAAAGGAAGTAAGGTACAC	362	TAGTTGCGCCACGTGCCATT	507	146
MKLN1	NM_013255	GAGGGCCGAAATTGGTGTTTGA	1169	ATTGTGGTTCACTGGCTCTGCT	1297	129
NIPBL	NM_015384	AGTGTACGCCACTTTGCCCTAA	6886	ATCAGCCTTGTTCCGCATAGCA	7017	132
PPP1R2	NM_006241	AAGATGCCTGTAGTGACACCGA	250	ATCCGATACTTTGGCTCCAAGC	349	100

TABLE 7

	AJ36h		Blind test	
	No Polyp	Polyp	No Polyp	Polyp
Sample Size	110	68	40	40
Gender (F/M)	55/54*	22/45*	21/19	13/27
Age mean (range)	57 (23~83)	57 (38~82)	57 (40~79)	60 (38~76)
Polyp Subtype				
Tubular adenoma		21 (31%)		14 (35%)
Hyperplastic		18 (27%)		15 (38%)
High risk pathology		7 (10%)		3 (7.5%)
Others		22 (32%)		8 (20%)

* one sample missing information

TABLE 8

Equ #	# ratios	ROC area	Constant	MGC45871-APEH	MKLN1-APEH	MGC45871-FLJ23091	MKLN1-FLJ23091	NIPBL-FLJ23091	MGC45871-MGC40157	MKLN1-MGC40157	NIPBL-MGC40157	MGC45871-PPP1R2	MKLN1-PPP1R2	Thresh
26692	5	0.718	-2.483	0	0.173	0	-0.291	0	0	0	-0.173	-0.863	-0.929	-0.481
26690	5	0.718	-2.483	0.173	0	0	-0.291	0	0	0	-0.173	-1.036	-0.766	-0.481
26658	5	0.718	-2.483	0.173	0	-0.291	0	0	0	0	-0.173	-0.745	-1.047	-0.481
26660	5	0.718	-2.483	0	0.173	-0.291	0	0	0	0	-0.173	-0.572	-1.220	-0.481
25732	5	0.718	-3.284	0	0.441	0	0	-0.230	0	-0.514	0	-0.793	-0.916	-0.014
25218	5	0.718	-3.285	0.441	0	0	0	-0.230	-0.514	0	0	-0.720	-0.989	-0.014
25730	5	0.718	-3.284	0.441	0	0	0	-0.230	0	-0.514	0	-1.234	-0.475	-0.014
25220	5	0.718	-3.285	0	0.441	0	0	-0.230	-0.514	0	0	-0.279	-1.430	-0.014
17030	5	0.718	-3.285	-0.279	0.720	0	0	-0.230	-0.514	0	0	0	-1.709	-0.014
18062	5	0.718	-3.284	0	0.441	0	0	-0.230	-0.793	0.279	0	0	-1.709	-0.014

TABLE 9

Parameter	Blind
Number of Samples	80
Number of Equations	10
Sensitivity (TPF)	43 % (17/40)
Specificity (TNF)	80 % (32/40)
Overall accuracy	61 % (49/80)

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TABLE 10

Reporter Gene	Protein Activity & Measurement
CAT (chloramphenicol acetyltransferase)	Transfers radioactive acetyl groups to chloramphenicol or detection by thin layer chromatography and autoradiography
GAL (beta-galactosidase)	Hydrolyzes colorless galactosides to yield colored products.
GUS (beta-glucuronidase)	Hydrolyzes colorless glucuronides to yield colored products.
LUC (luciferase)	Oxidizes luciferin, emitting photons
GFP (green fluorescent protein)	Fluorescent protein without substrate
SEAP (secreted alkaline phosphatase)	Luminescence reaction with suitable substrates or with substrates that generate chromophores
HRP (horseradish peroxidase)	In the presence of hydrogen oxide, oxidation of 3,3',5,5'-tetramethylbenzidine to form a colored complex
AP (alkaline phosphatase)	Luminescence reaction with suitable substrates or with substrates that generate chromophores

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Table 11 is found in the instant specification after Tables 17 and 1, and before the sequence listing and claims.

TABLE 12

AffySpotID	Gene	GENE ID	p value	CCa/Ctrl	direction	DEFAULTGENEDESCRIPTION
219073_s_at	OSBPL10	114884	3.8499E-08	0.451209844	downregulated	oxysterol binding protein-like 10
1563498_s_at	LOC283130	283130	8.1224E-06	0.628849872	downregulated	hypothetical protein LOC283130
219667_s_at	BANK1	55024	1.0668E-10	0.430259207	downregulated	B-cell scaffold protein with ankyrin repeats 1
205547_s_at	TAGLN	6876	0.40991641	0.889953014	downregulated	transgelin
203642_s_at	COBLL1	22837	5.3941E-07	0.474077388	downregulated	COBL-like 1
228551_at	MGC24039	160518	0.05283113	0.695785002	downregulated	hypothetical protein MGC24039
235866_at	C9orf85	138241	4.2656E-06	0.649259289	downregulated	chromosome 9 open reading frame 85
207655_s_at	BLNK	29760	4.7146E-09	0.508654531	downregulated	B-cell linker
230983_at	BCNP1	199786	1.8615E-11	0.422871727	downregulated	B-cell novel protein 1
208591_s_at	PDE3B	5140	0.05166031	0.826542405	downregulated	phosphodiesterase 3B, cGMP-inhibited
201340_s_at	ENC1	8507	0.62995039	0.93326798	downregulated	ectodermal-neural cortex (with BTB-like domain)
208325_s_at	AKAP13	11214	0.00033172	0.80202517	downregulated	A kinase (PRKA) anchor protein 13
233559_s_at	WDFY1	57590	0.00920709	0.845905759	downregulated	WD repeat and FYVE domain containing 1
205627_at	CDA	978	9.2103E-05	1.343547864	upregulated	cytidine deaminase
1555736_a_at	AGTRAP	57085	0.09637521	0.906895763	downregulated	angiotensin II receptor-associated protein
1554390_s_at	ACTR2	10097	0.03306275	0.892740407	downregulated	ARP2 actin-related protein 2 homolog (yeast)
201554_x_at	GYG	2992	0.51537492	1.055438457	upregulated	glycogenin 1
1559051_s_at	C6orf150	115004	0.97824175	1.002133453	upregulated	chromosome 6 open reading frame 150
207795_s_at	KLRD1	3824	0.19904885	0.861882517	downregulated	killer cell lectin-like receptor subfamily D, member 1

220784_s_at	UTS2	10911	0.04243446	0.627549503	downregulated	urotensin 2
217418_x_at	MS4A1	931	1.3139E-09	0.423617526	downregulated	membrane-spanning 4-domains, subfamily A, member 1
1563674_at	SPAP1	79368	9.3602E-09	0.400736546	downregulated	Fc receptor-like 2
1570259_at	LIMS1	3987	0.92270088	0.990561902	downregulated	LIM and senescent cell antigen-like domains 1
228988_at	ZNF6	7552	0.26569378	0.691253833	downregulated	zinc finger protein 6 (CMPX1)
215314_at	ANK3	288	0.03458547	0.655571614	downregulated	ankyrin 3, node of Ranvier (ankyrin G)
232911_at	KIAA1559	57677	2.7111E-07	0.640258188	downregulated	mouse zinc finger protein 14-like
200661_at	PPGB	5476	0.6034369	1.039669304	upregulated	protective protein for beta-galactosidase (galactosialidosis)
238581_at	GBP5	115362	0.03263835	1.323760479	upregulated	guanylate binding protein 5
212859_x_at	MT1E	4493	0.46242859	0.892029229	downregulated	metallothionein 1E (functional)
229893_at	MGC20553 (FRMD3)	257019	0.02322844	1.294641476	upregulated	FERM domain containing 3
204415_at	G1P3	2537	0.98563356	1.003662309	upregulated	interferon, alpha-inducible protein (clone IFI-6-16)
211889_x_at	CEACAM1	634	0.12181619	1.155086057	upregulated	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)
1558733_at	FLJ35036	253461	0.9989125	1.000149237	¾	zinc finger and BTB domain containing 38
235885_at	P2RY12	64805	0.64527963	1.061974664	upregulated	purinergic receptor P2Y, G-protein coupled, 12
208180_s_at	HIST1H4H	8365	1.275E-05	0.673893846	downregulated	histone 1, H4h
204627_s_at	ITGB3	3690	0.27856391	1.238694854	upregulated	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
1554676_at	PRG1	5552	0.14822954	1.10791216	upregulated	proteoglycan 1, secretory granule
208685_x_at	BRD2	6046	0.01411177	0.840822417	downregulated	bromodomain containing 2
219922_s_at	LTBP3	4054	0.00028011	0.553407885	downregulated	latent transforming growth factor beta binding protein 3

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218311_at	MAP4K3	8491	5.0346E-06	0.680583549	downregulated	mitogen-activated protein kinase kinase kinase 3
212129_at	NIPA2	81614	0.00333649	0.8287373	downregulated	non imprinted in Prader-Willi/Angelman syndrome 2
229039_at	SYN2	6854	0.3194711	1.139160086	upregulated	synapsin II
203645_s_at	CD163	9332	0.76	0.98	downregulated	CD163 molecule
221557_s_at	LEF1	51176	0.28	0.87	downregulated	lymphoid enhancer-binding factor 1
1552772_at	CLEC4D	362432	0.01	1.31	upregulated	C-type lectin domain family 4, member d
220001_at	PADI4	23569	0.06	1.18	upregulated	peptidyl arginine deiminase, type IV
206026_s_a	TNFAIP6	460097	0.03	1.29	upregulated	tumor necrosis factor, alpha-induced protein 6
202431_s_at	MYC	4609	0.06	0.84	downregulated	v-myc myelocytomatosis viral oncogene homolog (avian)

TABLE 13

AffySpotID	GeneSymbolCG	RNA Sequence	RNA Acc'n	Protein Acc'n
1554390_s_at	ACTR2	SEQ ID NO 1	NM_001005386	NP_001005386
1554390_s_at	ACTR2	SEQ ID NO 2	NM_005722	NP_005713
1555736_a_at	AGTRAP	SEQ ID NO 3	NM_020350	NP_065083
1559051_s_at	C6orf150	SEQ ID NO 4	NM_138441	NP_612450
1563674_at	SPAP1	SEQ ID NO 5	NM_030764	NP_110391
200661_at	PPGB	SEQ ID NO 6	NM_000308	NP_000299
201340_s_at	ENC1	SEQ ID NO 7	NM_003633	NP_003624
201554_x_at	GYG	SEQ ID NO 8	NM_004130	NP_004121
203642_s_at	COBLL1	SEQ ID NO 9	NM_014900	NP_055715
203645_s_at	CD163	SEQ ID NO 10	NM_004244	NP_004235
203645_s_at	CD163	SEQ ID NO 11	NM_203416	NP_981961
204415_at	G1P3	SEQ ID NO 12	NM_002038	NP_002029
204415_at	G1P3	SEQ ID NO 13	NM_022872	NP_075010
204415_at	G1P3	SEQ ID NO 14	NM_022873	NP_075011
204627_s_at	ITGB3	SEQ ID NO 15	NM_000212	NP_000203
205547_s_at	TAGLN	SEQ ID NO 16	NM_001001522	NP_001001522
205547_s_at	TAGLN	SEQ ID NO 17	NM_003186	NP_003177
205627_at	CDA	SEQ ID NO 18	NM_001785	NP_001776
207655_s_at	BLNK	SEQ ID NO 19	NM_013314	NP_037446
207795_s_at	KLRD1	SEQ ID NO 20	NM_002262	NP_002253
207795_s_at	KLRD1	SEQ ID NO 21	NM_007334	NP_031360

208180_s_at	HIST1H4H	SEQ ID NO 22	NM_003543	NP_003534
208325_s_at	AKAP13	SEQ ID NO 23	NM_006738	NP_006729
208325_s_at	AKAP13	SEQ ID NO 24	NM_007200	NP_009131
208325_s_at	AKAP13	SEQ ID NO 25	NM_144767	NP_658913
208591_s_at	PDE3B	SEQ ID NO 26	NM_000922	NP_000913
208685_x_at	BRD2	SEQ ID NO 27	NM_005104	NP_005095
211889_x_at	CEACAM1	SEQ ID NO 28	NM_001712	NP_001703
212129_at	NIPA2	SEQ ID NO 29	NM_001008860	NP_001008860
212129_at	NIPA2	SEQ ID NO 30	NM_001008892	NP_001008892
212129_at	NIPA2	SEQ ID NO 31	NM_001008894	NP_001008894
212129_at	NIPA2	SEQ ID NO 32	NM_030922	NP_112184
217418_x_at	MS4A1	SEQ ID NO 33	NM_021950	NP_068769
217418_x_at	MS4A1	SEQ ID NO 34	NM_152866	NP_690605
218311_at	MAP4K3	SEQ ID NO 35	NM_003618	NP_003609
219073_s_at	OSBPL10	SEQ ID NO 36	NM_017784	NP_060254
219667_s_at	BANK1	SEQ ID NO 37	NM_017935	NP_060405
219922_s_at	LTBP3	SEQ ID NO 38	NM_021070	NP_066548
220784_s_at	UTS2	SEQ ID NO 39	NM_006786	NP_006777
220784_s_at	UTS2	SEQ ID NO 40	NM_021995	NP_068835
228988_at	ZNF6	SEQ ID NO 41	NM_021998	NP_068838
229039_at	SYN2	SEQ ID NO 42	NM_003178	NP_003169
230983_at	BCNP1	SEQ ID NO 43	NM_173544	NP_775815
232911_at	KIAA1559	SEQ ID NO 44	NM_020917	NP_065968
233559_s_at	WDFY1	SEQ ID	NM_020830	NP_065881

		NO 45		
235885_at	P2RY12	SEQ ID NO 46	NM_022788	NP_073625
235885_at	P2RY12	SEQ ID NO 47	NM_176876	NP_795345
229893_at	MGC20553 (FRMD3)	SEQ ID NO 48	NM_174938	NP_777598
221557_s_at	LEF1	SEQ ID NO 49	NM_016269	NP_057353
1552772_at	CLEC4D	SEQ ID NO 50	NM_080387	NP_525126
220001_at	PADI4	SEQ ID NO 51	NM_012387	NP_036519
206026_s_a	TNFAIP6	SEQ ID NO 52	NM_007115	NP_009046
202431_s_at	MYC	SEQ ID NO 53	NM_002467	NP_002458

TABLE 14

Gene	GeneID	RNA Acc'n	Sense Primer (5' Primer)	Antisense Primer (3' Primer)	TaqMan Probe
OSBPL10	114884	NM_017784	GCTGGTGGTGTACTCTGCTA	CATTTCCATGTGGTATTTGG	CAAGCTCGAAGCTGAGTCACCCA
OSBPL10	114884	NM_017784	GTGCCTCAACTTGTTACAGC	CTGCTCTGTGGAATGTGACT	CAGCCCAGCCAGAAGCCAGG
OSBPL10	114884	NM_017784	TCTATGGAGGGAAAGTCCAC	TGACTTTGGTTTCTCCATTG	CCGCAGAAGTGAAGCACAACCC
LOC283130	283130	NM_182556	TGGTCTTGATCTCCTGACTT	AGGGACTCTCAGAAGTGGAG	
LOC283130	283130	NM_182556	TTCTTCAAGGGAATGAGCTT	GGAAGATGTGCATGTAGCTG	CTGCTGGTGCTCACGGCCAC
LOC283130	283130	NM_182556	TCAACTCTGTCTCCTCTGCT	TTACAGTGTCAAACGGGTGT	CCAGTTCCCGCAAGCCCAGA
BANK1	55024	AK091523	ACAGGCATCACTACTTCCAA	ACCATCTTCACCATATGCAA	TGAGGATCCCACATCCTGAGATCAA
BANK1	55024	AK091523	TGAAAGCAGGAAGACATACG	ACCTCTAGTGGGCTGTGTTT	CATTTGCCTCAGCTCCATCTGCA
BANK1	55024	AK091523	TATCCAGCTTCACTTTCTGC	TGTCAAGTACAGAGCCCATT	CCCATGGTCAACTGCCATCTGAA
TAGLN	6876	NM_003186	AACCCAGACACAAGTCTTCA	TCCAGCTCCTCGTCATACTT	CTGCACTTCGCGGCTCATGC
TAGLN	6876	NM_003186	AGCAATGGTAACTGCACCT	CCAGGGAGGAGACAGTAGAG	
TAGLN	6876	NM_003186	TGACATGTTCCAGACTGTTG	GCGCTTTCTTCATAAACCA	CTGCCAAGCTGCCCAAAGCC
COBLL1	22837	NM_014900	ATGGCTAGATGTCCCAAGTT	AATGACACAGCCAGTAGTGC	
COBLL1	22837	NM_014900	GCTTGGTGTGTCTGATAAGG	ACTCTGTCGCATCTGTTCTG	ACCAACTCCAACTGATGGCCCA
COBLL1	22837	NM_014900	CAGAACAGATGCGACAGAGT	AATGGCTGAGTCTTGACCTT	
MGC24039	160518	AK125323	TTGACAAAGCTTCCTTTCTG	TTTCTCTTCCCACTGAGACA	CCAGCCTGAGCCTTACCTGCCA
MGC24039	160518	AK125323	ACCTTTGAGTGCCAGAACTT	TCATTTCTGACCATGACACA	
MGC24039	160518	AK125323	GGACACAAACGGACAATAAA	GCTGTGCAGATTTGCTTACT	CCAGGGAAGATGGTTCTCGCACC
C9orf85	138241	NM_182505	GCACCAGAATACGTTTAGCTT	TTTACACGCCACTCAAGAAC	CAGCGCTGACATACTCCATCATGAAG
C9orf85	138241	NM_182505	CTGGGAGTAGTTCGTTGGTT	CGTATTCTGGTGCTTCTGAG	TCTGGAACGAGCCACGTTGCC
C9orf85	138241	NM_182505	GGAGATTGAAGTGAGCTGAG	AAGGTGGTCAGAATTTCACA	CGTGCCATTACACTCCAGCCTGG
BLNK	29760	NM_013314	CTTGAGACCAGAGGCTTACC	AAGCTTGTCCATTCTGTTTG	CACGTCAGCAGTTCCTGGCCC
BLNK	29760	NM_013314	GCTATTGAAGTGGTCATCCA	CATGATAACTCAACCTCACCA	CAGGTCAGGCAATAGAACAAGTCCACA
BLNK	29760	NM_013314	CCGTGGAAGATAATGATGAA	GAATTTGGCTTGGTTGATCT	TCCCACAGAAAGCAGTTCACCTCCA
BCNP1	199786	NM_173544	ACTGGATATTGGCAGCTTCT	TCTCCAGGGAGTGTGAAAG	CCCACTCCGGAAGCAGCTGC
BCNP1	199786	NM_173544	GCAGCTCCAAATCTTAACTTG	AGAAGCTGCCAATATCCAGT	CCGACTTCCTCTGCTTGCCAGC
BCNP1	199786	NM_173544	TTTCCTCCCATTCTGTCTG	AGCAAATGTATTTCGGAAGG	TGCCCTTTCCTCCTATTTCCCTCCA
PDE3B	5140	NM_000922	AATGGCTATCGAGACATTCC	TTCATTTCCTGTTCCACAAC	CAACACGGCCAGTTCCTGGC
PDE3B	5140	NM_000922	CTTCCACCACAAGTCATTTC	CTCAGCTGGGTCCTCTATTT	TGCTTTCTCAGGTTCCTGTAGGCCA
PDE3B	5140	NM_000922	AGGTGGGATCGTAATAATGG	TGCTTCGGGATAGTCAGTAG	AAAGGCCTCACCAAGAATTTGGCA
ENC1	8507	NM_003633	TGCCGTCGTAGGTATTAGTG	GTGAGAAACATGGACGAAAG	TCGAGTTGCAAACTTTGGTCTTCCC
ENC1	8507	NM_003633	TGTGCCGTCGTAGGTATTAG	GTGAGAAACATGGACGAAAG	TCGAGTTGCAAACTTTGGTCTTCCC
ENC1	8507	NM_003633	CAAACCATCAGGAAGAATGA	TCCAGTTAATTGCAGACTCG	CAAGCCTTTCATCCTCTGTCTCCAGC
AKAP13	11214	NM_006738	CTCCTGGTCATGATTGTTGT	ATCCTGGACGAAATGAAAGT	CCACAAACACGGGAAGGCCC

AKAP13	11214	NM_006738	AGGTTCTGGTTGGACAAGTT	GGGAAGAGAGATGACAAAGG	
AKAP13	11214	NM_006738	GTTGCACAGACTGAAAGTCC	TCCAGAGTCCACAATAGGTG	CAGGAACGGTCTGTATTCTCCTCCTCA
WDFY1	57590	NM_020830	GACAAGTGTGTGAGCTGGAT	TGATCTGCCCAGAATAATCA	TGCCTCCCCGAGCATGTTCCC
WDFY1	57590	NM_020830	GCTGAAGCTTGAACAGAACA	TCAGATGCTCCTGAGAAGAG	TCGCCTGCCTCTGGTGGGAC
WDFY1	57590	NM_020830	CTGTGCTACCTTCAGCTCAC	ACTTTCCAACCACTGAGGAG	TTCCGCCGTCCGAGGAACAG
CDA	978	NM_001785	CAAAGGGTGCAACATAGAAA	TTGCCCTGAAATCCTTGTA	ACCCGCTGGGCATCTGTGCT
CDA	978	NM_001785	TACAAGGATTTCAGGGCAAT	AGTTGGTGCCAAACTCTCTC	TGCTATCGCCAGTGACATGCAAGA
CDA	978	NM_001785	TGCCTTGGGACTTAGAACAC	CAGGATAGAACCTTGGGAAG	TCCTTTCCTTCCTGTGGGCCC
AGTRAP	57085	NM_020350	GTTCTAGGGATGCTCCTGAC	GGAGTGTGCATGGTACTGG	CCCAGCTCAGGGATTGCCTGA
AGTRAP	57085	NM_020350	CTCCTGCTGCTTCGTCTAC	CCTCTGCTGAGTCAATCGT	CCGCGCTCCCGGTACATGTG
AGTRAP	57085	NM_020350	CACCATCTTCCTGGACATC	CTCCCGGTACATGTGGTAG	CTACCCGCGGGTCAGCCTCA
ACTR2	10097	NM_005722	GTGCTTTCTGGAGGGTCTAC	TCTTCAATGCGGATCTTAAA	ATCCTGGCCTGCCATCACGG
ACTR2	10097	NM_005722	AGACTCTGGAGATGGTGTGA	CTCGCAACAGAAGTAGCTTG	TCCCTCCCAGCAATATCCAGTCTCC
ACTR2	10097	NM_005722	AGAGCAGAAACTGGCCTTAG	GGCTGAAATAAAGCTTCTGG	CCCAACTTTGATGATACGTCCATCTGG
GYG1	2992	NM_004130	TGTGTACCTTTCACGAGACC	TGGGTTAATGCTATTGGTTG	TCACTCTGGCAGCACTGGGCA
GYG1	2992	NM_004130	CCAAAGTTGTGCATTTCCT	GGTAAAGATGTTCCACCACA	TGAGGCCCATGATCCCAACATG
GYG1	2992	NM_004130	TGTGGCTTCTGTAGAAAGGA	TCTGCTCCCATATAATCAGC	TCCCAGCTATGGCACAGCCG
C6orf150	115004	NM_138441	TATAACCCTGGCTTTGGAAT	ATGGCTTTAGTCGTAGTTGCT	AGCACCCAAGAAGGCCTGCG
C6orf150	115004	NM_138441	GATATAACCCTGGCTTTGGA	ATGCTTGGGTACAAGGTAAA	AGCACCCAAGAAGGCCTGCG
C6orf150	115004	NM_138441	ACTGCCTTCTTTCACGTATG	CCTGAGGCACTGAAGAAAG	CCCAGGTCTTTGCGGTCCCA
KLRD1	3824	AF498040	ACAATTCAACGCTGTTCTTT	TTATCCCTAAGGTCCCAGAA	CGTGCCTTCTCTACTTCGCTCTTGGA
KLRD1	3824	NM_007334	CGGTGCAACTGTTACTTCAT	AATTGTTGACTGGAGCTCAT	TGTGCTTCTCAGAAATCCAGCCTGC
KLRD1	3824	NM_007334	CACATCGTGCCTTCTCTACT	TCTATGTTGGGTCCTGGAGT	CGCTCTTGGAACATAATTTCTCATGGC
UTS2	10911	NM_021995	TTATGCTCTGCGTCACTTCT	GAGGTGCTGAGAGTTGAAAG	TCCACGTCTCTTTGCTTTGGCCA
UTS2	10911	NM_021995	CACTTCTGCTCGGACTCATA	GTCTTCATGAGGTGCTGAGA	TCCACGTCTCTTTGCTTTGGCCA
UTS2	10911	NM_021995	CTTTCAACTCTCAGCACCTC	TGAGTCTGCTTTCCTGAGAA	
MS4A1	931	NM_021950	TCGTTGAGAATGAATGGAAA	ATGTTTCAGTTAGCCCAACC	
MS4A1	931	NM_021950	ACCGATCTGTGTGACTGTGT	CTTTGACCAAACACTTCCTG	CCGGATCACTCCTGGCAGCA
MS4A1	931	NM_021950	GTGTTGTCACGCTTCTTCTT	AAAGCCTATCCAAGGAACAG	TCACATTCTGAAGCACTCATTCTGCCT
SPATA1	64173	NM_022354	AAGTCACAGCATCAATGGAG	AGTCTGTGATGTTTGCCAGA	CCCTGGCTTCAAGTTGCATGAGC
SPATA1	64173	NM_022354	CTGATGGAACAATCCACAGA	CCAGCTTCTTCCTGATTCTT	TGGGATCTCTTCCAAGTTCCTCCTTGA
SPATA1	64173	NM_022354	CGATATCATGCCTACAATGG	CTTCAAGTTGCATGAGCAGT	CCTCCTCCATTGATGCTGTGACTTTC
LIMS1	3987	NM_004987	AGCTGTACCATGAGCAGTGT	GGCAAAGAGCATCTGAAAG	TGCGCTCAGTGCTTCCAGCA
LIMS1	3987	NM_004987	TATCGGGTTTGTCAAGAATG	TGAATATCAGAGGCTGCTCA	TGGGAGACACCTGTGTCGCCC
LIMS1	3987	NM_004987	GTGATGTGGTCTCTGCTCTT	TACAGACTGGCTTCATGTCA	AGCAGTTCACGCACCAGGCC
ZNF6	7552	NM_021998	GATGGGTTTGGTTCTGAAGT	CTCCAGCTACTGAATGTCCA	TTCAACATCATCTTCAGCCTCCGC
ZNF6	7552	NM_021998	TCAGCTTGAGGACTCTGATG	TTTGAAGGTACTGTGCTGCT	TGCCGCAGCCCAGACAACAG

ZNF6	7552	NM_021998	AAGACCCATACTGGAAGGAA	CCTTCTTGCAGAATTCACAC	TCACATGTCGTTTAAAGCCAGATGCA
ANK3	288	NM_001149	TTGATCATCCAAGCCTAGTG	GAATCATCACCCAATTCCTT	CGGTCATTGCATCTTCACTCTGCG
ANK3	288	NM_001149	AATTCACCGAGAAGTGTGTG	TGAAAGTGATTTCCATGCTC	CGCTGCTTCCACACATTAATGGCA
ANK3	288	NM_001149	ATGGACCTCCAGTCGTAACT	CTGGCTCTCATCTACATCCA	TGCCTTTAACAGAAATGCCTGAAGCA
KIAA1559	57677	NM_020917.1	AAAATTAGCCAGGCATGGTG	GCGATCTCAACTCACCACAA	TCCGCCTCCTGGATTCAAGTGA
KIAA1559	57677	NM_020917.1	ACCAAATTTCAGGGTCACCA	CTCAAACTCCTGGCCTCAAG	CCCTGTGCCAGGCCAAATTCA
KIAA1559	57677	NM_020917.1	ACCAAATTTCAGGGTCACCA	CTCAAGTGATCCACCCACCT	CCCTGTGCCAGGCCAAATTCA
PPGB	5476	NM_000308	GAGAGCTATGCTGGCATCTA	GACCAGGGAGTTGTCATTCT	TCCTGCATGACCAGCACGGC
PPGB	5476	NM_000308	ACAGGCTTTGGTCTTCTCTC	TTGTAGATGTTGAGGCCAGA	CACGATGCGGGCCACTTCCT
PPGB	5476	NM_000308	AACAAGCAGCCATACTGATG	GGCACTTTGCTTAGAAGAGG	CAGCTCCACGGCCTGATGCA
GBP5	115362	NM_052942	CCTACCTGATGAACAAGCTG	GATGAGGCACACACCATATC	CGGTGCAGTCTCACACCAAGGG
GBP5	115362	NM_052942	ACCAAGGGAATTTGGATATG	AGTAAGAGTGCCAGTGCAAA	CTCCCAGGCCCTCGGTGTCA
GBP5	115362	NM_052942	GAAGAAAGAGGCACAAGTGA	TGTTTGGCTATCTCCATTTG	TCTGCCTTTGAATCGCCGCC
MT1E	4493	NM_175617	AAGTCTACTGCCACCTCTCAC	AAGAGCTGTTCCCACATCA	CCCTGGGCACACTTGGCACA
MT1E	4493	NM_175617	CCTATGGTTTCAGAACAGAGC	AGTGAGAGGTGGCAGTAGAC	CGGGCACCTCCCTGCCCTAA
MT1E	4493	NM_175617	ACTGCCACCTCTCACTCTC	AGAGCTGTTCCCACATCAG	CCCTGGGCACACTTGGCACA
FRMD3	257019	NM_174938	GAACCCACTGGTCAAGAGTT	ACTGCTCAAACTCTGGTGTC	CCAGGCCCACCACAAGGAGC
FRMD3	257019	NM_174938	TTGTGGTCTTTCAGGGAAAT	AGTATTGAATGCCAACATGG	TCTCCTTCTGGGTGCCAATCACA
FRMD3	257019	NM_174938	AACATTTCTGCTCCCTTGAT	GGCACTTGGGTTGTACACTA	CTCCCGGGCTGCCTTCACTG
G1P3	2537	NM_022873	GGTAATATTGGTGCCCTGA	TTAGGCCAAGAAGGAAGAAG	TGGGCTACGCCACCCACAAG
G1P3	2537	NM_022873	TATTGTCCAGGCTAGAGTGC	CTACTTGGGAGGTTGAGACA	TGCAGCCTCCAACTCCTAGCCTCA
G1P3	2537	NM_022873	TCTTCTCTCCTCCAAGGTCT	TCTTACCTGCATCCTTACCC	TACCGCCTTCTGCCGCATGG
CEACAM1	634	NM_001712	CAACCTACCTGTGGTGGATA	TTCACACTCATAGGGTCCTG	TCCCAGGCTGCAGCTGTCCA
CEACAM1	634	NM_001712	CACTTCACAGAGTGCGTGTA	GAATGGCATGGATTCAGTAG	CTTCTGGAACCCGCCCACCA
CEACAM1	634	NM_001712	AGGTTCTTCTCCTTGTCCAC	GGGTAGCTTGTTGAGTTCCT	CGGTTGCCATCCACTCTTTCCC
ZBTB38	253461	XM_172341.5	AGGGACCTCAAGGACGACTT	TTGAAGCTGCCAGAACATTG	CCCGAATGCGCTGCTCATTTAA
ZBTB38	253461	XM_172341.5	ACCAACGCTGAATTTCCAAG	TCCATTTTCAATGCCTCCTC	CAACAGTCCAGCCATCCCATTGG
ZBTB38	253461	XM_172341.5	ATGGAGGAGGTTCACACCAG	GGATTATGGGGCTCATGCTA	TCATGCTGCACCCTGACCGG
P2RY12	64805	NM_176876	TGGTAACACCAGTCTGTGC	GCCATTTGTGATAAGTCCAA	CACCCAGGTCCTCTTCCCACTGC
P2RY12	64805	NM_022788	GCTGCAGAACAGAACACTTT	TGCCAAACCTCTTTGTGATA	TGCTCTTGTAATCTGACCCTGGACATG
P2RY12	64805	NM_022788	ACATTCAAACCCTCCAGAAT	GGTGCACAGACTGGTGTTAC	CGACAACCTCACCTCTGCGCC
HIST1H4H	8365	NM_003543	GTGTTCTGAAGGTGTTCCTG	GTAAAGAGTGCGTCCCTGTC	CGCCAAACGCAAGACCGTGA
HIST1H4H	8365	NM_003543	TAACATCCAGGGCATCACTA	GAACACCTTCAGAACACCAC	TATCCGGCGCCTTGCTCGTC
HIST1H4H	8365	NM_003543	ATAACATCCAGGGCATCACT	AGAACACCACGAGTCTCCTC	TATCCGGCGCCTTGCTCGTC
ITGB3	3690	NM_000212	GACTCAAGATTGGAGACACG	AGGCACAGTCACAATCAAAG	TGTCCTTGAAGCCCACGGGC
ITGB3	3690	NM_000212	TTACCACTGATGCCAAGACT	TGGAGGCAGAGTAATGATTG	CCTGCCAGCCTTCCGTCCAA
ITGB3	3690	NM_000212	AACCCTTCAGATTTGCCTTA	CAGTGAGGGTGTGGAATTAG	TGTCACCCTTAGGCCAGCACCA

PRG1	5552	NM_002727	CTTCCCACTTTCTGAGGACT	ATCCTGTTCCATTTCCGTTA	CGGCTCCGGCTCTGGATCAG
PRG1	5552	NM_002727	GGTTCTGGAATCCTCAGTTC	TTGGATTCACCTGGAAGTAG	TCTGGATTGCAGCGCACCCA
PRG1	5552	NM_002727	TCGAACTACTTCCAGGTGAA	GTCCTCAGAAAGTGGGAAGA	TCCAAAGACGAGAATCCAGGACTTGA
BRD2	6046	NM_005104	GATTCAGAGGAGGAGGAAGA	TGGGTTTGAATCACGTAAAG	TCCAGGCTCAGCTGCCGCTT
BRD2	6046	NM_005104	ATGCCAGATGAACCACTAGA	ATCTTCCTCCTCCTCTTCCT	CCCTGGCTTGGCCAAATCGTC
BRD2	6046	NM_005104	ACGGCTTATGTTCTCCAACT	CCCTGGTTCTAGTGGTTCAT	CGTGCCATTGCCACACAACATCG
LTBP3	4054	AF318354	ACCTTCAGGGCTCCTATGT	CACTGTGTCATCGAAGTTCA	CCACCCAGGACCAGCACGGT
LTBP3	4054	AF318354	GGACAACAACATCGTCAACT	GCTTGCAGTAGCACTCGTAG	CCAGCCCACCGTGACATCGA
LTBP3	4054	AF318354	CTCTGGCTACCATCTGTCC	TGTAGGAGCCATTGGTATTG	TCCTCGCAGTGGCTCCGGTC
MAP4K3	8491	NM_003618	TGAAATTTGATCCACCCTTA	TGGTGTCCTTGTCCATATTC	CCACATCATGAACTTCCCGACAGTG
MAP4K3	8491	NM_003618	TAAAGTGCATATGGGTGCAT	TCGGCACCAAATATCAAGTA	CACTGTGCATCATCATGGATAAACCCA
MAP4K3	8491	NM_003618	CTGGAATATGGACAAGGACA	CTTCTAAATGTGCGACGTGT	CCTCGCTGATGCAATTCTTCTTCAACA
NIPA2	81614	NM_030922	TATCAAGGAGCTGTTTGCAG	TGGAGTCACAATGGAAGTGT	AAGCCTGTGCTGCGGCATCC
NIPA2	81614	NM_030922	AACACTTCCATTGTGACTCC	GCCACTCAAAGTACCAATGA	CATCGTCAACAGGCATATCTTGCCA
NIPA2	81614	NM_030922	CTCACAAGCTAGGTGATCCA	CCGATTACAGAGCAGATTGT	CCATGGCGAGGACCCACCAC
SYN2	6854	NM_003178	GAACTGGAAGACGAACACTG	TACAGCTTTGACAGCACAGA	CCAGGCCGCCAAACATCTCA
SYN2	6854	NM_003178	CATAATGGGAGACCAAATCA	GGAAAGAGAAAGCTCCTCAA	CCACAGCCCTCCAGGGTCCA
SYN2	6854	NM_003178	TCTGTGCTGTCAAAGCTGTA	CTAGTTCGGTGATGAGTTGC	TGGCATGCTACAGTCCATGACCTCA
LEF1	51176	NM_016269	GATGTCAACTCCAAACAAGGC	AGTGAGGATGGGTAGGGTTG	TTATCCCTTGTCTCCGGGTGGT
LEF1	51176	NM_016269	TGGATTCAGGCAACCCTAC	TGTGGGGATGTTCCTGTTTG	ATGTCCAGGTTTTCCCATCA
LEF1	51176	NM_016269	AGGCTGGTCTGCAAGAGACA	GAATGAGCTTCGTTTTCCACC	TGCATCAGGTACAGGTCCAAGA
CLEC4D	362432	NM_080387	TTCACGCTGTAAGAGAGGCAC	AGTTGGACTGGAAGGCTCTC	GAACTGAAAAGTGCTGAAGGGA
CLEC4D	362432	NM_080387	GAACTGAAAAGTGCTGAAGGG	TCCTTTCACTCTCAGCCCAC	AGCACCTGGAACTGTTGTCCT
CLEC4D	362432	NM_080387	GGGCTGAGAGTGAAAGGAAC	CCACTGACCTTTGGCATTC	ATGACCATCAGCACGGAAGC
PADI4	23569	NM_012387	CTCCACCAGTCAAAGCTCTA	TCCAGGTCCTCTGATCTTTC	CTACATCCAAGCCCCACACAAAAC
PADI4	23569	NM_012387	ATGCAGGATGAAATGGAGAT	GTTTGATGGGAAACTCCTTC	CTACATCCAAGCCCCACACAAAA
PADI4	23569	NM_012387	GAAAGATCAGAGGACCTGGA	TCAAGCACTTCATCATCCTC	TACATCCAAGCCCCACACAAAA
TNFAIP6	23569	NM_007115	CAGGTTGCTTGGCTGATTATG	TTGATTTGGAAACCTCCAGC	TGGCTTTGTGGGAAGATACTGTGG
TNFAIP6	23569	NM_007115	CATTAGACTCAAGTATGGTCAGCG	TCCACAGTATCTTCCCACAAAG	CAGGTTGCTTGGCTGATTATGT
TNFAIP6	23569	NM_007115	TACCACAGAGAAGCACGGTC	ATCCATCCAGCAGCACAGA	GCAGAAGCTAAGGCGGTGTGTGAA
MYC	4609	NM_002467	GAGGCTATTCTGCCCATTTG	TCCTGTTGGTGAAGCTAACG	TTTCGGGTAGTGGAAAACCA
MYC	4609	NM_002467	TTTCGGGTAGTGGAAAACCAG	CGTCGCAGTAGAAATACGGCT	CTATGACCTCGACTACGACTCGGT
MYC	4609	NM_002467	AGTGGAAAACCAGCAGCCTC	CGTCGCAGTAGAAATACGGCT	ATGACCTCGACTACGACTCGGT
CD163	9332	NM_203416	TGAGTCTTCCTTGTGGGATTGT	CGACCTGTTGTGGCTTTTT	TTCAGTGCAGAAAACCCCACA
CD163	9332	NM_203416	TCTTCCTTGTGGGATTGTCC	AGGATGACTGACGGGATGA	CAGTGCAGAAAACCCCACAAA
CD163	9332	NM_203416	CCCACAAAAAGCCACAACA	CTTGAGGAAACTGCAAGCC	TCATCCCGTCAGTCATCCTTTATTGC

TABLE 15

Gene Symbol	Protein Description	Commercially Available Antibody Reference	Scientific Reference
OSBPL10	oxysterol binding protein-like 10		
LOC283130	hypothetical protein LOC283130		
BANK1	B-cell scaffold protein with ankyrin repeats 1		
TAGLN	Transgelin (alternative name smooth muscle 22 Protein SM22)	Abcam Ab14106 AntiHuman Rabbit Polyclonal Antibody	Nishida W *et al.* Gene cloning and nucleotide sequence of SM22 alpha from the chicken gizzard smooth muscle. *Biochem Int* **23**:663-8 (1991).
COBLL1	COBL-like 1		
MGC24039	hypothetical protein MGC24039		
C9orf85	chromosome 9 open reading frame 85		
BLNK	B-cell linker	Abcam Ab4474 AntiHuman Rabbit Polyclonal Antibody	Kabak S *et al.* The direct recruitment of BLNK to immunoglobulin alpha couples the B-cell antigen receptor to distal signaling pathways. *Mol Cell Biol* **22**:2524-35 (2002).
BCNP1	B-cell novel protein 1		
PDE3B	phosphodiesterase 3B, cGMP-inhibited	SantaCruz Biotechnology AntiHuman Rabbit Polyclonal Antibody	Liu H, and Maurel D.H. 1998 Expression of cyclic GMP-Inhibited phosphodiesterase 3A and 3B (PDE3A and PDE 3B) in rat tissues: differential subcellular localization and regulated expression Br. J. Pharmacol 125 1501:1510.
ENC1	ectodermal-neural cortex (with BTB-like domain)		

AKAP13	A kinase (PRKA) anchor protein 13		Other Family Antibodies Available including: Abcam Ab10346 AKAP12 AntiRat Rabbit Polyclonal Antibody Abcam Ab 25805 AKAP 9 AntiHuman Rabbit Polyclonal Antibody Abcam AB14096 AKAP 3 Goat Polyclonal Antibody
WDFY1	WD repeat and FYVE domain containing 1 (aka FENS-1)	Abcam Ab21695 AntiHuman Goat Polyclonal Antibody	
CDA	cytidine deaminase	Abcam Ab5197 Antihuman Rabbit Polyclonal Antibody	Duquette ML *et al.* AID binds to transcription-induced structures in c-MYC that map to regions associated with translocation and hypermutation. *Oncogene* **24**:5791-8 (2005).
AGTRAP	angiotensin II receptor-associated protein		
ACTR2	ARP2 actin-related protein 2 homolog (yeast)		
GYG	glycogenin 1		
C6orf150	chromosome 6 open reading frame 150		
KLRD1	killer cell lectin-like receptor subfamily D, member 1	Abcam Ab19740 CD94 Ab (aka KLRD1 Ab) AntiHuman Mouse Monoclonal Antibody	Moretta A *et al.* Human natural killer cell receptors for HLA-class I molecules, Evidence that the Kp43 (CD94) molecule functions as receptor for HLA-B alleles. *J Exp Med* **180**:545-55 (1994).
UTS2	urotensin 2	Abcam Ab14200 Antihuman Rabbit Polyclonal Antibody	
MS4A1	membrane-spanning 4-domains, subfamily A, member 1	Abcam Ab9475 AntiHuman Mouse Monoclonal Antibody	Mason DY *et al.* Antibody L26 recognizes an intracellular epitope on the B-cell-associated CD20 antigen. *Am J Pathol* **136**:1215-22 (1990).
SPAP1	Fc receptor-like 2		
LIMS1	LIM and senescent cell antigen-like domains 1		
ZNF6	zinc finger protein 6 (CMPX1)		

ANK3	ankyrin 3, node of Ranvier (ankyrin G)		
KIAA1559	mouse zinc finger protein 14-like		
PPGB	protective protein for beta-galactosidase (galactosialidosis)		
GBP5	guanylate binding protein 5		
MT1E	metallothionein 1E (functional)		
MGC20553 (FRMD3)	FERM domain containing 3		
G1P3	interferon, alpha-inducible protein (clone IFI-6-16)		
CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	Abcam Ab26279 Antihuman mouse monoclonal Antibody	
FLJ35036 (ZBTB38)	zinc finger and BTB domain containing 38		
P2RY12	purinergic receptor P2Y, G-protein coupled, 12	Alamone Labs #APR-012 AntiHuman Mouse Polyclonal Antibody	Queiroz, G. *et al.* (2003) *J. Pharmacol. Exp. Ther.* **307**, 809.
HIST1H4H	histone 1, H4h		
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	Abcam Ab7167 AntiHumanMouse Monoclonal Antibody	Pittier R *et al.* Neurite extension and in vitro myelination within three-dimensional modified fibrin matrices. *J Neurobiol* **63**:1-14 (2005).; Soldi R *et al.* Role of alphavbeta3 integrin in the activation of vascular endothelial growth factor receptor-2. *EMBO J* **18**:882-92 (1999).
PRG1	proteoglycan 1, secretory granule		

BRD2	bromodomain containing 2	Abcam Ab19276 Antihuman Rabbit PolyClonal Antibody	
LTBP3	latent transforming growth factor beta binding protein 3	Abcam Ab21621 Antibovine Rabbit Polyclonal	
MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3		
NIPA2	non imprinted in Prader-Willi/Angelman syndrome 2		
SYN2	synapsin II	Abcam Ab12240 Antihuman Rabbit Monoclonal	
LEF1	Lymphoid enhancer-binding factor 1	Abcam Ab22884 Antihuman Rabbit Polyclonal; Ab12037 Antihuman Mouse Monoclonal;	
CLEC4D	C-type lectin domain family 4, member d		
PADI4	peptidyl arginine deiminase, type IV	Abcam AB26071 Anithuman goat polyclonal	
TNFAIP6	tumor necrosis factor, alpha-induced protein 6	Abcam Ab36380 Antihuman chicken polyclonal	
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	Abcam Ab1383 Antihuman rabbit polyclonal	

TABLE 16

Symbol	5' Primer (Sense Primer) Primer Sequence		3' Primer (Antisense Primer) Primer Sequence	Position	Product
LOC283130	AAGGCCAGAATCCCAGCTCAG	934	ATCCATCTGCATCCGGGACTTGAT	1044	111
MGC24039	AACAAGGGATCGCCTGCTCC	3717	ATAAGGGAGTTGACAGTCATGCGG	3833	117
ACTR2	ACCGGGTTTGTGAAGTGTGGAT	109	CACTTGCCTCATCACCAACCAT	253	145
AGTRAP	CATGGCCATCCTCAGCTTGC	325	AAGACCCAAGGAAACCAGTGTGGA	434	110
AKAP13	TCTCAGCCCGGTGATGGTC	8562	TGTAAGAGACTTGTGCACGCGG	8710	149
ANK3	ATACGCCATTACATCAAGCAGCAC		CCAAGGGCAGTATTCCCATTCACA		
BANK1	TGCTGAAAGGCATGGTCACAAAG	1303	GCTGGGTTCTGTGTGGAAGGAATA	1449	147
BCNP1	GGCGCGTGCTGAAGAAATTCAA	1664	TTTGCAGCCTGGCTCGAGTTG	1782	119
BLNK	TTTCAGAACAGGAAGCTGGCGT	1172	GTTGTTTGGAATCATGGCCAGAGC	1315	144
BRD2	TGCCTATGCTTGGCCTTTCT	2799	ATCTTCCGCTTGACAGTGCTGA	2909	111
C6orf150	CAAGAAGGCCTGCGCATTCAAA	1098	AGCCGCCATGTTTCTTCTTGGA	1225	128
C9orf85	TTATTCCGTTGAATAAAGAAACAGA	545	TTTGATGGTCTCCTCCTGTG	694	150
CDA	ATCGCCAGTGACATGCAAGA	376	TACCATCCGGCTTGGTCATGTA	484	109
CEACAM1	ATTGGAGTAGTGGCCCTGGTTG		ATTGGAGTGGTCCTGAGTGTGGT		
COBLL1	AGGAAGAGTGAGGGCAGGTTCA	375	GCTGTAAGGCAGTCACACGACTAT	523	149
ENC1	CATGAGCTCACTCCATCACTCGAT	2196	AGCATTTACAAGGTGCAGCAGAT	2325	130
FLJ35036	CTCCGAGTTGTCTTGAAGTGAGG		TTGGCAAAGATTGGGCAGCAAG		
G1P3	CCTCCAAGGTCTAGTGACGGA	68	CCCACTGCAAGTGAAGAGCA	167	100
GBP5	CTGACTCTGCGAGCTTCTTCC		GATCACTACCTTGCTTTGGCCTT		
GYG	GGGACCAAGGCATACTGAACACA	538	TGGCACTTGCACCAAACACTTT	678	141
HIST1H4H	CACTTACACAGAGCACGCCAAA		TTAGCCACCGAAGCCGTAAAGA		
ITGB3	AGCTCATTGTTGATGCTTATGGGA	1118	ATACAAGACTTGAGGCCAGGGA	1232	
KIAA1559	TGTGGGAGAACTACAGCAAC	95	TGGACTCCAAATCAGGGCAGTA	238	144
KLRD1	cccagtatctatttccatcatttg	670	tctctgccccaagaaacatt	819	150
LIMS1	AGGTGATGTGGTCTCTGCTCTT		CAGACTGGCTTCATGTCAAACTCC		
LTBP3	TCTGCATCAACTTTCCCGGTCA	2024	TTGTTCTCGCATTTGCCATCCG	2162	139
MAP4K3	TGAACTTCCCGACAGTGATGGT	1141	AACCACCTTGGTGTCCTTGT	1250	110
MGC20553	AGGTGCACAGAGCCAACATTAC		AATGGAACACCCTCACCCAGA		
MS4A1	AAAGAACGTGCTCCAGACCC		TTCAGTTAGCCCAACCACTTCTTC		
MT1E	CTTGTTCGTCTCACTGGTGT	1	ACTCTTCTTGCAGGAGGTGCAT	142	142
NIPA2	CTGGACTGCTGTCAATGGGA	471	ACTTACTAGCACGCTGAGAGC	577	107
OSBPL10	ATGGAGTCCAGGAACCTCTGG	2467	TTTGGGCTTCCATGGTGTGC	2616	150
P2RY12	GAACACTTTCTCATGTCCAGGGT		CCTGCAGAGTGGCATCTGGTATTT		
PDE3B	TGAGCAGGGAGATGAAGAAGCAA	3171	GCAAACCAGCAGCATCATAGGAG	3316	146
PPGB	GACACTGTTGTGGTCCAGGATTTG		TGGAAGCAGCTGTTGTGTTGG		
PRG1	TACTCAAATGCAGTCGGCTTGTCC		ACCCATTGGTACCTGGCTCTCT		
SPAP1	AGCCAGTGTATGTCAATGTGGG		GGAGTCCTTGTTCTCCAGAAGTGT		
SYN2	ACAGCTCAACAAGTCGCAGT	1470	AAAGAGGCTGGCAAAGGACT	1605	136
TAGLN	TGAAGGCAAAGACATGGCAG	429	TTCCCTCTTATGCTCCTGCG	561	133
UTS2	AAGCCGTCTATCTTGTGGCGAT	10	CGTCTTCATGAGGTGCTGAGAGTT	150	141
WDFY1	AAGGACATGAAGGTAGTGTCGCCT	632	ATGGCCCTGAAGTAACAGCGT	768	137
ZNF6	TGCAGGGCTGATCTGGGTCT		CTTCCACCGCCTGAATCCATACTT		

Table 17

Symbol	RefSeq	Affy ID	5' Primer Primer Sequence	Taqman Probe	3' Primer Primer Sequence
BANK1	NM_017935	219667_s_at	CTGAAAGGCATGGTCACAAA	TCCTTCCACACAGAACCCAGCA	TCAGCTCCATCTGCACTCTG
BCNP1	NM_173544	230983_at	CGCGTGCTGAAGAAATTCAA	TTGGCGCAGAGGAGGTTCAT	ACTCAGGCAGCTCCTTTTTG
CD163	NM_004244; NM_203416	203645_s_at; 215049_x_at	GCAGCACATGGGAGATTGTCCTGTAA	AGCAAGTGGCCTCTGTAATCTGCTCA	ATTGCACGAGGACAGTGTTTGGGA
CDA	NM_001785	205627_at	GCCGTCTCAGAAGGGTACAA	CAGGGCAATTGCTATCGCCA	CCAGTTGGTGCCAAACTCTC
MGC20553	NM_174938	229893_at	AGGTGCACAGAGCCAACATTAC	CTCATCATTAACATGGAACCCCTGC	AATGGAACACCCTCACCCAGA
MS4A1	NM_152866	217418_x_at	AAAGAACGTGCTCCAGACCC	CATAGTTCTCCTGTCAGCAGAAGA	TTCAGTTAGCCCAACCACTTCTTC

Table 1

AffySpotID	GeneSymbol	GeneID	pvalue	RNAAccess'nNo.	ProteinAcc'nNo.	FoldChange	GeneDescription
1552256_a_at	SCARB1	949	0.04	NM_005505	NP_005496	1.15	scavenger receptor class B, member 1
1552283_s_at	ZDHHC11	79844	9.69e-03	NM_024786	NP_079062	0.85	zinc finger, DHHC domain containing 11
1552287_s_at	AFG3L1	172	2.95e-03	NM_001132	NP_001123	0.89	AFG3 ATPase family gene 3-like 1 (yeast)
1552302_at	MGC20235	113277	0.04	NM_145041	NP_659478	1.17	hypothetical protein MGC20235
1552303_a_at	MGC20235	113277	0.01	NM_145041	NP_659478	1.13	hypothetical protein MGC20235
1552310_at	MGC29937	123207	0.04	NM_144597	NP_653198	0.91	hypothetical protein MGC29937
1552312_a_at	MFAP3	4238	0.03	NM_005927	NP_005918	0.89	microfibrillar-associated protein 3
1552315_at	GIMAP1	170575	1.77e-04	NM_130759	NP_570115	0.83	GTPase, IMAP family member 1
1552316_a_at	GIMAP1	170575	4.31e-03	NM_130759	NP_570115	0.92	GTPase, IMAP family member 1
1552318_at	GIMAP1	170575	6.71e-03	AK091818	BAC03754	0.88	GTPase, IMAP family member 1
1552320_a_at	NYD-SP28	85478	0.03	NM_033124	NP_149115	0.84	NYD-SP28 protein
1552364_s_at	MSI2	124540	0.03	NM_138962	NP_620412	1.14	musashi homolog 2 (Drosophila)
1552497_a_at	SLAMF6	114836	6.4e-03	NM_052931	NP_443163	0.89	SLAM family member 6
1552536_at	VTI1A	143187	5.01e-04	NM_145206	NP_660207	1.20	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)
1552554_a_at	CARD12	58484	0.02	NM_021209	NP_067032	0.83	caspase recruitment domain family, member 12
1552584_at	IL12RB1	3594	0.02	NM_153701	NP_714912	0.85	interleukin 12 receptor, beta 1
1552607_at	CXorf52	286967	7.16e-03	AY168775	AAO11658	0.89	chromosome X open reading frame 52
1552610_a_at	JAK1	3716	0.03	NM_002227	NP_002218	0.92	Janus kinase 1 (a protein tyrosine kinase)
1552612_at	CDC42SE2	56990	0.04	NM_020240	NP_064625	0.86	CDC42 small effector 2
1552613_s_at	CDC42SE2	56990	0.02	NM_020240	NP_064625	0.86	CDC42 small effector 2
1552633_at	ZNF101	94039	0.03	NM_033204	NP_149981	0.89	zinc finger protein 101
1552634_a_at	ZNF101	94039	0.01	NM_033204	NP_149981	0.89	zinc finger protein 101
1552660_a_at	FLJ11193	55322	0.01	NM_018356	NP_060826	0.88	hypothetical protein FLJ11193
1552701_a_at	COPI	114769	0.01	NM_052889	NP_443121	0.84	CARD only protein
1552703_s_at	COPI	114769	0.03	NM_052889	NP_443121	0.86	CARD only protein
1552719_at	H63	113201	0.02	NM_138423	NP_612432	1.17	H63 breast cancer expressed gene
1552772_at	CLEC4D	338339	0.01	NM_080387	NP_525126	0.79	C-type lectin domain family 4, member D
1552773_at	CLEC4D	338339	0.04	NM_080387	NP_525126	0.85	C-type lectin domain family 4, member D
1552789_at	FLJ32803	151826	0.04	AK057365	BAB71453	0.87	hypothetical protein FLJ32803
1552889_a_at	XTP7 (HBxAg)	90332	0.04	NM_138568	NP_612635	1.04	protein 7 transactivated by hepatitis B virus X antigen
1552928_s_at	TAB3	257397	0.01	NM_152787	NP_690000	0.90	TAK1-binding protein 3
1552942_at	FLJ30430	149373	0.03	AK054992	BAB70837	1.09	hypothetical protein FLJ30430
1553048_a_at	PIP5K2B	8396	5.95e-03	NM_138687	NP_619632	0.85	phosphatidylinositol-4-phosphate 5-kinase, type II, beta
1553112_s_at	CDK8	1024	2.96e-03	NM_001260	NP_001251	0.86	cyclin-dependent kinase 8
1553117_a_at	STK38	11329	9.2e-03	NM_007271	NP_009202	0.91	serine/threonine kinase 38
1553133_at	C9orf72	203228	0.02	NM_145005	NP_659442	0.85	chromosome 9 open reading frame 72
1553153_at	ATP6V0D2 subunit d isoform 2	245972	8.33e-03	NM_152565	NP_689778	1.29	ATPase, H+ transporting, lysosomal 38kDa, V0
1553167_a_at	SLA/LP	51091	0.01	NM_153825	NP_722547	0.85	soluble liver antigen/liver pancreas antigen

1553167_a_at	SLA/LP	51091	0.01	NM_016955	NP_058651	0.85	soluble liver antigen/liver pancreas antigen
1553177_at	EAT2	117157	7.62e-03	NM_053282	NP_444512	0.73	SH2 domain-containing molecule EAT2
1553185_at	RASEF	158158	0.03	NM_152573	NP_689786	0.83	RAS and EF hand domain containing
1553193_at	ZNF441	126068	0.01	NM_152355	NP_689568	0.81	zinc finger protein 441
1553216_at	ZNF41	7592	0.01	NM_007130	NP_009061	0.87	zinc finger protein 41
1553222_at	OXER1	165140	0.03	NM_148962	NP_683765	1.16	oxoeicosanoid (OXE) receptor 1
1553225_s_at	ZNF75	7626	0.03	NM_007131	NP_009062	0.84	zinc finger protein 75 (D8C6)
1553227_s_at	WDR9	54014	0.02	NM_018963	NP_061836	0.88	WD repeat domain 9
1553252_a_at	BRWD3	254065	0.04	NM_153252	NP_694984	0.90	bromodomain and WD repeat domain containing 3
1553292_s_at	FLJ25006	124923	0.01	NM_144610	NP_653211	0.90	hypothetical protein FLJ25006
1553380_at	PARP15	165631	7.17e-03	NM_152615	NP_689828	0.83	poly (ADP-ribose) polymerase family, member 15
1553387_at	ATM	472	0.01	NM_138293	NP_612150	0.84	ataxia telangiectasia mutated (includes complementation groups A, C and D)
1553417_at	FLJ39058	283171	2.32e-03	NM_173580	NP_775851	1.17	hypothetical protein FLJ39058
1553530_a_at	ITGB1	3688	2.51e-04	NM_033669	NP_391989	0.91	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)
1553533_at	JPH1	56704	0.01	NM_020647	NP_065698	1.19	junctophilin 1
1553581_s_at	FLJ36754	285672	8.82e-03	NM_173829	NP_776190	0.88	hypothetical protein FLJ36754
1553587_a_at	POLE4	56655	3.48e-03	NM_019896	NP_063949	0.92	polymerase (DNA-directed), epsilon 4 (p12 subunit)
1553612_at	ZNF354B	117608	0.02	NM_058230	NP_478137	1.15	zinc finger protein 354B
1553647_at	CDYL2	124359	0.03	NM_152342	NP_689555	1.10	chromodomain protein, Y-like 2
1553678_a_at	ITGB1	3688	3.6e-03	NM_133376	NP_596867	0.92	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)
1553694_a_at	PIK3C2A	5286	0.04	NM_002645	NP_002636	0.91	phosphoinositide-3-kinase, class 2, alpha polypeptide
1553698_a_at	LOC126731	126731	0.04	NM_145257	NP_660300	0.83	LOC126731
1553703_at	FLJ90396	163049	0.04	NM_153358	NP_699189	1.05	hypothetical protein FLJ90396
1553709_a_at	FLJ14936	84950	6.11e-03	NM_032284	NP_115660	0.93	hypothetical protein FLJ14936
1553719_s_at	ZNF548	147694	0.01	NM_152909	NP_690873	0.90	zinc finger protein 548
1553750_a_at	MGC33371	143684	0.04	NM_144664	NP_653265	0.85	hypothetical protein MGC33371
1553861_at	MGC40368	255394	0.02	NM_152772	NP_689985	1.27	hypothetical protein MGC40368
1553881_at	MGC16142	84849	0.03	BC007365		0.93	hypothetical protein MGC16142
1553901_x_at	ZNF486	90649	0.03	BC008936	AAH08936	1.14	zinc finger protein 486
1553920_at	C9orf84	158401	0.01	NM_173521	NP_775792	1.21	chromosome 9 open reading frame 84
1553954_at	MGC19780	199857	0.02	NM_144988	NP_659425	0.87	hypothetical protein MGC19780
1553957_at	ZNF564	163050	1.31e-03	NM_144976	NP_659413	0.78	zinc finger protein 564
1553987_at	FLJ39616	51275	0.03	NM_016534	NP_057618	0.95	apoptosis-related protein PNAS-1
1554021_a_at	ZNF12	7559	0.01	NM_006956	NP_008887	0.89	zinc finger protein 12 (KOX 3)
1554039_at	C14orf159	80017	0.01	BC009182	AAH09182	1.19	chromosome 14 open reading frame 159
1554078_s_at	DNAJA3	9093	0.01	NM_005147	NP_005138	0.91	DnaJ (Hsp40) homolog, subfamily A, member 3
1554080_at	RQCD1	9125	0.04	BC007102	AAH07102	0.87	RCD1 required for cell differentiation1 homolog (S. pombe)
1554086_at	TUBGCP3	10426	0.01	BC007763	AAH07763	1.18	tubulin, gamma complex associated protein 3
1554089_s_at	SBDS	51119	1.26e-03	NM_016038	NP_057122	0.87	Shwachman-Bodian-Diamond syndrome
1554093_a_at	SNAPC5	10302	2.78e-03	NM_006049	NP_006040	0.93	small nuclear RNA activating complex, polypeptide 5, 19kDa

1554105_at	FAM11A	84548	0.01	NM_032508	NP_115897	0.88	family with sequence similarity 11, member A
1554116_s_at	PARP11	57097	0.01	BC031073	AAH31073	0.84	poly (ADP-ribose) polymerase family, member 11
1554149_at	C3orf4	56650	0.02	NM_019895	NP_063948	0.88	chromosome 3 open reading frame 4
1554153_a_at	PHF21A	51317	0.02	NM_016621	NP_057705	1.08	PHD finger protein 21A
1554167_a_at	GOLGA7	51125	0.01	NM_016099	NP_057183	0.95	golgi autoantigen, golgin subfamily a, 7
1554178_a_at	MGC39518	285172	1.41e-03	NM_173822	NP_776183	1.26	hypothetical protein MGC39518
1554182_at	TRIM50C	378108	5.81e-04	NM_198853	NP_942150	0.82	tripartite motif-containing 50C
1554205_s_at	ALS2CR15	130026	1.17e-03	NM_138468	NP_612477	1.23	amyotrophic lateral sclerosis 2 (juvenile)
chromosome region, candidate 15							
1554250_s_at	MGC45477	387277	0.03	BC033812	AAH33812	0.86	hypothetical protein MGC45477
1554306_at	ITPKB	3707	4.36e-03	BC015009	AAH15009	1.27	inositol 1,4,5-trisphosphate 3-kinase B
1554335_at	PSCD4	27128	0.02	BC017780	AAH17780	1.17	pleckstrin homology, Sec7 and coiled-coil domains 4
1554339_a_at	COG3	83548	0.02	NM_031431	NP_113619	0.89	component of oligomeric golgi complex 3
1554342_s_at	HEL308	113510	0.01	NM_133636	NP_598375	0.87	DNA helicase HEL308
1554406_a_at	CLEC7A	64581	0.03	NM_197947	NP_922938	0.83	C-type lectin domain family 7, member A
1554410_a_at	WBSCR16	81554	0.03	NM_030798	NP_110425	0.87	Williams-Beuren syndrome chromosome region 16
1554423_a_at	FBXO7	25793	0.01	NM_012179	NP_036311	0.92	F-box protein 7
1554424_at	FIP1L1	81608	0.03	NM_030917	NP_112179	0.88	FIP1 like 1 (S. cerevisiae)
1554451_s_at	DNAJC14	85406	2.27e-04	NM_032364	NP_115740	0.79	DnaJ (Hsp40) homolog, subfamily C, member 14
1554455_at	WINS1	55180	0.02	NM_181739	NP_859523	0.82	WINS1 protein with Drosophila Lines (Lin) homologous
domain							
1554462_a_at	DNAJB9	4189	0.03	NM_012328	NP_036460	0.92	DnaJ (Hsp40) homolog, subfamily B, member 9
1554464_a_at	CRTAP	10491	3.94e-03	NM_006371	NP_006362	0.78	cartilage associated protein
1554465_s_at	FLJ20344	55634	0.04	NM_017776	NP_060246	0.88	hypothetical protein FLJ20344
1554482_a_at	SARA2	51128	0.04	NM_016103	NP_057187	0.89	SAR1a gene homolog 2 (S. cerevisiae)
1554493_s_at	THADA	63892	8.65e-03	NM_198554	NP_940956	0.88	thyroid adenoma associated
1554493_s_at	THADA	63892	8.65e-03	NM_022065	NP_071348	0.88	thyroid adenoma associated
1554510_s_at	GHITM	27069	0.01	NM_014394	NP_055209	0.93	growth hormone inducible transmembrane protein
1554538_at	RHOF	54509	0.02	BC018208	AAH18208	0.89	ras homolog gene family, member F (in filopodia)
1554545_at	MGC26594	403314	0.04	NM_203454	NP_982279	1.09	hypothetical protein MGC26594
1554549_a_at	WDR20	91833	0.01	BC030654	AAH30654	1.16	WD repeat domain 20
1554557_at	ATP11B	23200	0.01	BC033880	AAH33880	0.80	ATPase, Class VI, type 11B
1554577_a_at	PSMD10	5716	5.57e-03	NM_002814	NP_002805	0.95	proteasome (prosome, macropain) 26S subunit, non-
ATPase, 10							
1554606_at	FLJ36090	153241	0.03	BC040527	AAH40527	0.90	hypothetical protein FLJ36090
1554616_at	SERPINB8	5271	3.88e-03	BC034528	AAH34528	1.11	serine (or cysteine) proteinase inhibitor, clade B
(ovalbumin), member 8							
1554627_a_at	ASCC1	51008	1.11e-04	NM_015947	NP_057031	0.91	activating signal cointegrator 1 complex subunit 1
1554637_a_at	CBFA2T2	9139	0.02	NM_175864	NP_787060	0.92	core-binding factor, runt domain, alpha subunit 2;
translocated to, 2							
1554661_s_at	FLJ32001	163882	0.02	NM_152609	NP_689822	0.93	hypothetical protein FLJ32001
1554670_at	GGA1	26088	0.02	NM_001001561	NP_001001561	0.90	golgi associated, gamma adaptin ear containing, ARF
binding protein 1							
1554678_s_at	HNRPDL	9987	0.01	NM_005463	NP_005454	0.88	heterogeneous nuclear ribonucleoprotein D-like
1554726_at	ZNF655	79027	0.02	NM_138494	NP_612503	0.87	zinc finger protein 655

1554747_a_at	SEPT2	4735	0.03	NM_004404	NP_004395	0.90	septin 2
1554783_s_at	ARHGEF2	9181	9.54e-03	NM_004723	NP_004714	0.82	rho/rac guanine nucleotide exchange factor (GEF) 2
1554794_a_at	UBE3C	9690	0.01	BC014029	AAH14029	0.86	ubiquitin protein ligase E3C
1554806_a_at	FBXO8	26269	0.03	NM_012180	NP_036312	0.91	F-box protein 8
1554821_a_at	ZBED1	9189	7.29e-03	NM_004729	NP_004720	1.21	zinc finger, BED domain containing 1
1554866_at	FLJ22104	65084	8.99e-03	BC030952	AAH30952	1.19	hypothetical protein FLJ22104
1554878_a_at	ABCD3	5825	0.02	NM_002858	NP_002849	0.86	ATP-binding cassette, sub-family D (ALD), member 3
1554890_a_at	TIA1	7072	0.03	NM_022037	NP_071320	0.80	TIA1 cytotoxic granule-associated RNA binding protein
1554899_s_at	FCER1G	2207	0.03	NM_004106	NP_004097	0.87	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
1554930_a_at	FUT8	2530	0.02	NM_178155	NP_835368	0.90	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
1554952_s_at	NALP12	91662	0.02	NM_144687	NP_653288	1.22	NACHT, leucine rich repeat and PYD containing 12
1554952_s_at	NALP12	91662	0.02	NM_033297	NP_150639	1.22	NACHT, leucine rich repeat and PYD containing 12
1554986_a_at	SNX19	399979	0.04	BC031620	AAH31620	0.93	sorting nexin 19
1554997_a_at	PTGS2	5743	0.03	NM_000963	NP_000954	0.70	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
1555001_at	IQCF1	132141	0.01	BC034228	AAH34228	1.17	IQ motif containing F1
1555016_at	IL16	3603	4.58e-03	BC040272	AAH40272	0.84	interleukin 16 (lymphocyte chemoattractant factor)
1555037_a_at	IDH1	3417	0.01	NM_005896	NP_005887	0.88	isocitrate dehydrogenase 1 (NADP+), soluble
1555042_at	TRPV5	56302	0.01	BC034740	AAH34740	1.16	transient receptor potential cation channel, subfamily V, member 5
1555088_x_at	STAT5B	6777	0.01	BC020868	AAH20868	1.29	signal transducer and activator of transcription 5B
1555091_at	PPM1F	9647	0.03	NM_014634	NP_055449	1.19	protein phosphatase 1F (PP2C domain containing)
1555092_at	FLJ12505	79805	0.03	BC028194	AAH28194	1.12	hypothetical protein FLJ12505
1555106_a_at	HSPC129	51496	7.34e-03	NM_016396	NP_057480	0.88	hypothetical protein HSPC129
1555141_a_at	LOC150159	150159	0.04	NM_139173	NP_631912	0.80	CG10806-like
1555192_at	ZNF277	11179	0.01	BC020626	AAH20626	0.80	zinc finger protein (C2H2 type) 277
1555193_a_at	ZNF277	11179	3.27e-03	NM_021994	NP_068834	0.84	zinc finger protein (C2H2 type) 277
1555226_s_at	C1orf43	25912	0.01	NM_138740	NP_620077	0.96	chromosome 1 open reading frame 43
1555226_s_at	C1orf43	25912	0.01	NM_015449	NP_056264	0.96	chromosome 1 open reading frame 43
1555241_at	LOC401466	401466	0.04	BC032347		0.82	hypothetical gene supported by BC055092
1555243_x_at	LOC401466	401466	0.04	BC032347		0.81	hypothetical gene supported by BC055092
1555247_a_at	RAPGEF6	51735	0.04	NM_016340	NP_057424	0.88	Rap guanine nucleotide exchange factor (GEF) 6
1555250_a_at	CPEB3	22849	0.04	NM_014912	NP_055727	1.14	cytoplasmic polyadenylation element binding protein 3
1555289_at	RGPR	89866	3.49e-03	BC009106	AAH09106	1.24	regucalcin gene promotor region related protein
1555301_a_at	C21orf106	23181	0.04	NM_206890	NP_996773	0.83	chromosome 21 open reading frame 106
1555334_s_at	SLC30A5	64924	2.8e-03	NM_022902	NP_075053	0.93	solute carrier family 30 (zinc transporter), member 5
1555334_s_at	SLC30A5	64924	2.8e-03	NM_024055	NP_076960	0.93	solute carrier family 30 (zinc transporter), member 5
1555351_s_at	PPHLN1	51535	4.61e-03	NM_016488	NP_057572	1.30	periphilin 1
1555355_a_at	ETS1	2113	2.8e-03	NM_005238	NP_005229	0.80	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)
1555372_at	BCL2L11	10018	0.01	AF455755	AAL57868	1.17	BCL2-like 11 (apoptosis facilitator)
1555373_at	C21orf114	378826	0.01	AF304443		1.14	chromosome 21 open reading frame 114
1555374_at	TTL	150465	0.03	AB071393	BAC06832	0.91	tubulin tyrosine ligase
1555423_at	SSH2	85464	0.04	AB072358	BAB84117	0.89	slingshot homolog 2 (Drosophila)

1555427_s_at	SYNCRIP	10492	3.29e-03	NM_006372	NP_006363	0.81	synaptotagmin binding, cytoplasmic RNA interacting protein
1555446_s_at	TMEM1	7109	0.01	NM_001001723	NP_001001723	1.12	transmembrane protein 1
1555467_a_at	CUGBP1	10658	0.02	NM_006560	NP_006551	0.80	CUG triplet repeat, RNA binding protein 1
1555468_at	NRP2	8828	0.01	BC009222	AAH09222	1.19	neuropilin 2
1555554_at	BASE	317716	0.02	NM_173859	NP_776258	1.14	breast cancer and salivary gland expression gene
1555559_s_at	USP25	29761	0.02	NM_013396	NP_037528	0.82	ubiquitin specific protease 25
1555613_a_at	ZAP70	7535	0.01	NM_001079	NP_001070	0.83	zeta-chain (TCR) associated protein kinase 70kDa
1555630_a_at	RAB34	83871	0.02	NM_031934	NP_114140	0.87	RAB34, member RAS oncogene family
1555638_a_at	SAMSN1	64092	0.02	NM_022136	NP_071419	0.91	SAM domain, SH3 domain and nuclear localisation signals, 1
1555691_a_at	KLRK1	22914	0.01	NM_007360	NP_031386	0.81	killer cell lectin-like receptor subfamily K, member 1
1555705_a_at	CKLFSF3	123920	0.02	NM_144601	NP_653202	0.93	chemokine-like factor super family 3
1555745_a_at	LYZ	4069	0.04	NM_000239	NP_000230	0.78	lysozyme (renal amyloidosis)
1555760_a_at	RBM15	64783	0.02	NM_022768	NP_073605	0.90	RNA binding motif protein 15
1555762_s_at	RBM15	64783	0.01	NM_022768	NP_073605	0.84	RNA binding motif protein 15
1555764_s_at	TIMM10	26519	5.48e-03	NM_012456	NP_036588	0.77	translocase of inner mitochondrial membrane 10 homolog (yeast)
1555780_a_at	RHEB	6009	6.83e-05	NM_005614	NP_005605	0.94	Ras homolog enriched in brain
1555785_a_at	XRN1	54464	0.04	NM_019001	NP_061874	0.82	5'-3' exoribonuclease 1
1555797_a_at	ARPC5	10092	0.02	NM_005717	NP_005708	0.91	actin related protein 2/3 complex, subunit 5, 16kDa
1555803_a_at	FLJ10726	55216	3.1e-03	NM_018195	NP_060665	0.83	hypothetical protein FLJ10726
1555815_a_at	L3MBTL2	83746	0.02	NM_031488	NP_113676	0.91	l(3)mbt-like 2 (Drosophila)
1555827_at	CCNL1	57018	0.01	AY034790	AAK61551	0.94	cyclin L1
1555830_s_at	CHR2SYT	57488	4.6e-03	NM_020728	NP_065779	0.80	chr2 synaptotagmin
1555837_s_at	POLR2B	5431	0.01	NM_000938	NP_000929	0.95	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa
1555851_s_at	SEPW1	6415	0.01	NM_003009	NP_003000	0.94	selenoprotein W, 1
1555852_at	PSMB8	5696	0.02	AI375915		0.94	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)
1555878_at	RPS24	6229	7.19e-03	AK094613		0.74	ribosomal protein S24
1555881_s_at	LZTS2	84445	2.95e-03	NM_032429	NP_115805	0.90	leucine zipper, putative tumor suppressor 2
1555882_at	SPIN3	169981	0.01	AL832091		0.85	spindlin family, member 3
1555886_at	C6orf210	57107	1.75e-03	BC029491		0.85	chromosome 6 open reading frame 210
1555889_a_at	CRTAP	10491	0.02	NM_006371	NP_006362	0.93	cartilage associated protein
1555933_at	MGC33867	90231	0.04	AB095933	BAC23109	1.13	hypothetical protein MGC33867
1555960_at	HINT1	3094	3.33e-03	AK054976		0.89	histidine triad nucleotide binding protein 1
1555961_a_at	HINT1	3094	0.01	NM_005340	NP_005331	0.87	histidine triad nucleotide binding protein 1
1555981_at	DKFZp762C2414	339201	1.98e-03	NM_178542	NP_848637	0.85	hypothetical protein DKFZp762C2414
1555996_s_at	EIF4A2	1974	0.01	AL137681		0.83	eukaryotic translation initiation factor 4A, isoform 2
1555998_at	ATP5H	10476	0.01	AK095671		0.87	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d
1556009_at	PEX13	5194	0.02	NM_002618	NP_002609	0.88	peroxisome biogenesis factor 13
1556035_s_at	ZNF207	7756	0.03	AL834501	CAD39159	0.94	zinc finger protein 207
1556090_at	HSMPP8	54737	0.01	BM970306		0.86	M-phase phosphoprotein, mpp8

1556105_at	PARD3	56288	0.03	AW079553		1.12	par-3 partitioning defective 3 homolog (C. elegans)
1556285_s_at	PPA2	27068	5.93e-03	NM_176869	NP_789845	0.89	inorganic pyrophosphatase 2
1556389_at	TNRC5	10695	4.39e-03	AF161347	AAF28907	0.82	trinucleotide repeat containing 5
1556420_s_at	YPEL2	388403	0.01	AK097253		1.14	yippee-like 2 (Drosophila)
1556471_at	SCML4	256380	2.72e-03	AK093571	BAC04198	0.82	sex comb on midleg-like 4 (Drosophila)
1556472_s_at	SCML4	256380	6.73e-04	AK093571	BAC04198	0.82	sex comb on midleg-like 4 (Drosophila)
1556588_at	LOC283687	283687	0.01	NM_175898	NP_787094	1.21	hypothetical protein LOC283687
1556732_at	EML4	27436	1.95e-03	BC039354		1.16	echinoderm microtubule associated protein like 4
1556787_s_at	PDE5A	8654	0.03	AW975338		1.14	phosphodiesterase 5A, cGMP-specific
1557036_at	ZBTB1	22890	0.02	BU950380		1.22	zinc finger and BTB domain containing 1
1557059_at	MKI67IP	84365	0.02	AK098264		1.12	MKI67 (FHA domain) interacting nucleolar phosphoprotein
1557066_at	LUC7L	55692	0.01	BX647161		0.86	LUC7-like (S. cerevisiae)
1557067_s_at	LUC7L	55692	6.71e-03	NM_018032	NP_060502	0.85	LUC7-like (S. cerevisiae)
1557145_at	STK38	11329	5.07e-03	BU617137		1.12	serine/threonine kinase 38
1557170_at	NEK8	284086	0.03	NM_178170	NP_835464	1.15	NIMA (never in mitosis gene a)- related kinase 8
1557227_s_at	TPR	7175	0.01	NM_003292	NP_003283	0.91	translocated promoter region (to activated MET oncogene)
1557246_at	KIDINS220	57498	0.04	AA992480		0.83	likely homolog of rat kinase D-interacting substance of 220
kDa							
1557300_s_at	WHSC2	7469	0.02	AI741292		1.11	Wolf-Hirschhorn syndrome candidate 2
1557309_at	FAM31B	163486	0.01	BC016588	AAH16588	1.24	family with sequence similarity 31, member B
1557360_at	LRPPRC	10128	7.07e-05	BC038181		0.83	leucine-rich PPR-motif containing
1557394_at	DLGAP4	22839	0.03	AK057672		1.07	discs, large (Drosophila) homolog-associated protein 4
1557477_at	STIM1	6786	0.01	BQ022900		1.15	stromal interaction molecule 1
1557527_at	RUNX1	861	0.01	BU789637		1.17	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1
oncogene)							
1557539_at	KIAA1545	57666	0.02	BC008052		1.09	KIAA1545 protein
1557551_at	PSCD1	9267	2.39e-03	CA442689		1.27	pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin
1)							
1557586_s_at	ATP6V1H	51606	0.01	AW468382		1.08	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H
1557611_at	TTLL4	9654	9.89e-03	AW779022		1.21	tubulin tyrosine ligase-like family, member 4
1557666_s_at	C9orf98	158067	5.7e-03	AW511637		1.16	chromosome 9 open reading frame 98
1557684_at	ZNF286	57335	0.04	AK021478		0.93	zinc finger protein 286
1557706_at	ZHX2	22882	2.67e-03	AF075099		1.18	zinc fingers and homeoboxes 2
1557749_at	EHBP1L1	254102	0.04	AK092750		1.13	EH domain binding protein 1-like 1
1557799_at	C11orf31	280636	0.04	AF085883		0.91	chromosome 11 open reading frame 31
1557820_at	AFG3L2	10939	0.01	AA905788		0.88	AFG3 ATPase family gene 3-like 2 (yeast)
1557852_at	PHC2	1912	0.04	AW418842		0.85	polyhomeotic-like 2 (Drosophila)
1557915_s_at	GSTO1	9446	6.92e-03	NM_004832	NP_004823	0.95	glutathione S-transferase omega 1
1557945_at	TCTE3	6991	0.04	BC043594		0.91	t-complex-associated-testis-expressed 3
1557950_at	SDCCAG1	9147	2.28e-03	NM_004713	NP_004704	0.87	serologically defined colon cancer antigen 1
1557954_at	RBBP7	5931	0.02	BM757251		0.94	retinoblastoma binding protein 7
1557965_at	MGC61716	130916	0.02	NM_182501	NP_872307	0.86	hypothetical protein MGC61716
1557987_at	LOC23117	23117	0.02	BC042832		0.77	KIAA0220-like protein
1558014_s_at	MLSTD2	84188	0.02	NM_032228	NP_115604	0.90	male sterility domain containing 2
1558094_s_at	C3orf19	51244	0.04	NM_016474	NP_057558	0.90	chromosome 3 open reading frame 19

1558097_at	MGC50372	253143	0.02	BX647272		0.93	hypothetical protein MGC50372
1558120_at	DDX3X	1654	1.99e-04	BE379787		1.29	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
1558136_s_at	TAF11	6882	0.01	NM_005643	NP_005634	0.87	TAF11 RNA polymerase II, TATA box binding protein
(TBP)-associated factor, 28kDa							
1558199_at	FN1	2335	0.04	BX641150		1.11	fibronectin 1
1558208_at	TARDBP	23435	0.01	AL039795		0.79	TAR DNA binding protein
1558217_at	FLJ31952	146857	0.01	NM_144682	NP_653283	0.83	hypothetical protein FLJ31952
1558233_s_at	ATF1	466	0.04	NM_005171	NP_005162	0.90	activating transcription factor 1
1558289_at	RFT1	91869	9.2e-03	NM_052859	NP_443091	1.13	RFT1 homolog (S. cerevisiae)
1558292_s_at	PIGW	284098	3.28e-03	NM_178517	NP_848612	0.82	phosphatidylinositol glycan, class W
1558304_s_at	SEN54L	283989	0.01	NM_207346	NP_997229	0.86	likely homolog of yeast SEN54
1558327_at	ZDHHC18	84243	7.35e-03	NM_032283	NP_115659	1.21	zinc finger, DHHC domain containing 18
1558392_at	SYNE2	23224	0.04	NM_015180	NP_055995	0.89	spectrin repeat containing, nuclear envelope 2
1558409_at	LOC442612	442612	0.02	AW974642		0.82	LOC442612
1558448_a_at	JMJD2B	23030	8.05e-03	BC032415		1.18	jumonji domain containing 2B
1558450_at	A2M	2	0.01	NM_000014	NP_000005	1.18	alpha-2-macroglobulin
1558511_s_at	CHR2SYT	57488	8.42e-03	NM_020728	NP_065779	0.80	chr2 synaptotagmin
1558648_at	MGC20481	90416	0.01	AL832032	CAD89911	1.14	hypothetical protein MGC20481
1558675_s_at	SDCCAG1	9147	0.04	NM_004713	NP_004704	0.92	serologically defined colon cancer antigen 1
1558685_a_at	LOC158960	158960	0.03	BC009467	AAH09467	1.08	hypothetical protein BC009467
1558692_at	MGC31963	112770	0.02	AW090182		0.87	kidney predominant protein NCU-G1
1558693_s_at	MGC31963	112770	0.01	NM_144580	NP_653181	0.84	kidney predominant protein NCU-G1
1558742_at	DEXI	28955	7.02e-03	BE899474		1.10	dexamethasone-induced transcript
1558745_at	LOC92017	92017	0.02	BC029857	AAH29857	0.87	similar to RIKEN cDNA 4933437K13
1558759_s_at	CLASP2	23122	0.04	AB014527	BAA31602	1.09	cytoplasmic linker associated protein 2
1558761_a_at	C9orf10OS	158293	1.75e-03	AK093641		1.16	chromosome 9 open reading frame 10 opposite strand
1558802_at	BBP	83941	9.61e-03	BG401696		0.83	beta-amyloid binding protein precursor
1558953_s_at	Cep164	22897	0.04	NM_014956	NP_055771	0.87	KIAA1052 protein
1558996_at	FOXP1	27086	0.02	BX647682		0.89	forkhead box P1
1559025_at	SEPT9	10801	0.03	AL833770		0.86	septin 9
1559064_at	NUP153	9972	0.02	BC035502		0.88	nucleoporin 153kDa
1559094_at	FBXO9	26268	1.11e-03	AK095307		0.90	F-box protein 9
1559096_x_at	FBXO9	26268	5.53e-04	AK095307		0.92	F-box protein 9
1559101_at	FYN	2534	0.02	AK090692		0.76	FYN oncogene related to SRC, FGR, YES
1559128_at	HSDL2	84263	0.02	BC036620		1.25	hydroxysteroid dehydrogenase like 2
1559203_s_at	KRAS	3845	0.04	BC029545	AAH29545	1.27	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
1559347_at	CNOT4	4850	0.03	BI599409		1.11	CCR4-NOT transcription complex, subunit 4
1559391_s_at	B4GALT5	9334	0.01	AI084451		1.19	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase,
polypeptide 5							
1559399_s_at	ZCCHC10	54819	7.35e-03	BC015986		0.86	zinc finger, CCHC domain containing 10
1559413_at	MGC40368	255394	0.04	AF306858		1.13	hypothetical protein MGC40368
1559441_s_at	CYP4V2	285440	0.03	AK095895		1.21	cytochrome P450, family 4, subfamily V, polypeptide 2
1559502_s_at	LRRC25	126364	0.02	NM_145256	NP_660299	1.13	leucine rich repeat containing 25
1559582_at	RHOQ	23433	0.01	BC033251		1.15	ras homolog gene family, member Q
1559716_at	C18orf37	125476	0.02	AK095502	BAC04560	1.10	chromosome 18 open reading frame 37

1559739_at	CHPT1	56994	2.79e-03	AK025141		0.83	choline phosphotransferase 1
1559756_at	DKFZp667F0711	399716	0.02	AL713753	CAD28526	1.21	hypothetical protein DKFZp667F0711
1559881_s_at	ZNF12	7559	0.04	NM_006956	NP_008887	0.87	zinc finger protein 12 (KOX 3)
1559883_s_at	SAMHD1	25939	0.02	NM_015474	NP_056289	0.83	SAM domain and HD domain 1
1559942_at	HIC	29969	0.02	NM_199072	NP_951038	1.14	I-mfa domain-containing protein
1559946_s_at	RUVBL2	10856	0.03	NM_006666	NP_006657	1.12	RuvB-like 2 (E. coli)
1559954_s_at	DDX42	11325	7.69e-03	NM_007372	NP_031398	0.88	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42
1560069_at	LOC389072	389072	0.02	BC020812	AAH20812	0.89	hypothetical protein LOC389072
1560474_at	NIPBL	25836	3.9e-03	BM728509		1.36	Nipped-B homolog (Drosophila)
1560486_at	STXBP3	6814	8.05e-03	BC028028	AAH28028	1.22	syntaxin binding protein 3
1560622_at	TPARL	55858	0.04	AK000203		0.90	TPA regulated locus
1560679_at	LOC151438	151438	0.02	AK055877		0.74	hypothetical protein LOC151438
1560741_at	UBE3A	7337	6.77e-03	AL832250		1.18	ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome)
1560776_at	LOC201158	201158	0.03	AU121725		1.12	similar to CGI-148 protein
1560986_a_at	EHBP1	23301	9.33e-03	AF086019		1.15	EH domain binding protein 1
1561128_at	STK10	6793	0.03	AF088069		1.08	serine/threonine kinase 10
1561135_at	FLJ34870	401013	0.01	AF085980		1.15	FLJ34870 protein
1561303_at	LOC440384	440384	0.02	XM_498646	XP_498646	1.17	hypothetical gene supported by BC042734
1561442_at	LOC283585	283585	4.01e-04	BC034577	AAH34577	1.33	hypothetical protein LOC283585
1561453_at	KIAA1276	27146	0.03	BC037915		1.10	KIAA1276 protein
1561467_at	KIAA0804	23355	0.01	BC039111		1.17	KIAA0804 protein
1561502_x_at	LOC348180	348180	0.04	AW575915		0.88	hypothetical protein LOC348180
1561654_at	LIMK2	3985	0.03	AF085978		1.23	LIM domain kinase 2
1561690_at	SSBP2	23635	0.01	BC041991		1.19	single-stranded DNA binding protein 2
1561890_at	C10orf128	170371	0.02	BC037922		1.18	chromosome 10 open reading frame 128
1561908_a_at	HS3ST3B1	9953	0.02	AL832823		0.87	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1
1562051_at	LOC284757	284757	0.02	AK092805		0.89	hypothetical protein LOC284757
1562059_at	SVIL	6840	0.03	AW020871		1.21	supervillin
1562256_at	NALP1	22861	5.97e-03	AL832400		1.15	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1
1562257_x_at	NALP1	22861	1.54e-03	AL832400		1.14	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1
1562259_at	TEX9	374618	0.03	AL832050		0.80	testis expressed gene 9
1562305_x_at	ZNF306	80317	0.01	AK091225		1.18	zinc finger protein 306
1562314_at	NCOA1	8648	1.16e-03	AL713641		1.20	nuclear receptor coactivator 1
1562416_at	FLNB	2317	0.01	AI524619		0.89	filamin B, beta (actin binding protein 278)
1562505_at	STK35	140901	0.03	BC035700		1.18	serine/threonine kinase 35
1562612_at	ME2	4200	0.03	BC020933		0.88	malic enzyme 2, NAD(+)-dependent, mitochondrial
1562619_at	TXNDC6	347736	0.03	NM_178130	NP_835231	1.11	thioredoxin domain containing 6
1562650_at	LOC285527	285527	0.01	AL833444		0.82	hypothetical protein LOC285527
1562673_at	CHES1	1112	0.01	BC043161		1.17	checkpoint suppressor 1
1562733_at	LOC401544	401544	3.57e-03	BC043559		0.89	hypothetical gene supported by BC043559
1562894_at	ELMO1	9844	0.02	BC022406		1.16	engulfment and cell motility 1 (ced-12 homolog, C. elegans)
1562898_at	ATP11A	23250	0.04	AL713719		1.16	ATPase, Class VI, type 11A

1563455_at	KIAA0999	23387	0.01	NM_025164	NP_079440	1.12	KIAA0999 protein
1563498_s_at	LOC283130	283130	0.02	AK090434	BAC03415	0.83	hypothetical protein LOC283130
1563621_at	KIAA1706	80820	0.04	AL713724		1.18	KIAA1706 protein
1563657_at	PLXND1	23129	7.09e-03	NM_015103	NP_055918	1.18	plexin D1
1563687_a_at	KIAA0826	23045	0.02	U80082	AAD00351	0.87	KIAA0826
1563796_s_at	KIAA1970	124454	0.03	AK095998		0.91	KIAA1970 protein
1564063_a_at	ATP11B	23200	0.04	BC033880	AAH33880	0.84	ATPase, Class VI, type 11B
1564093_at	NEK1	4750	0.01	AK024912		0.88	NIMA (never in mitosis gene a)-related kinase 1
1564139_at	LOC144571	144571	0.01	AK056852		0.70	hypothetical protein LOC144571
1564203_at	LOC147004	147004	0.02	AK057317		1.10	hypothetical protein LOC147004
1564301_a_at	RIP	84268	0.02	AK096001		1.14	RPA interacting protein
1564310_a_at	PARP15	165631	0.01	NM_152615	NP_689828	0.87	poly (ADP-ribose) polymerase family, member 15
1564443_at	RFP2OS	448961	0.02	AF529010		1.11	ret finger protein 2 opposite strand
1564494_s_at	P4HB	5034	0.01	NM_000918	NP_000909	0.89	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline
4-hydroxylase), beta polypeptide (protein disulfide isomerase; thy							
1564521_x_at	SKB1	10419	0.02	NM_006109	NP_006100	0.81	SKB1 homolog (S. pombe)
1564798_at	EEA1	8411	0.01	AK000811		1.09	early endosome antigen 1, 162kD
1565269_s_at	ATF1	466	0.01	NM_005171	NP_005162	0.89	activating transcription factor 1
1565358_at	RARA	5914	0.01	AJ417079		1.17	retinoic acid receptor, alpha
1565657_at	CKLFSF6	54918	0.04	BC042995		0.75	chemokine-like factor super family 6
1565672_at	LOC440703	440703	0.01	BC031957		1.14	hypothetical gene supported by AK026359
1565673_at	FCGR2A	2212	3.78e-03	AF416711	AAL78867	1.30	Fc fragment of IgG, low affinity IIa, receptor (CD32)
1565717_s_at	FUS	2521	2.44e-05	NM_004960	NP_004951	0.77	fusion (involved in t(12;16) in malignant liposarcoma)
1565804_at	LOC360030	360030	5.07e-03	AK025161		1.24	homeobox C14
1565830_at	KIAA1731	85459	0.01	AL833615		0.83	KIAA1731 protein
1565978_a_at	FCHO2	115548	0.01	N33616		1.18	FCH domain only 2
1566142_at	GBF1	8729	2.98e-03	AK095268		1.15	golgi-specific brefeldin A resistance factor 1
1566144_at	LOC401131	401131	9.73e-03	AK098337		1.15	hypothetical LOC401131
1566509_s_at	FBXO9	26268	8.32e-03	NM_012347	NP_036479	0.93	F-box protein 9
1566577_at	DPYSL5	56896	0.03	AL831879		1.20	dihydropyrimidinase-like 5
1566959_at	GAB2	9846	0.02	AL049273		1.34	GRB2-associated binding protein 2
1567032_s_at	ZNF160	90338	0.02	NM_033288	NP_150630	1.19	zinc finger protein 160
1567044_s_at	C19orf13	26065	0.02	AF085866		1.13	chromosome 19 open reading frame 13
1567107_s_at	TPM4	7171	0.01	NM_003290	NP_003281	1.08	tropomyosin 4
1567213_at	PNN	5411	0.01	U59479	AAB03391	0.92	pinin, desmosome associated protein
1567214_a_at	PNN	5411	0.02	NM_002687	NP_002678	0.90	pinin, desmosome associated protein
1568592_at	LOC400368	400368	0.02	XM_378511	XP_378511	0.85	hypothetical gene supported by BC031266
1568619_s_at	LOC162073	162073	0.01	BC015343		1.17	hypothetical protein LOC162073
1568620_at	CSAD	51380	0.04	BC018042		1.16	cysteine sulfinic acid decarboxylase
1568704_a_at	CHERP	10523	0.03	NM_006387	NP_006378	1.06	calcium homeostasis endoplasmic reticulum protein
1568720_at	ZNF505	81931	0.01	NM_031218	NP_112495	1.24	zinc finger protein 505
1568780_at	LOC389634	389634	5.93e-03	AK124896		1.25	hypothetical LOC389634
1568830_at	IRAK3	11213	0.03	BC029493		0.88	interleukin-1 receptor-associated kinase 3
1568836_at	CLK4	57396	9.75e-03	BC034633		0.84	CDC-like kinase 4
1568856_at	NBR1	4077	0.04	NM_005899	NP_005890	0.77	neighbor of BRCA1 gene 1

1568877_a_at	ACBD5	91452	0.02	NM_145698	NP_663736	0.88	acyl-Coenzyme A binding domain containing 5
1568903_at	EDD	51366	2.11e-03	BC014866		1.20	E3 identified by differential display
1568938_at	LOC388628	388628	0.03	XM_373843	XP_373843	1.13	hypothetical gene supported by BC021746
1568949_at	PITPNC1	26207	0.01	BC067095	AAH67095	0.92	phosphatidylinositol transfer protein, cytoplasmic 1
1569077_x_at	FLJ16287	162962	8.05e-03	BE791720		1.09	FLJ16287 protein
1569091_at	ZNF198	7750	0.03	BC039458		1.13	zinc finger protein 198
1569206_at	MGC40368	255394	0.04	NM_152772	NP_689985	1.12	hypothetical protein MGC40368
1569225_a_at	SCML4	256380	0.01	AK093571	BAC04198	0.84	sex comb on midleg-like 4 (Drosophila)
1569369_at	ZFYVE28	57732	0.02	BC053664	AAH53664	0.83	zinc finger, FYVE domain containing 28
1569374_at	FLJ43654	375341	0.02	NM_198562	NP_940964	1.18	FLJ43654 protein
1569594_a_at	SDCCAG1	9147	0.02	NM_004713	NP_004704	0.91	serologically defined colon cancer antigen 1
1569669_at	FOXR2	139628	0.03	NM_198451	NP_940853	1.15	forkhead box R2
1569714_at	ZFYVE20	64145	0.03	NM_022340	NP_071735	0.88	zinc finger, FYVE domain containing 20
1569791_at	STK4	6789	0.01	NM_006282	NP_006273	0.92	serine/threonine kinase 4
1569792_a_at	MGC50559	254013	0.01	NM_173802	NP_776163	1.14	hypothetical protein MGC50559
1569857_s_at	TPP2	7174	0.02	NM_003291	NP_003282	0.90	tripeptidyl peptidase II
1570078_a_at	DOCK5	80005	0.01	BC011877	AAH11877	1.21	dedicator of cytokinesis 5
1570108_at	GNB1	2782	2.34e-03	BC037848		1.19	guanine nucleotide binding protein (G protein), beta polypeptide
1							
1570342_at	NKTR	4820	0.04	BC020672		0.85	natural killer-tumor recognition sequence
1570523_s_at	APG10L	83734	2.58e-03	NM_031482	NP_113670	0.84	APG10 autophagy 10-like (S. cerevisiae)
1729_at	TRADD	8717	0.02	NM_003789	NP_003780	0.91	TNFRSF1A-associated via death domain
200003_s_at	RPL28	6158	0.04	NM_000991	NP_000982	0.91	ribosomal protein L28
200005_at	EIF3S7	8664	0.01	NM_003753	NP_003744	0.93	eukaryotic translation initiation factor 3, subunit 7 zeta,
66/67kDa							
200006_at	PARK7	11315	7.66e-03	NM_007262	NP_009193	0.94	Parkinson disease (autosomal recessive, early onset) 7
200011_s_at	ARF3	377	0.01	NM_001659	NP_001650	0.94	ADP-ribosylation factor 3
200013_at	RPL24	6152	6.41e-03	NM_000986	NP_000977	0.88	ribosomal protein L24
200015_s_at	SEPT2	4735	0.04	NM_004404	NP_004395	0.90	septin 2
200016_x_at	HNRPA1	3178	0.02	NM_002136	NP_002127	0.95	heterogeneous nuclear ribonucleoprotein A1
200018_at	RPS13	6207	0.04	NM_001017	NP_001008	0.92	ribosomal protein S13
200020_at	TARDBP	23435	1.33e-03	NM_007375	NP_031401	0.93	TAR DNA binding protein
200027_at	NARS	4677	5.31e-03	NM_004539	NP_004530	0.95	asparaginyl-tRNA synthetase
200030_s_at	SLC25A3	5250	2.76e-03	NM_002635	NP_002626	0.93	solute carrier family 25 (mitochondrial carrier;
phosphate carrier), member 3							
200035_at	DULLARD	23399	4.31e-03	NM_015343	NP_056158	1.16	dullard homolog (Xenopus laevis)
200037_s_at	CBX3	11335	8.52e-03	NM_016587	NP_057671	0.89	chromobox homolog 3 (HP1 gamma homolog,
Drosophila)							
200038_s_at	RPL17	6139	0.04	NM_000985	NP_000976	0.91	ribosomal protein L17
200039_s_at	PSMB2	5690	7.84e-03	NM_002794	NP_002785	0.93	proteasome (prosome, macropain) subunit, beta type, 2
200040_at	KHDRBS1	10657	0.03	NM_006559	NP_006550	0.93	KH domain containing, RNA binding, signal
transduction associated 1							
200042_at	HSPC117	51493	6.55e-03	NM_014306	NP_055121	0.83	hypothetical protein HSPC117
200043_at	ERH	2079	0.02	NM_004450	NP_004441	0.91	enhancer of rudimentary homolog (Drosophila)
200044_at	SFRS9	8683	6.18e-03	NM_003769	NP_003760	0.94	splicing factor, arginine/serine-rich 9

200046_at	DAD1	1603	0.01	NM_001344	NP_001335	0.90	defender against cell death 1
200050_at	ZNF146	7705	0.02	NM_007145	NP_009076	0.88	zinc finger protein 146
200051_at	SART1	9092	0.01	NM_005146	NP_005137	0.87	squamous cell carcinoma antigen recognised by T cells
200052_s_at	ILF2	3608	4.11e-03	NM_004515	NP_004506	0.90	interleukin enhancer binding factor 2, 45kDa
200054_at	ZNF259	8882	0.01	NM_003904	NP_003895	0.92	zinc finger protein 259
200056_s_at	C1D	10438	0.04	NM_006333	NP_006324	0.92	nuclear DNA-binding protein
200057_s_at	NONO	4841	5.83e-03	NM_007363	NP_031389	0.94	non-POU domain containing, octamer-binding
200066_at	IK	3550	9.59e-03	NM_006083	NP_006074	0.88	IK cytokine, down-regulator of HLA II
200068_s_at	CANX	821	0.01	NM_001746	NP_001737	0.95	calnexin
200072_s_at	HNRPM	4670	0.01	NM_005968	NP_005959	0.91	heterogeneous nuclear ribonucleoprotein M
200073_s_at	HNRPD	3184	4.1e-05	NM_001003810	NP_001003810	0.84	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
200074_s_at	RPL14	9045	0.03	NM_003973	NP_003964	0.90	ribosomal protein L14
200076_s_at	MGC2749	79036	0.02	NM_024069	NP_076974	0.95	hypothetical protein MGC2749
200079_s_at	KARS	3735	0.02	NM_005548	NP_005539	0.94	lysyl-tRNA synthetase
200081_s_at	RPS6	6194	0.04	NM_001010	NP_001001	0.92	ribosomal protein S6
200084_at	SMAP	10944	2.82e-03	NM_014267	NP_055082	0.95	small acidic protein
200088_x_at	RPL12	6136	0.03	NM_000976	NP_000967	0.90	ribosomal protein L12
200089_s_at	RPL4	6124	0.02	NM_000968	NP_000959	0.89	ribosomal protein L4
200090_at	FNTA	2339	0.02	NM_002027	NP_002018	0.95	farnesyltransferase, CAAX box, alpha
200092_s_at	RPL37	6167	0.01	NM_000997	NP_000988	0.90	ribosomal protein L37
200093_s_at	HINT1	3094	0.02	NM_005340	NP_005331	0.87	histidine triad nucleotide binding protein 1
200098_s_at	ANAPC5	51433	0.02	NM_016237	NP_057321	0.92	anaphase promoting complex subunit 5
200593_s_at	HNRPU	3192	0.03	NM_031844	NP_114032	0.93	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
200595_s_at	EIF3S10	8661	0.02	NM_003750	NP_003741	0.90	eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa
200596_s_at	EIF3S10	8661	0.03	NM_003750	NP_003741	0.86	eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa
200597_at	EIF3S10	8661	0.02	NM_003750	NP_003741	0.86	eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa
200599_s_at	TRA1	7184	0.01	NM_003299	NP_003290	0.91	tumor rejection antigen (gp96) 1
200606_at	DSP	1832	3.32e-03	NM_004415	NP_004406	1.39	desmoplakin
200609_s_at	WDR1	9948	0.04	NM_017491	NP_059830	0.96	WD repeat domain 1
200613_at	AP2M1	1173	6.4e-03	NM_004068	NP_004059	0.92	adaptor-related protein complex 2, mu 1 subunit
200614_at	CLTC	1213	0.02	NM_004859	NP_004850	0.95	clathrin, heavy polypeptide (Hc)
200618_at	LASP1	3927	0.02	NM_006148	NP_006139	1.09	LIM and SH3 protein 1
200620_at	C1orf8	9528	0.04	NM_004872	NP_004863	0.96	chromosome 1 open reading frame 8
200623_s_at	CALM3	808	0.01	NM_005184	NP_005175	0.89	calmodulin 3 (phosphorylase kinase, delta)
200624_s_at	MATR3	9782	0.01	NM_018834	NP_061322	0.90	matrin 3
200626_s_at	MATR3	9782	9.07e-03	NM_018834	NP_061322	0.92	matrin 3
200629_at	WARS	7453	0.04	NM_004184	NP_004175	0.83	tryptophanyl-tRNA synthetase
200631_s_at	SET	6418	0.01	NM_003011	NP_003002	0.93	SET translocation (myeloid leukemia-associated)
200642_at	SOD1	6647	0.04	NM_000454	NP_000445	0.90	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))

200647_x_at	EIF3S8	8663	0.02	NM_003752	NP_003743	0.86	eukaryotic translation initiation factor 3, subunit 8, 110kDa
200650_s_at	LDHA	3939	0.02	NM_005566	NP_005557	0.95	lactate dehydrogenase A
200651_at	GNB2L1	10399	0.01	NM_006098	NP_006089	0.89	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
200652_at	SSR2	6746	8.57e-03	NM_003145	NP_003136	0.93	signal sequence receptor, beta (translocon-associated protein beta)
200653_s_at	CALM1	801	0.04	NM_006888	NP_008819	0.92	calmodulin 1 (phosphorylase kinase, delta)
200654_at	P4HB	5034	0.02	NM_000918	NP_000909	0.94	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thy
200657_at	SLC25A5	292	0.04	NM_001152	NP_001143	0.92	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
200658_s_at	PHB	5245	0.04	NM_002634	NP_002625	0.87	prohibitin
200661_at	PPGB	5476	0.02	NM_000308	NP_000299	0.93	protective protein for beta-galactosidase (galactosialidosis)
200662_s_at	TOMM20	9804	9.2e-03	NM_014765	NP_055580	0.94	translocase of outer mitochondrial membrane 20 homolog (yeast)
200664_s_at	DNAJB1	3337	0.04	NM_006145	NP_006136	0.91	DnaJ (Hsp40) homolog, subfamily B, member 1
200667_at	UBE2D3	7323	0.03	NM_003340	NP_003331	0.90	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
200668_s_at	UBE2D3	7323	0.02	NM_003340	NP_003331	0.94	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
200669_s_at	UBE2D3	7323	0.04	NM_003340	NP_003331	0.94	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
200670_at	XBP1	7494	0.01	NM_005080	NP_005071	0.87	X-box binding protein 1
200673_at	LAPTM4A	9741	0.04	NM_014713	NP_055528	0.92	lysosomal-associated protein transmembrane 4 alpha
200685_at	SFRS11	9295	0.01	BX641004	CAE46007	0.85	splicing factor, arginine/serine-rich 11
200687_s_at	SF3B3	23450	0.02	NM_012426	NP_036558	0.85	splicing factor 3b, subunit 3, 130kDa
200691_s_at	HSPA9B	3313	0.02	NM_004134	NP_004125	0.89	heat shock 70kDa protein 9B (mortalin-2)
200698_at	KDELR2	11014	0.02	AK093917		0.94	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
200701_at	NPC2	10577	0.03	NM_006432	NP_006423	0.89	Niemann-Pick disease, type C2
200702_s_at	DDX24	57062	0.02	NM_020414	NP_065147	0.86	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24
200705_s_at	EEF1B2	1933	0.02	NM_001959	NP_001950	0.90	eukaryotic translation elongation factor 1 beta 2
200707_at	PRKCSH	5589	0.03	NM_002743	NP_002734	1.11	protein kinase C substrate 80K-H
200708_at	GOT2	2806	0.04	NM_002080	NP_002071	0.93	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
200711_s_at	SKP1A	6500	6.35e-03	NM_006930	NP_008861	0.96	S-phase kinase-associated protein 1A (p19A)
200712_s_at	MAPRE1	22919	0.01	NM_012325	NP_036457	0.95	microtubule-associated protein, RP/EB family, member 1
200713_s_at	MAPRE1	22919	4.8e-03	NM_012325	NP_036457	0.94	microtubule-associated protein, RP/EB family, member 1
200717_x_at	RPL7	6129	0.03	NM_000971	NP_000962	0.92	ribosomal protein L7
200718_s_at	SKP1A	6500	0.03	NM_006930	NP_008861	0.91	S-phase kinase-associated protein 1A (p19A)
200719_at	SKP1A	6500	0.03	NM_006930	NP_008861	0.92	S-phase kinase-associated protein 1A (p19A)
200722_s_at	M11S1	4076	0.03	NM_005898	NP_005889	0.92	membrane component, chromosome 11, surface marker 1
200726_at	PPP1CC	5501	0.03	NM_002710	NP_002701	0.90	protein phosphatase 1, catalytic subunit, gamma isoform

200728_at	ACTR2	10097	0.04	NM_001005386	NP_001005386	1.07	ARP2 actin-related protein 2 homolog (yeast)
200731_s_at	PTP4A1	7803	0.02	NM_003463	NP_003454	1.10	protein tyrosine phosphatase type IVA, member 1
200733_s_at	PTP4A1	7803	0.04	NM_003463	NP_003454	0.85	protein tyrosine phosphatase type IVA, member 1
200735_x_at	NACA	4666	0.01	NM_005594	NP_005585	0.91	nascent-polypeptide-associated complex alpha polypeptide
200737_at	PGK1	5230	0.02	NM_000291	NP_000282	0.96	phosphoglycerate kinase 1
200739_s_at	SUMO3	6612	0.01	NM_006936	NP_008867	0.90	SMT3 suppressor of mif two 3 homolog 3 (yeast)
200740_s_at	SUMO3	6612	0.01	NM_006936	NP_008867	0.88	SMT3 suppressor of mif two 3 homolog 3 (yeast)
200742_s_at	TPP1	1200	0.04	NM_000391	NP_000382	0.95	tripeptidyl peptidase I
200743_s_at	TPP1	1200	0.04	NM_000391	NP_000382	0.95	tripeptidyl peptidase I
200750_s_at	RAN	5901	0.01	NM_006325	NP_006316	0.91	RAN, member RAS oncogene family
200751_s_at	HNRPC	3183	0.03	NM_031314	NP_112604	0.91	heterogeneous nuclear ribonucleoprotein C (C1/C2)
200753_x_at	SFRS2	6427	0.04	NM_003016	NP_003007	0.93	splicing factor, arginine/serine-rich 2
200754_x_at	SFRS2	6427	9.2e-03	NM_003016	NP_003007	0.90	splicing factor, arginine/serine-rich 2
200760_s_at	ARL6IP5	10550	0.03	NM_006407	NP_006398	0.92	ADP-ribosylation-like factor 6 interacting protein 5
200761_s_at	ARL6IP5	10550	4.68e-03	NM_006407	NP_006398	0.92	ADP-ribosylation-like factor 6 interacting protein 5
200762_at	DPYSL2	1808	0.03	NM_001386	NP_001377	0.85	dihydropyrimidinase-like 2
200768_s_at	MAT2A	4144	9.33e-03	NM_005911	NP_005902	0.88	methionine adenosyltransferase II, alpha
200773_x_at	PTMA	5757	3.1e-03	NM_002823	NP_002814	0.91	prothymosin, alpha (gene sequence 28)
200776_s_at	BZW1	9689	0.03	NM_014670	NP_055485	0.92	basic leucine zipper and W2 domains 1
200777_s_at	BZW1	9689	0.02	NM_014670	NP_055485	0.95	basic leucine zipper and W2 domains 1
200778_s_at	SEPT2	4735	0.03	NM_004404	NP_004395	0.92	septin 2
200779_at	ATF4	468	0.01	NM_001675	NP_001666	0.90	activating transcription factor 4 (tax-responsive enhancer element B67)
200786_at	PSMB7	5695	0.04	NM_002799	NP_002790	0.94	proteasome (prosome, macropain) subunit, beta type, 7
200787_s_at	PEA15	8682	0.03	NM_003768	NP_003759	0.85	phosphoprotein enriched in astrocytes 15
200792_at	G22P1	2547	0.01	NM_001469	NP_001460	0.95	thyroid autoantigen 70kDa (Ku antigen)
200799_at	HSPA1A	3303	3.43e-03	NM_005345	NP_005336	1.08	heat shock 70kDa protein 1A
200800_s_at	HSPA1A	3303	0.02	NM_005345	NP_005336	1.10	heat shock 70kDa protein 1A
200806_s_at	HSPD1	3329	0.04	NM_002156	NP_002147	0.88	heat shock 60kDa protein 1 (chaperonin)
200807_s_at	HSPD1	3329	0.01	NM_002156	NP_002147	0.93	heat shock 60kDa protein 1 (chaperonin)
200809_x_at	RPL12	6136	0.02	NM_000976	NP_000967	0.90	ribosomal protein L12
200811_at	CIRBP	1153	3.43e-03	NM_001280	NP_001271	0.87	cold inducible RNA binding protein
200814_at	PSME1	5720	0.02	NM_006263	NP_006254	0.90	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
200816_s_at	PAFAH1B1	5048	7.16e-03	NM_000430	NP_000421	0.93	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa
200818_at	ATP5O	539	0.04	NM_001697	NP_001688	0.92	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
200820_at	PSMD8	5714	0.02	NM_002812	NP_002803	0.90	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
200824_at	GSTP1	2950	0.01	NM_000852	NP_000843	0.88	glutathione S-transferase pi
200828_s_at	ZNF207	7756	0.01	NM_003457	NP_003448	0.93	zinc finger protein 207
200829_x_at	ZNF207	7756	0.01	NM_003457	NP_003448	0.93	zinc finger protein 207
200841_s_at	EPRS	2058	7.71e-03	NM_004446	NP_004437	0.86	glutamyl-prolyl-tRNA synthetase

200842_s_at	EPRS	2058	2.28e-03	NM_004446	NP_004437	0.86	glutamyl-prolyl-tRNA synthetase
200844_s_at	PRDX6	9588	0.03	NM_004905	NP_004896	0.88	peroxiredoxin 6
200848_at	AHCYL1	10768	0.04	NM_006621	NP_006612	1.16	S-adenosylhomocysteine hydrolase-like 1
200850_s_at	AHCYL1	10768	3.66e-03	NM_006621	NP_006612	0.92	S-adenosylhomocysteine hydrolase-like 1
200851_s_at	KIAA0174	9798	0.01	NM_014761	NP_055576	0.94	KIAA0174 gene product
200853_at	H2AFZ	3015	0.01	NM_002106	NP_002097	0.93	H2A histone family, member Z
200855_at	NCOR1	9611	0.01	NM_006311	NP_006302	0.90	nuclear receptor co-repressor 1
200860_s_at	CNOT1	23019	0.04	NM_016284	NP_057368	0.94	CCR4-NOT transcription complex, subunit 1
200870_at	STRAP	11171	1.39e-03	NM_007178	NP_009109	0.95	serine/threonine kinase receptor associated protein
200873_s_at	CCT8	10694	0.03	NM_006585	NP_006576	0.88	chaperonin containing TCP1, subunit 8 (theta)
200875_s_at	NOL5A	10528	0.02	NM_006392	NP_006383	0.87	nucleolar protein 5A (56kDa with KKE/D repeat)
200876_s_at	PSMB1	5689	0.01	NM_002793	NP_002784	0.94	proteasome (prosome, macropain) subunit, beta type, 1
200877_at	CCT4	10575	2.16e-03	NM_006430	NP_006421	0.86	chaperonin containing TCP1, subunit 4 (delta)
200881_s_at	DNAJA1	3301	0.04	NM_001539	NP_001530	0.93	DnaJ (Hsp40) homolog, subfamily A, member 1
200883_at	UQCRC2	7385	2.39e-03	NM_003366	NP_003357	0.95	ubiquinol-cytochrome c reductase core protein II
200887_s_at	STAT1	6772	0.03	NM_007315	NP_009330	0.82	signal transducer and activator of transcription 1, 91kDa
200892_s_at	SFRS10	6434	9.2e-03	NM_004593	NP_004584	0.86	splicing factor, arginine/serine-rich 10 (transformer 2
homolog, Drosophila)							
200893_at	SFRS10	6434	8.67e-03	NM_004593	NP_004584	0.91	splicing factor, arginine/serine-rich 10 (transformer 2
homolog, Drosophila)							
200900_s_at	M6PR	4074	3.26e-03	NM_002355	NP_002346	0.89	mannose-6-phosphate receptor (cation dependent)
200902_at	SEP15	9403	0.04	NM_004261	NP_004252	0.94	15 kDa selenoprotein
200903_s_at	AHCY	191	0.03	NM_000687	NP_000678	0.90	S-adenosylhomocysteine hydrolase
200912_s_at	EIF4A2	1974	0.01	NM_001967	NP_001958	0.90	eukaryotic translation initiation factor 4A, isoform 2
200913_at	PPM1G	5496	0.02	NM_002707	NP_002698	0.88	protein phosphatase 1G (formerly 2C), magnesium-
dependent, gamma isoform							
200915_x_at	KTN1	3895	0.01	NM_182926	NP_891556	0.94	kinectin 1 (kinesin receptor)
200918_s_at	SRPR	6734	0.01	NM_003139	NP_003130	0.91	signal recognition particle receptor ('docking protein')
200923_at	LGALS3BP	3959	0.03	NM_005567	NP_005558	0.74	lectin, galactoside-binding, soluble, 3 binding protein
200927_s_at	RAB14	51552	0.01	NM_016322	NP_057406	0.91	RAB14, member RAS oncogene family
200928_s_at	RAB14	51552	9.33e-03	NM_016322	NP_057406	0.87	RAB14, member RAS oncogene family
200929_at	TMP21	10972	0.01	NM_006827	NP_006818	0.91	transmembrane trafficking protein
200934_at	DEK	7913	0.02	NM_003472	NP_003463	0.89	DEK oncogene (DNA binding)
200936_at	RPL8	6132	4.42e-03	NM_000973	NP_000964	0.86	ribosomal protein L8
200942_s_at	HSBP1	3281	0.03	NM_001537	NP_001528	0.93	heat shock factor binding protein 1
200944_s_at	HMGN1	3150	0.01	NM_004965	NP_004956	0.87	high-mobility group nucleosome binding domain 1
200945_s_at	SEC31L1	22872	0.02	NM_014933	NP_055748	0.92	SEC31-like 1 (S. cerevisiae)
200946_x_at	GLUD1	2746	9.61e-03	NM_005271	NP_005262	0.89	glutamate dehydrogenase 1
200948_at	MLF2	8079	0.04	NM_005439	NP_005430	1.09	myeloid leukemia factor 2
200953_s_at	CCND2	894	0.04	NM_001759	NP_001750	0.87	cyclin D2
200955_at	IMMT	10989	8.05e-03	NM_006839	NP_006830	0.92	inner membrane protein, mitochondrial (mitofilin)
200956_s_at	SSRP1	6749	0.01	NM_003146	NP_003137	0.89	structure specific recognition protein 1
200959_at	FUS	2521	0.01	NM_004960	NP_004951	0.90	fusion (involved in t(12;16) in malignant liposarcoma)
200965_s_at	ABLIM1	3983	0.02	NM_006720	NP_006711	0.84	actin binding LIM protein 1
200969_at	SERP1	27230	0.04	AK093929		0.92	stress-associated endoplasmic reticulum protein 1

200970_s_at	SERP1	27230	8.57e-03	NM_014445	NP_055260	0.95	stress-associated endoplasmic reticulum protein 1
200978_at	MDH1	4190	6.71e-03	NM_005917	NP_005908	0.87	malate dehydrogenase 1, NAD (soluble)
200980_s_at	PDHA1	5160	0.01	NM_000284	NP_000275	0.89	pyruvate dehydrogenase (lipoamide) alpha 1
200987_x_at	PSME3	10197	0.03	NM_005789	NP_005780	0.91	proteasome (prosome, macropain) activator subunit 3
(PA28 gamma; Ki)							
200988_s_at	PSME3	10197	7.35e-03	NM_005789	NP_005780	0.90	proteasome (prosome, macropain) activator subunit 3
(PA28 gamma; Ki)							
200991_s_at	SNX17	9784	0.02	NM_014748	NP_055563	0.93	sorting nexin 17
200993_at	IPO7	10527	0.01	AK074908	0.88	importin 7	
200994_at	IPO7	10527	0.01	BG291787	0.91	importin 7	
200996_at	ACTR3	10096	0.03	NM_005721	NP_005712	0.92	ARP3 actin-related protein 3 homolog (yeast)
201001_s_at	Kua-UEV	387522	6.11e-03	NM_199203	NP_954673	0.91	ubiquitin-conjugating enzyme E2 variant 1
201002_s_at	Kua-UEV	387522	1.01e-03	NM_199203	NP_954673	0.91	ubiquitin-conjugating enzyme E2 variant 1
201004_at	SSR4	6748	8.67e-03	NM_006280	NP_006271	0.91	signal sequence receptor, delta (translocon-associated
protein delta)							
201007_at	HADHB	3032	0.01	NM_000183	NP_000174	0.96	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-
Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta							
201014_s_at	PAICS	10606	0.01	NM_006452	NP_006443	0.88	phosphoribosylaminoimidazole carboxylase,
phosphoribosylaminoimidazole succinocarboxamide synthetase							
201022_s_at	DSTN	11034	0.03	NM_006870	NP_006861	0.92	destrin (actin depolymerizing factor)
201030_x_at	LDHB	3945	3.43e-03	NM_002300	NP_002291	0.86	lactate dehydrogenase B
201047_x_at	RAB6A	5870	0.02	NM_002869	NP_002860	0.95	RAB6A, member RAS oncogene family
201048_x_at	RAB6A	5870	0.02	NM_002869	NP_002860	0.94	RAB6A, member RAS oncogene family
201053_s_at	PSMF1	9491	0.01	NM_006814	NP_006805	0.92	proteasome (prosome, macropain) inhibitor subunit 1
(PI31)							
201054_at	HNRPA0	10949	0.02	NM_006805	NP_006796	0.92	heterogeneous nuclear ribonucleoprotein A0
201055_s_at	HNRPA0	10949	0.04	NM_006805	NP_006796	0.95	heterogeneous nuclear ribonucleoprotein A0
201064_s_at	PABPC4	8761	0.01	NM_003819	NP_003810	0.85	poly(A) binding protein, cytoplasmic 4 (inducible form)
201068_s_at	PSMC2	5701	4.38e-03	NM_002803	NP_002794	0.92	proteasome (prosome, macropain) 26S subunit, ATPase,
2							
201076_at	NHP2L1	4809	0.03	NM_005008	NP_004999	1.06	NHP2 non-histone chromosome protein 2-like 1 (S.
cerevisiae)							
201078_at	TM9SF2	9375	0.03	NM_004800	NP_004791	0.94	transmembrane 9 superfamily member 2
201082_s_at	DCTN1	1639	0.03	NM_004082	NP_004073	1.10	dynactin 1 (p150, glued homolog, Drosophila)
201085_s_at	SON	6651	5.83e-03	NM_138925	NP_620303	0.87	SON DNA binding protein
201086_x_at	SON	6651	0.04	NM_003103	NP_003094	0.92	SON DNA binding protein
201091_s_at	CBX3	11335	2.69e-03	NM_007276	NP_009207	0.88	chromobox homolog 3 (HP1 gamma homolog,
Drosophila)							
201092_at	RBBP7	5931	0.02	NM_002893	NP_002884	0.91	retinoblastoma binding protein 7
201095_at	DAP	1611	0.03	NM_004394	NP_004385	1.14	death-associated protein
201096_s_at	ARF4	378	2.86e-03	NM_001660	NP_001651	0.93	ADP-ribosylation factor 4
201098_at	COPB2	9276	0.01	NM_004766	NP_004757	0.91	coatomer protein complex, subunit beta 2 (beta prime)
201099_at	USP9X	8239	0.03	AA824386	0.94	ubiquitin specific protease 9, X-linked (fat facets-like, Drosophila)	
201101_s_at	BCLAF1	9774	0.02	NM_014739	NP_055554	0.92	BCL2-associated transcription factor 1
201111_at	CSE1L	1434	0.04	NM_001316	NP_001307	0.84	CSE1 chromosome segregation 1-like (yeast)

201112_s_at	CSE1L	1434	0.01	NM_001316	NP_001307	0.94	CSE1 chromosome segregation 1-like (yeast)
201128_s_at	ACLY	47	0.04	NM_001096	NP_001087	0.93	ATP citrate lyase
201129_at	SFRS7	6432	0.02	NM_006276	NP_006267	0.89	splicing factor, arginine/serine-rich 7, 35kDa
201134_x_at	COX7C	1350	0.02	NM_001867	NP_001858	0.93	cytochrome c oxidase subunit VIIc
201142_at	EIF2S1	1965	0.04	AA577698		0.90	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
201143_s_at	EIF2S1	1965	0.01	NM_004094	NP_004085	0.90	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
201144_s_at	EIF2S1	1965	4.61e-03	NM_004094	NP_004085	0.93	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
201145_at	HAX1	10456	2.84e-03	NM_006118	NP_006109	0.91	HS1 binding protein
201146_at	NFE2L2	4780	0.01	NM_006164	NP_006155	0.89	nuclear factor (erythroid-derived 2)-like 2
201153_s_at	MBNL1	4154	0.04	NM_021038	NP_066368	0.93	muscleblind-like (Drosophila)
201154_x_at	RPL4	6124	0.02	NM_000968	NP_000959	0.94	ribosomal protein L4
201155_s_at	MFN2	9927	0.02	NM_014874	NP_055689	0.88	mitofusin 2
201157_s_at	NMT1	4836	0.01	NM_021079	NP_066565	0.95	N-myristoyltransferase 1
201163_s_at	IGFBP7	3490	6.3e-03	NM_001553	NP_001544	0.76	insulin-like growth factor binding protein 7
201164_s_at	PUM1	9698	0.04	NM_014676	NP_055491	0.89	pumilio homolog 1 (Drosophila)
201166_s_at	PUM1	9698	0.01	NM_014676	NP_055491	0.92	pumilio homolog 1 (Drosophila)
201174_s_at	TERF2IP	54386	0.01	NM_018975	NP_061848	0.95	telomeric repeat binding factor 2, interacting protein
201175_at	TMX2	51075	0.04	NM_015959	NP_057043	0.92	thioredoxin-related transmembrane protein 2
201177_s_at	UBA2	10054	0.01	NM_005499	NP_005490	0.89	SUMO-1 activating enzyme subunit 2
201178_at	FBXO7	25793	0.01	NM_012179	NP_036311	0.91	F-box protein 7
201179_s_at	GNAI3	2773	6.53e-03	NM_006496	NP_006487	0.90	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3
201182_s_at	CHD4	1108	0.02	NM_001273	NP_001264	0.91	chromodomain helicase DNA binding protein 4
201194_at	SEPW1	6415	0.03	NM_003009	NP_003000	0.90	selenoprotein W, 1
201198_s_at	PSMD1	5707	0.04	NM_002807	NP_002798	0.96	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1
201202_at	PCNA	5111	0.03	NM_002592	NP_002583	0.86	proliferating cell nuclear antigen
201204_s_at	RRBP1	6238	0.04	AA706065		0.89	ribosome binding protein 1 homolog 180kDa (dog)
201207_at	TNFAIP1	7126	0.01	NM_021137	NP_066960	0.86	tumor necrosis factor, alpha-induced protein 1 (endothelial)
201209_at	HDAC1	3065	0.02	NM_004964	NP_004955	0.89	histone deacetylase 1
201216_at	C12orf8	10961	0.01	NM_006817	NP_006808	0.90	chromosome 12 open reading frame 8
201226_at	NDUFB8	4714	0.01	NM_005004	NP_004995	0.81	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
201232_s_at	PSMD13	5719	0.01	NM_002817	NP_002808	0.93	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13
201233_at	PSMD13	5719	2.19e-03	NM_002817	NP_002808	0.89	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13
201235_s_at	BTG2	7832	5.31e-03	NM_006763	NP_006754	0.75	BTG family, member 2
201239_s_at	SPCS2	9789	8.8e-03	NM_014752	NP_055567	0.91	signal peptidase complex subunit 2 homolog (S. cerevisiae)
201240_s_at	SPCS2	9789	0.02	NM_014752	NP_055567	0.94	signal peptidase complex subunit 2 homolog (S. cerevisiae)
201241_at	DDX1	1653	3.98e-03	NM_004939	NP_004930	0.91	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1

201245_s_at	OTUB1	55611	0.03	NM_017670	NP_060140	0.93	OTU domain, ubiquitin aldehyde binding 1
201253_s_at	CDIPT	10423	0.01	NM_006319	NP_006310	0.92	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
(phosphatidylinositol synthase)							
201256_at	COX7A2L	9167	0.03	NM_004718	NP_004709	0.91	cytochrome c oxidase subunit VIIa polypeptide 2 like
201258_at	RPS16	6217	9.86e-03	NM_001020	NP_001011	0.88	ribosomal protein S16
201259_s_at	SYPL	6856	0.01	NM_006754	NP_006745	0.90	synaptophysin-like protein
201260_s_at	SYPL	6856	0.03	NM_006754	NP_006745	0.91	synaptophysin-like protein
201266_at	TXNRD1	7296	0.01	NM_003330	NP_003321	0.92	thioredoxin reductase 1
201268_at	NME2	4831	2.39e-03	NM_002512	NP_002503	0.80	non-metastatic cells 2, protein (NM23B) expressed in
201273_s_at	SRP9	6726	0.01	NM_003133	NP_003124	0.94	signal recognition particle 9kDa
201274_at	PSMA5	5686	4.38e-03	NM_002790	NP_002781	0.93	proteasome (prosome, macropain) subunit, alpha type, 5
201277_s_at	HNRPAB	3182	0.04	NM_004499	NP_004490	0.88	heterogeneous nuclear ribonucleoprotein A/B
201284_s_at	APEH	327	8.74e-05	NM_001640	NP_001631	0.87	N-acylaminoacyl-peptide hydrolase
201290_at	SEC11L1	23478	0.02	NM_014300	NP_055115	0.95	SEC11-like 1 (S. cerevisiae)
201301_s_at	ANXA4	307	0.01	NM_001153	NP_001144	0.91	annexin A4
201302_at	ANXA4	307	0.02	NM_001153	NP_001144	0.92	annexin A4
201304_at	NDUFA5	4698	1.05e-03	NM_005000	NP_004991	0.83	NADH dehydrogenase (ubiquinone) 1 alpha
subcomplex, 5, 13kDa							
201305_x_at	ANP32B	10541	0.01	NM_006401	NP_006392	0.85	acidic (leucine-rich) nuclear phosphoprotein 32 family,
member B							
201306_s_at	ANP32B	10541	0.01	NM_006401	NP_006392	0.91	acidic (leucine-rich) nuclear phosphoprotein 32 family,
member B							
201310_s_at	C5orf13	9315	0.02	NM_004772	NP_004763	0.91	chromosome 5 open reading frame 13
201311_s_at	SH3BGRL	6451	0.01	NM_003022	NP_003013	0.92	SH3 domain binding glutamic acid-rich protein like
201317_s_at	PSMA2	5683	6.48e-03	NM_002787	NP_002778	0.96	proteasome (prosome, macropain) subunit, alpha type, 2
201318_s_at	MRCL3	10627	0.02	NM_006471	NP_006462	0.91	myosin regulatory light chain MRCL3
201320_at	SMARCC2	6601	0.01	NM_003075	NP_003066	0.88	SWI/SNF related, matrix associated, actin dependent
regulator of chromatin, subfamily c, member 2							
201323_at	EBNA1BP2	10969	0.03	NM_006824	NP_006815	0.85	EBNA1 binding protein 2
201327_s_at	CCT6A	908	0.03	NM_001762	NP_001753	0.85	chaperonin containing TCP1, subunit 6A (zeta 1)
201329_s_at	ETS2	2114	0.04	NM_005239	NP_005230	0.88	v-ets erythroblastosis virus E26 oncogene homolog 2
(avian)							
201336_at	VAMP3	9341	0.04	NM_004781	NP_004772	0.95	vesicle-associated membrane protein 3 (cellubrevin)
201338_x_at	GTF3A	2971	0.03	NM_002097	NP_002088	0.93	general transcription factor IIIA
201339_s_at	SCP2	6342	0.01	NM_002979	NP_002970	0.85	sterol carrier protein 2
201348_at	GPX3	2878	2.3e-03	NM_002084	NP_002075	1.41	glutathione peroxidase 3 (plasma)
201351_s_at	YME1L1	10730	0.01	NM_139312	NP_647473	0.94	YME1-like 1 (S. cerevisiae)
201370_s_at	CUL3	8452	0.01	NM_003590	NP_003581	0.93	cullin 3
201376_s_at	HNRPF	3185	4.19e-03	NM_004966	NP_004957	0.89	heterogeneous nuclear ribonucleoprotein F
201378_s_at	UBAP2L	9898	0.02	NM_014847	NP_055662	0.91	ubiquitin associated protein 2-like
201384_s_at	NBR1	4077	9.63e-03	NM_005899	NP_005890	0.96	neighbor of BRCA1 gene 1
201385_at	DHX15	1665	8.42e-03	NM_001358	NP_001349	0.93	DEAH (Asp-Glu-Ala-His) box polypeptide 15
201386_s_at	DHX15	1665	7.57e-04	NM_001358	NP_001349	0.95	DEAH (Asp-Glu-Ala-His) box polypeptide 15
201389_at	ITGA5	3678	0.03	NM_002205	NP_002196	1.13	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
201395_at	RBM5	10181	0.02	NM_005778	NP_005769	0.93	RNA binding motif protein 5

201398_s_at	TRAM1	23471	0.04	NM_014294	NP_055109	0.89	translocation associated membrane protein 1
201404_x_at	PSMB2	5690	5.21e-03	NM_002794	NP_002785	0.82	proteasome (prosome, macropain) subunit, beta type, 2
201408_at	PPP1CB	5500	8.32e-03	NM_002709	NP_002700	0.91	protein phosphatase 1, catalytic subunit, beta isoform
201410_at	PLEKHB2	55041	0.01	AI983043		0.95	pleckstrin homology domain containing, family B (evectins) member 2
201417_at	SOX4	6659	5.44e-03	NM_003107	NP_003098	0.89	SRY (sex determining region Y)-box 4
201432_at	CAT	847	0.01	NM_001752	NP_001743	0.89	catalase
201435_s_at	EIF4E	1977	0.04	NM_001968	NP_001959	0.92	eukaryotic translation initiation factor 4E
201436_at	EIF4E	1977	4.38e-03	NM_001968	NP_001959	0.82	eukaryotic translation initiation factor 4E
201437_s_at	EIF4E	1977	6.44e-04	NM_001968	NP_001959	0.83	eukaryotic translation initiation factor 4E
201440_at	DDX23	9416	0.03	NM_004818	NP_004809	0.91	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23
201441_at	COX6B1 (ubiquitous)	1340	0.04	NM_001863	NP_001854	0.95	cytochrome c oxidase subunit Vib polypeptide 1
201447_at	TIA1	7072	0.02	H96549		0.89	TIA1 cytotoxic granule-associated RNA binding protein
201448_at	TIA1	7072	0.04	AL046419		0.92	TIA1 cytotoxic granule-associated RNA binding protein
201449_at	TIA1	7072	0.03	AL567227		0.91	TIA1 cytotoxic granule-associated RNA binding protein
201453_x_at	RHEB	6009	0.03	NM_005614	NP_005605	0.91	Ras homolog enriched in brain
201455_s_at	NPEPPS	9520	0.04	NM_006310	NP_006301	0.94	aminopeptidase puromycin sensitive
201456_s_at	BUB3 (yeast)	9184	0.01	NM_004725	NP_004716	0.88	BUB3 budding uninhibited by benzimidazoles 3 homolog
201457_x_at	BUB3 (yeast)	9184	3.1e-03	NM_004725	NP_004716	0.91	BUB3 budding uninhibited by benzimidazoles 3 homolog
201458_s_at	BUB3 (yeast)	9184	1.33e-03	NM_004725	NP_004716	0.85	BUB3 budding uninhibited by benzimidazoles 3 homolog
201469_s_at	SHC1 protein 1	6464	4.83e-03	NM_003029	NP_003020	0.90	SHC (Src homology 2 domain containing) transforming
201470_at	GSTO1	9446	0.01	NM_004832	NP_004823	0.94	glutathione S-transferase omega 1
201472_at	VBP1	7411	0.01	NM_003372	NP_003363	0.95	von Hippel-Lindau binding protein 1
201477_s_at	RRM1	6240	0.01	NM_001033	NP_001024	0.91	ribonucleotide reductase M1 polypeptide
201478_s_at	DKC1	1736	3.84e-03	NM_001363	NP_001354	0.84	dyskeratosis congenita 1, dyskerin
201479_at	DKC1	1736	0.01	NM_001363	NP_001354	0.88	dyskeratosis congenita 1, dyskerin
201491_at	AHSA1 homolog 1 (yeast)	10598	0.04	NM_012111	NP_036243	0.92	AHA1, activator of heat shock 90kDa protein ATPase
201494_at	PRCP	5547	0.03	NM_005040	NP_005031	0.92	prolylcarboxypeptidase (angiotensinase C)
201501_s_at	GRSF1	2926	0.02	NM_002092	NP_002083	0.94	G-rich RNA sequence binding factor 1
201511_at	AAMP	14	6.57e-03	NM_001087	NP_001078	0.93	angio-associated, migratory cell protein
201512_s_at	TOMM70A homolog A (yeast)	9868	1.56e-04	NM_014820	NP_055635	0.93	translocase of outer mitochondrial membrane 70
201513_at	TSN	7247	0.04	NM_004622	NP_004613	0.87	translin
201515_s_at	TSN	7247	0.04	NM_004622	NP_004613	0.93	translin
201517_at	NCBP2	22916	0.03	NM_007362	NP_031388	0.86	nuclear cap binding protein subunit 2, 20kDa
201519_at	TOMM70A homolog A (yeast)	9868	0.01	NM_014820	NP_055635	0.92	translocase of outer mitochondrial membrane 70
201520_s_at	GRSF1	2926	1.01e-03	NM_002092	NP_002083	0.95	G-rich RNA sequence binding factor 1
201521_s_at	NCBP2	22916	6.51e-03	NM_007362	NP_031388	0.90	nuclear cap binding protein subunit 2, 20kDa

201528_at	RPA1	6117	0.01	NM_002945	NP_002936	0.90	replication protein A1, 70kDa
201529_s_at	RPA1	6117	0.01	NM_002945	NP_002936	0.87	replication protein A1, 70kDa
201530_x_at	EIF4A1	1973	0.03	NM_001416	NP_001407	0.96	eukaryotic translation initiation factor 4A, isoform 1
201532_at	PSMA3	5684	4.31e-03	NM_002788	NP_002779	0.92	proteasome (prosome, macropain) subunit, alpha type, 3
201544_x_at	PABPN1	8106	1.01e-03	NM_004643	NP_004634	0.86	poly(A) binding protein, nuclear 1
201546_at	TRIP12	9320	0.03	NM_004238	NP_004229	0.96	thyroid hormone receptor interactor 12
201551_s_at	LAMP1	3916	1.13e-03	NM_005561	NP_005552	0.77	lysosomal-associated membrane protein 1
201552_at	LAMP1	3916	0.01	NM_005561	NP_005552	0.94	lysosomal-associated membrane protein 1
201553_s_at	LAMP1	3916	0.02	NM_005561	NP_005552	0.94	lysosomal-associated membrane protein 1
201555_at	MCM3	4172	0.03	NM_002388	NP_002379	0.91	MCM3 minichromosome maintenance deficient 3 (S.
cerevisiae)							
201557_at	VAMP2	6844	0.04	NM_014232	NP_055047	1.04	vesicle-associated membrane protein 2 (synaptobrevin 2)
201567_s_at	GOLGA4	2803	4.38e-03	NM_002078	NP_002069	0.90	golgi autoantigen, golgin subfamily a, 4
201568_at	QP-C	27089	0.03	NM_014402	NP_055217	0.88	low molecular mass ubiquinone-binding protein (9.5kD)
201570_at	CGI-51	25813	5.57e-03	NM_015380	NP_056195	0.89	CGI-51 protein
201571_s_at	DCTD	1635	0.01	NM_001921	NP_001912	0.86	dCMP deaminase
201572_x_at	DCTD	1635	0.02	NM_001921	NP_001912	0.84	dCMP deaminase
201573_s_at	ETF1	2107	0.01	NM_004730	NP_004721	0.91	eukaryotic translation termination factor 1
201574_at	ETF1	2107	0.01	NM_004730	NP_004721	0.94	eukaryotic translation termination factor 1
201575_at	SKIIP	22938	0.01	NM_012245	NP_036377	0.95	SKI interacting protein
201577_at	NME1	4830	6.3e-03	NM_000269	NP_000260	0.90	non-metastatic cells 1, protein (NM23A) expressed in
201583_s_at	SEC23B	10483	8.07e-03	NM_006363	NP_006354	0.93	Sec23 homolog B (S. cerevisiae)
201584_s_at	DDX39	10212	0.01	NM_005804	NP_005795	0.93	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
201585_s_at	SFPQ	6421	0.01	NM_005066	NP_005057	0.95	splicing factor proline/glutamine rich (polypyrimidine tract
binding protein associated)							
201588_at	TXNL1	9352	5.44e-03	NM_004786	NP_004777	0.94	thioredoxin-like 1
201589_at	SMC1L1	8243	0.04	NM_006306	NP_006297	0.91	SMC1 structural maintenance of chromosomes 1-like 1
(yeast)							
201590_x_at	ANXA2	302	0.03	NM_004039	NP_004030	0.87	annexin A2
201591_s_at	NISCH	11188	0.02	NM_007184	NP_009115	0.92	nischarin
201592_at	EIF3S3	8667	9.61e-03	NM_003756	NP_003747	0.94	eukaryotic translation initiation factor 3, subunit 3 gamma,
40kDa							
201593_s_at	LEREPO4	55854	0.04	NM_018471	NP_060941	0.93	likely ortholog of mouse immediate early response,
erythropoietin 4							
201595_s_at	LEREPO4	55854	0.01	NM_018471	NP_060941	0.87	likely ortholog of mouse immediate early response,
erythropoietin 4							
201597_at	COX7A2	1347	8.67e-03	NM_001865	NP_001856	0.95	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
201601_x_at	IFITM1	8519	5.07e-03	NM_003641	NP_003632	0.86	interferon induced transmembrane protein 1 (9-27)
201608_s_at	PWP1	11137	0.02	NM_007062	NP_008993	0.89	nuclear phosphoprotein similar to S. cerevisiae PWP1
201611_s_at	ICMT	23463	0.03	NM_012405	NP_036537	0.92	isoprenylcysteine carboxyl methyltransferase
201612_at	ALDH9A1	223	0.04	NM_000696	NP_000687	0.92	aldehyde dehydrogenase 9 family, member A1
201613_s_at	AP1G2	8906	0.02	NM_003917	NP_003908	0.88	adaptor-related protein complex 1, gamma 2 subunit
201619_at	PRDX3	10935	0.01	NM_006793	NP_006784	0.93	peroxiredoxin 3
201620_at	MBTPS1	8720	0.04	NM_003791	NP_003782	0.91	membrane-bound transcription factor protease, site 1
201623_s_at	DARS	1615	0.01	NM_001349	NP_001340	0.89	aspartyl-tRNA synthetase

201624_at	DARS	1615	0.04	NM_001349	NP_001340	0.87	aspartyl-tRNA synthetase
201626_at	INSIG1	3638	0.02	NM_005542	NP_005533	0.86	insulin induced gene 1
201628_s_at	RRAGA	10670	0.01	NM_006570	NP_006561	0.95	Ras-related GTP binding A
201629_s_at	ACP1	52	0.04	NM_004300	NP_004291	0.92	acid phosphatase 1, soluble
201630_s_at	ACP1	52	0.01	NM_004300	NP_004291	0.88	acid phosphatase 1, soluble
201633_s_at	CYB5-M	80777	0.02	NM_030579	NP_085056	0.91	outer mitochondrial membrane cytochrome b5
201637_s_at	FXR1	8087	0.01	NM_005087	NP_005078	0.89	fragile X mental retardation, autosomal homolog 1
201641_at	BST2	684	0.02	NM_004335	NP_004326	0.77	bone marrow stromal cell antigen 2
201643_x_at	JMJD1B	51780	0.04	NM_016604	NP_057688	0.95	jumonji domain containing 1B
201653_at	CNIH	10175	0.03	NM_005776	NP_005767	0.96	cornichon homolog (Drosophila)
201656_at	ITGA6	3655	0.01	NM_000210	NP_000201	0.78	integrin, alpha 6
201657_at	ARL1	400	0.01	NM_001177	NP_001168	0.87	ADP-ribosylation factor-like 1
201659_s_at	ARL1	400	0.01	NM_001177	NP_001168	0.89	ADP-ribosylation factor-like 1
201663_s_at	SMC4L1	10051	0.02	NM_005496	NP_005487	0.91	SMC4 structural maintenance of chromosomes 4-like 1
(yeast)							
201671_x_at	USP14	9097	7.25e-03	NM_005151	NP_005142	0.86	ubiquitin specific protease 14 (tRNA-guanine
transglycosylase)							
201672_s_at	USP14	9097	0.01	NM_005151	NP_005142	0.90	ubiquitin specific protease 14 (tRNA-guanine
transglycosylase)							
201673_s_at	GYS1	2997	8.5e-04	NM_002103	NP_002094	0.88	glycogen synthase 1 (muscle)
201676_x_at	PSMA1	5682	0.01	NM_002786	NP_002777	0.92	proteasome (prosome, macropain) subunit, alpha type, 1
201680_x_at	ARS2	51593	0.02	NM_015908	NP_056992	0.90	arsenate resistance protein ARS2
201682_at	PMPCB	9512	0.03	NM_004279	NP_004270	0.86	peptidase (mitochondrial processing) beta
201685_s_at	C14orf92	9878	6.92e-03	NM_014828	NP_055643	0.89	chromosome 14 open reading frame 92
201687_s_at	API5	8539	0.04	NM_006595	NP_006586	0.88	apoptosis inhibitor 5
201692_at	OPRS1	10280	0.03	NM_005866	NP_005857	0.90	opioid receptor, sigma 1
201693_s_at	EGR1	1958	0.04	NM_001964	NP_001955	1.29	early growth response 1
201697_s_at	DNMT1	1786	0.03	NM_001379	NP_001370	0.89	DNA (cytosine-5-)-methyltransferase 1
201698_s_at	SFRS9	8683	0.01	NM_003769	NP_003760	0.93	splicing factor, arginine/serine-rich 9
201699_at	PSMC6	5706	2.29e-03	NM_002806	NP_002797	0.92	proteasome (prosome, macropain) 26S subunit, ATPase,
6							
201700_at	CCND3	896	4.38e-03	NM_001760	NP_001751	0.93	cyclin D3
201701_s_at	PGRMC2	10424	6.7e-03	NM_006320	NP_006311	0.77	progesterone receptor membrane component 2
201707_at	PEX19	5824	0.01	NM_002857	NP_002848	0.84	peroxisomal biogenesis factor 19
201711_x_at	RANBP2	5903	2.19e-03	NM_006267	NP_006258	0.82	RAN binding protein 2
201713_s_at	RANBP2	5903	0.01	NM_006267	NP_006258	0.91	RAN binding protein 2
201717_at	MRPL49	740	0.01	NM_004927	NP_004918	0.94	mitochondrial ribosomal protein L49
201728_s_at	KIAA0100	9703	0.02	AK130007	BAC85274	0.91	KIAA0100 gene product
201734_at	CLCN3	1182	8.42e-03	AI760629	0.95		chloride channel 3
201735_s_at	CLCN3	1182	5.57e-03	NM_001829	NP_001820	0.89	chloride channel 3
201736_s_at	MARCH6	10299	8.42e-03	NM_005885	NP_005876	0.93	membrane-associated ring finger (C3HC4) 6
201737_s_at	MARCH6	10299	0.03	NM_005885	NP_005876	0.94	membrane-associated ring finger (C3HC4) 6
201739_at	SGK	6446	0.04	NM_005627	NP_005618	0.89	serum/glucocorticoid regulated kinase
201740_at	NDUFS3	4722	0.01	NM_004551	NP_004542	0.93	NADH dehydrogenase (ubiquinone) Fe-S protein 3,
30kDa (NADH-coenzyme Q reductase)							

201742_x_at	SFRS1	6426	1.66e-03	NM_006924	NP_008855	0.92	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
201745_at	PTK9	5756	0.02	NM_002822	NP_002813	0.89	PTK9 protein tyrosine kinase 9
201748_s_at	SAFB	6294	2.39e-03	NM_002967	NP_002958	0.89	scaffold attachment factor B
201753_s_at	ADD3	120	0.02	NM_019903	NP_063968	0.91	adducin 3 (gamma)
201754_at	COX6C	1345	0.04	NM_004374	NP_004365	0.91	cytochrome c oxidase subunit VIc
201757_at	NDUFS5	4725	0.01	NM_004552	NP_004543	0.91	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)
201761_at	MTHFD2	10797	0.01	NM_006636	NP_006627	0.83	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
201762_s_at	PSME2	5721	0.01	NM_002818	NP_002809	0.81	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
201765_s_at	HEXA	3073	5.48e-03	NM_000520	NP_000511	0.86	hexosaminidase A (alpha polypeptide)
201767_s_at	ELAC2	60528	0.04	NM_018127	NP_060597	0.80	elaC homolog 2 (E. coli)
201768_s_at	ENTH	9685	0.01	NM_014666	NP_055481	0.92	enthoprotin
201769_at	ENTH	9685	0.02	NM_014666	NP_055481	0.94	enthoprotin
201771_at	SCAMP3	10067	0.04	NM_005698	NP_005689	0.91	secretory carrier membrane protein 3
201775_s_at	KIAA0494	9813	0.03	AB007963	BAA32328	0.94	KIAA0494 gene product
201776_s_at	KIAA0494	9813	0.01	AK001487		0.91	KIAA0494 gene product
201777_s_at	KIAA0494	9813	0.03	BC002525	AAH02525	0.92	KIAA0494 gene product
201778_s_at	KIAA0494	9813	1.41e-03	NM_014774	NP_055589	0.94	KIAA0494 gene product
201779_s_at	RNF13	11342	9.61e-03	NM_007282	NP_009213	1.14	ring finger protein 13
201781_s_at	AIP	9049	0.03	NM_003977	NP_003968	0.90	aryl hydrocarbon receptor interacting protein
201784_s_at	SMAP	10944	5.93e-03	NM_014267	NP_055082	0.86	small acidic protein
201799_s_at	OSBP	5007	0.03	NM_002556	NP_002547	0.90	oxysterol binding protein
201800_s_at	OSBP	5007	0.01	NM_002556	NP_002547	0.92	oxysterol binding protein
201803_at	POLR2B	5431	5.97e-03	NM_000938	NP_000929	0.93	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa
201807_at	VPS26	9559	0.02	NM_004896	NP_004887	0.96	vacuolar protein sorting 26 (yeast)
201812_s_at	TOMM7	54543	0.02	NM_019059	NP_061932	0.86	translocase of outer mitochondrial membrane 7 homolog (yeast)
201816_s_at	GBAS	2631	0.04	NM_001483	NP_001474	0.91	glioblastoma amplified sequence
201818_at	FLJ12443	79888	7.35e-03	NM_024830	NP_079106	0.84	hypothetical protein FLJ12443
201823_s_at	RNF14	9604	2.91e-03	NM_004290	NP_004281	0.93	ring finger protein 14
201828_x_at	CXX1	8933	0.02	NM_003928	NP_003919	0.94	CAAX box 1
201830_s_at	NET1	10276	0.03	NM_005863	NP_005854	0.79	neuroepithelial cell transforming gene 1
201832_s_at	VDP	8615	0.01	NM_003715	NP_003706	0.93	vesicle docking protein p115
201833_at	HDAC2	3066	0.01	NM_001527	NP_001518	0.91	histone deacetylase 2
201836_s_at	STAF65(gamma)	9913	0.03	NM_014860	NP_055675	0.91	SPTF-associated factor 65 gamma
201837_s_at	STAF65(gamma)	9913	0.01	NM_014860	NP_055675	0.90	SPTF-associated factor 65 gamma
201840_at	NEDD8	4738	0.03	NM_006156	NP_006147	0.92	neural precursor cell expressed, developmentally down-regulated 8
201847_at	LIPA	3988	0.02	NM_000235	NP_000226	0.84	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)
201849_at	BNIP3	664	3.26e-03	NM_004052	NP_004043	0.81	BCL2/adenovirus E1B 19kDa interacting protein 3

201856_s_at	ZFR	51663	9.33e-03	NM_016107	NP_057191	0.92	zinc finger RNA binding protein
201857_at	ZFR	51663	0.01	NM_016107	NP_057191	0.89	zinc finger RNA binding protein
201862_s_at	LRRFIP1	9208	0.04	NM_004735	NP_004726	1.10	leucine rich repeat (in FLII) interacting protein 1
201863_at	FAM32A	26017	0.02	NM_014077	NP_054796	0.95	family with sequence similarity 32, member A
201867_s_at	TBL1X	6907	0.04	NM_005647	NP_005638	0.89	transducin (beta)-like 1X-linked
201869_s_at	TBL1X	6907	0.03	NM_005647	NP_005638	1.15	transducin (beta)-like 1X-linked
201871_s_at	LOC51035	51035	0.01	NM_015853	NP_056937	0.87	ORF
201872_s_at	ABCE1	6059	0.02	NM_002940	NP_002931	0.91	ATP-binding cassette, sub-family E (OABP), member 1
201873_s_at	ABCE1	6059	0.01	NM_002940	NP_002931	0.83	ATP-binding cassette, sub-family E (OABP), member 1
201874_at	MPZL1	9019	0.04	NM_003953	NP_003944	1.23	myelin protein zero-like 1
201875_s_at	MPZL1	9019	0.01	NM_024569	NP_078845	1.27	myelin protein zero-like 1
201885_s_at	DIA1	1727	0.04	NM_000398	NP_000389	0.91	diaphorase (NADH) (cytochrome b-5 reductase)
201886_at	WDR23	80344	0.02	NM_025230	NP_079506	1.10	WD repeat domain 23
201898_s_at	UBE2A	7319	0.03	NM_003336	NP_003327	0.94	ubiquitin-conjugating enzyme E2A (RAD6 homolog)
201908_at	DVL3	1857	0.03	NM_004423	NP_004414	1.09	dishevelled, dsh homolog 3 (Drosophila)
201916_s_at	SEC63	11231	0.01	NM_007214	NP_009145	0.95	SEC63-like (S. cerevisiae)
201917_s_at	FLJ10618	55186	2.05e-03	NM_018155	NP_060625	0.84	hypothetical protein FLJ10618
201919_at	FLJ10618	55186	9.53e-04	AL049246		0.91	hypothetical protein FLJ10618
201920_at	SLC20A1	6574	0.02	NM_005415	NP_005406	0.85	solute carrier family 20 (phosphate transporter), member 1
201922_at	TINP1	10412	0.01	NM_014886	NP_055701	0.89	TGF beta-inducible nuclear protein 1
201923_at	PRDX4	10549	0.01	NM_006406	NP_006397	0.97	peroxiredoxin 4
201924_at	MLLT2	4299	0.04	NM_005935	NP_005926	0.90	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2
201931_at	ETFA	2108	6.92e-03	NM_000126	NP_000117	0.95	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)
201934_at	PRO2730	80335	0.03	AY358264	AAQ88631	0.92	hypothetical protein PRO2730
201946_s_at	CCT2	10576	2.05e-03	NM_006431	NP_006422	0.90	chaperonin containing TCP1, subunit 2 (beta)
201947_s_at	CCT2	10576	0.01	NM_006431	NP_006422	0.89	chaperonin containing TCP1, subunit 2 (beta)
201948_at	GNL2	29889	0.01	NM_013285	NP_037417	0.85	guanine nucleotide binding protein-like 2 (nucleolar)
201955_at	CCNC	892	3.71e-03	NM_005190	NP_005181	0.90	cyclin C
201956_s_at	GNPAT	8443	4.6e-03	NM_014236	NP_055051	0.93	glyceronephosphate O-acyltransferase
201963_at	ACSL1	2180	0.03	NM_001995	NP_001986	1.08	acyl-CoA synthetase long-chain family member 1
201970_s_at	NASP	4678	3.95e-03	NM_002482	NP_002473	0.81	nuclear autoantigenic sperm protein (histone-binding)
201973_s_at	C7orf28A	51622	1.38e-03	NM_015622	NP_056437	0.91	chromosome 7 open reading frame 28A
201988_s_at	CREBL2	1389	0.04	NM_001310	NP_001301	0.91	cAMP responsive element binding protein-like 2
201989_s_at	CREBL2	1389	0.01	NM_001310	NP_001301	0.95	cAMP responsive element binding protein-like 2
201990_s_at	CREBL2	1389	2.01e-03	NM_001310	NP_001301	0.85	cAMP responsive element binding protein-like 2
201993_x_at	HNRPDL	9987	0.01	NM_005463	NP_005454	0.87	heterogeneous nuclear ribonucleoprotein D-like
201995_at	EXT1	2131	0.02	NM_000127	NP_000118	1.19	exostoses (multiple) 1
202000_at	NDUFA6	4700	0.01	NM_002490	NP_002481	0.93	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
202001_s_at	NDUFA6	4700	4.14e-03	NM_002490	NP_002481	0.81	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
202011_at	TJP1	7082	0.03	NM_003257	NP_003248	1.24	tight junction protein 1 (zona occludens 1)
202013_s_at	EXT2	2132	0.04	NM_000401	NP_000392	0.86	exostoses (multiple) 2

202015_x_at	METAP2	10988	0.03	NM_006838	NP_006829	1.23	methionyl aminopeptidase 2
202021_x_at	SUI1	10209	0.01	NM_005801	NP_005792	0.92	putative translation initiation factor
202025_x_at	ACAA1	30	1.68e-03	NM_001607	NP_001598	0.93	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
202026_at	SDHD	6392	1.35e-03	NM_003002	NP_002993	0.88	succinate dehydrogenase complex, subunit D, integral membrane protein
202030_at	BCKDK	10295	0.02	NM_005881	NP_005872	0.93	branched chain ketoacid dehydrogenase kinase
202038_at	UBE4A	9354	0.02	NM_004788	NP_004779	0.95	ubiquitination factor E4A (UFD2 homolog, yeast)
202046_s_at	GRLF1	2909	0.02	NM_004491	NP_004482	1.16	glucocorticoid receptor DNA binding factor 1
202049_s_at	ZNF262	9202	4.07e-03	NM_005095	NP_005086	0.84	zinc finger protein 262
202054_s_at	ALDH3A2	224	0.02	NM_000382	NP_000373	0.85	aldehyde dehydrogenase 3 family, member A2
202058_s_at	KPNA1	3836	0.03	NM_002264	NP_002255	0.92	karyopherin alpha 1 (importin alpha 5)
202059_s_at	KPNA1	3836	0.02	NM_002264	NP_002255	0.90	karyopherin alpha 1 (importin alpha 5)
202069_s_at	IDH3A	3419	3.43e-04	NM_005530	NP_005521	0.90	isocitrate dehydrogenase 3 (NAD+) alpha
202070_s_at	IDH3A	3419	9.1e-03	NM_005530	NP_005521	0.87	isocitrate dehydrogenase 3 (NAD+) alpha
202076_at	BIRC2	329	0.02	NM_001166	NP_001157	0.92	baculoviral IAP repeat-containing 2
202077_at	NDUFAB1	4706	0.01	NM_005003	NP_004994	0.92	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
202078_at	COPS3	8533	0.03	NM_003653	NP_003644	0.93	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
202079_s_at	OIP106	22906	0.02	AB028965	BAA82994	1.10	OGT(O-Glc-NAc transferase)-interacting protein 106 KDa
202087_s_at	CTSL	1514	0.02	NM_001912	NP_001903	0.72	cathepsin L
202088_at	SLC39A6	25800	0.02	BC008317	AAH08317	0.87	solute carrier family 39 (zinc transporter), member 6
202092_s_at	ARL2BP	23568	0.04	NM_012106	NP_036238	0.95	ADP-ribosylation factor-like 2 binding protein
202104_s_at	SPG7	6687	0.01	NM_003119	NP_003110	0.81	spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)
202110_at	COX7B	1349	0.04	NM_001866	NP_001857	0.97	cytochrome c oxidase subunit VIIb
202117_at	ARHGAP1	392	0.04	NM_004308	NP_004299	0.92	Rho GTPase activating protein 1
202118_s_at	CPNE3	8895	0.01	NM_003909	NP_003900	0.90	copine III
202125_s_at	ALS2CR3	66008	0.02	NM_015049	NP_055864	0.89	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3
202126_at	PRPF4B	8899	0.01	NM_003913	NP_003904	0.89	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
202128_at	KIAA0317	9870	4.51e-03	NM_014821	NP_055636	0.92	KIAA0317
202129_s_at	RIOK3	8780	9.61e-03	NM_003831	NP_003822	1.14	RIO kinase 3 (yeast)
202130_at	RIOK3	8780	0.04	NM_003831	NP_003822	0.96	RIO kinase 3 (yeast)
202135_s_at	ACTR1B	10120	6.4e-03	NM_005735	NP_005726	0.90	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)
202138_x_at	JTV1	7965	0.01	NM_006303	NP_006294	0.90	JTV1 gene
202141_s_at	COPS8	10920	0.02	NM_006710	NP_006701	0.91	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)
202144_s_at	ADSL	158	0.01	NM_000026	NP_000017	0.92	adenylosuccinate lyase
202163_s_at	CNOT8	9337	4.51e-03	NM_004779	NP_004770	0.88	CCR4-NOT transcription complex, subunit 8
202164_s_at	CNOT8	9337	0.01	NM_004779	NP_004770	0.94	CCR4-NOT transcription complex, subunit 8
202165_at	PPP1R2	5504	0.03	NM_006241	NP_006232	0.91	protein phosphatase 1, regulatory (inhibitor) subunit 2
202166_s_at	PPP1R2	5504	7.73e-05	NM_006241	NP_006232	0.87	protein phosphatase 1, regulatory (inhibitor) subunit 2

202168_at	TAF9	6880	0.02	NM_003187	NP_003178	0.90	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa
202169_s_at	AASDHPPT	60496	0.02	NM_015423	NP_056238	0.90	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
202172_at	ZNF161	7716	0.04	BX648862		0.94	zinc finger protein 161
202174_s_at	PCM1	5108	0.01	NM_006197	NP_006188	0.89	pericentriolar material 1
202176_at	ERCC3	2071	0.04	NM_000122	NP_000113	0.92	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B compleme
202181_at	KIAA0247	9766	0.01	NM_014734	NP_055549	0.92	KIAA0247
202182_at	GCN5L2	2648	0.04	NM_021078	NP_066564	0.86	GCN5 general control of amino-acid synthesis 5-like 2 (yeast)
202184_s_at	NUP133	55746	0.02	NM_018230	NP_060700	0.90	nucleoporin 133kDa
202188_at	NUP93	9688	0.03	NM_014669	NP_055484	0.84	nucleoporin 93kDa
202189_x_at	PTBP1	5725	0.01	NM_002819	NP_002810	0.90	polypyrimidine tract binding protein 1
202195_s_at	TMED5	50999	9.3e-04	NM_016040	NP_057124	0.86	transmembrane emp24 protein transport domain containing 5
202205_at	VASP	7408	0.04	NM_003370	NP_003361	1.06	vasodilator-stimulated phosphoprotein
202206_at	ARL7	10123	8.05e-03	NM_005737	NP_005728	0.88	ADP-ribosylation factor-like 7
202207_at	ARL7	10123	3.26e-03	NM_005737	NP_005728	0.84	ADP-ribosylation factor-like 7
202220_at	KIAA0907	22889	0.03	NM_014949	NP_055764	0.92	KIAA0907 protein
202221_s_at	EP300	2033	0.02	NM_001429	NP_001420	0.87	E1A binding protein p300
202224_at	CRK	1398	5.48e-03	NM_005206	NP_005197	1.18	v-crk sarcoma virus CT10 oncogene homolog (avian)
202231_at	GA17	10480	0.01	NM_006360	NP_006351	0.87	dendritic cell protein
202232_s_at	GA17	10480	0.01	NM_006360	NP_006351	0.88	dendritic cell protein
202233_s_at	UQCRH	7388	0.03	NM_006004	NP_005995	0.95	ubiquinol-cytochrome c reductase hinge protein
202243_s_at	PSMB4	5692	0.03	NM_002796	NP_002787	0.95	proteasome (prosome, macropain) subunit, beta type, 4
202245_at	LSS	4047	3.06e-03	NM_002340	NP_002331	0.85	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
202251_at	PRPF3	9129	0.04	NM_004698	NP_004689	0.88	PRP3 pre-mRNA processing factor 3 homolog (yeast)
202255_s_at	SIPA1L1	26037	0.01	NM_015556	NP_056371	1.11	signal-induced proliferation-associated 1 like 1
202256_at	CD2BP2	10421	0.01	AB033004	BAA86492	0.91	CD2 antigen (cytoplasmic tail) binding protein 2
202257_s_at	CD2BP2	10421	0.02	NM_006110	NP_006101	0.84	CD2 antigen (cytoplasmic tail) binding protein 2
202258_s_at	PFAAP5	10443	0.03	NM_014887	NP_055702	0.93	phosphonoformate immuno-associated protein 5
202264_s_at	TOMM40	10452	0.04	NM_006114	NP_006105	0.90	translocase of outer mitochondrial membrane 40 homolog (yeast)
202265_at	PCGF4	648	0.01	NM_005180	NP_005171	0.86	polycomb group ring finger 4
202268_s_at	APPBP1	8883	0.04	NM_003905	NP_003896	0.90	amyloid beta precursor protein binding protein 1, 59kDa
202270_at	GBP1	2633	0.04	NM_002053	NP_002044	0.74	guanylate binding protein 1, interferon-inducible, 67kDa
202276_at	SHFM1	7979	7.69e-03	NM_006304	NP_006295	0.93	split hand/foot malformation (ectrodactyly) type 1
202282_at	HADH2	3028	0.04	NM_004493	NP_004484	0.87	hydroxyacyl-Coenzyme A dehydrogenase, type II
202290_at	PDAP1	11333	0.03	NM_014891	NP_055706	0.87	PDGFA associated protein 1
202296_s_at	RER1	11079	0.03	NM_007033	NP_008964	0.96	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)
202298_at	NDUFA1	4694	4.6e-03	NM_004541	NP_004532	0.90	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
202301_s_at	FLJ11021	65117	2.33e-03	NM_023012	NP_075388	0.92	similar to splicing factor, arginine/serine-rich 4

202302_s_at	FLJ11021	65117	4.37e-03	NM_023012	NP_075388	0.93	similar to splicing factor, arginine/serine-rich 4
202303_x_at	SMARCA5	8467	0.01	NM_003601	NP_003592	0.90	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
202306_at	POLR2G	5436	8.09e-03	NM_002696	NP_002687	0.90	polymerase (RNA) II (DNA directed) polypeptide G
202307_s_at	TAP1	6890	0.01	NM_000593	NP_000584	0.80	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
202313_at	PPP2R2A	5520	0.02	NM_002717	NP_002708	0.93	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
202322_s_at	GGPS1	9453	0.01	NM_004837	NP_004828	0.95	geranylgeranyl diphosphate synthase 1
202325_s_at	ATP5J	522	0.01	NM_001685	NP_001676	0.90	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6
202330_s_at	UNG	7374	0.03	NM_003362	NP_003353	0.82	uracil-DNA glycosylase
202333_s_at	UBE2B	7320	1.13e-03	NM_003337	NP_003328	1.15	ubiquitin-conjugating enzyme E2B (RAD6 homolog)
202335_s_at	UBE2B	7320	0.02	NM_003337	NP_003328	1.14	ubiquitin-conjugating enzyme E2B (RAD6 homolog)
202343_x_at	COX5B	1329	0.03	NM_001862	NP_001853	0.90	cytochrome c oxidase subunit Vb
202345_s_at	FABP5	2171	2.39e-03	NM_001444	NP_001435	0.70	fatty acid binding protein 5 (psoriasis-associated)
202348_s_at	TOR1A	1861	3.72e-04	NM_000113	NP_000104	0.86	torsin family 1, member A (torsin A)
202349_at	TOR1A	1861	0.02	NM_000113	NP_000104	0.91	torsin family 1, member A (torsin A)
202353_s_at	PSMD12	5718	0.03	NM_002816	NP_002807	0.94	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
202354_s_at	GTF2F1	2962	5.57e-03	NM_002096	NP_002087	0.84	general transcription factor IIF, polypeptide 1, 74kDa
202355_s_at	GTF2F1	2962	0.04	NM_002096	NP_002087	0.93	general transcription factor IIF, polypeptide 1, 74kDa
202358_s_at	SNX19	399979	0.02	D87443	BAA13384	0.91	sorting nexin 19
202359_s_at	SNX19	399979	0.02	D87443	BAA13384	0.90	sorting nexin 19
202362_at	RAP1A	5906	0.02	NM_002884	NP_002875	0.89	RAP1A, member of RAS oncogene family
202365_at	MGC5139	84747	1.65e-03	BC004815	AAH04815	0.89	hypothetical protein MGC5139
202367_at	CUTL1	1523	0.02	NM_001913	NP_001904	0.87	cut-like 1, CCAAT displacement protein (Drosophila)
202369_s_at	TRAM2	9697	4.16e-04	NM_012288	NP_036420	0.93	translocation associated membrane protein 2
202370_s_at	CBFB	865	1.57e-03	NM_001755	NP_001746	0.93	core-binding factor, beta subunit
202374_s_at	RAB3-GAP150	25782	0.02	NM_012414	NP_036546	0.92	rab3 GTPase-activating protein, non-catalytic subunit (150kD)
202380_s_at	NKTR	4820	0.04	NM_005385	NP_005376	0.91	natural killer-tumor recognition sequence
202382_s_at	GNPDA1	10007	5.61e-03	NM_005471	NP_005462	0.90	glucosamine-6-phosphate deaminase 1
202386_s_at	LKAP	9665	0.01	NM_019081	NP_061954	0.94	limkain b1
202391_at	BASP1	10409	9.61e-03	NM_006317	NP_006308	1.11	brain abundant, membrane attached signal protein 1
202394_s_at	ABCF3	55324	0.04	NM_018358	NP_060828	0.91	ATP-binding cassette, sub-family F (GCN20), member 3
202395_at	NSF	4905	0.02	NM_006178	NP_006169	0.93	N-ethylmaleimide-sensitive factor
202396_at	TCERG1	10915	2.53e-03	NM_006706	NP_006697	0.85	transcription elongation regulator 1
202405_at	TIAL1	7073	0.03	BF432532		0.87	TIA1 cytotoxic granule-associated RNA binding protein-like 1
202406_s_at	TIAL1	7073	0.01	NM_003252	NP_003243	0.91	TIA1 cytotoxic granule-associated RNA binding protein-like 1
202407_s_at	PRPF31	26121	0.04	NM_015629	NP_056444	0.90	PRP31 pre-mRNA processing factor 31 homolog (yeast)
202413_s_at	USP1	7398	3.43e-03	NM_003368	NP_003359	0.94	ubiquitin specific protease 1
202414_at	ERCC5	2073	0.03	NM_000123	NP_000114	0.91	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation

202416_at	DNAJC7	7266	0.04	NM_003315	NP_003306	0.86	DnaJ (Hsp40) homolog, subfamily C, member 7
202418_at	YIF1	10897	0.02	NM_020470	NP_065203	0.89	Yip1 interacting factor homolog (S. cerevisiae)
202430_s_at	PLSCR1	5359	0.02	NM_021105	NP_066928	0.70	phospholipid scramblase 1
202431_s_at	MYC	4609	0.02	NM_002467	NP_002458	0.86	v-myc myelocytomatosis viral oncogene homolog (avian)
202433_at	SLC35B1	10237	5.63e-04	NM_005827	NP_005818	0.93	solute carrier family 35, member B1
202439_s_at	IDS	3423	0.03	NM_000202	NP_000193	1.11	iduronate 2-sulfatase (Hunter syndrome)
202441_at	SPFH1	10613	0.01	NM_006459	NP_006450	0.92	SPFH domain family, member 1
202442_at	AP3S1	1176	0.02	NM_001284	NP_001275	0.95	adaptor-related protein complex 3, sigma 1 subunit
202447_at	DECR1	1666	0.02	NM_001359	NP_001350	0.95	2,4-dienoyl CoA reductase 1, mitochondrial
202450_s_at	CTSK	1513	0.01	NM_000396	NP_000387	1.10	cathepsin K (pycnodysostosis)
202451_at	GTF2H1	2965	0.03	NM_005316	NP_005307	0.87	general transcription factor IIH, polypeptide 1, 62kDa
202453_s_at	GTF2H1	2965	0.02	NM_005316	NP_005307	0.90	general transcription factor IIH, polypeptide 1, 62kDa
202460_s_at	LPIN2	9663	0.04	NM_014646	NP_055461	0.87	lipin 2
202461_at	EIF2B2	8892	1.95e-03	NM_014239	NP_055054	0.93	eukaryotic translation initiation factor 2B, subunit 2 beta,
39kDa							
202466_at	POLS	11044	5.06e-03	NM_006999	NP_008930	0.87	polymerase (DNA directed) sigma
202467_s_at	COPS2	9318	0.01	NM_004236	NP_004227	0.89	COP9 constitutive photomorphogenic homolog subunit 2
(Arabidopsis)							
202468_s_at	CTNNAL1	8727	0.01	NM_003798	NP_003789	1.25	catenin (cadherin-associated protein), alpha-like 1
202469_s_at	CPSF6	11052	0.04	NM_007007	NP_008938	0.89	cleavage and polyadenylation specific factor 6, 68kDa
202478_at	TRIB2	28951	0.04	NM_021643	NP_067675	0.85	tribbles homolog 2 (Drosophila)
202479_s_at	TRIB2	28951	0.02	NM_021643	NP_067675	0.87	tribbles homolog 2 (Drosophila)
202481_at	DHRS3	9249	0.02	NM_004753	NP_004744	0.87	dehydrogenase/reductase (SDR family) member 3
202491_s_at	IKBKAP	8518	4.6e-03	NM_003640	NP_003631	0.83	inhibitor of kappa light polypeptide gene enhancer in B-
cells, kinase complex-associated protein							
202502_at	ACADM	34	0.01	NM_000016	NP_000007	0.86	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight
chain							
202503_s_at	KIAA0101	9768	0.02	NM_014736	NP_055551	1.09	KIAA0101
202505_at	SNRPB2	6629	0.03	NM_003092	NP_003083	0.92	small nuclear ribonucleoprotein polypeptide B"
202511_s_at	APG5L	9474	0.02	NM_004849	NP_004840	0.94	APG5 autophagy 5-like (S. cerevisiae)
202514_at	DLG1	1739	1.19e-03	AL831922	CAD38582	0.87	discs, large homolog 1 (Drosophila)
202515_at	DLG1	1739	0.01	AL831922	CAD38582	0.91	discs, large homolog 1 (Drosophila)
202518_at	BCL7B	9275	6.4e-03	NM_001707	NP_001698	0.87	B-cell CLL/lymphoma 7B
202520_s_at	MLH1	4292	0.01	NM_000249	NP_000240	0.94	mutL homolog 1, colon cancer, nonpolyposis type 2 (E.
coli)							
202522_at	PITPNB	23760	0.03	NM_012399	NP_036531	0.94	phosphatidylinositol transfer protein, beta
202526_at	SMAD4	4089	0.02	U44378	AAA91041	1.07	SMAD, mothers against DPP homolog 4 (Drosophila)
202527_s_at	SMAD4	4089	0.02	NM_005359	NP_005350	0.95	SMAD, mothers against DPP homolog 4 (Drosophila)
202537_s_at	DKFZP564O123	25978	0.03	NM_014043	NP_054762	0.90	DKFZP564O123 protein
202538_s_at	DKFZP564O123	25978	0.03	NM_014043	NP_054762	0.91	DKFZP564O123 protein
202541_at	SCYE1	9255	6.11e-03	NM_004757	NP_004748	0.87	small inducible cytokine subfamily E, member 1
(endothelial monocyte-activating)							
202542_s_at	SCYE1	9255	1.66e-03	NM_004757	NP_004748	0.91	small inducible cytokine subfamily E, member 1
(endothelial monocyte-activating)							
202556_s_at	MCRS1	10445	0.03	NM_006337	NP_006328	0.94	microspherule protein 1

202557_at	STCH	6782	0.03	NM_006948	NP_008879	0.87	stress 70 protein chaperone, microsome-associated, 60kDa
202558_s_at	STCH	6782	7.04e-03	NM_006948	NP_008879	0.83	stress 70 protein chaperone, microsome-associated, 60kDa
202560_s_at	DKFZP547E1010	26097	0.04	NM_015607	NP_056422	0.92	DKFZP547E1010 protein
202561_at	TNKS	8658	1.66e-03	AF082557	AAC79842	0.89	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
202567_at	SNRPD3	6634	0.01	NM_004175	NP_004166	0.86	small nuclear ribonucleoprotein D3 polypeptide 18kDa
202581_at	HSPA1B	3304	0.04	NM_005346	NP_005337	1.28	heat shock 70kDa protein 1B
202582_s_at	RANBP9	10048	0.02	NM_005493	NP_005484	0.93	RAN binding protein 9
202585_s_at	NFX1	4799	0.02	NM_002504	NP_002495	0.92	nuclear transcription factor, X-box binding 1
202591_s_at	SSBP1	6742	0.01	NM_003143	NP_003134	0.90	single-stranded DNA binding protein 1
202595_s_at	LEPROTL1	23484	4.51e-03	NM_015344	NP_056159	0.93	leptin receptor overlapping transcript-like 1
202599_s_at	NRIP1	8204	0.03	NM_003489	NP_003480	0.90	nuclear receptor interacting protein 1
202600_s_at	NRIP1	8204	0.04	NM_003489	NP_003480	0.88	nuclear receptor interacting protein 1
202604_x_at	ADAM10	102	0.04	NM_001110	NP_001101	0.93	a disintegrin and metalloproteinase domain 10
202610_s_at	CRSP2	9282	5.44e-03	NM_004229	NP_004220	0.92	cofactor required for Sp1 transcriptional activation, subunit 2, 150kDa
202611_s_at	CRSP2	9282	0.02	NM_004229	NP_004220	0.90	cofactor required for Sp1 transcriptional activation, subunit 2, 150kDa
202613_at	CTPS	1503	0.01	NM_001905	NP_001896	0.90	CTP synthase
202614_at	SLC30A9	10463	0.02	NM_006345	NP_006336	0.90	solute carrier family 30 (zinc transporter), member 9
202623_at	C14orf11	55837	0.03	NM_018453	NP_060923	0.92	chromosome 14 open reading frame 11
202633_at	TOPBP1	11073	0.01	NM_007027	NP_008958	0.96	topoisomerase (DNA) II binding protein 1
202635_s_at	POLR2K	5440	0.01	NM_005034	NP_005025	0.86	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
202636_at	RNF103	7844	0.02	NM_005667	NP_005658	0.95	ring finger protein 103
202642_s_at	TRRAP	8295	0.01	NM_003496	NP_003487	0.85	transformation/transcription domain-associated protein
202647_s_at	NRAS	4893	0.01	NM_002524	NP_002515	0.89	neuroblastoma RAS viral (v-ras) oncogene homolog
202655_at	ARMET	7873	0.03	NM_006010	NP_006001	0.93	arginine-rich, mutated in early stage tumors
202658_at	PEX11B	8799	5.57e-03	NM_003846	NP_003837	0.91	peroxisomal biogenesis factor 11B
202659_at	PSMB10	5699	0.01	NM_002801	NP_002792	0.86	proteasome (prosome, macropain) subunit, beta type, 10
202663_at	WASPIP	7456	0.02	NM_003387	NP_003378	0.90	Wiskott-Aldrich syndrome protein interacting protein
202666_s_at	ACTL6A	86	0.02	NM_004301	NP_004292	0.88	actin-like 6A
202667_s_at	SLC39A7	7922	5.07e-03	NM_006979	NP_008910	0.88	solute carrier family 39 (zinc transporter), member 7
202670_at	MAP2K1	5604	9.08e-03	NM_002755	NP_002746	0.89	mitogen-activated protein kinase kinase 1
202675_at	SDHB	6390	0.04	NM_003000	NP_002991	0.97	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
202677_at	RASA1	5921	0.02	NM_002890	NP_002881	0.93	RAS p21 protein activator (GTPase activating protein) 1
202678_at	GTF2A2	2958	6.4e-03	NM_004492	NP_004483	0.91	general transcription factor IIA, 2, 12kDa
202679_at	NPC1	4864	0.03	NM_000271	NP_000262	0.83	Niemann-Pick disease, type C1
202691_at	SNRPD1	6632	0.02	NM_006938	NP_008869	0.84	small nuclear ribonucleoprotein D1 polypeptide 16kDa
202694_at	STK17A	9263	0.03	NM_004760	NP_004751	0.86	serine/threonine kinase 17a (apoptosis-inducing)
202696_at	OXSR1	9943	0.01	NM_005109	NP_005100	0.91	oxidative-stress responsive 1
202697_at	CPSF5	11051	0.01	NM_007006	NP_008937	0.86	cleavage and polyadenylation specific factor 5, 25 kDa

202706_s_at	UMPS	7372	8.26e-04	NM_000373	NP_000364	0.95	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)
202710_at	BET1	10282	0.02	NM_005868	NP_005859	0.86	BET1 homolog (S. cerevisiae)
202713_s_at	KIAA0391	9692	0.03	XM_375074	XP_375074	0.92	KIAA0391
202716_at	PTPN1	5770	3.43e-03	NM_002827	NP_002818	1.10	protein tyrosine phosphatase, non-receptor type 1
202717_s_at	CDC16	8881	0.03	NM_003903	NP_003894	0.88	CDC16 cell division cycle 16 homolog (S. cerevisiae)
202720_at	TES	26136	2.16e-03	NM_015641	NP_056456	0.91	testis derived transcript (3 LIM domains)
202730_s_at	PDCD4	27250	0.02	NM_014456	NP_055271	0.89	programmed cell death 4 (neoplastic transformation inhibitor)
202731_at	PDCD4	27250	0.02	NM_014456	NP_055271	0.92	programmed cell death 4 (neoplastic transformation inhibitor)
202735_at	EBP	10682	0.02	NM_006579	NP_006570	0.79	emopamil binding protein (sterol isomerase)
202736_s_at	LSM4	25804	0.02	NM_012321	NP_036453	0.90	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)
202738_s_at	PHKB	5257	0.01	NM_000293	NP_000284	0.90	phosphorylase kinase, beta
202741_at	PRKACB	5567	0.01	NM_182948	NP_891993	0.88	protein kinase, cAMP-dependent, catalytic, beta
202742_s_at	PRKACB	5567	0.04	NM_002731	NP_002722	0.88	protein kinase, cAMP-dependent, catalytic, beta
202753_at	p44S10	9861	0.02	NM_014814	NP_055629	0.95	proteasome regulatory particle subunit p44S10
202758_s_at	RFXANK	8625	0.01	NM_003721	NP_003712	0.81	regulatory factor X-associated ankyrin-containing protein
202761_s_at	SYNE2	23224	0.02	NM_015180	NP_055995	0.88	spectrin repeat containing, nuclear envelope 2
202767_at	ACP2	53	0.03	NM_001610	NP_001601	0.92	acid phosphatase 2, lysosomal
202771_at	FAM38A	9780	0.02	NM_014745	NP_055560	0.88	family with sequence similarity 38, member A
202774_s_at	SFRS8	6433	0.03	NM_004592	NP_004583	0.89	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)
202775_s_at	SFRS8	6433	0.03	NM_004592	NP_004583	0.89	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)
202778_s_at	ZNF198	7750	0.02	NM_003453	NP_003444	0.95	zinc finger protein 198
202780_at	OXCT1	5019	0.03	NM_000436	NP_000427	0.90	3-oxoacid CoA transferase 1
202783_at	NNT	23530	0.02	NM_182977	NP_892022	0.84	nicotinamide nucleotide transhydrogenase
202783_at	NNT	23530	0.02	NM_012343	NP_036475	0.84	nicotinamide nucleotide transhydrogenase
202784_s_at	NNT	23530	8.5e-04	NM_012343	NP_036475	0.86	nicotinamide nucleotide transhydrogenase
202791_s_at	KIAA0685	9701	0.04	NM_014678	NP_055493	0.94	KIAA0685
202797_at	SACM1L	22908	0.01	NM_014016	NP_054735	0.85	SAC1 suppressor of actin mutations 1-like (yeast)
202798_at	SEC24B	10427	0.02	NM_006323	NP_006314	0.94	SEC24 related gene family, member B (S. cerevisiae)
2028_s_at	E2F1	1869	0.02	NM_005225	NP_005216	1.12	E2F transcription factor 1
202801_at	PRKACA	5566	0.04	NM_002730	NP_002721	1.12	protein kinase, cAMP-dependent, catalytic, alpha
202810_at	DRG1	4733	0.01	NM_004147	NP_004138	0.90	developmentally regulated GTP binding protein 1
202813_at	TARBP1	6894	2.78e-04	NM_005646	NP_005637	0.84	TAR (HIV) RNA binding protein 1
202814_s_at	HIS1	10614	0.02	NM_006460	NP_006451	0.90	HMBA-inducible
202816_s_at	SS18	6760	2.66e-03	NM_005637	NP_005628	0.84	synovial sarcoma translocation, chromosome 18
202817_s_at	SS18	6760	2.4e-03	NM_005637	NP_005628	0.77	synovial sarcoma translocation, chromosome 18
202826_at	SPINT1	6692	0.01	NM_003710	NP_003701	1.17	serine protease inhibitor, Kunitz type 1
202836_s_at	TXNL4A	10907	0.04	NM_006701	NP_006692	0.93	thioredoxin-like 4A
202841_x_at	OGFR	11054	0.04	NM_007346	NP_031372	1.05	opioid growth factor receptor

202842_s_at	DNAJB9	4189	0.03	NM_012328	NP_036460	0.93	DnaJ (Hsp40) homolog, subfamily B, member 9
202843_at	DNAJB9	4189	0.03	NM_012328	NP_036460	0.91	DnaJ (Hsp40) homolog, subfamily B, member 9
202846_s_at	PIGC	5279	0.02	NM_002642	NP_002633	0.92	phosphatidylinositol glycan, class C
202847_at	PCK2	5106	1.68e-03	NM_004563	NP_004554	0.81	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
202850_at	ABCD3	5825	0.02	NM_002858	NP_002849	0.91	ATP-binding cassette, sub-family D (ALD), member 3
202852_s_at	FLJ11506	79719	0.02	NM_024666	NP_078942	0.94	hypothetical protein FLJ11506
202854_at	HPRT1	3251	0.01	NM_000194	NP_000185	0.86	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)
202858_at	U2AF1	7307	0.02	NM_006758	NP_006749	0.91	U2(RNU2) small nuclear RNA auxiliary factor 1
202862_at	FAH	2184	9.37e-03	NM_000137	NP_000128	0.89	fumarylacetoacetate hydrolase (fumarylacetoacetase)
202864_s_at	SP100	6672	0.02	NM_003113	NP_003104	1.12	nuclear antigen Sp100
202868_s_at	POP4	10775	0.04	NM_006627	NP_006618	0.95	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)
202869_at	OAS1	4938	0.01	NM_016816	NP_058132	0.51	2',5'-oligoadenylate synthetase 1, 40/46kDa
202878_s_at	C1QR1	22918	0.03	NM_012072	NP_036204	0.89	complement component 1, q subcomponent, receptor 1
202882_x_at	NOL7	51406	0.01	NM_016167	NP_057251	0.88	nucleolar protein 7, 27kDa
202886_s_at	PPP2R1B	5519	7.69e-03	NM_002716	NP_002707	0.92	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform
202887_s_at	DDIT4	54541	0.03	NM_019058	NP_061931	0.80	DNA-damage-inducible transcript 4
202892_at	CDC23	8697	0.03	NM_004661	NP_004652	0.91	CDC23 (cell division cycle 23, yeast, homolog)
202899_s_at	SFRS3	6428	0.03	NM_003017	NP_003008	0.94	splicing factor, arginine/serine-rich 3
202900_s_at	NUP88	4927	0.02	NM_002532	NP_002523	0.86	nucleoporin 88kDa
202904_s_at	LSM5	23658	0.03	NM_012322	NP_036454	0.88	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
202905_x_at	NBS1	4683	5.45e-03	NM_002485	NP_002476	0.82	Nijmegen breakage syndrome 1 (nibrin)
202906_s_at	NBS1	4683	0.01	NM_002485	NP_002476	0.83	Nijmegen breakage syndrome 1 (nibrin)
202907_s_at	NBS1	4683	7.65e-03	NM_002485	NP_002476	0.85	Nijmegen breakage syndrome 1 (nibrin)
202909_at	EPM2AIP1	9852	3.1e-03	NM_014805	NP_055620	0.92	EPM2A (laforin) interacting protein 1
202910_s_at	CD97	976	7.02e-03	NM_001784	NP_001775	1.12	CD97 antigen
202911_at	MSH6	2956	0.02	NM_000179	NP_000170	0.92	mutS homolog 6 (E. coli)
202915_s_at	FAM20B	9917	0.02	NM_014864	NP_055679	0.91	family with sequence similarity 20, member B
202916_s_at	FAM20B	9917	0.01	NM_014864	NP_055679	0.86	family with sequence similarity 20, member B
202918_s_at	PREI3	25843	0.01	NM_015387	NP_056202	0.90	preimplantation protein 3
202922_at	GCLC	2729	0.02	NM_001498	NP_001489	0.89	glutamate-cysteine ligase, catalytic subunit
202923_s_at	GCLC	2729	0.04	NM_001498	NP_001489	0.91	glutamate-cysteine ligase, catalytic subunit
202927_at	PIN1	5300	2.28e-03	NM_006221	NP_006212	0.79	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1
202930_s_at	SUCLA2	8803	0.03	NM_003850	NP_003841	0.90	succinate-CoA ligase, ADP-forming, beta subunit
202932_at	YES1	7525	0.01	NM_005433	NP_005424	0.76	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
202941_at	NDUFV2	4729	0.01	NM_021074	NP_066552	0.96	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa
202942_at	ETFB	2109	0.02	NM_001985	NP_001976	0.84	electron-transfer-flavoprotein, beta polypeptide
202951_at	STK38	11329	0.04	NM_007271	NP_009202	0.94	serine/threonine kinase 38
202955_s_at	ARFGEF1	10565	9.22e-03	NM_006421	NP_006412	0.93	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)

202956_at	ARFGEF1	10565	0.02	NM_006421	NP_006412	0.92	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)
202959_at	MUT	4594	0.03	NM_000255	NP_000246	0.92	methylmalonyl Coenzyme A mutase
202963_at	RFX5	5993	0.02	NM_000449	NP_000440	0.83	regulatory factor X, 5 (influences HLA class II expression)
202968_s_at	DYRK2	8445	0.03	NM_003583	NP_003574	0.85	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
202969_at	DYRK2	8445	2.8e-03	AI216690		0.83	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
202971_s_at	DYRK2	8445	0.01	NM_006482	NP_006473	0.84	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
202976_s_at	RHOBTB3	22836	0.02	NM_014899	NP_055714	0.77	Rho-related BTB domain containing 3
202978_s_at	ZF	58487	1.13e-03	NM_021212	NP_067035	0.87	HCF-binding transcription factor Zhangfei
202979_s_at	ZF	58487	0.01	NM_021212	NP_067035	0.91	HCF-binding transcription factor Zhangfei
202984_s_at	BAG5	9529	0.02	NM_004873	NP_004864	0.88	BCL2-associated athanogene 5
202985_s_at	BAG5	9529	0.03	NM_004873	NP_004864	0.93	BCL2-associated athanogene 5
203003_at	MEF2D	4209	0.02	NM_005920	NP_005911	1.16	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D)
203008_x_at	TXNDC9	10190	4.31e-03	NM_005783	NP_005774	0.90	thioredoxin domain containing 9
203011_at	IMPA1	3612	0.02	NM_005536	NP_005527	0.89	inositol(myo)-1(or 4)-monophosphatase 1
203013_at	HSGT1	11319	0.01	NM_007265	NP_009196	0.94	suppressor of S. cerevisiae gcr2
203021_at	SLPI	6590	0.04	NM_003064	NP_003055	0.81	secretory leukocyte protease inhibitor (antileukoproteinase)
203022_at	RNASEH2A	10535	0.01	NM_006397	NP_006388	0.87	ribonuclease H2, large subunit
203023_at	HSPC111	51491	0.04	NM_016391	NP_057475	0.89	hypothetical protein HSPC111
203024_s_at	C5orf15	56951	0.02	NM_020199	NP_064584	0.90	chromosome 5 open reading frame 15
203026_at	ZBTB5	9925	0.04	NM_014872	NP_055687	0.89	zinc finger and BTB domain containing 5
203037_s_at	MTSS1	9788	0.03	NM_014751	NP_055566	0.85	metastasis suppressor 1
203053_at	BCAS2	10286	0.01	NM_005872	NP_005863	0.89	breast carcinoma amplified sequence 2
203067_at	PDHX	8050	0.01	NM_003477	NP_003468	0.94	pyruvate dehydrogenase complex, component X
203076_s_at	SMAD2	4087	1.95e-03	NM_005901	NP_005892	0.96	SMAD, mothers against DPP homolog 2 (Drosophila)
203078_at	CUL2	8453	0.02	NM_003591	NP_003582	0.81	cullin 2
203079_s_at	CUL2	8453	2.28e-03	NM_003591	NP_003582	0.91	cullin 2
203084_at	TGFB1	7040	0.04	NM_000660	NP_000651	1.12	transforming growth factor, beta 1 (Camurati-Engelmann disease)
203087_s_at	KIF2	3796	0.03	NM_004520	NP_004511	0.90	kinesin heavy chain member 2
203091_at	FUBP1	8880	0.02	NM_003902	NP_003893	0.89	far upstream element (FUSE) binding protein 1
203094_at	MAD2L1BP	9587	0.01	NM_014628	NP_055443	0.92	MAD2L1 binding protein
203100_s_at	CDYL	9425	0.02	NM_004824	NP_004815	0.89	chromodomain protein, Y-like
203102_s_at	MGAT2	4247	0.02	NM_002408	NP_002399	0.88	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
203105_s_at	DNM1L	10059	0.01	NM_012062	NP_036192	0.90	dynamin 1-like
203112_s_at	WHSC2	7469	0.02	NM_005663	NP_005654	0.92	Wolf-Hirschhorn syndrome candidate 2
203133_at	SEC61B	10952	0.01	NM_006808	NP_006799	0.83	Sec61 beta subunit
203135_at	TBP	6908	0.01	NM_003194	NP_003185	0.92	TATA box binding protein
203137_at	WTAP	9589	0.02	NM_004906	NP_004897	0.93	Wilms tumor 1 associated protein
203139_at	DAPK1	1612	0.04	NM_004938	NP_004929	0.91	death-associated protein kinase 1
203140_at	BCL6	604	0.04	NM_001706	NP_001697	1.07	B-cell CLL/lymphoma 6 (zinc finger protein 51)

203148_s_at	TRIM14	9830	0.01	NM_014788	NP_055603	0.80	tripartite motif-containing 14
203152_at	MRPL40	64976	5.21e-03	NM_003776	NP_003767	0.82	mitochondrial ribosomal protein L40
203156_at	AKAP11	11215	0.03	NM_016248	NP_057332	0.91	A kinase (PRKA) anchor protein 11
203164_at	SLC33A1	9197	0.01	NM_004733	NP_004724	0.88	solute carrier family 33 (acetyl-CoA transporter), member 1
203165_s_at	SLC33A1	9197	0.01	NM_004733	NP_004724	0.86	solute carrier family 33 (acetyl-CoA transporter), member 1
203177_x_at	TFAM	7019	0.03	NM_003201	NP_003192	0.86	transcription factor A, mitochondrial
203179_at	GALT	2592	0.02	NM_000155	NP_000146	0.90	galactose-1-phosphate uridylyltransferase
203189_s_at	NDUFS8	4728	0.01	NM_002496	NP_002487	0.81	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
203190_at	NDUFS8	4728	0.01	NM_002496	NP_002487	0.92	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
203196_at	ABCC4	10257	3.96e-03	NM_005845	NP_005836	0.83	ATP-binding cassette, sub-family C (CFTR/MRP), member 4
203198_at	CDK9	1025	0.03	NM_001261	NP_001252	0.91	cyclin-dependent kinase 9 (CDC2-related kinase)
203200_s_at	MTRR	4552	7.57e-04	NM_024010	NP_076915	0.86	5-methyltetrahydrofolate-homocysteine methyltransferase reductase
203201_at	PMM2	5373	0.02	NM_000303	NP_000294	1.18	phosphomannomutase 2
203218_at	MAPK9	5601	6.71e-03	NM_002752	NP_002743	0.91	mitogen-activated protein kinase 9
203219_s_at	APRT	353	0.02	NM_000485	NP_000476	0.86	adenine phosphoribosyltransferase
203224_at	RFK	55312	3.8e-03	NM_018339	NP_060809	0.80	riboflavin kinase
203226_s_at	SAS	6302	0.01	NM_005981	NP_005972	0.90	sarcoma amplified sequence
203229_s_at	CLK2	1196	0.01	NM_003993	NP_003984	0.86	CDC-like kinase 2
203232_s_at	ATXN1	6310	0.02	NM_000332	NP_000323	0.92	ataxin 1
203234_at	UPP1	7378	0.04	NM_003364	NP_003355	0.84	uridine phosphorylase 1
203239_s_at	CNOT3	4849	0.02	NM_014516	NP_055331	1.14	CCR4-NOT transcription complex, subunit 3
203241_at	UVRAG	7405	0.03	NM_003369	NP_003360	0.92	UV radiation resistance associated gene
203246_s_at	TUSC4	10641	0.01	NM_006545	NP_006536	0.86	tumor suppressor candidate 4
203250_at	RBM16	22828	0.04	NM_014892	NP_055707	0.94	RNA binding motif protein 16
203254_s_at	TLN1	7094	0.03	NM_006289	NP_006280	1.11	talin 1
203259_s_at	C6orf74	51020	0.02	NM_016063	NP_057147	0.86	chromosome 6 open reading frame 74
203264_s_at	ARHGEF9	23229	2.13e-03	NM_015185	NP_056000	0.81	Cdc42 guanine nucleotide exchange factor (GEF) 9
203269_at	NSMAF	8439	3.37e-03	NM_003580	NP_003571	0.91	neutral sphingomyelinase (N-SMase) activation associated factor
203274_at	F8A1	8263	0.02	NM_012151	NP_036283	0.92	coagulation factor VIII-associated (intronic transcript) 1
203279_at	EDEM1	9695	0.03	NM_014674	NP_055489	0.91	ER degradation enhancer, mannosidase alpha-like 1
203285_s_at	HS2ST1	9653	0.03	NM_012262	NP_036394	0.86	heparan sulfate 2-O-sulfotransferase 1
203291_at	CNOT4	4850	3.37e-03	NM_013316	NP_037448	0.92	CCR4-NOT transcription complex, subunit 4
203302_at	DCK	1633	0.03	NM_000788	NP_000779	0.89	deoxycytidine kinase
203309_s_at	HPS1	3257	9.33e-03	NM_000195	NP_000186	1.09	Hermansky-Pudlak syndrome 1
203311_s_at	ARF6	382	0.03	NM_001663	NP_001654	0.85	ADP-ribosylation factor 6
203315_at	NCK2	8440	0.01	NM_003581	NP_003572	0.91	NCK adaptor protein 2
203316_s_at	SNRPE	6635	7.35e-03	NM_003094	NP_003085	0.87	small nuclear ribonucleoprotein polypeptide E
203322_at	KIAA0863	22850	3.45e-03	NM_014913	NP_055728	0.89	KIAA0863 protein

203327_at	IDE	3416	0.01	NM_004969	NP_004960	0.90	insulin-degrading enzyme
203333_at	KIFAP3	22920	0.02	NM_014970	NP_055785	0.88	kinesin-associated protein 3
203334_at	DHX8	1659	0.03	NM_004941	NP_004932	0.93	DEAH (Asp-Glu-Ala-His) box polypeptide 8
203336_s_at	ITGB1BP1	9270	0.03	NM_004763	NP_004754	0.88	integrin beta 1 binding protein 1
203341_at	CEBPZ	10153	0.04	NM_005760	NP_005751	0.87	CCAAT/enhancer binding protein zeta
203345_s_at	M96	22823	0.02	NM_007358	NP_031384	0.89	likely ortholog of mouse metal response element binding
transcription factor 2							
203347_s_at	M96	22823	9.61e-03	NM_007358	NP_031384	0.85	likely ortholog of mouse metal response element binding
transcription factor 2							
203353_s_at	MBD1	4152	0.01	NM_015846	NP_056671	0.93	methyl-CpG binding domain protein 1
203356_at	CAPN7	23473	0.01	NM_014296	NP_055111	0.88	calpain 7
203357_s_at	CAPN7	23473	0.03	NM_014296	NP_055111	0.91	calpain 7
203359_s_at	MYCBP	26292	0.01	NM_012333	NP_036465	0.93	c-myc binding protein
203362_s_at	MAD2L1	4085	0.04	NM_002358	NP_002349	0.80	MAD2 mitotic arrest deficient-like 1 (yeast)
203363_s_at	KIAA0652	9776	9.61e-03	NM_014741	NP_055556	0.91	KIAA0652 gene product
203364_s_at	KIAA0652	9776	0.03	NM_014741	NP_055556	0.95	KIAA0652 gene product
203374_s_at	TPP2	7174	0.03	NM_003291	NP_003282	0.85	tripeptidyl peptidase II
203378_at	PCF11	51585	0.02	NM_015885	NP_056969	0.88	pre-mRNA cleavage complex II protein Pcf11
203380_x_at	SFRS5	6430	1.48e-04	NM_006925	NP_008856	0.92	splicing factor, arginine/serine-rich 5
203383_s_at	GOLGA1	2800	0.03	NM_002077	NP_002068	1.11	golgi autoantigen, golgin subfamily a, 1
203385_at	DGKA	1606	0.02	NM_001345	NP_001336	0.86	diacylglycerol kinase, alpha 80kDa
203386_at	TBC1D4	9882	0.01	AB011175	BAA25529	0.80	TBC1 domain family, member 4
203387_s_at	TBC1D4	9882	8.02e-04	NM_014832	NP_055647	0.84	TBC1 domain family, member 4
203396_at	PSMA4	5685	4.57e-03	NM_002789	NP_002780	0.93	proteasome (prosome, macropain) subunit, alpha type, 4
203401_at	PRPS2	5634	7.47e-03	NM_002765	NP_002756	0.83	phosphoribosyl pyrophosphate synthetase 2
203403_s_at	RNF6	6049	0.01	NM_005977	NP_005968	0.91	ring finger protein (C3H2C3 type) 6
203405_at	DSCR2	8624	0.03	NM_003720	NP_003711	0.90	Down syndrome critical region gene 2
203406_at	MFAP1	4236	0.01	NM_005926	NP_005917	0.95	microfibrillar-associated protein 1
203413_at	NELL2	4753	5.3e-04	NM_006159	NP_006150	0.84	NEL-like 2 (chicken)
203420_at	FAM8A1	51439	0.04	NM_016255	NP_057339	0.88	family with sequence similarity 8, member A1
203432_at	TMPO	7112	0.02	NM_003276	NP_003267	0.89	thymopoietin
203436_at	RPP30	10556	0.02	NM_006413	NP_006404	0.90	ribonuclease P/MRP 30kDa subunit
203447_at	PSMD5	5711	0.03	NM_005047	NP_005038	0.91	proteasome (prosome, macropain) 26S subunit, non-
ATPase, 5							
203478_at	NDUFC1	4717	4.42e-04	NM_002494	NP_002485	0.86	NADH dehydrogenase (ubiquinone) 1, subcomplex
unknown, 1, 6kDa							
203481_at	C10orf6	55719	0.02	NM_018121	NP_060591	0.88	chromosome 10 open reading frame 6
203482_at	C10orf6	55719	0.03	NM_018121	NP_060591	0.89	chromosome 10 open reading frame 6
203484_at	SEC61G	23480	3.76e-03	NM_014302	NP_055117	0.94	Sec61 gamma subunit
203486_s_at	ARMC8	25852	0.01	NM_213654	NP_998819	0.92	armadillo repeat containing 8
203486_s_at	ARMC8	25852	0.01	NM_015396	NP_056211	0.92	armadillo repeat containing 8
203486_s_at	ARMC8	25852	0.01	NM_014154	NP_054873	0.92	armadillo repeat containing 8
203493_s_at	PIG8	9702	0.03	D42054	BAA07654	0.86	translokin
203494_s_at	PIG8	9702	0.04	NM_014679	NP_055494	0.87	translokin
203502_at	BPGM	669	0.04	NM_001724	NP_001715	0.89	2,3-bisphosphoglycerate mutase

203512_at	TRAPPC3	27095	0.01	NM_014408	NP_055223	0.88	trafficking protein particle complex 3
203521_s_at	ZNF318	24149	4.83e-03	NM_014345	NP_055160	0.86	zinc finger protein 318
203526_s_at	APC	324	0.02	NM_000038	NP_000029	0.92	adenomatosis polyposis coli
203529_at	PPP6C	5537	0.01	NM_002721	NP_002712	0.95	protein phosphatase 6, catalytic subunit
203530_s_at	STX4A	6810	0.04	NM_004604	NP_004595	0.92	syntaxin 4A (placental)
203531_at	CUL5	8065	2.56e-03	BF435809		0.93	cullin 5
203537_at	PRPSAP2	5636	0.02	NM_002767	NP_002758	0.90	phosphoribosyl pyrophosphate synthetase-associated protein 2
203543_s_at	KLF9	687	0.03	NM_001206	NP_001197	0.82	Kruppel-like factor 9
203545_at	ALG8	79053	0.01	NM_024079	NP_076984	0.89	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)
203555_at	PTPN18	26469	0.01	NM_014369	NP_055184	0.89	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)
203563_at	AFAP	60312	0.04	NM_021638	NP_067651	1.36	actin filament associated protein
203566_s_at	AGL	178	0.01	NM_000645	NP_000636	0.86	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)
203567_s_at	TRIM38	10475	0.02	NM_006355	NP_006346	1.09	tripartite motif-containing 38
203568_s_at	TRIM38	10475	3.43e-03	NM_006355	NP_006346	1.16	tripartite motif-containing 38
203569_s_at	OFD1	8481	0.01	NM_003611	NP_003602	0.89	oral-facial-digital syndrome 1
203577_at	GTF2H4	2968	0.01	NM_001517	NP_001508	0.84	general transcription factor IIH, polypeptide 4, 52kDa
203579_s_at	SLC7A6	9057	7.02e-03	NM_003983	NP_003974	0.89	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
203583_at	UNC50	25972	5.95e-03	NM_014044	NP_054763	0.94	unc-50 homolog (C. elegans)
203584_at	KIAA0103	9694	9.24e-03	NM_014673	NP_055488	0.89	KIAA0103
203593_at	CD2AP	23607	7.47e-03	NM_012120	NP_036252	0.76	CD2-associated protein
203594_at	RTCD1	8634	2.28e-03	NM_003729	NP_003720	0.91	RNA terminal phosphate cyclase domain 1
203598_s_at	WBP4	11193	0.03	NM_007187	NP_009118	0.91	WW domain binding protein 4 (formin binding protein 21)
203605_at	SRP54	6729	4.03e-03	NM_003136	NP_003127	0.93	signal recognition particle 54kDa
203606_at	NDUFS6	4726	0.02	NM_004553	NP_004544	0.84	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
203610_s_at	TRIM38	10475	0.02	NM_006355	NP_006346	1.08	tripartite motif-containing 38
203611_at	TERF2	7014	9.61e-03	NM_005652	NP_005643	0.89	telomeric repeat binding factor 2
203614_at	UTP14C	9724	0.04	NM_021645	NP_067677	0.92	UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)
203616_at	POLB	5423	0.02	NM_002690	NP_002681	0.90	polymerase (DNA directed), beta
203617_x_at	ELK1	2002	2.42e-03	NM_005229	NP_005220	1.11	ELK1, member of ETS oncogene family
203621_at	NDUFB5	4711	7.89e-03	NM_002492	NP_002483	0.96	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa
203624_at	DXYS155E	8227	0.02	NM_005088	NP_005079	0.93	DNA segment on chromosome X and Y (unique) 155 expressed sequence
203630_s_at	COG5	10466	0.01	NM_006348	NP_006339	0.86	component of oligomeric golgi complex 5
203635_at	DSCR3	10311	0.01	NM_006052	NP_006043	0.94	Down syndrome critical region gene 3
203647_s_at	FDX1	2230	0.03	NM_004109	NP_004100	0.88	ferredoxin 1
203648_at	TATDN2	9797	0.02	D86972	BAA13208	0.93	TatD DNase domain containing 2
203650_at	PROCR	10544	0.03	NM_006404	NP_006395	0.82	protein C receptor, endothelial (EPCR)

203659_s_at	RFP2	10206	0.01	NM_005798	NP_005789	0.93	ret finger protein 2
203663_s_at	COX5A	9377	0.02	NM_004255	NP_004246	0.88	cytochrome c oxidase subunit Va
203675_at	NUCB2	4925	0.02	NM_005013	NP_005004	0.87	nucleobindin 2
203678_at	KIAA1018	22909	5.75e-03	NM_014967	NP_055782	0.79	KIAA1018 protein
203685_at	BCL2	596	0.02	NM_000633	NP_000624	0.87	B-cell CLL/lymphoma 2
203686_at	MPG	4350	0.04	NM_002434	NP_002425	0.89	N-methylpurine-DNA glycosylase
203689_s_at	FMR1	2332	8.67e-03	NM_002024	NP_002015	0.93	fragile X mental retardation 1
203690_at	TUBGCP3	10426	0.01	NM_006322	NP_006313	0.95	tubulin, gamma complex associated protein 3
203694_s_at	DHX16	8449	0.01	NM_003587	NP_003578	0.94	DEAH (Asp-Glu-Ala-His) box polypeptide 16
203702_s_at	TTLL4	9654	0.02	NM_014640	NP_055455	1.12	tubulin tyrosine ligase-like family, member 4
203703_s_at	TTLL4	9654	0.01	NM_014640	NP_055455	1.11	tubulin tyrosine ligase-like family, member 4
203704_s_at	RREB1	6239	0.03	NM_001003699	NP_001003699	0.96	ras responsive element binding protein 1
203707_at	ZNF263	10127	5.62e-06	NM_005741	NP_005732	0.91	zinc finger protein 263
203712_at	KIAA0020	9933	1.26e-03	NM_014878	NP_055693	0.86	KIAA0020
203719_at	ERCC1	2067	3.63e-03	NM_001983	NP_001974	1.14	excision repair cross-complementing rodent repair
deficiency, complementation group 1 (includes overlapping antisense sequenc							
203721_s_at	WDR50	51096	0.02	NM_016001	NP_057085	0.92	WD repeat domain 50
203732_at	TRIP4	9325	0.03	NM_016213	NP_057297	0.95	thyroid hormone receptor interactor 4
203743_s_at	TDG	6996	6.69e-03	NM_003211	NP_003202	0.83	thymine-DNA glycosylase
203745_at	HCCS	3052	0.01	NM_005333	NP_005324	0.92	holocytochrome c synthase (cytochrome c heme-lyase)
203746_s_at	HCCS	3052	0.01	NM_005333	NP_005324	0.94	holocytochrome c synthase (cytochrome c heme-lyase)
203758_at	CTSO	1519	0.03	NM_001334	NP_001325	0.90	cathepsin O
203760_s_at	SLA	6503	0.03	NM_006748	NP_006739	1.15	Src-like-adaptor
203765_at	GCA	25801	0.02	NM_012198	NP_036330	1.07	grancalcin, EF-hand calcium binding protein
203774_at	MTR	4548	0.01	NM_000254	NP_000245	0.84	5-methyltetrahydrofolate-homocysteine methyltransferase
203776_at	GPKOW	27238	8.7e-03	NM_015698	NP_056513	0.85	G patch domain and KOW motifs
203777_s_at	RPS6KB2	6199	0.04	NM_003952	NP_003943	0.91	ribosomal protein S6 kinase, 70kDa, polypeptide 2
203785_s_at	DDX28	55794	0.01	NM_018380	NP_060850	0.88	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28
203790_s_at	HRSP12	10247	0.01	NM_005836	NP_005827	0.89	heat-responsive protein 12
203791_at	DMXL1	1657	2.61e-03	NM_005509	NP_005500	0.84	Dmx-like 1
203802_x_at	NSUN5	55695	0.04	NM_018044	NP_060514	0.89	NOL1/NOP2/Sun domain family, member 5
203804_s_at	CROP	51747	0.01	NM_006107	NP_006098	0.93	cisplatin resistance-associated overexpressed protein
203810_at	DNAJB4	11080	0.03	NM_007034	NP_008965	0.83	DnaJ (Hsp40) homolog, subfamily B, member 4
203816_at	DGUOK	1716	4.59e-03	NM_001929	NP_001920	0.86	deoxyguanosine kinase
203829_at	ELP4	26610	0.03	NM_019040	NP_061913	0.88	elongation protein 4 homolog (S. cerevisiae)
203848_at	AKAP8	10270	0.01	NM_005858	NP_005849	0.91	A kinase (PRKA) anchor protein 8
203857_s_at	PDIR	10954	0.02	NM_006810	NP_006801	0.90	for protein disulfide isomerase-related
203858_s_at	COX10	1352	0.01	NM_001303	NP_001294	0.90	COX10 homolog, cytochrome c oxidase assembly protein,
heme A: farnesyltransferase (yeast)							
203864_s_at	ACTN2	88	1.99e-04	NM_001103	NP_001094	1.20	actinin, alpha 2
203870_at	USP46	64854	0.04	AK021861		0.81	ubiquitin specific protease 46
203884_s_at	RAB11FIP2	22841	9.61e-03	NM_014904	NP_055719	0.86	RAB11 family interacting protein 2 (class I)
203888_at	THBD	7056	0.04	NM_000361	NP_000352	1.19	thrombomodulin
203890_s_at	DAPK3	1613	0.02	NM_001348	NP_001339	0.89	death-associated protein kinase 3
203897_at	LOC57149	57149	0.03	NM_020424	NP_065157	0.87	hypothetical protein A-211C6.1

203921_at	CHST2	9435	0.03	NM_004267	NP_004258	0.91	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
203922_s_at	CYBB	1536	0.03	NM_000397	NP_000388	0.83	cytochrome b-245, beta polypeptide (chronic granulomatous disease)
203931_s_at	MRPL12	6182	7.12e-04	NM_002949	NP_002940	0.82	mitochondrial ribosomal protein L12
203947_at	CSTF3	1479	0.01	NM_001326	NP_001317	0.93	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa
203965_at	USP20	10868	0.04	NM_006676	NP_006667	0.92	ubiquitin specific protease 20
203972_s_at	PEX3	8504	8.05e-03	NM_003630	NP_003621	0.88	peroxisomal biogenesis factor 3
203975_s_at	CHAF1A	10036	0.03	NM_005483	NP_005474	1.10	chromatin assembly factor 1, subunit A (p150)
203987_at	FZD6	8323	0.03	NM_003506	NP_003497	0.83	frizzled homolog 6 (Drosophila)
204001_at	SNAPC3	6619	6.46e-05	NM_003084	NP_003075	0.93	small nuclear RNA activating complex, polypeptide 3, 50kDa
204003_s_at	NUPL2	11097	6.41e-03	NM_007342	NP_031368	0.84	nucleoporin like 2
204006_s_at	FCGR3B	2215	0.02	NM_000570	NP_000561	1.12	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)
204012_s_at	LCMT2	9836	0.02	NM_014793	NP_055608	0.92	leucine carboxyl methyltransferase 2
204021_s_at	PURA	5813	2.05e-03	NM_005859	NP_005850	0.81	purine-rich element binding protein A
204024_at	C8orf1	734	0.01	NM_004337	NP_004328	1.11	chromosome 8 open reading frame 1
204025_s_at	PDCD2	5134	0.04	NM_002598	NP_002589	0.85	programmed cell death 2
204040_at	RNF144	9781	0.04	NM_014746	NP_055561	0.89	ring finger protein 144
204046_at	PLCB2	5330	0.01	NM_004573	NP_004564	1.16	phospholipase C, beta 2
204049_s_at	PHACTR2	9749	0.02	NM_014721	NP_055536	0.86	phosphatase and actin regulator 2
204063_s_at	ULK2	9706	0.04	NM_014683	NP_055498	0.91	unc-51-like kinase 2 (C. elegans)
204068_at	STK3	6788	7.12e-04	NM_006281	NP_006272	0.79	serine/threonine kinase 3 (STE20 homolog, yeast)
204069_at	MEIS1	4211	0.02	NM_002398	NP_002389	1.18	Meis1, myeloid ecotropic viral integration site 1 homolog (mouse)
204070_at	RARRES3	5920	0.03	NM_004585	NP_004576	0.92	retinoic acid receptor responder (tazarotene induced) 3
204076_at	ENTPD4	9583	8.07e-03	AB002390	BAA21575	0.91	ectonucleoside triphosphate diphosphohydrolase 4
204077_x_at	ENTPD4	9583	0.01	NM_004901	NP_004892	1.16	ectonucleoside triphosphate diphosphohydrolase 4
204079_at	TPST2	8459	0.02	NM_003595	NP_003586	0.87	tyrosylprotein sulfotransferase 2
204085_s_at	CLN5	1203	0.02	NM_006493	NP_006484	0.88	ceroid-lipofuscinosis, neuronal 5
204093_at	CCNH	902	0.03	NM_001239	NP_001230	0.95	cyclin H
204096_s_at	ELL	8178	0.03	NM_006532	NP_006523	1.18	elongation factor RNA polymerase II
204099_at	SMARCD3	6604	0.03	NM_003078	NP_003069	1.10	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
204103_at	CCL4	6351	5.31e-03	NM_002984	NP_002975	0.78	chemokine (C-C motif) ligand 4
204107_at	NFYA	4800	0.03	NM_002505	NP_002496	0.91	nuclear transcription factor Y, alpha
204116_at	IL2RG	3561	0.01	NM_000206	NP_000197	0.94	interleukin 2 receptor, gamma (severe combined immunodeficiency)
204117_at	PREP	5550	0.02	NM_002726	NP_002717	0.88	prolyl endopeptidase
204118_at	CD48	962	0.01	NM_001778	NP_001769	0.94	CD48 antigen (B-cell membrane protein)
204146_at	RAD51AP1	10635	4.1e-03	NM_006479	NP_006470	0.77	RAD51 associated protein 1
204151_x_at	AKR1C1	1645	0.01	NM_001353	NP_001344	0.87	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
204153_s_at	MFNG	4242	0.02	NM_002405	NP_002396	0.92	manic fringe homolog (Drosophila)
204162_at	KNTC2	10403	0.01	NM_006101	NP_006092	0.73	kinetochore associated 2
204171_at	RPS6KB1	6198	0.03	NM_003161	NP_003152	0.89	ribosomal protein S6 kinase, 70kDa, polypeptide 1

204185_x_at	PPID	5481	0.02	NM_005038	NP_005029	1.12	peptidylprolyl isomerase D (cyclophilin D)
204186_s_at	PPID	5481	0.02	NM_005038	NP_005029	1.13	peptidylprolyl isomerase D (cyclophilin D)
204190_at	C13orf22	10208	3.1e-03	NM_005800	NP_005791	0.92	chromosome 13 open reading frame 22
204205_at	APOBEC3G	60489	0.03	NM_021822	NP_068594	0.80	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G
204211_x_at	EIF2AK2	5610	7.02e-03	NM_002759	NP_002750	1.20	eukaryotic translation initiation factor 2-alpha kinase 2
204212_at	PTE1	10005	0.01	NM_005469	NP_005460	0.88	peroxisomal acyl-CoA thioesterase
204215_at	C7orf23	79161	0.01	NM_024315	NP_077291	0.88	chromosome 7 open reading frame 23
204218_at	DKFZP564M082	25906	0.04	NM_014042	NP_054761	0.87	DKFZP564M082 protein
204219_s_at	PSMC1	5700	7.02e-03	NM_002802	NP_002793	0.92	proteasome (prosome, macropain) 26S subunit, ATPase, 1
204224_s_at	GCH1	2643	3.32e-03	NM_000161	NP_000152	0.77	GTP cyclohydrolase 1 (dopa-responsive dystonia)
204226_at	STAU2	27067	0.04	NM_014393	NP_055208	1.11	staufen, RNA binding protein, homolog 2 (Drosophila)
204227_s_at	TK2	7084	0.04	NM_004614	NP_004605	0.92	thymidine kinase 2, mitochondrial
204228_at	PPIH	10465	0.02	NM_006347	NP_006338	0.79	peptidyl prolyl isomerase H (cyclophilin H)
204232_at	FCER1G	2207	0.01	NM_004106	NP_004097	0.87	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
204234_s_at	ZNF195	7748	0.01	NM_007152	NP_009083	0.89	zinc finger protein 195
204236_at	FLI1	2313	1.16e-03	NM_002017	NP_002008	0.86	Friend leukemia virus integration 1
204250_s_at	Cep164	22897	0.01	NM_014956	NP_055771	0.86	KIAA1052 protein
204252_at	CDK2	1017	8.82e-03	NM_001798	NP_001789	0.93	cyclin-dependent kinase 2
204256_at	ELOVL6	79071	0.04	NM_024090	NP_076995	0.85	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)
204258_at	CHD1	1105	7.38e-03	NM_001270	NP_001261	0.95	chromodomain helicase DNA binding protein 1
204274_at	EBAG9	9166	0.01	NM_004215	NP_004206	0.87	estrogen receptor binding site associated, antigen, 9
204276_at	TK2	7084	0.01	BC040667		0.90	thymidine kinase 2, mitochondrial
204297_at	PIK3C3	5289	8.5e-04	NM_002647	NP_002638	0.94	phosphoinositide-3-kinase, class 3
204313_s_at	CREB1	1385	0.03	NM_004379	NP_004370	1.09	cAMP responsive element binding protein 1
204319_s_at	RGS10	6001	0.04	NM_002925	NP_002916	0.91	regulator of G-protein signalling 10
204335_at	FLJ10374	55702	0.04	NM_018074	NP_060544	0.86	hypothetical protein FLJ10374
204349_at	CRSP9	9443	5.48e-03	NM_004270	NP_004261	0.81	cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa
204350_s_at	CRSP9	9443	0.01	NM_004270	NP_004261	0.94	cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa
204352_at	TRAF5	7188	0.02	NM_004619	NP_004610	0.84	TNF receptor-associated factor 5
204353_s_at	POT1	25913	0.04	NM_015450	NP_056265	0.89	POT1 protection of telomeres 1 homolog (S. pombe)
204354_at	POT1	25913	5.95e-03	NM_015450	NP_056265	0.92	POT1 protection of telomeres 1 homolog (S. pombe)
204366_s_at	GTF3C2	2976	0.01	NM_001521	NP_001512	0.90	general transcription factor IIIC, polypeptide 2, beta 110kDa
204367_at	SP2	6668	0.02	NM_003110	NP_003101	0.93	Sp2 transcription factor
204382_at	EBSP	26151	3.98e-03	NM_015654	NP_056469	0.84	embryo brain specific protein
204386_s_at	MRP63	78988	0.02	NM_024026	NP_076931	0.92	mitochondrial ribosomal protein 63
204392_at	CAMK1	8536	2.57e-03	NM_003656	NP_003647	0.84	calcium/calmodulin-dependent protein kinase I
204405_x_at	HSA9761	27292	0.01	NM_014473	NP_055288	0.86	putative dimethyladenosine transferase
204407_at	TTF2	8458	0.03	NM_003594	NP_003585	0.85	transcription termination factor, RNA polymerase II

204417_at	GALC	2581	0.03	NM_000153	NP_000144	0.91	galactosylceramidase (Krabbe disease)
204426_at	RNP24	10959	4.31e-03	NM_006815	NP_006806	0.88	coated vesicle membrane protein
204427_s_at	RNP24	10959	0.01	NM_006815	NP_006806	0.93	coated vesicle membrane protein
204436_at	pp9099	80301	0.04	NM_025201	NP_079477	1.08	PH domain-containing protein
204453_at	ZNF84	7637	0.02	NM_003428	NP_003419	0.82	zinc finger protein 84 (HPF2)
204458_at	LYPLA3	23659	0.02	NM_012320	NP_036452	0.89	lysophospholipase 3 (lysosomal phospholipase A2)
204490_s_at	CD44	960	0.02	NM_000610	NP_000601	0.93	CD44 antigen (homing function and Indian blood group system)
204494_s_at	DKFZP434H132	56905	0.01	NM_015492	NP_056307	1.10	DKFZP434H132 protein
204502_at	SAMHD1	25939	0.02	NM_015474	NP_056289	0.89	SAM domain and HD domain 1
204505_s_at	EPB49	2039	0.02	NM_001978	NP_001969	1.15	erythrocyte membrane protein band 4.9 (dematin)
204512_at	HIVEP1	3096	7.35e-03	NM_002114	NP_002105	1.09	human immunodeficiency virus type I enhancer binding protein 1
204523_at	ZNF140	7699	5.64e-03	NM_003440	NP_003431	0.88	zinc finger protein 140 (clone pHZ-39)
204526_s_at	TBC1D8	11138	0.02	NM_007063	NP_008994	0.81	TBC1 domain family, member 8 (with GRAM domain)
204528_s_at	NAP1L1	4673	3.19e-03	NM_004537	NP_004528	0.91	nucleosome assembly protein 1-like 1
204529_s_at	TOX	9760	0.02	NM_014729	NP_055544	0.81	thymus high mobility group box protein TOX
204531_s_at	BRCA1	672	0.04	NM_007295	NP_009226	0.88	breast cancer 1, early onset
204552_at	INPP4A	3631	0.02	AA355179		0.89	inositol polyphosphate-4-phosphatase, type I, 107kDa
204555_s_at	PPP1R3D	5509	0.02	NM_006242	NP_006233	1.16	protein phosphatase 1, regulatory subunit 3D
204559_s_at	LSM7	51690	0.01	NM_016199	NP_057283	0.87	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)
204560_at	FKBP5	2289	3.08e-03	NM_004117	NP_004108	0.72	FK506 binding protein 5
204565_at	THEM2	55856	0.04	NM_018473	NP_060943	0.92	thioesterase superfamily member 2
204566_at	PPM1D	8493	0.04	NM_003620	NP_003611	0.91	protein phosphatase 1D magnesium-dependent, delta isoform
204568_at	KIAA0831	22863	0.01	NM_014924	NP_055739	0.89	KIAA0831
204571_x_at	PIN4	5303	3.45e-04	NM_006223	NP_006214	0.93	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
204593_s_at	FLJ20232	54471	0.01	NM_019008	NP_061881	0.91	hypothetical protein FLJ20232
204605_at	CGRRF1	10668	0.02	NM_006568	NP_006559	0.89	cell growth regulator with ring finger domain 1
204610_s_at	DIPA	11007	0.02	NM_006848	NP_006839	0.79	hepatitis delta antigen-interacting protein A
204612_at	PKIA	5569	0.01	NM_006823	NP_006814	0.81	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
204615_x_at	IDI1	3422	0.02	NM_004508	NP_004499	0.91	isopentenyl-diphosphate delta isomerase
204635_at	RPS6KA5	9252	0.04	NM_004755	NP_004746	1.12	ribosomal protein S6 kinase, 90kDa, polypeptide 5
204645_at	CCNT2	905	0.04	NM_001241	NP_001232	0.91	cyclin T2
204646_at	DPYD	1806	0.04	NM_000110	NP_000101	0.89	dihydropyrimidine dehydrogenase
204650_s_at	APBB3	10307	0.04	NM_006051	NP_006042	1.11	amyloid beta (A4) precursor protein-binding, family B, member 3
204665_at	FLJ21168	80143	0.01	NM_025073	NP_079349	1.15	hypothetical protein FLJ21168
204671_s_at	ANKRD6	22881	0.02	AB023174	BAA76801	0.89	ankyrin repeat domain 6
204676_at	DKFZP564K2062	25880	5.93e-03	NM_015421	NP_056236	0.84	DKFZP564K2062 protein
204683_at	ICAM2	3384	1.68e-03	NM_000873	NP_000864	0.85	intercellular adhesion molecule 2
204690_at	STX8	9482	0.01	NM_004853	NP_004844	0.88	syntaxin 8

204692_at	LRCH4	4034	0.01	NM_002319	NP_002310	1.18	leucine-rich repeats and calponin homology (CH) domain containing 4
204725_s_at	NCK1	4690	0.04	NM_006153	NP_006144	0.92	NCK adaptor protein 1
204739_at	CENPC1	1060	0.01	NM_001812	NP_001803	0.86	centromere protein C 1
204744_s_at	IARS	3376	0.02	NM_013417	NP_038203	0.90	isoleucine-tRNA synthetase
204759_at	CHC1L	1102	0.02	NM_001268	NP_001259	0.93	chromosome condensation 1-like
204777_s_at	MAL	4118	0.03	NM_002371	NP_002362	0.85	mal, T-cell differentiation protein
204780_s_at	FAS	355	0.01	NM_000043	NP_000034	0.85	Fas (TNF receptor superfamily, member 6)
204781_s_at	FAS	355	0.03	NM_000043	NP_000034	0.87	Fas (TNF receptor superfamily, member 6)
204786_s_at	IFNAR2	3455	0.03	NM_207585	NP_997468	1.14	interferon (alpha, beta and omega) receptor 2
204788_s_at	PPOX	5498	0.03	NM_000309	NP_000300	0.90	protoporphyrinogen oxidase
204791_at	NR2C1	7181	2.05e-03	NM_003297	NP_003288	0.81	nuclear receptor subfamily 2, group C, member 1
204793_at	GPRASP1	9737	0.02	NM_014710	NP_055525	0.80	G protein-coupled receptor associated sorting protein 1
204807_at	TMEM5	10329	0.01	BX647105		0.78	transmembrane protein 5
204831_at	CDK8	1024	9.3e-03	R59697		0.84	cyclin-dependent kinase 8
204839_at	POP5	51367	0.01	NM_015918	NP_057002	0.88	processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)
204847_at	ZBTB11	27107	9.58e-03	NM_014415	NP_055230	0.89	zinc finger and BTB domain containing 11
204864_s_at	IL6ST	3572	9.7e-03	NM_002184	NP_002175	0.85	interleukin 6 signal transducer (gp130, oncostatin M receptor)
204868_at	ICT1	3396	9.57e-03	NM_001545	NP_001536	0.86	immature colon carcinoma transcript 1
204884_s_at	HUS1	3364	0.03	NM_004507	NP_004498	1.18	HUS1 checkpoint homolog (S. pombe)
204906_at	RPS6KA2	6196	0.04	NM_021135	NP_066958	1.12	ribosomal protein S6 kinase, 90kDa, polypeptide 2
204912_at	IL10RA	3587	0.04	NM_001558	NP_001549	0.89	interleukin 10 receptor, alpha
204924_at	TLR2	7097	0.03	NM_003264	NP_003255	0.92	toll-like receptor 2
204929_s_at	VAMP5	10791	0.03	NM_006634	NP_006625	0.80	vesicle-associated membrane protein 5 (myobrevin)
204956_at	MTAP	4507	0.02	NM_002451	NP_002442	0.85	methylthioadenosine phosphorylase
204976_s_at	AMMECR1	9949	3.43e-03	AK023637		0.80	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1
204985_s_at	MGC2650	79090	9.61e-03	NM_024108	NP_077013	0.89	hypothetical protein MGC2650
205004_at	NKRF	55922	0.02	NM_017544	NP_060014	0.89	NF-kappaB repressing factor
205005_s_at	NMT2	9397	0.01	NM_004808	NP_004799	0.78	N-myristoyltransferase 2
205018_s_at	MBNL2	10150	0.01	NM_144778	NP_659002	0.91	muscleblind-like 2 (Drosophila)
205020_s_at	ARL4A	10124	3.18e-03	NM_005738	NP_005729	0.84	ADP-ribosylation factor-like 4A
205038_at	ZNFN1A1	10320	6.41e-03	BG540504		0.86	zinc finger protein, subfamily 1A, 1 (Ikaros)
205042_at	GNE	10020	0.02	NM_005476	NP_005467	0.91	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase
205053_at	PRIM1	5557	0.01	NM_000946	NP_000937	0.87	primase, polypeptide 1, 49kDa
205060_at	PARG	8505	0.01	NM_003631	NP_003622	0.78	poly (ADP-ribose) glycohydrolase
205061_s_at	EXOSC9	5393	0.04	NM_005033	NP_005024	0.82	exosome component 9
205063_at	SIP1	8487	0.01	NM_003616	NP_003607	0.83	survival of motor neuron protein interacting protein 1
205074_at	SLC22A5	6584	0.02	NM_003060	NP_003051	0.90	solute carrier family 22 (organic cation transporter), member 5
205076_s_at	CRA	10903	4.07e-03	NM_006697	NP_006688	0.89	cisplatin resistance associated
205077_s_at	PIGF	5281	3.84e-04	NM_002643	NP_002634	0.95	phosphatidylinositol glycan, class F

205078_at	PIGF	5281	0.03	NM_002643	NP_002634	0.94	phosphatidylinositol glycan, class F
205084_at	BCAP29	55973	0.04	NM_018844	NP_061332	0.87	B-cell receptor-associated protein 29
205087_at	RWDD3	25950	9.2e-03	NM_015485	NP_056300	0.79	RWD domain containing 3
205094_at	PEX12	5193	0.01	NM_000286	NP_000277	0.88	peroxisomal biogenesis factor 12
205097_at	SLC26A2	1836	1.55e-03	NM_000112	NP_000103	0.85	solute carrier family 26 (sulfate transporter), member 2
205099_s_at	CCR1	1230	0.01	NM_001295	NP_001286	1.23	chemokine (C-C motif) receptor 1
205107_s_at	EFNA4	1945	0.04	NM_005227	NP_005218	0.88	ephrin-A4
205118_at	FPR1	2357	0.02	M60626	AAA35846	1.14	formyl peptide receptor 1
205133_s_at	HSPE1	3336	0.01	NM_002157	NP_002148	0.87	heat shock 10kDa protein 1 (chaperonin 10)
205140_at	FPGT	8790	6.58e-04	NM_003838	NP_003829	0.83	fucose-1-phosphate guanylyltransferase
205176_s_at	ITGB3BP	23421	0.03	NM_014288	NP_055103	0.87	integrin beta 3 binding protein (beta3-endonexin)
205178_s_at	RBBP6	5930	0.04	NM_006910	NP_008841	0.93	retinoblastoma binding protein 6
205219_s_at	GALK2	2585	1.83e-03	NM_002044	NP_002035	0.84	galactokinase 2
205232_s_at	PAFAH2	5051	2.8e-03	NM_000437	NP_000428	0.85	platelet-activating factor acetylhydrolase 2, 40kDa
205248_at	C21orf5	9980	0.01	NM_005128	NP_005119	1.09	chromosome 21 open reading frame 5
205255_x_at	TCF7	6932	0.02	NM_003202	NP_003193	0.85	transcription factor 7 (T-cell specific, HMG-box)
205269_at	LCP2	3937	3.37e-03	NM_005565	NP_005556	0.87	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)
205273_s_at	PITRM1	10531	0.01	NM_014889	NP_055704	0.86	pitrilysin metalloproteinase 1
205285_s_at	FYB	2533	0.04	NM_199335	NP_955367	0.93	FYN binding protein (FYB-120/130)
205285_s_at	FYB	2533	0.04	NM_001465	NP_001456	0.93	FYN binding protein (FYB-120/130)
205291_at	IL2RB	3560	0.01	NM_000878	NP_000869	0.82	interleukin 2 receptor, beta
205292_s_at	HNRPA2B1	3181	4.67e-05	NM_002137	NP_002128	0.85	heterogeneous nuclear ribonucleoprotein A2/B1
205294_at	BAIAP2	10458	0.01	NM_017450	NP_059344	1.14	BAI1-associated protein 2
205298_s_at	BTN2A2	10385	3.1e-03	NM_006995	NP_008926	0.85	butyrophilin, subfamily 2, member A2
205300_s_at	U1SNRNPBP	11066	0.01	NM_022717	NP_073208	0.91	U11/U12 snRNP 35K
205310_at	FBXO46	23403	0.02	BC008046		0.91	F-box protein 46
205321_at	EIF2S3	1968	0.02	NM_001415	NP_001406	0.76	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa
205324_s_at	FTSJ1	24140	0.01	NM_012280	NP_036412	0.87	FtsJ homolog 1 (E. coli)
205329_s_at	SNX4	8723	2.19e-03	NM_003794	NP_003785	0.87	sorting nexin 4
205353_s_at	PBP	5037	0.01	NM_002567	NP_002558	0.81	prostatic binding protein
205361_s_at	PFDN4	5203	0.04	NM_002623	NP_002614	0.84	prefoldin 4
205372_at	PLAG1	5324	0.03	NM_002655	NP_002646	0.86	pleiomorphic adenoma gene 1
205376_at	INPP4B	8821	0.04	NM_003866	NP_003857	0.86	inositol polyphosphate-4-phosphatase, type II, 105kDa
205395_s_at	MRE11A	4361	0.01	NM_005590	NP_005581	0.91	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
205400_at	WAS	7454	8.05e-03	NM_000377	NP_000368	1.22	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
205401_at	AGPS	8540	0.03	NM_003659	NP_003650	0.92	alkylglycerone phosphate synthase
205410_s_at	ATP2B4	493	0.04	NM_001684	NP_001675	0.89	ATPase, Ca++ transporting, plasma membrane 4
205419_at	EBI2	1880	0.03	NM_004951	NP_004942	0.78	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)
205425_at	HIP1	3092	2.26e-03	NM_005338	NP_005329	0.74	huntingtin interacting protein 1
205435_s_at	AAK1	22848	0.02	NM_014911	NP_055726	0.84	AP2 associated kinase 1

205443_at	SNAPC1	6617	0.02	NM_003082	NP_003073	0.86	small nuclear RNA activating complex, polypeptide 1, 43kDa
205456_at	CD3E	916	0.02	NM_000733	NP_000724	0.84	CD3E antigen, epsilon polypeptide (TiT3 complex)
205461_at	RAB35	11021	1.65e-03	NM_006861	NP_006852	0.83	RAB35, member RAS oncogene family
205467_at	CASP10	843	0.04	NM_001230	NP_001221	0.91	caspase 10, apoptosis-related cysteine protease
205469_s_at	IRF5	3663	0.03	NM_002200	NP_002191	0.99	interferon regulatory factor 5
205471_s_at	DACH1	1602	0.04	NM_080759	NP_542937	1.18	dachshund homolog 1 (Drosophila)
205480_s_at	UGP2	7360	8.05e-03	NM_006759	NP_006750	0.92	UDP-glucose pyrophosphorylase 2
205482_x_at	SNX15	29907	0.01	NM_013306	NP_037438	0.89	sorting nexin 15
205483_s_at	G1P2	9636	0.04	NM_005101	NP_005092	0.65	interferon, alpha-inducible protein (clone IFI-15K)
205504_at	BTK	695	8.07e-03	NM_000061	NP_000052	0.90	Bruton agammaglobulinemia tyrosine kinase
205510_s_at	FLJ10038	55056	6.39e-03	AK000900	BAA91415	0.89	hypothetical protein FLJ10038
205512_s_at	PDCD8	9131	8.39e-03	NM_004208	NP_004199	0.85	programmed cell death 8 (apoptosis-inducing factor)
205541_s_at	GSPT2	23708	0.02	NM_018094	NP_060564	0.86	G1 to S phase transition 2
205545_x_at	DNAJC8	22826	0.01	NM_014280	NP_055095	0.91	DnaJ (Hsp40) homolog, subfamily C, member 8
205552_s_at	OAS1	4938	2.19e-03	NM_002534	NP_002525	0.55	2',5'-oligoadenylate synthetase 1, 40/46kDa
205558_at	TRAF6	7189	8.33e-03	NM_004620	NP_004611	0.90	TNF receptor-associated factor 6
205559_s_at	PCSK5	5125	6.11e-03	NM_006200	NP_006191	0.83	proprotein convertase subtilisin/kexin type 5
205562_at	RPP38	10557	0.04	NM_006414	NP_006405	0.86	ribonuclease P/MRP 38kDa subunit
205565_s_at	FXN	2395	9.49e-03	NM_000144	NP_000135	0.86	frataxin
205571_at	LIPT1	51601	3.61e-03	NM_015929	NP_057013	0.91	lipoyltransferase 1
205575_at	C1QL1	10882	7.08e-03	NM_006688	NP_006679	1.17	complement component 1, q subcomponent-like 1
205583_s_at	CXorf45	79868	0.03	NM_024810	NP_079086	0.84	chromosome X open reading frame 45
205584_at	CXorf45	79868	0.04	NM_024810	NP_079086	0.83	chromosome X open reading frame 45
205588_s_at	FGFR1OP	11116	0.01	NM_007045	NP_008976	1.12	FGFR1 oncogene partner
205603_s_at	DIAPH2	1730	0.04	NM_007309	NP_009293	0.89	diaphanous homolog 2 (Drosophila)
205621_at	ALKBH	8846	0.03	NM_006020	NP_006011	0.92	alkB, alkylation repair homolog (E. coli)
205627_at	CDA	978	0.01	NM_001785	NP_001776	1.30	cytidine deaminase
205642_at	CEP1	11064	4.36e-03	NM_007018	NP_008949	0.93	centrosomal protein 1
205644_s_at	SNRPG	6637	0.04	NM_003096	NP_003087	0.87	small nuclear ribonucleoprotein polypeptide G
205661_s_at	PP591	80308	0.03	NM_025207	NP_079483	0.95	FAD-synthetase
205668_at	LY75	4065	0.02	NM_002349	NP_002340	0.89	lymphocyte antigen 75
205672_at	XPA	7507	0.03	NM_000380	NP_000371	0.87	xeroderma pigmentosum, complementation group A
205685_at	CD86	942	0.03	NM_175862	NP_787058	0.88	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)
205711_x_at	ATP5C1	509	1.75e-03	NM_005174	NP_005165	0.90	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
205716_at	MCFP	55972	2.44e-03	NM_018843	NP_061331	0.87	mitochondrial carrier family protein
205763_s_at	DDX18	8886	0.02	NM_006773	NP_006764	0.86	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
205771_s_at	AKAP7	9465	7.86e-04	NM_004842	NP_004833	0.81	A kinase (PRKA) anchor protein 7
205781_at	C16orf7	9605	0.03	NM_004913	NP_004904	0.89	chromosome 16 open reading frame 7
205786_s_at	ITGAM	3684	0.01	NM_000632	NP_000623	0.91	integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide)
205788_s_at	KIAA0663	9877	0.02	NM_014827	NP_055642	0.91	KIAA0663 gene product
205798_at	IL7R	3575	7.47e-03	NM_002185	NP_002176	0.86	interleukin 7 receptor

205804_s_at	T3JAM	80342	0.01	NM_025228	NP_079504	0.84	TRAF3-interacting Jun N-terminal kinase (JNK)-activating modulator
205822_s_at	HMGCS1	3157	0.04	NM_002130	NP_002121	0.92	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
205835_s_at	YTHDC2	64848	0.01	NM_022828	NP_073739	0.87	YTH domain containing 2
205836_s_at	YTHDC2	64848	0.01	NM_022828	NP_073739	0.89	YTH domain containing 2
205849_s_at	UQCRB	7381	0.01	NM_006294	NP_006285	0.89	ubiquinol-cytochrome c reductase binding protein
205851_at	NME6	10201	0.02	NM_005793	NP_005784	1.09	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)
205861_at	SPIB	6689	0.03	NM_003121	NP_003112	1.17	Spi-B transcription factor (Spi-1/PU.1 related)
205865_at	ARID3A	1820	0.04	NM_005224	NP_005215	1.11	AT rich interactive domain 3A (BRIGHT- like)
205871_at	PLGL	5342	0.03	NM_002665	NP_002656	1.38	plasminogen-like
205883_at	ZBTB16	7704	9.75e-03	NM_006006	NP_005997	0.83	zinc finger and BTB domain containing 16
205898_at	CX3CR1	1524	0.03	NM_001337	NP_001328	0.84	chemokine (C-X3-C motif) receptor 1
205904_at	MICA	4276	7.64e-03	NM_000247	NP_000238	0.85	MHC class I polypeptide-related sequence A
205905_s_at	MICA	4276	0.04	NM_000247	NP_000238	0.85	MHC class I polypeptide-related sequence A
205934_at	PLCL1	5334	0.02	NM_006226	NP_006217	0.81	phospholipase C-like 1
205953_at	LRIG2	9860	0.04	NM_014813	NP_055628	0.93	leucine-rich repeats and immunoglobulin-like domains 2
205961_s_at	PSIP1	11168	0.01	NM_021144	NP_066967	0.86	PC4 and SFRS1 interacting protein 1
205961_s_at	PSIP1	11168	0.01	NM_033222	NP_150091	0.86	PC4 and SFRS1 interacting protein 1
205981_s_at	ING2	3622	3.48e-03	NM_001564	NP_001555	0.88	inhibitor of growth family, member 2
205987_at	CD1C	911	0.04	NM_001765	NP_001756	0.85	CD1C antigen, c polypeptide
205992_s_at	IL15	3600	5.48e-03	NM_000585	NP_000576	0.83	interleukin 15
205996_s_at	AK2	204	5.93e-03	NM_013411	NP_037543	0.87	adenylate kinase 2
206003_at	KIAA0635	9662	0.04	NM_025009	NP_079285	0.92	KIAA0635
206015_s_at	FOXJ3	22887	1.48e-03	NM_014947	NP_055762	0.91	forkhead box J3
206035_at	REL	5966	0.01	NM_002908	NP_002899	1.19	v-rel reticuloendotheliosis viral oncogene homolog (avian)
206055_s_at	SNRPA1	6627	0.04	NM_003090	NP_003081	0.85	small nuclear ribonucleoprotein polypeptide A'
206059_at	ZNF91	7644	0.04	NM_003430	NP_003421	0.89	zinc finger protein 91 (HPF7, HTF10)
206082_at	HCP5	10866	0.01	NM_006674	NP_006665	0.85	HLA complex P5
206095_s_at	FUSIP1	10772	3.66e-03	NM_006625	NP_006616	0.87	FUS interacting protein (serine-arginine rich) 1
206096_at	ZNF35	7584	0.01	NM_003420	NP_003411	0.87	zinc finger protein 35 (clone HF.10)
206099_at	PRKCH	5583	0.04	NM_006255	NP_006246	0.89	protein kinase C, eta
206118_at	STAT4	6775	3.43e-03	NM_003151	NP_003142	0.84	signal transducer and activator of transcription 4
206129_s_at	ARSB	411	0.04	NM_000046	NP_000037	1.11	arylsulfatase B
206133_at	HSXIAPAF1	54739	0.03	NM_017523	NP_059993	1.19	XIAP associated factor-1
206138_s_at	PIK4CB	5298	9.91e-03	NM_002651	NP_002642	0.94	phosphatidylinositol 4-kinase, catalytic, beta polypeptide
206139_at	PIK4CB	5298	0.04	NM_002651	NP_002642	0.92	phosphatidylinositol 4-kinase, catalytic, beta polypeptide
206150_at	TNFRSF7	939	0.02	NM_001242	NP_001233	0.81	tumor necrosis factor receptor superfamily, member 7
206158_s_at	ZNF9	7555	0.01	NM_003418	NP_003409	0.91	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)
206169_x_at	RoXaN	23264	0.03	AK023849	BAB14701	1.09	rotavirus X protein associated with NSP3
206174_s_at	PPP6C	5537	0.01	NM_002721	NP_002712	0.94	protein phosphatase 6, catalytic subunit
206184_at	CRKL	1399	0.02	NM_005207	NP_005198	1.13	v-crk sarcoma virus CT10 oncogene homolog (avian)-like

206200_s_at	ANXA11	311	0.03	NM_001157	NP_001148	0.96	annexin A11
206218_at	MAGEB2	4113	0.04	NM_002364	NP_002355	1.16	melanoma antigen family B, 2
206235_at	LIG4	3981	8.05e-03	NM_002312	NP_002303	0.89	ligase IV, DNA, ATP-dependent
206241_at	KPNA5	3841	0.04	NM_002269	NP_002260	0.90	karyopherin alpha 5 (importin alpha 6)
206257_at	CCDC9	26093	0.02	NM_015603	NP_056418	1.07	coiled-coil domain containing 9
206267_s_at	MATK	4145	3.43e-03	NM_002378	NP_002369	0.86	megakaryocyte-associated tyrosine kinase
206302_s_at	NUDT4	11163	0.01	NM_019094	NP_061967	0.86	nudix (nucleoside diphosphate linked moiety X)-type motif 4
206316_s_at	KNTC1	9735	3.2e-03	NM_014708	NP_055523	0.82	kinetochore associated 1
206332_s_at	IFI16	3428	0.01	NM_005531	NP_005522	0.82	interferon, gamma-inducible protein 16
206336_at	CXCL6	6372	0.03	NM_002993	NP_002984	1.23	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
206337_at	CCR7	1236	0.03	NM_001838	NP_001829	0.84	chemokine (C-C motif) receptor 7
206341_at	IL2RA	3559	5.76e-03	NM_000417	NP_000408	0.76	interleukin 2 receptor, alpha
206357_at	OPA3	80207	0.01	NM_025136	NP_079412	1.17	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)
206371_at	FOLR3	2352	8.35e-04	NM_000804	NP_000795	1.31	folate receptor 3 (gamma)
206398_s_at	CD19	930	0.04	NM_001770	NP_001761	1.17	CD19 antigen
206445_s_at	HRMT1L2	3276	0.02	NM_001536	NP_001527	0.90	HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae)
206474_at	PCTK2	5128	0.02	NM_002595	NP_002586	0.92	PCTAIRE protein kinase 2
206499_s_at	CHC1	1104	0.02	NM_001269	NP_001260	0.86	chromosome condensation 1
206513_at	AIM2	9447	0.03	NM_004833	NP_004824	0.75	absent in melanoma 2
206540_at	GLB1L	79411	0.04	NM_024506	NP_078782	0.95	galactosidase, beta 1-like
206544_x_at	SMARCA2	6595	0.04	NM_003070	NP_003061	0.93	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
206553_at	OAS2	4939	0.03	NM_002535	NP_002526	0.73	2'-5'-oligoadenylate synthetase 2, 69/71kDa
206555_s_at	THUMPD1	55623	0.01	NM_017736	NP_060206	0.88	THUMP domain containing 1
206583_at	FLJ20344	55634	0.02	NM_017776	NP_060246	0.87	hypothetical protein FLJ20344
206590_x_at	DRD2	1813	0.03	NM_000795	NP_000786	0.88	dopamine receptor D2
206613_s_at	TAF1A	9015	0.01	NM_005681	NP_005672	0.84	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa
206637_at	P2RY14	9934	7.05e-03	NM_014879	NP_055694	0.66	purinergic receptor P2Y, G-protein coupled, 14
206667_s_at	SCAMP1	9522	4.31e-03	NM_004866	NP_004857	0.85	secretory carrier membrane protein 1
206668_s_at	SCAMP1	9522	6.44e-04	NM_004866	NP_004857	0.91	secretory carrier membrane protein 1
206688_s_at	CPSF4	10898	0.02	NM_006693	NP_006684	0.92	cleavage and polyadenylation specific factor 4, 30kDa
206693_at	IL7	3574	2.29e-03	NM_000880	NP_000871	1.24	interleukin 7
206722_s_at	EDG4	9170	0.03	NM_004720	NP_004711	0.90	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4
206723_s_at	EDG4	9170	0.01	NM_004720	NP_004711	0.87	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4
206761_at	CD96	10225	0.01	NM_005816	NP_005807	0.84	CD96 antigen
206766_at	ITGA10	8515	0.02	NM_003637	NP_003628	1.07	integrin, alpha 10
206788_s_at	CBFB	865	1.26e-03	NM_022845	NP_074036	0.85	core-binding factor, beta subunit
206790_s_at	NDUFB1	4707	0.02	NM_004545	NP_004536	0.94	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa

206792_x_at	PDE4C	5143	0.01	NM_000923	NP_000914	1.07	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)
206807_s_at	ADD2	119	0.04	NM_017482	NP_059516	1.16	adducin 2 (beta)
206809_s_at	HNRPA3	220988	0.03	BC032437		0.89	heterogeneous nuclear ribonucleoprotein A3
206828_at	TXK	7294	0.02	NM_003328	NP_003319	0.86	TXK tyrosine kinase
206846_s_at	HDAC6	10013	5.93e-03	NM_006044	NP_006035	1.09	histone deacetylase 6
206854_s_at	MAP3K7	6885	0.02	NM_003188	NP_003179	0.92	mitogen-activated protein kinase kinase kinase 7
206917_at	GNA13	10672	0.04	NM_006572	NP_006563	0.91	guanine nucleotide binding protein (G protein), alpha 13
206943_at	TGFBR1	7046	0.03	NM_004612	NP_004603	0.87	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)
206958_s_at	UPF3A	65110	0.01	NM_023011	NP_075387	0.84	UPF3 regulator of nonsense transcripts homolog A (yeast)
206976_s_at	HSPH1	10808	0.01	NM_006644	NP_006635	0.88	heat shock 105kDa/110kDa protein 1
206978_at	CCR2	1231	0.03	NM_000647	NP_000638	0.94	chemokine (C-C motif) receptor 2
206995_x_at	SCARF1	8578	0.02	NM_003693	NP_003684	0.81	scavenger receptor class F, member 1
207000_s_at	PPP3CC	5533	0.04	NM_005605	NP_005596	0.83	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)
207008_at	IL8RB	3579	6.71e-03	NM_001557	NP_001548	1.11	interleukin 8 receptor, beta
207040_s_at	ST13	6767	4.6e-03	NM_003932	NP_003923	0.89	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)
207057_at	SLC16A7	9194	0.04	NM_004731	NP_004722	0.81	solute carrier family 16 (monocarboxylic acid transporters), member 7
207079_s_at	MED6	10001	4.7e-04	NM_005466	NP_005457	0.83	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)
207093_s_at	OMG	4974	0.03	NM_002544	NP_002535	1.18	oligodendrocyte myelin glycoprotein
207094_at	IL8RA	3577	0.02	NM_000634	NP_000625	1.10	interleukin 8 receptor, alpha
207101_at	VAMP1	6843	0.01	NM_016830	NP_058439	0.85	vesicle-associated membrane protein 1 (synaptobrevin 1)
207104_x_at	LILRB1	10859	0.02	NM_006669	NP_006660	1.10	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1
207111_at	EMR1	2015	0.04	NM_001974	NP_001965	0.88	egf-like module containing, mucin-like, hormone receptor-like 1
207121_s_at	MAPK6	5597	8.67e-03	NM_002748	NP_002739	0.79	mitogen-activated protein kinase 6
207127_s_at	HNRPH3	3189	0.01	NM_021644	NP_067676	0.92	heterogeneous nuclear ribonucleoprotein H3 (2H9)
207128_s_at	ZNF223	7766	0.04	NM_013361	NP_037493	1.08	zinc finger protein 223
207132_x_at	PFDN5	5204	0.02	NM_002624	NP_002615	0.92	prefoldin 5
207153_s_at	GLMN	11146	0.04	NM_007070	NP_009001	0.88	glomulin, FKBP associated protein
207170_s_at	LETMD1	25875	7.89e-03	NM_015416	NP_056231	0.90	LETM1 domain containing 1
207176_s_at	CD80	941	0.02	NM_005191	NP_005182	1.08	CD80 antigen (CD28 antigen ligand 1, B7-1 antigen)
207187_at	JAK3	3718	4.19e-03	NM_000215	NP_000206	1.19	Janus kinase 3 (a protein tyrosine kinase, leukocyte)
207223_s_at	ROD1	9991	0.01	NM_005156	NP_005147	0.85	ROD1 regulator of differentiation 1 (S. pombe)
207269_at	DEFA4	1669	0.03	NM_001925	NP_001916	1.39	defensin, alpha 4, corticostatin
207283_at	RPL23AP13	56969	0.01	NM_020217		1.14	ribosomal protein L23a pseudogene 13
207304_at	ZNF45	7596	9.48e-03	NM_003425	NP_003416	0.86	zinc finger protein 45
207308_at	SLCO1A2	6579	0.02	NM_021094	NP_066580	1.14	solute carrier organic anion transporter family, member 1A2
207323_s_at	MBP	4155	0.02	NM_002385	NP_002376	1.15	myelin basic protein

207332_s_at	TFRC	7037	0.01	NM_003234	NP_003225	0.86	transferrin receptor (p90, CD71)
207334_s_at	TGFBR2	7048	0.01	NM_003242	NP_003233	0.87	transforming growth factor, beta receptor II (70/80kDa)
207338_s_at	ZNF200	7752	0.01	NM_003454	NP_003445	1.11	zinc finger protein 200
207347_at	ERCC6	2074	3.98e-03	NM_000124	NP_000115	0.89	excision repair cross-complementing rodent repair deficiency, complementation group 6
207358_x_at	MACF1	23499	0.02	NM_012090	NP_036222	0.89	microtubule-actin crosslinking factor 1
207375_s_at	IL15RA	3601	0.01	NM_002189	NP_002180	0.86	interleukin 15 receptor, alpha
207391_s_at	PIP5K1A	8394	0.03	NM_003557	NP_003548	0.86	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha
207405_s_at	RAD17	5884	0.04	NM_002873	NP_002864	0.87	RAD17 homolog (S. pombe)
207425_s_at	SEPT9	10801	0.02	NM_006640	NP_006631	0.82	septin 9
207426_s_at	TNFSF4	7292	0.04	NM_003326	NP_003317	1.10	tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa)
207438_s_at	RNUT1	10073	0.03	NM_005701	NP_005692	0.84	RNA, U transporter 1
207483_s_at	TIP120A	55832	0.02	NM_018448	NP_060918	0.89	TBP-interacting protein
207507_s_at	ATP5G3	518	0.01	NM_001689	NP_001680	0.85	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
207521_s_at	ATP2A3	489	0.02	NM_005173	NP_005164	1.21	ATPase, Ca++ transporting, ubiquitous
207522_s_at	ATP2A3	489	0.03	NM_005173	NP_005164	1.10	ATPase, Ca++ transporting, ubiquitous
207563_s_at	OGT	8473	0.02	NM_003605	NP_003596	0.88	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
207564_x_at	OGT	8473	0.02	NM_003605	NP_003596	0.89	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
207573_x_at	ATP5L	10632	4.95e-03	NM_006476	NP_006467	0.94	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g
207583_at	ABCD2	225	7.18e-03	NM_005164	NP_005155	1.22	ATP-binding cassette, sub-family D (ALD), member 2
207585_s_at	RPL36AL	6166	0.03	NM_001001	NP_000992	0.90	ribosomal protein L36a-like
207606_s_at	ARHGAP12	94134	0.01	NM_018287	NP_060757	0.90	Rho GTPase activating protein 12.
207608_x_at	CYP1A2	1544	0.03	NM_000761	NP_000752	1.10	cytochrome P450, family 1, subfamily A, polypeptide 2
207614_s_at	CUL1	8454	0.01	NM_003592	NP_003583	0.86	cullin 1
207627_s_at	TFCP2	7024	2.16e-03	NM_005653	NP_005644	0.93	transcription factor CP2
207628_s_at	WBSCR22	114049	0.02	NM_017528	NP_059998	0.93	Williams Beuren syndrome chromosome region 22
207654_x_at	DR1	1810	0.01	NM_001938	NP_001929	0.96	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
207657_x_at	TNPO1	3842	0.04	NM_002270	NP_002261	0.95	transportin 1
207668_x_at	TXNDC7	10130	0.01	NM_005742	NP_005733	0.87	thioredoxin domain containing 7 (protein disulfide isomerase)
207674_at	FCAR	2204	8.05e-03	NM_002000	NP_001991	1.26	Fc fragment of IgA, receptor for
207688_s_at	INHBC	3626	0.01	NM_005538	NP_005529	0.85	inhibin, beta C
207707_s_at	SEC13L1	6396	0.03	NM_030673	NP_109598	0.92	SEC13-like 1 (S. cerevisiae)
207711_at	KIAA0889	25781	0.02	AB020696	BAA74912	1.09	KIAA0889 protein
207721_x_at	HINT1	3094	0.01	NM_005340	NP_005331	0.90	histidine triad nucleotide binding protein 1
207728_at	ATF7IP	55729	0.01	AK001001	BAA91461	1.12	activating transcription factor 7 interacting protein
207734_at	LAX	54900	0.04	NM_017773	NP_060243	0.88	hypothetical protein FLJ20340
207735_at	RNF125	54941	0.01	NM_017831	NP_060301	0.85	ring finger protein 125
207740_s_at	NUP62	23636	0.01	NM_012346	NP_036478	0.85	nucleoporin 62kDa

207761_s_at	DKFZP586A0522	25840	0.03	NM_014033	NP_054752	0.89	DKFZP586A0522 protein		
207769_s_at	PQBP1	10084	0.01	NM_005710	NP_005701	0.95	polyglutamine binding protein 1		
207791_s_at	RAB1A	5861	0.04	NM_004161	NP_004152	0.93	RAB1A, member RAS oncogene family		
207796_x_at	KLRD1	3824	0.04	NM_007334	NP_031360	0.79	killer cell lectin-like receptor subfamily D, member 1		
207801_s_at	RNF10	9921	0.03	NM_014868	NP_055683	0.91	ring finger protein 10		
207805_s_at	PSMD9	5715	0.03	NM_002813	NP_002804	0.93	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9		
207809_s_at	ATP6AP1	537	0.01	NM_001183	NP_001174	0.93	ATPase, H+ transporting, lysosomal accessory protein 1		
207812_s_at	GORASP2	26003	0.01	NM_015530	NP_056345	0.89	golgi reassembly stacking protein 2, 55kDa		
207845_s_at	ANAPC10	10393	2.35e-03	NM_014885	NP_055700	0.80	anaphase promoting complex subunit 10		
207855_s_at	MCLC	23155	0.01	NM_015127	NP_055942	0.85	Mid-1-related chloride channel 1		
207953_at	AD7C-NTP	27308	7.89e-03	AF010144	AAC08737	1.13	neuronal thread protein AD7c-NTP		
207956_x_at	APRIN	23047	3.6e-03	NM_015928	NP_057012	0.93	androgen-induced proliferation inhibitor		
207971_s_at	KIAA0582	23177	0.01	NM_015147	NP_055962	1.15	KIAA0582		
207974_s_at	SKP1A	6500	1.16e-03	NM_006930	NP_008861	0.96	S-phase kinase-associated protein 1A (p19A)		
207992_s_at	AMPD3	272	0.02	NM_000480	NP_000471	0.91	adenosine monophosphate deaminase (isoform E)		
208002_s_at	BACH	11332	0.04	NM_007274	NP_009205	0.83	brain acyl-CoA hydrolase		
208035_at	GRM6	2916	1.43e-03	NM_000843	NP_000834	1.19	glutamate receptor, metabotropic 6		
208047_s_at	NAB1	4664	5.47e-03	NM_005966	NP_005957	0.82	NGFI-A binding protein 1 (EGR1 binding protein 1)		
208066_s_at	GTF2B	2959	0.04	NM_001514	NP_001505	0.96	general transcription factor IIB		
208073_x_at	TTC3	7267	0.02	NM_003316	NP_003307	0.87	tetratricopeptide repeat domain 3		
208074_s_at	AP2S1	1175	6.35e-03	NM_021575	NP_067586	0.94	adaptor-related protein complex 2, sigma 1 subunit		
208097_s_at	TXNDC	81542	0.04	NM_030755	NP_110382	0.93	thioredoxin domain containing		
208099_x_at	KIAA0998	23093	0.01	NM_015072	NP_055887	1.14	KIAA0998		
208103_s_at	ANP32E	81611	0.03	NM_030920	NP_112182	0.84	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E		
208114_s_at	FLJ12671	81875	2.78e-04	NM_030980	NP_112242	1.12	hypothetical protein FLJ12671		
208146_s_at	CPVL	54504	0.01	NM_031311	NP_112601	0.83	carboxypeptidase, vitellogenic-like		
208151_x_at	DDX17	10521	0.03	NM_030881	NP_112020	1.25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17		
208152_s_at	DDX21	9188	0.02	NM_004728	NP_004719	0.90	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21		
208184_s_at	TMEM1	7109	3.79e-03	NM_003274	NP_003265	0.87	transmembrane protein 1		
208246_x_at	TK2	7084	0.01	NM_017618	1.08	thymidine kinase 2, mitochondrial			
208249_s_at	TGDS	23483	6.92e-03	NM_014305	NP_055120	0.91	TDP-glucose 4,6-dehydratase		
208289_s_at	EI24	9538	0.01	NM_004879	NP_004870	0.81	etoposide induced 2.4 mRNA		
208296_x_at	TNFAIP8	25816	5.07e-03	NM_014350	NP_055165	0.91	tumor necrosis factor, alpha-induced protein 8		
208297_s_at	EVI5	7813	0.03	NM_005665	NP_005656	1.14	ecotropic viral integration site 5		
208308_s_at	GPI	2821	0.01	NM_000175	NP_000166	0.87	glucose phosphate isomerase		
208309_s_at	MALT1	10892	0.01	NM_006785	NP_006776	0.87	mucosa associated lymphoid tissue lymphoma translocation gene 1		
208310_s_at	FSTL1	11167	7.71e-03	NM_007085	NP_009016	0.89	follistatin-like 1		
208398_s_at	TBPL1	9519	0.02	NM_004865	NP_004856	0.90	TBP-like 1		
208403_x_at	MAX	4149	0.01	NM_002382	NP_002373	0.92	MYC associated factor X		
208405_s_at	CD164	8763	0.01	NM_006016	NP_006007	0.89	CD164 antigen, sialomucin		
208415_x_at	ING1	3621	0.02	NM_005537	NP_005528	0.90	inhibitor of growth family, member 1		
208424_s_at	CIAPIN1	57019	0.02	NM_020313	NP_064709	0.89	cytokine induced apoptosis inhibitor 1		

208442_s_at	ATM	472	7.35e-03	NM_000051	NP_000042	0.86	ataxia telangiectasia mutated (includes complementation groups A, C and D)
208445_s_at	BAZ1B	9031	0.01	NM_023005	NP_075381	0.89	bromodomain adjacent to zinc finger domain, 1B
208447_s_at	PRPS1	5631	5.31e-03	NM_002764	NP_002755	0.82	phosphoribosyl pyrophosphate synthetase 1
208453_s_at	XPNPEP1	7511	8.5e-04	NM_020383	NP_065116	0.92	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
208456_s_at	RRAS2	22800	0.03	NM_012250	NP_036382	0.76	related RAS viral (r-ras) oncogene homolog 2
208459_s_at	XPO7	23039	0.04	NM_015024	NP_055839	0.90	exportin 7
208478_s_at	BAX	581	6.71e-03	NM_004324	NP_004315	0.86	BCL2-associated X protein
208490_x_at	HIST1H2BF	8343	4.83e-03	NM_003522	NP_003513	1.20	histone 1, H2bf
208523_x_at	HIST1H2BI	8346	7.19e-03	NM_003525	NP_003516	1.23	histone 1, H2bi
208527_x_at	HIST1H2BE	8344	1.59e-04	NM_003523	NP_003514	1.26	histone 1, H2be
208546_x_at	HIST1H2BH	8345	0.01	NM_003524	NP_003515	1.26	histone 1, H2bh
208549_x_at	PTMA	5757	0.04	NM_002823	NP_002814	0.82	prothymosin, alpha (gene sequence 28)
208598_s_at	HUWE1	10075	4.83e-03	AB002310	BAA20771	0.94	HECT, UBA and WWE domain containing 1
208612_at	GRP58	2923	2.39e-03	NM_005313	NP_005304	0.83	glucose regulated protein, 58kDa
208616_s_at	PTP4A2	8073	0.04	NM_003479	NP_003470	0.95	protein tyrosine phosphatase type IVA, member 2
208624_s_at	EIF4G1	1981	4.83e-03	NM_182917	NP_886553	0.93	eukaryotic translation initiation factor 4 gamma, 1
208627_s_at	NSEP1	4904	3.83e-03	NM_004559	NP_004550	0.94	nuclease sensitive element binding protein 1
208628_s_at	NSEP1	4904	0.02	NM_004559	NP_004550	0.88	nuclease sensitive element binding protein 1
208631_s_at	HADHA	3030	5.83e-03	NM_000182	NP_000173	0.91	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha
208632_at	RNF10	9921	0.02	NM_014868	NP_055683	0.88	ring finger protein 10
208633_s_at	MACF1	23499	8.8e-03	NM_012090	NP_036222	0.88	microtubule-actin crosslinking factor 1
208634_s_at	MACF1	23499	0.01	NM_012090	NP_036222	0.88	microtubule-actin crosslinking factor 1
208635_x_at	NACA	4666	0.02	NM_005594	NP_005585	0.90	nascent-polypeptide-associated complex alpha polypeptide
208639_x_at	TXNDC7	10130	5.48e-03	NM_005742	NP_005733	0.85	thioredoxin domain containing 7 (protein disulfide isomerase)
208642_s_at	XRCC5	7520	0.01	NM_021141	NP_066964	0.94	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa)
208643_s_at	XRCC5	7520	2.26e-03	NM_021141	NP_066964	0.95	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa)
208649_s_at	VCP	7415	0.01	NM_007126	NP_009057	0.91	valosin-containing protein
208653_s_at	CD164	8763	0.01	NM_006016	NP_006007	0.83	CD164 antigen, sialomucin
208654_s_at	CD164	8763	0.03	NM_006016	NP_006007	0.90	CD164 antigen, sialomucin
208660_at	CS	1431	0.02	NM_004077	NP_004068	0.93	citrate synthase
208667_s_at	ST13	6767	0.02	NM_003932	NP_003923	0.91	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)
208669_s_at	CRI1	23741	0.03	NM_014335	NP_055150	0.88	CREBBP/EP300 inhibitor 1
208675_s_at	DDOST	1650	0.02	NM_005216	NP_005207	0.90	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
208680_at	PRDX1	5052	0.01	NM_002574	NP_002565	0.96	peroxiredoxin 1
208682_s_at	MAGED2	10916	0.01	NM_014599	NP_055414	0.87	melanoma antigen family D, 2
208683_at	CAPN2	824	0.04	NM_001748	NP_001739	0.94	calpain 2, (m/II) large subunit
208691_at	TFRC	7037	0.01	BC001188	AAH01188	0.87	transferrin receptor (p90, CD71)

208696_at	CCT5	22948	0.03	NM_012073	NP_036205	0.88	chaperonin containing TCP1, subunit 5 (epsilon)
208697_s_at	EIF3S6	3646	0.01	NM_001568	NP_001559	0.91	eukaryotic translation initiation factor 3, subunit 6 48kDa
208698_s_at	NONO	4841	2.66e-03	NM_007363	NP_031389	0.87	non-POU domain containing, octamer-binding
208706_s_at	EIF5	1983	5.61e-03	NM_001969	NP_001960	0.93	eukaryotic translation initiation factor 5
208707_at	EIF5	1983	0.01	NM_001969	NP_001960	0.87	eukaryotic translation initiation factor 5
208708_x_at	EIF5	1983	3.1e-03	NM_001969	NP_001960	0.91	eukaryotic translation initiation factor 5
208713_at	HNRPUL1	11100	9.2e-03	NM_007040	NP_008971	0.82	heterogeneous nuclear ribonucleoprotein U-like 1
208716_s_at	LOC54499	54499	7.96e-03	NM_019026	NP_061899	0.93	putative membrane protein
208717_at	OXA1L	5018	0.01	NM_005015	NP_005006	0.94	oxidase (cytochrome c) assembly 1-like
208721_s_at	ANAPC5	51433	0.03	NM_016237	NP_057321	0.91	anaphase promoting complex subunit 5
208722_s_at	ANAPC5	51433	0.01	NM_016237	NP_057321	0.91	anaphase promoting complex subunit 5
208723_at	USP11	8237	0.04	NM_004651	NP_004642	0.91	ubiquitin specific protease 11
208724_s_at	RAB1A	5861	0.04	NM_004161	NP_004152	0.92	RAB1A, member RAS oncogene family
208726_s_at	EIF2S2	8894	0.01	NM_003908	NP_003899	0.96	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
208727_s_at	CDC42	998	0.01	NM_001791	NP_001782	0.80	cell division cycle 42 (GTP binding protein, 25kDa)
208728_s_at	CDC42	998	0.04	NM_001791	NP_001782	0.96	cell division cycle 42 (GTP binding protein, 25kDa)
208734_x_at	RAB2	5862	0.01	NM_002865	NP_002856	0.94	RAB2, member RAS oncogene family
208738_x_at	SUMO2	6613	0.01	NM_006937	NP_008868	0.90	SMT3 suppressor of mif two 3 homolog 2 (yeast)
208739_x_at	SUMO2	6613	8.49e-03	NM_006937	NP_008868	0.95	SMT3 suppressor of mif two 3 homolog 2 (yeast)
208742_s_at	SAP18	10284	9.33e-03	NM_005870	NP_005861	0.90	sin3-associated polypeptide, 18kDa
208745_at	ATP5L	10632	0.03	NM_006476	NP_006467	0.84	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g
208746_x_at	ATP5L	10632	5.36e-03	NM_006476	NP_006467	0.95	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g
208752_x_at	NAP1L1	4673	0.01	NM_139207	NP_631946	0.90	nucleosome assembly protein 1-like 1
208753_s_at	NAP1L1	4673	3.1e-03	NM_139207	NP_631946	0.91	nucleosome assembly protein 1-like 1
208754_s_at	NAP1L1	4673	0.01	NM_139207	NP_631946	0.86	nucleosome assembly protein 1-like 1
208756_at	EIF3S2	8668	4.18e-03	NM_003757	NP_003748	0.90	eukaryotic translation initiation factor 3, subunit 2 beta, 36kDa
208757_at	TMED9	54732	6.71e-03	NM_017510	NP_059980	0.84	transmembrane emp24 protein transport domain containing 9
208758_at	ATIC	471	1.41e-03	NM_004044	NP_004035	0.89	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
208761_s_at	SUMO1	7341	0.02	NM_003352	NP_003343	0.95	SMT3 suppressor of mif two 3 homolog 1 (yeast)
208762_at	SUMO1	7341	0.02	NM_003352	NP_003343	0.89	SMT3 suppressor of mif two 3 homolog 1 (yeast)
208764_s_at	ATP5G2	517	0.04	NM_001002031	NP_001002031	0.95	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
208766_s_at	HNRPR	10236	0.01	NM_005826	NP_005817	0.89	heterogeneous nuclear ribonucleoprotein R
208771_s_at	LTA4H	4048	0.02	NM_000895	NP_000886	0.90	leukotriene A4 hydrolase
208772_at	ANKHD1	54882	0.02	NM_017747	NP_060217	0.88	ankyrin repeat and KH domain containing 1
208773_s_at	ANKHD1	54882	4.09e-03	NM_017747	NP_060217	0.94	ankyrin repeat and KH domain containing 1
208778_s_at	TCP1	6950	0.04	NM_030752	NP_110379	0.91	t-complex 1
208787_at	MRPL3	11222	8.8e-03	NM_007208	NP_009139	0.93	mitochondrial ribosomal protein L3

208795_s_at	MCM7	4176	8.58e-03	NM_005916	NP_005907	0.89	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)
208797_s_at	GOLGIN-67	23015	1.07e-03	NM_015003	NP_055818	0.79	golgin-67
208798_x_at	GOLGIN-67	23015	0.03	NM_015003	NP_055818	0.86	golgin-67
208801_at	SRP72	6731	9.55e-04	NM_006947	NP_008878	0.94	signal recognition particle 72kDa
208805_at	PSMA6	5687	5.99e-03	NM_002791	NP_002782	0.95	proteasome (prosome, macropain) subunit, alpha type, 6
208809_s_at	C6orf62	81688	2.19e-03	NM_030939	NP_112201	0.89	chromosome 6 open reading frame 62
208818_s_at	COMT	1312	7.86e-04	NM_000754	NP_000745	0.94	catechol-O-methyltransferase
208819_at	RAB8A	4218	0.04	NM_005370	NP_005361	1.13	RAB8A, member RAS oncogene family
208826_x_at	HINT1	3094	0.02	NM_005340	NP_005331	0.89	histidine triad nucleotide binding protein 1
208827_at	PSMB6	5694	0.03	NM_002798	NP_002789	0.94	proteasome (prosome, macropain) subunit, beta type, 6
208828_at	POLE3	54107	7.02e-03	NM_017443	NP_059139	0.86	polymerase (DNA directed), epsilon 3 (p17 subunit)
208833_s_at	ATXN10	25814	0.01	NM_013236	NP_037368	0.94	ataxin 10
208835_s_at	CROP	51747	0.03	NM_016424	NP_057508	0.90	cisplatin resistance-associated overexpressed protein
208837_at	TMED3	23423	0.01	NM_007364	NP_031390	0.86	transmembrane emp24 domain containing 3
208838_at	TIP120A	55832	8.66e-03	AB020636	BAA74852	0.85	TBP-interacting protein
208839_s_at	TIP120A	55832	0.02	NM_018448	NP_060918	0.87	TBP-interacting protein
208840_s_at	G3BP2	9908	3.43e-03	NM_203505	NP_987101	0.90	Ras-GTPase activating protein SH3 domain-binding protein 2
208841_s_at	G3BP2	9908	0.01	NM_203505	NP_987101	0.90	Ras-GTPase activating protein SH3 domain-binding protein 2
208842_s_at	GORASP2	26003	0.01	NM_015530	NP_056345	0.94	golgi reassembly stacking protein 2, 55kDa
208843_s_at	GORASP2	26003	9.61e-03	NM_015530	NP_056345	0.88	golgi reassembly stacking protein 2, 55kDa
208845_at	VDAC3	7419	4.31e-03	NM_005662	NP_005653	0.87	voltage-dependent anion channel 3
208846_s_at	VDAC3	7419	1.42e-03	NM_005662	NP_005653	0.94	voltage-dependent anion channel 3
208847_s_at	ADH5	128	0.01	NM_000671	NP_000662	0.89	alcohol dehydrogenase 5 (class III), chi polypeptide
208848_at	ADH5	128	3.43e-03	NM_000671	NP_000662	0.87	alcohol dehydrogenase 5 (class III), chi polypeptide
208852_s_at	CANX	821	0.01	NM_001746	NP_001737	0.92	calnexin
208853_s_at	CANX	821	1.33e-03	NM_001746	NP_001737	0.93	calnexin
208854_s_at	STK24	8428	0.01	NM_003576	NP_003567	0.94	serine/threonine kinase 24 (STE20 homolog, yeast)
208860_s_at	ATRX	546	0.03	NM_000489	NP_000480	0.92	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
208863_s_at	SFRS1	6426	7.27e-03	NM_006924	NP_008855	0.91	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
208865_at	CSNK1A1	1452	0.04	AF447582	AAL60204	0.96	casein kinase 1, alpha 1
208866_at	CSNK1A1	1452	0.04	AF447582	AAL60204	0.93	casein kinase 1, alpha 1
208870_x_at	ATP5C1	509	2.51e-04	NM_001001973	NP_001001973	0.95	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
208873_s_at	C5orf18	7905	0.01	NM_005669	NP_005660	0.92	chromosome 5 open reading frame 18
208874_x_at	PPP2R4	5524	0.02	NM_178001	NP_821068	0.92	protein phosphatase 2A, regulatory subunit B' (PR 53)
208880_s_at	C20orf14	24148	0.02	NM_012469	NP_036601	0.91	chromosome 20 open reading frame 14
208882_s_at	EDD	51366	2.33e-03	NM_015902	NP_056986	0.93	E3 identified by differential display
208883_at	EDD	51366	6.92e-03	AL833555		0.87	E3 identified by differential display
208887_at	EIF3S4	8666	5.99e-03	NM_003755	NP_003746	0.87	eukaryotic translation initiation factor 3, subunit 4 delta, 44kDa

208891_at	DUSP6	1848	0.03	NM_001946	NP_001937	0.95	dual specificity phosphatase 6
208894_at	HLA-DRA	3122	0.02	NM_019111	NP_061984	0.91	major histocompatibility complex, class II, DR alpha
208895_s_at	DDX18	8886	6.46e-03	NM_006773	NP_006764	0.84	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
208896_at	DDX18	8886	0.03	NM_006773	NP_006764	0.87	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
208897_s_at	DDX18	8886	3.37e-03	NM_006773	NP_006764	0.82	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
208901_s_at	TOP1	7150	0.03	NM_003286	NP_003277	0.95	topoisomerase (DNA) I
208905_at	CYCS	54205	0.02	NM_018947	NP_061820	0.91	cytochrome c, somatic
208909_at	UQCRFS1	7386	0.04	NM_006003	NP_005994	0.96	ubiquinol-cytochrome c reductase, Rieske iron-sulfur
polypeptide 1							
208910_s_at	C1QBP	708	0.03	NM_001212	NP_001203	0.86	complement component 1, q subcomponent binding protein
208911_s_at	PDHB	5162	9.2e-03	NM_000925	NP_000916	0.90	pyruvate dehydrogenase (lipoamide) beta
208912_s_at	CNP	1267	4.31e-03	NM_033133	NP_149124	0.82	2',3'-cyclic nucleotide 3' phosphodiesterase
208921_s_at	SRI	6717	0.01	NM_003130	NP_003121	0.94	sorcin
208923_at	CYFIP1	23191	0.04	NM_014608	NP_055423	0.88	cytoplasmic FMR1 interacting protein 1
208927_at	SPOP	8405	0.03	BF673888		1.06	speckle-type POZ protein
208928_at	POR	5447	0.04	NM_000941	NP_000932	0.94	P450 (cytochrome) oxidoreductase
208930_s_at	ILF3	3609	0.02	NM_012218	NP_036350	0.89	interleukin enhancer binding factor 3, 90kDa
208933_s_at	LGALS8	3964	6.14e-03	NM_006499	NP_006490	0.93	lectin, galactoside-binding, soluble, 8 (galectin 8)
208934_s_at	LGALS8	3964	4.48e-03	NM_006499	NP_006490	0.83	lectin, galactoside-binding, soluble, 8 (galectin 8)
208935_s_at	LGALS8	3964	6.76e-04	L78132	AAB51605	0.93	lectin, galactoside-binding, soluble, 8 (galectin 8)
208936_x_at	LGALS8	3964	0.01	NM_006499	NP_006490	0.92	lectin, galactoside-binding, soluble, 8 (galectin 8)
208945_s_at	BECN1	8678	0.04	NM_003766	NP_003757	0.92	beclin 1 (coiled-coil, myosin-like BCL2 interacting
protein)							
208946_s_at	BECN1	8678	0.04	NM_003766	NP_003757	0.96	beclin 1 (coiled-coil, myosin-like BCL2 interacting
protein)							
208952_s_at	KIAA0217	23185	9.63e-03	AA811923		0.92	KIAA0217
208953_at	KIAA0217	23185	0.02	AU154358		0.93	KIAA0217
208956_x_at	DUT	1854	0.01	NM_001948	NP_001939	0.89	dUTP pyrophosphatase
208957_at	TXNDC4	23071	0.03	NM_015051	NP_055866	0.94	thioredoxin domain containing 4 (endoplasmic reticulum)
208958_at	TXNDC4	23071	0.02	NM_015051	NP_055866	0.86	thioredoxin domain containing 4 (endoplasmic reticulum)
208959_s_at	TXNDC4	23071	0.04	NM_015051	NP_055866	0.93	thioredoxin domain containing 4 (endoplasmic
reticulum)							
208965_s_at	IFI16	3428	0.02	NM_005531	NP_005522	1.09	interferon, gamma-inducible protein 16
208966_x_at	IFI16	3428	0.01	AF208043	AAF20997	0.83	interferon, gamma-inducible protein 16
208967_s_at	AK2	204	0.03	NM_001625	NP_001616	0.93	adenylate kinase 2
208968_s_at	CIAPIN1	57019	3.45e-04	NM_020313	NP_064709	0.83	cytokine induced apoptosis inhibitor 1
208970_s_at	UROD	7389	0.02	NM_000374	NP_000365	0.93	uroporphyrinogen decarboxylase
208974_x_at	KPNB1	3837	0.02	NM_002265	NP_002256	1.14	karyopherin (importin) beta 1
208985_s_at	EIF3S1	8669	0.02	NM_003758	NP_003749	0.89	eukaryotic translation initiation factor 3, subunit 1 alpha,
35kDa							
208986_at	TCF12	6938	0.02	NM_207036	NP_996919	0.88	transcription factor 12 (HTF4, helix-loop-helix transcription
factors 4)							
208990_s_at	HNRPH3	3189	4.65e-03	NM_012207	NP_036339	0.94	heterogeneous nuclear ribonucleoprotein H3 (2H9)
209002_s_at	KIAA1536	57658	0.01	NM_020898	NP_065949	1.13	KIAA1536 protein
209009_at	ESD	2098	0.04	NM_001984	NP_001975	0.92	esterase D/formylglutathione hydrolase

209023_s_at	STAG2	10735	0.01	NM_006603	NP_006594	1.17	stromal antigen 2
209025_s_at	SYNCRIP	10492	3.43e-03	NM_006372	NP_006363	0.86	synaptotagmin binding, cytoplasmic RNA interacting protein
209027_s_at	ABI1	10006	4.68e-03	NM_005470	NP_005461	0.91	abl-interactor 1
209028_s_at	ABI1	10006	0.02	NM_005470	NP_005461	0.91	abl-interactor 1
209036_s_at	MDH2	4191	0.01	NM_005918	NP_005909	0.88	malate dehydrogenase 2, NAD (mitochondrial)
209040_s_at	PSMB8	5696	0.04	NM_004159	NP_004150	0.96	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)
209045_at	XPNPEP1	7511	0.04	NM_020383	NP_065116	0.91	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
209048_s_at	PRKCBP1	23613	0.01	NM_183047	NP_898868	0.89	protein kinase C binding protein 1
209055_s_at	CDC5L	988	0.01	NM_001253	NP_001244	0.88	CDC5 cell division cycle 5-like (S. pombe)
209063_x_at	PAIP1	10605	4.73e-04	NM_006451	NP_006442	0.84	poly(A) binding protein interacting protein 1
209067_s_at	HNRPDL	9987	0.01	NM_005463	NP_005454	0.88	heterogeneous nuclear ribonucleoprotein D-like
209068_at	HNRPDL	9987	9.51e-03	NM_005463	NP_005454	0.92	heterogeneous nuclear ribonucleoprotein D-like
209080_x_at	TXNL2	10539	0.03	NM_006541	NP_006532	0.92	thioredoxin-like 2
209082_s_at	COL18A1	80781	0.02	NM_030582	NP_085059	0.81	collagen, type XVIII, alpha 1
209085_x_at	RFC1	5981	0.01	NM_002913	NP_002904	0.91	replication factor C (activator 1) 1, 145kDa
209089_at	RAB5A	5868	0.02	NM_004162	NP_004153	0.94	RAB5A, member RAS oncogene family
209092_s_at	C17orf25	51031	0.03	NM_016080	NP_057164	0.85	chromosome 17 open reading frame 25
209095_at	DLD	1738	4.87e-06	NM_000108	NP_000099	0.90	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto
209096_at	UBE2V2	7336	2.4e-03	NM_003350	NP_003341	0.87	ubiquitin-conjugating enzyme E2 variant 2
209104_s_at	NOLA2	55651	0.02	NM_017838	NP_060308	0.93	nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs)
209112_at	CDKN1B	1027	0.01	NM_004064	NP_004055	0.90	cyclin-dependent kinase inhibitor 1B (p27, Kip1)
209113_s_at	HMG20B	10362	0.02	NM_006339	NP_006330	0.91	high-mobility group 20B
209115_at	UBE1C	9039	0.02	NM_003968	NP_003959	0.91	ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)
209122_at	ADFP	123	0.04	NM_001122	NP_001113	0.90	adipose differentiation-related protein
209124_at	MYD88	4615	0.03	NM_002468	NP_002459	0.94	myeloid differentiation primary response gene (88)
209143_s_at	CLNS1A	1207	0.01	NM_001293	NP_001284	0.94	chloride channel, nucleotide-sensitive, 1A
209160_at	AKR1C3	8644	9.55e-04	NM_003739	NP_003730	0.58	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)
209161_at	PRPF4	9128	0.03	NM_004697	NP_004688	0.93	PRP4 pre-mRNA processing factor 4 homolog (yeast)
209165_at	AATF	26574	0.01	NM_012138	NP_036270	1.06	apoptosis antagonizing transcription factor
209175_at	SEC23IP	11196	0.02	NM_007190	NP_009121	0.94	SEC23 interacting protein
209177_at	DKFZP564J0123	25915	5.83e-03	NM_199069	NP_951032	0.91	nuclear protein E3-3
209180_at	RABGGTB	5876	6.44e-04	NM_004582	NP_004573	0.77	Rab geranylgeranyltransferase, beta subunit
209181_s_at	RABGGTB	5876	0.01	NM_004582	NP_004573	0.82	Rab geranylgeranyltransferase, beta subunit
209184_s_at	IRS2	8660	0.02	NM_003749	NP_003740	1.25	insulin receptor substrate 2
209186_at	ATP2A2	488	0.02	NM_170665	NP_733765	0.91	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
209187_at	DR1	1810	0.03	NM_001938	NP_001929	0.91	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
209188_x_at	DR1	1810	0.04	NM_001938	NP_001929	0.93	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
209214_s_at	EWSR1	2130	9.29e-03	NM_005243	NP_005234	0.94	Ewing sarcoma breakpoint region 1

209216_at	WDR45	11152	0.01	NM_007075	NP_009006	0.92	WD repeat domain 45
209239_at	NFKB1	4790	0.02	NM_003998	NP_003989	0.91	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
209242_at	PEG3	5178	4.38e-03	BC037330		1.22	paternally expressed 3
209249_s_at	GHITM	27069	0.04	NM_014394	NP_055209	0.97	growth hormone inducible transmembrane protein
209257_s_at	CSPG6	9126	0.03	NM_005445	NP_005436	0.89	chondroitin sulfate proteoglycan 6 (bamacan)
209258_s_at	CSPG6	9126	0.02	NM_005445	NP_005436	0.87	chondroitin sulfate proteoglycan 6 (bamacan)
209267_s_at	SLC39A8	64116	8.67e-03	NM_022154	NP_071437	0.83	solute carrier family 39 (zinc transporter), member 8
209271_at	FALZ	2186	0.02	NM_182641	NP_872579	0.89	fetal Alzheimer antigen
209284_s_at	RAP140	23272	0.01	NM_015224	NP_056039	0.89	retinoblastoma-associated protein 140
209285_s_at	RAP140	23272	0.01	AB029028	BAA83057	0.89	retinoblastoma-associated protein 140
209287_s_at	CDC42EP3	10602	0.02	NM_006449	NP_006440	0.89	CDC42 effector protein (Rho GTPase binding) 3
209302_at	POLR2H	5437	0.03	NM_006232	NP_006223	0.92	polymerase (RNA) II (DNA directed) polypeptide H
209304_x_at	GADD45B	4616	0.03	AF087853	AAG48366	0.89	growth arrest and DNA-damage-inducible, beta
209305_s_at	GADD45B	4616	0.02	NM_015675	NP_056490	0.88	growth arrest and DNA-damage-inducible, beta
209308_s_at	BNIP2	663	0.02	NM_004330	NP_004321	0.90	BCL2/adenovirus E1B 19kDa interacting protein 2
209310_s_at	CASP4	837	0.03	NM_001225	NP_001216	0.86	caspase 4, apoptosis-related cysteine protease
209312_x_at	HLA-DRB1	3123	6.41e-03	U65585	AAD43827	0.88	major histocompatibility complex, class II, DR beta 1
209313_at	XAB1	11321	0.03	NM_007266	NP_009197	0.92	XPA binding protein 1
209316_s_at	HBS1L	10767	0.03	NM_006620	NP_006611	0.88	HBS1-like (S. cerevisiae)
209317_at	POLR1C	9533	0.04	NM_203290	NP_976035	0.87	polymerase (RNA) I polypeptide C, 30kDa
209322_s_at	SH2B	25970	6.0e-04	NM_015503	NP_056318	0.83	SH2-B homolog
209330_s_at	HNRPD	3184	2.99e-03	NM_031369	NP_112737	0.93	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
209331_s_at	MAX	4149	8.57e-03	NM_002382	NP_002373	0.88	MYC associated factor X
209332_s_at	MAX	4149	0.01	NM_002382	NP_002373	0.94	MYC associated factor X
209333_at	ULK1	8408	0.02	NM_003565	NP_003556	1.15	unc-51-like kinase 1 (C. elegans)
209337_at	PSIP1	11168	0.03	NM_021144	NP_066967	0.89	PC4 and SFRS1 interacting protein 1
209337_at	PSIP1	11168	0.03	NM_033222	NP_150091	0.89	PC4 and SFRS1 interacting protein 1
209338_at	TFCP2	7024	9.61e-03	NM_005653	NP_005644	0.93	transcription factor CP2
209340_at	UAP1	6675	0.04	NM_003115	NP_003106	0.89	UDP-N-acteylglucosamine pyrophosphorylase 1
209341_s_at	IKBKB	3551	0.01	NM_001556	NP_001547	0.93	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
209344_at	TPM4	7171	0.01	NM_003290	NP_003281	1.16	tropomyosin 4
209350_s_at	GPS2	2874	4.38e-03	NM_004489	NP_004480	0.89	G protein pathway suppressor 2
209352_s_at	SIN3B	23309	0.04	NM_015260	NP_056075	0.87	SIN3 homolog B, transcription regulator (yeast)
209358_at	TAF11	6882	0.02	NM_005643	NP_005634	0.88	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa
209377_s_at	HMGN3	9324	3.43e-03	NM_004242	NP_004233	0.85	high mobility group nucleosomal binding domain 3
209382_at	POLR3C	10623	1.53e-03	NM_006468	NP_006459	0.87	polymerase (RNA) III (DNA directed) polypeptide C (62kD)
209384_at	PROSC	11212	0.02	NM_007198	NP_009129	0.95	proline synthetase co-transcribed homolog (bacterial)
209390_at	TSC1	7248	0.03	NM_000368	NP_000359	0.90	tuberous sclerosis 1
209393_s_at	EIF4E2	9470	0.04	NM_004846	NP_004837	0.93	eukaryotic translation initiation factor 4E member 2
209397_at	ME2	4200	0.01	BC000147	AAH00147	0.92	malic enzyme 2, NAD(+)-dependent, mitochondrial

209405_s_at	FAM3A	60343	0.04	NM_021806	NP_068578	1.09	family with sequence similarity 3, member A
209417_s_at	IFI35	3430	5.89e-03	NM_005533	NP_005524	0.69	interferon-induced protein 35
209419_at	C22orf19	8563	8.27e-04	NM_001002878	NP_001002878	0.78	chromosome 22 open reading frame 19
209421_at	MSH2	4436	0.03	NM_000251	NP_000242	0.87	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
209429_x_at	EIF2B4	8890	6.71e-03	AF112207	AAF17195	0.92	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa
209430_at	BTAF1	9044	4.68e-03	NM_003972	NP_003963	0.91	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae)
209431_s_at	ZNF278	23598	7.37e-03	NM_014323	NP_055138	0.83	zinc finger protein 278
209439_s_at	PHKA2	5256	8.02e-03	NM_000292	NP_000283	1.12	phosphorylase kinase, alpha 2 (liver)
209440_at	PRPS1	5631	0.02	NM_002764	NP_002755	0.89	phosphoribosyl pyrophosphate synthetase 1
209444_at	RAP1GDS1	5910	0.02	NM_021159	NP_066982	0.88	RAP1, GTP-GDP dissociation stimulator 1
209450_at	OSGEP	55644	0.01	NM_017807	NP_060277	0.85	O-sialoglycoprotein endopeptidase
209451_at	TANK	10010	0.03	NM_004180	NP_004171	0.91	TRAF family member-associated NFKB activator
209452_s_at	VTI1B	10490	3.37e-03	NM_006370	NP_006361	0.91	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)
209455_at	FBXW11	23291	1.57e-03	NM_033645	NP_387449	0.93	F-box and WD-40 domain protein 11
209456_s_at	FBXW11	23291	2.51e-04	NM_033645	NP_387449	0.92	F-box and WD-40 domain protein 11
209463_s_at	TAF12	6883	0.02	NM_005644	NP_005635	0.92	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa
209476_at	TXNDC	81542	0.02	NM_030755	NP_110382	0.92	thioredoxin domain containing
209477_at	EMD	2010	7.35e-03	NM_000117	NP_000108	0.86	emerin (Emery-Dreifuss muscular dystrophy)
209486_at	SAS10	57050	0.03	NM_020368	NP_065101	0.88	disrupter of silencing 10
209489_at	CUGBP1	10658	0.03	AK056024		0.86	CUG triplet repeat, RNA binding protein 1
209503_s_at	PSMC5	5705	6.71e-03	NM_002805	NP_002796	0.92	proteasome (prosome, macropain) 26S subunit, ATPase, 5
209507_at	RPA3	6119	3.66e-03	NM_002947	NP_002938	0.83	replication protein A3, 14kDa
209520_s_at	NCBP1	4686	5.83e-03	NM_002486	NP_002477	0.88	nuclear cap binding protein subunit 1, 80kDa
209522_s_at	CRAT	1384	0.03	NM_000755	NP_000746	0.86	carnitine acetyltransferase
209523_at	TAF2	6873	0.01	NM_003184	NP_003175	0.94	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa
209538_at	ZNF32	7580	0.03	NM_006973	NP_008904	0.90	zinc finger protein 32 (KOX 30)
209539_at	ARHGEF6	9459	1.26e-03	NM_004840	NP_004831	0.91	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
209545_s_at	RIPK2	8767	0.04	NM_003821	NP_003812	0.87	receptor-interacting serine-threonine kinase 2
209546_s_at	APOL1	8542	0.04	AF323540	AAG53690	0.78	apolipoprotein L, 1
209549_s_at	DGUOK	1716	7.47e-03	NM_080916	NP_550438	0.89	deoxyguanosine kinase
209555_s_at	CD36	948	0.01	NM_001001548	NP_001001548	0.84	CD36 antigen (collagen type I receptor, thrombospondin receptor)
209561_at	THBS3	7059	0.04	NM_007112	NP_009043	0.91	thrombospondin 3
209565_at	ZNF183	7737	0.03	NM_006978	NP_008909	0.89	zinc finger protein 183 (RING finger, C3HC4 type)
209566_at	INSIG2	51141	3.79e-03	NM_016133	NP_057217	0.91	insulin induced gene 2
209571_at	CIR	9541	0.04	NM_004882	NP_004873	0.90	CBF1 interacting corepressor
209572_s_at	EED	8726	2.59e-03	NM_003797	NP_003788	0.92	embryonic ectoderm development

209574_s_at	C18orf1	753	0.01	NM_181481	NP_852146	0.90	chromosome 18 open reading frame 1
209575_at	IL10RB	3588	0.03	NM_000628	NP_000619	1.11	interleukin 10 receptor, beta
209585_s_at	MINPP1	9562	0.04	NM_004897	NP_004888	0.83	multiple inositol polyphosphate histidine phosphatase, 1
209606_at	PSCDBP	9595	0.01	NM_004288	NP_004279	0.89	pleckstrin homology, Sec7 and coiled-coil domains,
binding protein							
209620_s_at	ABCB7	22	4.43e-03	NM_004299	NP_004290	0.91	ATP-binding cassette, sub-family B (MDR/TAP),
member 7							
209623_at	MCCC2	64087	4.06e-03	AK025591		0.91	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)
209625_at	PIGH	5283	0.01	NM_004569	NP_004560	0.91	phosphatidylinositol glycan, class H
209628_at	NXT2	55916	6.41e-03	NM_018698	NP_061168	0.83	nuclear transport factor 2-like export factor 2
209630_s_at	FBXW2	26190	1.49e-03	AL043967		0.92	F-box and WD-40 domain protein 2
209640_at	PML	5371	9.6e-03	NM_033238	NP_150241	0.80	promyelocytic leukemia
209647_s_at	SOCS5	9655	8.05e-03	NM_014011	NP_054730	0.90	suppressor of cytokine signaling 5
209654_at	KIAA0947	23379	8.8e-03	BC004902	AAH04902	0.87	KIAA0947 protein
209657_s_at	HSF2	3298	0.04	NM_004506	NP_004497	0.88	heat shock transcription factor 2
209659_s_at	CDC16	8881	0.01	NM_003903	NP_003894	0.85	CDC16 cell division cycle 16 homolog (S. cerevisiae)
209662_at	CETN3	1070	0.01	NM_004365	NP_004356	0.85	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)
209666_s_at	CHUK	1147	0.02	NM_001278	NP_001269	0.92	conserved helix-loop-helix ubiquitous kinase
209667_at	CES2	8824	8.5e-04	NM_003869	NP_003860	0.92	carboxylesterase 2 (intestine, liver)
209668_x_at	CES2	8824	0.04	NM_003869	NP_003860	0.94	carboxylesterase 2 (intestine, liver)
209669_s_at	PAI-RBP1	26135	0.01	NM_015640	NP_056455	0.91	PAI-1 mRNA-binding protein
209674_at	CRY1	1407	0.04	NM_004075	NP_004066	0.85	cryptochrome 1 (photolyase-like)
209689_at	FLJ10996	54520	0.04	BC005078	AAH05078	0.91	hypothetical protein FLJ10996
209696_at	FBP1	2203	0.04	NM_000507	NP_000498	0.88	fructose-1,6-bisphosphatase 1
209721_s_at	HOM-TES-103	25900	3.6e-03	NM_015438	NP_056253	0.89	HOM-TES-103 tumor antigen-like
209732_at	CLEC2B	9976	4.31e-03	NM_005127	NP_005118	0.82	C-type lectin domain family 2, member B
209734_at	HEM1	3071	0.04	NM_005337	NP_005328	0.92	hematopoietic protein 1
209741_x_at	ZNF291	49855	1.53e-03	NM_020843	NP_065894	0.90	zinc finger protein 291
209744_x_at	ITCH	83737	0.01	NM_031483	NP_113671	1.13	itchy homolog E3 ubiquitin protein ligase (mouse)
209746_s_at	COQ7	10229	3.1e-03	NM_016138	NP_057222	0.86	coenzyme Q7 homolog, ubiquinone (yeast)
209748_at	SPG4	6683	0.01	NM_014946	NP_055761	0.88	spastic paraplegia 4 (autosomal dominant; spastin)
209753_s_at	TMPO	7112	8.42e-03	BC053675	AAH53675	0.87	thymopoietin
209754_s_at	TMPO	7112	0.01	AF113682	AAF29583	0.86	thymopoietin
209761_s_at	SP110	3431	0.04	NM_004509	NP_004500	1.10	SP110 nuclear body protein
209765_at	ADAM19	8728	0.03	NM_033274	NP_150377	0.94	a disintegrin and metalloproteinase domain 19 (meltrin
beta)							
209780_at	PHTF2	57157	9.33e-03	NM_020432	NP_065165	0.87	putative homeodomain transcription factor 2
209787_s_at	HMGN4	10473	0.01	NM_006353	NP_006344	0.88	high mobility group nucleosomal binding domain 4
209788_s_at	ARTS-1	51752	4.18e-03	AF183569	AAF20384	0.79	type 1 tumor necrosis factor receptor shedding
aminopeptidase regulator							
209795_at	CD69	969	3.37e-03	NM_001781	NP_001772	0.79	CD69 antigen (p60, early T-cell activation antigen)
209798_at	NPAT	4863	0.01	NM_002519	NP_002510	0.87	nuclear protein, ataxia-telangiectasia locus
209799_at	PRKAA1	5562	0.01	NM_006251	NP_006242	0.86	protein kinase, AMP-activated, alpha 1 catalytic subunit
209814_at	ZNF330	27309	2.23e-04	NM_014487	NP_055302	0.91	zinc finger protein 330

209852_x_at	PSME3	10197	3.79e-03	NM_005789	NP_005780	0.90	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
209853_s_at	PSME3	10197	0.01	NM_005789	NP_005780	0.88	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
209861_s_at	METAP2	10988	1.27e-03	NM_006838	NP_006829	0.85	methionyl aminopeptidase 2
209862_s_at	PIG8	9702	0.02	NM_014679	NP_055494	0.89	translokin
209870_s_at	APBA2	321	3.2e-03	NM_005503	NP_005494	0.81	amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)
209875_s_at	SPP1	6696	0.04	NM_000582	NP_000573	1.30	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)
209881_s_at	LAT	27040	0.03	NM_014387	NP_055202	0.86	linker for activation of T cells
209894_at	LEPR	3953	0.03	NM_001003679	NP_001003679	0.87	leptin receptor
209896_s_at	PTPN11	5781	5.3e-04	NM_002834	NP_002825	0.88	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)
209899_s_at	SIAHBP1	22827	0.03	NM_078480	NP_510965	0.88	fuse-binding protein-interacting repressor
209901_x_at	AIF1	199	0.03	NM_004847	NP_004838	0.95	allograft inflammatory factor 1
209903_s_at	ATR	545	0.01	NM_001184	NP_001175	0.88	ataxia telangiectasia and Rad3 related
209911_x_at	HIST1H2BD	3017	8.05e-03	NM_138720	NP_619790	1.26	histone 1, H2bd
209912_s_at	KIAA0415	9907	0.03	AB007875	BAA24845	0.93	KIAA0415 protein
209916_at	DHTKD1	55526	0.01	NM_018706	NP_061176	1.16	dehydrogenase E1 and transketolase domain containing 1
209927_s_at	DKFZP547E1010	26097	0.04	NM_015607	NP_056422	0.91	DKFZP547E1010 protein
209943_at	FBXL4	26235	4.68e-03	NM_012160	NP_036292	0.86	F-box and leucine-rich repeat protein 4
209944_at	ZNF410	57862	0.02	BC000330		0.93	zinc finger protein 410
209945_s_at	GSK3B	2932	0.03	NM_002093	NP_002084	1.11	glycogen synthase kinase 3 beta
209971_x_at	JTV1	7965	4.74e-03	NM_006303	NP_006294	0.91	JTV1 gene
209972_s_at	JTV1	7965	3.67e-04	NM_006303	NP_006294	1.25	JTV1 gene
209974_s_at	BUB3	9184	9.2e-03	NM_004725	NP_004716	0.87	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)
209984_at	JMJD2C	23081	0.01	NM_015061	NP_055876	0.84	jumonji domain containing 2C
209989_at	ZNF268	10795	0.04	NM_003415	NP_003406	0.88	zinc finger protein 268
210005_at	GART	2618	0.02	NM_000819	NP_000810	0.90	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
210006_at	DKFZP564O243	25864	0.01	NM_015407	NP_056222	0.87	DKFZP564O243 protein
210007_s_at	GPD2	2820	0.04	NM_000408	NP_000399	0.86	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
210012_s_at	EWSR1	2130	0.03	BC000527	AAH00527	0.92	Ewing sarcoma breakpoint region 1
210018_x_at	MALT1	10892	0.01	NM_006785	NP_006776	0.90	mucosa associated lymphoid tissue lymphoma translocation gene 1
210027_s_at	APEX1	328	0.01	NM_001641	NP_001632	0.88	APEX nuclease (multifunctional DNA repair enzyme) 1
210028_s_at	ORC3L	23595	1.16e-03	NM_181837	NP_862820	0.82	origin recognition complex, subunit 3-like (yeast)
210031_at	CD3Z	919	0.03	NM_198053	NP_932170	0.87	CD3Z antigen, zeta polypeptide (TiT3 complex)
210038_at	PRKCQ	5588	2.63e-03	NM_006257	NP_006248	0.84	protein kinase C, theta
210039_s_at	PRKCQ	5588	0.02	NM_006257	NP_006248	0.87	protein kinase C, theta
210058_at	MAPK13	5603	1.07e-03	NM_002754	NP_002745	0.87	mitogen-activated protein kinase 13
210059_s_at	MAPK13	5603	0.02	NM_002754	NP_002745	1.10	mitogen-activated protein kinase 13
210062_s_at	ZNF589	51385	0.01	NM_016089	NP_057173	0.89	zinc finger protein 589

210076_x_at	PAI-RBP1	26135	0.03	NM_015640	NP_056455	0.89	PAI-1 mRNA-binding protein
210077_s_at	SFRS5	6430	1.1e-04	NM_006925	NP_008856	0.86	splicing factor, arginine/serine-rich 5
210087_s_at	MPZL1	9019	3.96e-03	NM_003953	NP_003944	1.22	myelin protein zero-like 1
210092_at	MAGOH	4116	0.02	NM_002370	NP_002361	0.96	mago-nashi homolog, proliferation-associated
(Drosophila)							
210097_s_at	NOL7	51406	6.68e-03	NM_016167	NP_057251	0.84	nucleolar protein 7, 27kDa
210110_x_at	HNRPH3	3189	0.01	NM_012207	NP_036339	0.96	heterogeneous nuclear ribonucleoprotein H3 (2H9)
210113_s_at	NALP1	22861	0.02	NM_033004	NP_127497	1.12	NACHT, leucine rich repeat and PYD (pyrin domain)
containing 1							
210137_s_at	DCTD	1635	0.01	NM_001921	NP_001912	0.87	dCMP deaminase
210149_s_at	ATP5H	10476	0.02	NM_001003785	NP_001003785	0.96	ATP synthase, H+ transporting, mitochondrial F0
complex, subunit d							
210153_s_at	ME2	4200	0.01	NM_002396	NP_002387	0.92	malic enzyme 2, NAD(+)-dependent, mitochondrial
210154_at	ME2	4200	0.04	NM_002396	NP_002387	0.94	malic enzyme 2, NAD(+)-dependent, mitochondrial
210156_s_at	PCMT1	5110	5.45e-03	NM_005389	NP_005380	0.93	protein-L-isoaspartate (D-aspartate) O-
methyltransferase							
210208_x_at	BAT3	7917	0.02	NM_004639	NP_004630	0.93	HLA-B associated transcript 3
210213_s_at	ITGB4BP	3692	2.61e-03	NM_002212	NP_002203	0.89	integrin beta 4 binding protein
210218_s_at	SP100	6672	0.02	NM_003113	NP_003104	1.24	nuclear antigen Sp100
210225_x_at	LILRB3	11025	0.03	NM_006864	NP_006855	1.11	leukocyte immunoglobulin-like receptor, subfamily B
(with TM and ITIM domains), member 3							
210235_s_at	PPFIA1	8500	0.03	NM_177423	NP_803172	1.14	protein tyrosine phosphatase, receptor type, f polypeptide
(PTPRF), interacting protein (liprin), alpha 1							
210236_at	PPFIA1	8500	0.02	NM_177423	NP_803172	1.10	protein tyrosine phosphatase, receptor type, f polypeptide
(PTPRF), interacting protein (liprin), alpha 1							
210257_x_at	CUL4B	8450	0.01	NM_003588	NP_003579	0.93	cullin 4B
210260_s_at	TNFAIP8	25816	0.02	NM_014350	NP_055165	0.90	tumor necrosis factor, alpha-induced protein 8
210264_at	GPR35	2859	0.03	NM_005301	NP_005292	0.91	G protein-coupled receptor 35
210269_s_at	DXYS155E	8227	0.01	NM_005088	NP_005079	0.88	DNA segment on chromosome X and Y (unique) 155
expressed sequence							
210277_at	AP4S1	11154	0.01	AF155159	AAD43329	0.93	adaptor-related protein complex 4, sigma 1 subunit
210283_x_at	PAIP1	10605	5.82e-04	NM_006451	NP_006442	0.86	poly(A) binding protein interacting protein 1
210286_s_at	SLC4A7	9497	7.02e-03	NM_003615	NP_003606	0.86	solute carrier family 4, sodium bicarbonate
cotransporter, member 7							
210293_s_at	SEC23B	10483	5.34e-03	NM_006363	NP_006354	0.92	Sec23 homolog B (S. cerevisiae)
210306_at	L3MBTL	26013	3.77e-03	NM_015478	NP_056293	0.80	l(3)mbt-like (Drosophila)
210312_s_at	IFT20	90410	0.02	NM_174887	NP_777547	0.95	intraflagellar transport protein IFT20
210317_s_at	YWHAE	7531	0.03	NM_006761	NP_006752	0.85	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
activation protein, epsilon polypeptide							
210337_s_at	ACLY	47	0.04	NM_001096	NP_001087	0.89	ATP citrate lyase
210360_s_at	MTSS1	9788	0.02	NM_014751	NP_055566	0.87	metastasis suppressor 1
210371_s_at	RBBP4	5928	3.98e-03	NM_005610	NP_005601	0.87	retinoblastoma binding protein 4
210376_x_at	ELK1	2002	5.35e-03	NM_005229	NP_005220	1.09	ELK1, member of ETS oncogene family
210384_at	HRMT1L1	3275	0.01	U79286	AAB50221	0.81	HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae)

210385_s_at	ARTS-1	51752	0.01	AF106037	AAF07395	0.86	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
210406_s_at	RAB6A	5870	0.03	NM_002869	NP_002860	0.90	RAB6A, member RAS oncogene family
210407_at	PPM1A	5494	1.49e-03	NM_177951	NP_808820	1.17	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform
210418_s_at	IDH3B	3420	0.01	NM_006899	NP_008830	0.91	isocitrate dehydrogenase 3 (NAD+) beta
210425_x_at	LOC440270	440270	6.34e-04	AF164622	AAF40308	0.80	similar to golgin-67 isoform c
210425_x_at	GOLGIN-67	23015	6.34e-04	AF164622	AAF40308	0.80	golgin-67
210426_x_at	RORA	6095	0.03	NM_134261	NP_599023	0.79	RAR-related orphan receptor A
210427_x_at	ANXA2	302	0.02	NM_001002858	NP_001002858	0.87	annexin A2
210428_s_at	HGS	9146	0.04	NM_004712	NP_004703	1.11	hepatocyte growth factor-regulated tyrosine kinase substrate
210434_x_at	JTB	10899	0.01	NM_006694	NP_006685	0.95	jumping translocation breakpoint
210453_x_at	ATP5L	10632	0.01	NM_006476	NP_006467	0.96	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g
210458_s_at	TANK	10010	0.02	NM_004180	NP_004171	0.87	TRAF family member-associated NFKB activator
210460_s_at	PSMD4	5710	0.01	NM_002810	NP_002801	0.86	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
210465_s_at	SNAPC3	6619	9.5e-03	NM_003084	NP_003075	0.87	small nuclear RNA activating complex, polypeptide 3, 50kDa
210466_s_at	PAI-RBP1	26135	0.01	NM_015640	NP_056455	0.83	PAI-1 mRNA-binding protein
210470_x_at	NONO	4841	5.57e-03	NM_007363	NP_031389	0.87	non-POU domain containing, octamer-binding
210479_s_at	RORA	6095	5.83e-03	NM_134261	NP_599023	0.79	RAR-related orphan receptor A
210483_at	MGC31957	254896	0.02	BC005043	AAH05043	1.37	hypothetical protein MGC31957
210484_s_at	TNFRSF10C	8794	0.01	NM_003841	NP_003832	1.16	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain
210512_s_at	VEGF	7422	0.03	AF022375	AAC63143	0.93	vascular endothelial growth factor
210514_x_at	HLA-G	3135	0.01	NM_002127	NP_002118	0.83	HLA-G histocompatibility antigen, class I, G
210527_x_at	TUBA2	7278	8.8e-03	NM_006001	NP_005992	1.10	tubulin, alpha 2
210532_s_at	C14orf2	9556	0.03	NM_004894	NP_004885	0.96	chromosome 14 open reading frame 2
210538_s_at	BIRC3	330	0.02	NM_001165	NP_001156	0.87	baculoviral IAP repeat-containing 3
210540_s_at	B4GALT4	8702	3.79e-03	NM_212543	NP_997708	0.84	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4
210555_s_at	NFATC3	4775	0.01	NM_173165	NP_775188	0.86	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3
210556_at	NFATC3	4775	0.01	NM_173164	NP_775187	0.88	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3
210567_s_at	SKP2	6502	0.01	NM_005983	NP_005974	0.86	S-phase kinase-associated protein 2 (p45)
210573_s_at	POLR3C	10623	1.26e-03	NM_006468	NP_006459	0.91	polymerase (RNA) III (DNA directed) polypeptide C (62kD)
210582_s_at	LIMK2	3985	0.03	NM_005569	NP_005560	1.10	LIM domain kinase 2
210592_s_at	SAT	6303	0.03	NM_002970	NP_002961	0.89	spermidine/spermine N1-acetyltransferase
210594_x_at	MPZL1	9019	7.47e-03	NM_003953	NP_003944	1.29	myelin protein zero-like 1
210596_at	DKFZp564K142	84061	0.02	AF130104	AAG35529	0.85	implantation-associated protein
210616_s_at	SEC31L1	22872	0.03	NM_014933	NP_055748	0.94	SEC31-like 1 (S. cerevisiae)

210620_s_at	GTF3C2	2976	0.01	NM_001521	NP_001512	0.88	general transcription factor IIIC, polypeptide 2, beta 110kDa
210621_s_at	RASA1	5921	6.11e-03	NM_002890	NP_002881	0.95	RAS p21 protein activator (GTPase activating protein) 1
210638_s_at	FBXO9	26268	5.63e-04	NM_012347	NP_036479	0.95	F-box protein 9
210639_s_at	APG5L	9474	0.01	NM_004849	NP_004840	0.90	APG5 autophagy 5-like (S. cerevisiae)
210645_s_at	TTC3	7267	0.01	NM_003316	NP_003307	0.88	tetratricopeptide repeat domain 3
210655_s_at	FOXO3A	2309	0.02	NM_001455	NP_001446	0.85	forkhead box O3A
210666_at	IDS	3423	0.04	AF050145	AAC05984	1.23	iduronate 2-sulfatase (Hunter syndrome)
210667_s_at	C21orf33	8209	6.11e-03	NM_004649	NP_004640	0.92	chromosome 21 open reading frame 33
210676_x_at	RANBP2L1	84220	7.47e-03	NM_005054	NP_005045	0.87	RAN binding protein 2-like 1
210695_s_at	WWOX	51741	0.01	NM_016373	NP_057457	1.11	WW domain containing oxidoreductase
210705_s_at	TRIM5	85363	0.01	NM_033034	NP_149023	0.80	tripartite motif-containing 5
210707_x_at	PMS2L11	5389	1.07e-03	U38980	AAA97460	0.86	postmeiotic segregation increased 2-like 11
210710_at	AGGF1	55109	0.01	BC002828	AAH02828	0.91	angiogenic factor with G patch and FHA domains 1
210718_s_at	LOC51326	51326	0.02	NM_016632	NP_057716	0.83	ADP-ribosylation factor-like
210734_x_at	MAX	4149	0.01	NM_002382	NP_002373	0.91	MYC associated factor X
210739_x_at	SLC4A4	8671	6.98e-03	NM_003759	NP_003750	1.13	solute carrier family 4, sodium bicarbonate cotransporter, member 4
210754_s_at	LYN	4067	0.03	NM_002350	NP_002341	1.08	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
210756_s_at	NOTCH2	4853	0.04	NM_024408	NP_077719	0.92	Notch homolog 2 (Drosophila)
210758_at	PSIP1	11168	0.02	NM_021144	NP_066967	0.87	PC4 and SFRS1 interacting protein 1
210758_at	PSIP1	11168	0.02	NM_033222	NP_150091	0.87	PC4 and SFRS1 interacting protein 1
210759_s_at	PSMA1	5682	6.62e-03	NM_148976	NP_683877	0.91	proteasome (prosome, macropain) subunit, alpha type, 1
210763_x_at	NCR3	259197	0.04	NM_147130	NP_667341	0.83	natural cytotoxicity triggering receptor 3
210768_x_at	LOC54499	54499	0.01	NM_019026	NP_061899	0.88	putative membrane protein
210784_x_at	LILRB3	11025	0.03	NM_006864	NP_006855	1.11	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3
210789_x_at	CEACAM3	1084	0.04	NM_001815	NP_001806	1.10	carcinoembryonic antigen-related cell adhesion molecule 3
210796_x_at	SIGLEC6	946	0.04	NM_001245	NP_001236	1.07	sialic acid binding Ig-like lectin 6
210813_s_at	XRCC4	7518	0.04	NM_003401	NP_003392	0.88	X-ray repair complementing defective repair in Chinese hamster cells 4
210820_x_at	COQ7	10229	0.02	NM_016138	NP_057222	0.90	coenzyme Q7 homolog, ubiquinone (yeast)
210825_s_at	PBP	5037	0.03	NM_002567	NP_002558	0.85	prostatic binding protein
210840_s_at	IQGAP1	8826	0.02	NM_003870	NP_003861	1.09	IQ motif containing GTPase activating protein 1
210847_x_at	TNFRSF25	8718	0.02	NM_148965	NP_683866	0.90	tumor necrosis factor receptor superfamily, member 25
210858_x_at	ATM	472	5.83e-03	NM_000051	NP_000042	0.86	ataxia telangiectasia mutated (includes complementation groups A, C and D)
210865_at	FASLG	356	0.04	NM_000639	NP_000630	0.91	Fas ligand (TNF superfamily, member 6)
210878_s_at	JMJD1B	51780	0.01	NM_016604	NP_057688	0.94	jumonji domain containing 1B
210879_s_at	RAB11FIP5	26056	0.04	NM_015470	NP_056285	1.05	RAB11 family interacting protein 5 (class I)
210886_x_at	TP53AP1	11257	0.03	NM_007233	NP_009164	0.93	TP53 activated protein 1
210892_s_at	GTF2I	2969	0.02	NM_032999	NP_127492	0.90	general transcription factor II, i
210896_s_at	ASPH	444	0.04	NM_032468	NP_115857	0.83	aspartate beta-hydroxylase

210908_s_at	PFDN5	5204	0.03	NM_002624	NP_002615	0.92	prefoldin 5
210926_at	LOC440915	440915	0.03	AY014272		1.10	similar to FKSG30
210927_x_at	JTB	10899	0.03	BC004239	AAH04239	0.92	jumping translocation breakpoint
210947_s_at	MSH3	4437	0.02	NM_002439	NP_002430	0.89	mutS homolog 3 (E. coli)
210949_s_at	EIF3S8	8663	0.04	NM_003752	NP_003743	0.92	eukaryotic translation initiation factor 3, subunit 8, 110kDa
210959_s_at	SRD5A1	6715	0.01	NM_001047	NP_001038	0.94	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)
210962_s_at	AKAP9	10142	0.02	NM_147171	NP_671700	0.92	A kinase (PRKA) anchor protein (yotiao) 9
210970_s_at	IBTK	25998	3.66e-03	AF235049	AAG27170	0.87	inhibitor of Bruton agammaglobulinemia tyrosine kinase
210982_s_at	HLA-DRA	3122	0.03	NM_019111	NP_061984	0.91	major histocompatibility complex, class II, DR alpha
210995_s_at	TRIM23	373	0.02	NM_001656	NP_001647	0.88	tripartite motif-containing 23
211005_at	LAT	27040	7.35e-03	NM_014387	NP_055202	0.83	linker for activation of T cells
211009_s_at	ZNF271	10778	5.98e-05	NM_006629	NP_006620	0.84	zinc finger protein 271
211012_s_at	PML	5371	0.02	NM_033250	NP_150253	0.71	promyelocytic leukemia
211014_s_at	PML	5371	0.03	NM_033250	NP_150253	0.94	promyelocytic leukemia
211015_s_at	HSPA4	3308	0.03	NM_002154	NP_002145	0.90	heat shock 70kDa protein 4
211022_s_at	ATRX	546	0.03	NM_000489	NP_000480	0.89	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
211025_x_at	COX5B	1329	0.04	NM_001862	NP_001853	0.91	cytochrome c oxidase subunit Vb
211026_s_at	MGLL	11343	0.02	NM_007283	NP_009214	0.89	monoglyceride lipase
211027_s_at	IKBKB	3551	0.02	NM_001556	NP_001547	0.89	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
211048_s_at	ERP70	9601	5.07e-03	NM_004911	NP_004902	0.85	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)
211060_x_at	GPAA1	8733	0.04	NM_003801	NP_003792	0.92	GPAA1P anchor attachment protein 1 homolog (yeast)
211061_s_at	MGAT2	4247	7.64e-03	NM_002408	NP_002399	0.89	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
211064_at	LOC115648	115648	0.03	NM_145326	NP_663299	1.13	similar to hypothetical protein FLJ13659
211074_at	FOLR1	2348	0.02	AF000381	AAB81938	0.89	folate receptor 1 (adult)
211075_s_at	CD47	961	5.44e-03	NM_001777	NP_001768	0.92	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)
211090_s_at	PRPF4B	8899	9.61e-03	NM_003913	NP_003904	0.88	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
211115_x_at	SIP1	8487	1.13e-03	NM_003616	NP_003607	0.93	survival of motor neuron protein interacting protein 1
211133_x_at	LILRB3	11025	0.03	NM_006864	NP_006855	1.11	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3
211135_x_at	LILRB3	11025	0.03	NM_006864	NP_006855	1.11	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3
211136_s_at	CLPTM1	1209	4.6e-03	NM_001294	NP_001285	0.87	cleft lip and palate associated transmembrane protein 1
211159_s_at	PPP2R5D	5528	1.33e-03	NM_006245	NP_006236	0.89	protein phosphatase 2, regulatory subunit B (B56), delta isoform
211168_s_at	RENT1	5976	0.03	NM_002911	NP_002902	0.90	regulator of nonsense transcripts 1
211202_s_at	JARID1B	10765	0.01	NM_006618	NP_006609	0.94	Jumonji, AT rich interactive domain 1B (RBP2-like)
211230_s_at	PIK3CD	5293	9.78e-03	NM_005026	NP_005017	1.25	phosphoinositide-3-kinase, catalytic, delta polypeptide
211256_x_at	BTN2A1	11120	0.04	NM_007049	NP_008980	0.90	butyrophilin, subfamily 2, member A1
211270_x_at	PTBP1	5725	1.75e-03	NM_002819	NP_002810	0.90	polypyrimidine tract binding protein 1

211271_x_at	PTBP1	5725	5.06e-03	NM_002819	NP_002810	0.88	polypyrimidine tract binding protein 1
211272_s_at	DGKA	1606	9.61e-03	NM_201444	NP_958852	0.81	diacylglycerol kinase, alpha 80kDa
211282_x_at	TNFRSF25	8718	0.03	NM_148965	NP_683866	0.90	tumor necrosis factor receptor superfamily, member 25
211285_s_at	UBE3A	7337	7.02e-03	NM_000462	NP_000453	0.86	ubiquitin protein ligase E3A (human papilloma virus
E6-associated protein, Angelman syndrome)							
211300_s_at	TP53	7157	0.04	NM_000546	NP_000537	0.87	tumor protein p53 (Li-Fraumeni syndrome)
211305_x_at	FCAR	2204	0.03	NM_133280	NP_579814	1.20	Fc fragment of IgA, receptor for
211318_s_at	RAE1	8480	0.02	NM_003610	NP_003601	0.92	RAE1 RNA export 1 homolog (S. pombe)
211323_s_at	ITPR1	3708	0.04	NM_002222	NP_002213	0.85	inositol 1,4,5-triphosphate receptor, type 1
211330_s_at	HFE	3077	0.04	NM_000410	NP_000401	1.09	hemochromatosis
211333_s_at	FASLG	356	6.05e-04	NM_000639	NP_000630	0.83	Fas ligand (TNF superfamily, member 6)
211336_x_at	LILRB1	10859	0.01	NM_006669	NP_006660	1.08	leukocyte immunoglobulin-like receptor, subfamily B
(with TM and ITIM domains), member 1							
211339_s_at	ITK	3702	5.98e-04	NM_005546	NP_005537	0.81	IL2-inducible T-cell kinase
211367_s_at	CASP1	834	0.01	NM_033292	NP_150634	0.93	caspase 1, apoptosis-related cysteine protease (interleukin
1, beta, convertase)							
211368_s_at	CASP1	834	0.03	NM_033292	NP_150634	0.90	caspase 1, apoptosis-related cysteine protease (interleukin
1, beta, convertase)							
211375_s_at	ILF3	3609	0.01	NM_012218	NP_036350	0.88	interleukin enhancer binding factor 3, 90kDa
211376_s_at	C10orf86	54780	3.91e-04	NM_017615	NP_060085	0.87	chromosome 10 open reading frame 86
211383_s_at	WDR37	22884	1.66e-03	NM_014023	NP_054742	0.91	WD repeat domain 37
211406_at	IER3IP1	51124	0.04	AF119875	AAF69629	0.93	immediate early response 3 interacting protein 1
211413_s_at	PADI4	23569	0.04	NM_012387	NP_036519	1.22	peptidyl arginine deiminase, type IV
211445_x_at	FKSG17	83955	0.02	AF315951		0.78	FKSG17
211450_s_at	MSH6	2956	0.02	NM_000179	NP_000170	0.89	mutS homolog 6 (E. coli)
211501_s_at	EIF3S9	8662	0.01	NM_003751	NP_003742	0.88	eukaryotic translation initiation factor 3, subunit 9 eta,
116kDa							
211513_s_at	OGFR	11054	0.02	NM_007346	NP_031372	0.86	opioid growth factor receptor
211536_x_at	MAP3K7	6885	0.03	NM_003188	NP_003179	0.92	mitogen-activated protein kinase kinase kinase 7
211553_x_at	APAF1	317	0.01	NM_013229	NP_037361	0.83	apoptotic protease activating factor
211563_s_at	C19orf2	8725	6.15e-03	NM_003796	NP_003787	0.88	chromosome 19 open reading frame 2
211594_s_at	MRPL9	65005	0.01	NM_031420	NP_113608	0.89	mitochondrial ribosomal protein L9
211609_x_at	PSMD4	5710	0.03	NM_002810	NP_002801	0.90	proteasome (prosome, macropain) 26S subunit, non-
ATPase, 4							
211610_at	KLF6	1316	0.03	U51869	AAB94793	0.88	Kruppel-like factor 6
211610_at	KLF6	1316	0.03	U51869	AAB94792	0.88	Kruppel-like factor 6
211615_s_at	LRPPRC	10128	0.04	NM_133259	NP_573566	0.90	leucine-rich PPR-motif containing
211630_s_at	GSS	2937	0.01	NM_000178	NP_000169	0.92	glutathione synthetase
211657_at	CEACAM6	4680	0.03	NM_002483	NP_002474	1.26	carcinoembryonic antigen-related cell adhesion
molecule 6 (non-specific cross reacting antigen)							
211675_s_at	HIC	29969	9.2e-03	NM_199072	NP_951038	0.88	I-mfa domain-containing protein
211684_s_at	DNCI2	1781	0.02	NM_001378	NP_001369	0.88	dynein, cytoplasmic, intermediate polypeptide 2
211692_s_at	BBC3	27113	0.02	NM_014417	NP_055232	1.17	BCL2 binding component 3
211698_at	CRI1	23741	0.02	NM_014335	NP_055150	0.85	CREBBP/EP300 inhibitor 1
211703_s_at	BBP	83941	0.03	NM_032027	NP_114416	0.91	beta-amyloid binding protein precursor

211707_s_at	IQCB1	9657	0.02	NM_014642	NP_055457	0.88	IQ motif containing B1
211710_x_at	RPL4	6124	0.04	NM_000968	NP_000959	0.90	ribosomal protein L4
211716_x_at	ARHGDIA	396	0.01	NM_004309	NP_004300	0.92	Rho GDP dissociation inhibitor (GDI) alpha
211717_at	MGC15396	91369	0.04	BC005853	AAH05853	0.89	hypothetical protein MGC15396
211724_x_at	FLJ20323	54468	0.04	NM_019005	NP_061878	0.88	hypothetical protein FLJ20323
211727_s_at	COX11	1353	3.6e-03	NM_004375	NP_004366	0.88	COX11 homolog, cytochrome c oxidase assembly protein (yeast)
211729_x_at	BLVRA	644	6.39e-03	NM_000712	NP_000703	0.83	biliverdin reductase A
211730_s_at	POLR2L	5441	0.01	NM_021128	NP_066951	0.93	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa
211733_x_at	SCP2	6342	0.03	NM_002979	NP_002970	0.88	sterol carrier protein 2
211734_s_at	FCER1A	2205	0.02	NM_002001	NP_001992	0.76	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
211746_x_at	PSMA1	5682	3.79e-03	NM_148976	NP_683877	0.89	proteasome (prosome, macropain) subunit, alpha type, 1
211747_s_at	LSM5	23658	0.02	NM_012322	NP_036454	0.91	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
211753_s_at	RLN1	6013	8.31e-03	NM_006911	NP_008842	1.12	relaxin 1
211755_s_at	ATP5F1	515	0.01	NM_001002014	NP_001002014	0.96	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1
211758_x_at	TXNDC9	10190	3.04e-03	NM_005783	NP_005774	0.97	thioredoxin domain containing 9
211760_s_at	VAMP4	8674	0.02	NM_003762	NP_003753	0.93	vesicle-associated membrane protein 4
211779_x_at	AP2A2	161	0.01	NM_012305	NP_036437	0.92	adaptor-related protein complex 2, alpha 2 subunit
211783_s_at	MTA1	9112	8.42e-03	NM_004689	NP_004680	0.81	metastasis associated 1
211784_s_at	SFRS1	6426	5.83e-03	NM_006924	NP_008855	0.90	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
211787_s_at	EIF4A1	1973	0.02	NM_001416	NP_001407	0.92	eukaryotic translation initiation factor 4A, isoform 1
211794_at	FYB	2533	0.03	NM_199335	NP_955367	1.15	FYN binding protein (FYB-120/130)
211794_at	FYB	2533	0.03	NM_001465	NP_001456	1.15	FYN binding protein (FYB-120/130)
211801_x_at	MFN1	55669	0.01	NM_033540	NP_284941	0.94	mitofusin 1
211810_s_at	GALC	2581	0.03	NM_000153	NP_000144	0.89	galactosylceramidase (Krabbe disease)
211824_x_at	NALP1	22861	0.02	NM_033004	NP_127497	1.13	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1
211833_s_at	BAX	581	0.01	NM_138761	NP_620116	0.83	BCL2-associated X protein
211841_s_at	TNFRSF25	8718	0.04	NM_148965	NP_683866	0.91	tumor necrosis factor receptor superfamily, member 25
211842_s_at	SLC24A1	9187	0.01	NM_004727	NP_004718	1.14	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1
211861_x_at	CD28	940	0.04	NM_006139	NP_006130	0.84	CD28 antigen (Tp44)
211902_x_at	TRA@	6955	0.01	BC070337	AAH70337	0.85	T cell receptor alpha locus
211913_s_at	MERTK	10461	7.46e-03	NM_006343	NP_006334	0.87	c-mer proto-oncogene tyrosine kinase
211916_s_at	MYO1A	4640	0.03	NM_005379	NP_005370	1.11	myosin IA
211922_s_at	CAT	847	7.5e-03	NM_001752	NP_001743	0.86	catalase
211931_s_at	HNRPA3	220988	7.02e-03	BC032437		0.89	heterogeneous nuclear ribonucleoprotein A3
211932_at	HNRPA3	220988	3.26e-03	BC032437		0.89	heterogeneous nuclear ribonucleoprotein A3
211933_s_at	HNRPA3	220988	0.01	BC032437		0.90	heterogeneous nuclear ribonucleoprotein A3
211934_x_at	GANAB	23193	2.05e-03	NM_198334	NP_938148	0.88	glucosidase, alpha; neutral AB

211934_x_at	GANAB	23193	2.05e-03	NM_198335	NP_938149	0.88	glucosidase, alpha; neutral AB
211934_x_at	GANAB	23193	2.05e-03	NM_014610	NP_055425	0.88	glucosidase, alpha; neutral AB
211935_at	ARL6IP	23204	0.01	NM_015161	NP_055976	0.90	ADP-ribosylation factor-like 6 interacting protein
211936_at	HSPA5	3309	1.27e-03	NM_005347	NP_005338	0.87	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
211938_at	EIF4B	1975	7.69e-03	NM_001417	NP_001408	0.89	eukaryotic translation initiation factor 4B
211939_x_at	BTF3	689	0.01	NM_001207	NP_001198	0.90	basic transcription factor 3
211941_s_at	PBP	5037	6.11e-03	NM_002567	NP_002558	0.86	prostatic binding protein
211946_s_at	BAT2D1	23215	0.03	NM_015172	NP_055987	0.93	BAT2 domain containing 1
211950_at	RBAF600	23352	0.01	AB007931	BAA32307	0.94	retinoblastoma-associated factor 600
211951_at	NOLC1	9221	0.03	NM_004741	NP_004732	0.89	nucleolar and coiled-body phosphoprotein 1
211953_s_at	RANBP5	3843	0.01	NM_002271	NP_002262	0.89	RAN binding protein 5
211954_s_at	RANBP5	3843	0.02	NM_002271	NP_002262	0.87	RAN binding protein 5
211955_at	RANBP5	3843	3.66e-03	NM_002271	NP_002262	0.86	RAN binding protein 5
211967_at	PORIMIN	114908	1.05e-03	NM_052932	NP_443164	0.82	pro-oncosis receptor inducing membrane injury gene
211969_at	HSPCA	3320	0.01	NM_005348	NP_005339	0.92	heat shock 90kDa protein 1, alpha
211976_at	LOC401255	401255	0.03	AK026168		0.92	hypothetical LOC401255
211979_at	GPR107	57720	1.09e-03	AB046844	BAB13450	0.85	G protein-coupled receptor 107
211987_at	TOP2B	7155	0.01	NM_001068	NP_001059	0.88	topoisomerase (DNA) II beta 180kDa
211988_at	SMARCE1	6605	0.01	NM_003079	NP_003070	0.89	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
211989_at	SMARCE1	6605	7.77e-03	NM_003079	NP_003070	0.85	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
211990_at	HLA-DPA1	3113	0.03	NM_033554	NP_291032	0.83	major histocompatibility complex, class II, DP alpha 1
211991_s_at	HLA-DPA1	3113	0.03	NM_033554	NP_291032	0.88	major histocompatibility complex, class II, DP alpha 1
212001_at	SFRS14	10147	1.66e-03	AV738039		0.84	splicing factor, arginine/serine-rich 14
212006_at	UBXD2	23190	0.02	NM_014607	NP_055422	0.91	UBX domain containing 2
212008_at	UBXD2	23190	0.02	NM_014607	NP_055422	0.93	UBX domain containing 2
212010_s_at	H41	55573	0.01	NM_017548	NP_060018	0.93	hypothetical protein H41
212014_x_at	CD44	960	0.01	NM_000610	NP_000601	0.93	CD44 antigen (homing function and Indian blood group system)
212015_x_at	PTBP1	5725	0.04	NM_002819	NP_002810	0.92	polypyrimidine tract binding protein 1
212016_s_at	PTBP1	5725	0.01	NM_002819	NP_002810	0.90	polypyrimidine tract binding protein 1
212017_at	LOC130074	130074	9.2e-03	AL137406		0.92	hypothetical protein LOC130074
212031_at	RBM25	58517	0.01	AL832314		0.91	RNA binding motif protein 25
212033_at	RBM25	58517	1.95e-03	AL833497		0.95	RNA binding motif protein 25
212036_s_at	PNN	5411	3.45e-04	NM_002687	NP_002678	0.92	pinin, desmosome associated protein
212037_at	PNN	5411	8.42e-03	NM_002687	NP_002678	0.90	pinin, desmosome associated protein
212038_s_at	VDAC1	7416	0.02	NM_003374	NP_003365	0.87	voltage-dependent anion channel 1
212042_x_at	RPL7	6129	0.02	NM_000971	NP_000962	0.91	ribosomal protein L7
212048_s_at	YARS	8565	0.03	NM_003680	NP_003671	0.89	tyrosyl-tRNA synthetase
212055_at	C18orf10	25941	8.65e-03	NM_015476	NP_056291	0.83	chromosome 18 open reading frame 10
212056_at	KIAA0182	23199	1.78e-03	NM_014615	NP_055430	1.26	KIAA0182 protein
212058_at	SR140	23350	9.33e-03	XM_031553	XP_031553	0.93	U2-associated SR140 protein
212060_at	SR140	23350	0.02	XM_031553	XP_031553	0.94	U2-associated SR140 protein

212061_at	SR140	23350	7.47e-03	AB002330	BAA20790	0.89	U2-associated SR140 protein
212071_s_at	SPTBN1	6711	4.18e-03	AK023762		0.82	spectrin, beta, non-erythrocytic 1
212072_s_at	CSNK2A1	1457	0.02	NM_177559	NP_808227	0.91	casein kinase 2, alpha 1 polypeptide
212074_at	UNC84A	23353	0.01	NM_025154	NP_079430	0.92	unc-84 homolog A (C. elegans)
212079_s_at	MLL	4297	0.04	NM_005933	NP_005924	0.87	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)
212081_x_at	BAT2	7916	0.04	NM_080686	NP_542417	1.13	HLA-B associated transcript 2
212096_s_at	MTUS1	57509	0.04	NM_001001924	NP_001001924	0.83	mitochondrial tumor suppressor 1
212103_at	KPNA6	23633	4.48e-03	BG403834		1.11	karyopherin alpha 6 (importin alpha 7)
212106_at	ETEA	23197	0.02	NM_014613	NP_055428	0.93	expressed in T-cells and eosinophils in atopic dermatitis
212107_s_at	DHX9	1660	0.02	NM_001357	NP_001348	0.88	DEAH (Asp-Glu-Ala-His) box polypeptide 9
212112_s_at	STX12	23673	7.61e-03	NM_177424	NP_803173	0.90	syntaxin 12
212122_at	RHOQ	23433	0.04	NM_012249	NP_036381	0.90	ras homolog gene family, member Q
212131_at	C19orf13	26065	0.01	NM_015578	NP_056393	0.92	chromosome 19 open reading frame 13
212133_at	NIPA2	81614	0.04	NM_030922	NP_112184	0.87	non imprinted in Prader-Willi/Angelman syndrome 2
212137_at	LARP	23367	0.01	BC038220		0.86	likely ortholog of mouse la related protein
212145_at	MRPS27	23107	0.04	NM_015084	NP_055899	0.89	mitochondrial ribosomal protein S27
212159_x_at	AP2A2	161	5.83e-03	NM_012305	NP_036437	0.89	adaptor-related protein complex 2, alpha 2 subunit
212160_at	XPOT	11260	0.04	NM_007235	NP_009166	0.90	exportin, tRNA (nuclear export receptor for tRNAs)
212174_at	AK2	204	3.1e-03	AK023758		0.95	adenylate kinase 2
212175_s_at	AK2	204	3.1e-03	NM_013411	NP_037543	0.95	adenylate kinase 2
212190_at	SERPINE2	5270	0.01	NM_006216	NP_006207	1.18	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2
212191_x_at	RPL13	6137	0.02	NM_000977	NP_000968	0.89	ribosomal protein L13
212195_at	IL6ST	3572	0.04	AL049265		0.88	interleukin 6 signal transducer (gp130, oncostatin M receptor)
212196_at	IL6ST	3572	0.04	AW242916		0.89	interleukin 6 signal transducer (gp130, oncostatin M receptor)
212197_x_at	M-RIP	23164	0.04	NM_201274	NP_958431	0.92	myosin phosphatase-Rho interacting protein
212197_x_at	M-RIP	23164	0.04	NM_015134	NP_055949	0.92	myosin phosphatase-Rho interacting protein
212204_at	DKFZP564G2022	25963	0.01	NM_015497	NP_056312	0.89	DKFZP564G2022 protein
212211_at	ANKRD17	26057	0.01	NM_032217	NP_115593	0.93	ankyrin repeat domain 17
212216_at	KIAA0436	9581	0.03	NM_006036	NP_006027	0.86	putative prolyl oligopeptidase
212219_at	PSME4	23198	0.04	NM_014614	NP_055429	0.91	proteasome (prosome, macropain) activator subunit 4
212220_at	PSME4	23198	0.02	NM_014614	NP_055429	0.89	proteasome (prosome, macropain) activator subunit 4
212222_at	PSME4	23198	0.04	NM_014614	NP_055429	0.93	proteasome (prosome, macropain) activator subunit 4
212223_at	IDS	3423	0.01	BX647357		1.17	iduronate 2-sulfatase (Hunter syndrome)
212227_x_at	SUI1	10209	0.04	NM_005801	NP_005792	0.94	putative translation initiation factor
212228_s_at	DKFZP434K046	57017	0.03	NM_020312	NP_064708	0.91	hypothetical protein DKFZp434K046
212231_at	FBXO21	23014	0.01	NM_033624	NP_296373	0.86	F-box protein 21
212232_at	FNBP4	23360	0.02	NM_015308	NP_056123	0.87	formin binding protein 4
212243_at	GRINL1A	81488	0.03	NM_015532	NP_056347	0.91	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A
212244_at	GRINL1A	81488	4.16e-04	NM_015532	NP_056347	0.90	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A
212247_at	NUP205	23165	0.04	D86978	BAA13214	0.90	nucleoporin 205kDa
212248_at	LYRIC	92140	7.35e-03	AI886796		0.85	LYRIC/3D3

212251_at	LYRIC	92140	0.02	NM_178812	NP_848927	0.90	LYRIC/3D3
212255_s_at	ATP2C1	27032	0.03	NM_014382	NP_055197	0.94	ATPase, Ca++ transporting, type 2C, member 1
212256_at	GALNT10	55568	0.04	AK023815		0.91	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)
212257_s_at	SMARCA2	6595	6.71e-03	NM_003070	NP_003061	0.89	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
212261_at	TNRC15	26058	0.03	NM_015575	NP_056390	0.94	trinucleotide repeat containing 15
212266_s_at	SFRS5	6430	1.01e-03	NM_006925	NP_008856	0.93	splicing factor, arginine/serine-rich 5
212267_at	KIAA0261	23063	0.02	NM_015045	NP_055860	0.95	KIAA0261
212276_at	LPIN1	23175	0.02	NM_145693	NP_663731	0.90	lipin 1
212277_at	MTMR4	9110	0.01	NM_004687	NP_004678	0.96	myotubularin related protein 4
212288_at	FNBP1	23048	9.35e-03	NM_015033	NP_055848	0.93	formin binding protein 1
212295_s_at	SLC7A1	6541	4.16e-04	NM_003045	NP_003036	0.89	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
212297_at	ATP13A3	79572	0.02	BF218804		0.85	ATPase type 13A3
212301_at	KIAA0252	23168	0.01	NM_015138	NP_055953	0.93	KIAA0252
212307_s_at	OGT	8473	0.02	NM_003605	NP_003596	0.88	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
212315_s_at	NUP210	23225	0.02	NM_024923	NP_079199	0.86	nucleoporin 210kDa
212316_at	NUP210	23225	0.03	NM_024923	NP_079199	0.91	nucleoporin 210kDa
212330_at	TFDP1	7027	0.01	NM_007111	NP_009042	0.95	transcription factor Dp-1
212331_at	RBL2	5934	0.04	NM_005611	NP_005602	0.89	retinoblastoma-like 2 (p130)
212333_at	DKFZP564F0522	25940	0.03	NM_015475	NP_056290	0.86	DKFZP564F0522 protein
212337_at	TI-227H	29793	1.75e-03	D50525		0.89	hypothetical protein TI-227H
212348_s_at	AOF2	23028	0.02	NM_015013	NP_055828	0.92	amine oxidase (flavin containing) domain 2
212351_at	EIF2B5	8893	0.01	NM_003907	NP_003898	0.85	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa
212352_s_at	TMP21	10972	0.03	NM_006827	NP_006818	0.94	transmembrane trafficking protein
212361_s_at	ATP2A2	488	0.01	NM_001681	NP_001672	0.89	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
212367_at	FEM1B	10116	0.01	AI799061		0.88	fem-1 homolog b (C. elegans)
212371_at	PNAS-4	51029	0.02	NM_016076	NP_057160	0.92	CGI-146 protein
212373_at	FEM1B	10116	6.92e-03	AW139179		0.92	fem-1 homolog b (C. elegans)
212377_s_at	NOTCH2	4853	0.03	NM_024408	NP_077719	0.90	Notch homolog 2 (Drosophila)
212378_at	GART	2618	0.04	NM_000819	NP_000810	0.90	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
212388_at	USP24	23358	0.01	AB028980	BAA83009	0.87	ubiquitin specific protease 24
212393_at	SBF1	6305	0.03	NM_002972	NP_002963	1.11	SET binding factor 1
212403_at	UBE3B	89910	9.91e-03	NM_130466	NP_569733	0.93	ubiquitin protein ligase E3B
212405_s_at	KIAA0859	51603	1.25e-03	NM_015935	NP_057019	0.87	KIAA0859
212406_s_at	C20orf36	55251	3.6e-03	NM_018257	NP_060727	0.90	chromosome 20 open reading frame 36
212407_at	KIAA0859	51603	0.02	NM_015935	NP_057019	0.87	KIAA0859
212413_at	SEPT6	23157	0.01	NM_145799	NP_665798	0.83	septin 6
212414_s_at	SEPT6	23157	3.43e-03	NM_145799	NP_665798	0.85	septin 6
212415_at	SEPT6	23157	0.02	NM_145799	NP_665798	0.85	septin 6
212418_at	ELF1	1997	1.16e-03	NM_172373	NP_758961	0.88	E74-like factor 1 (ets domain transcription factor)

212422_at	PDCD11	22984	0.02	D80007	BAA11502	0.92	programmed cell death 11
212426_s_at	YWHAQ	10971	0.04	NM_006826	NP_006817	0.91	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide
212429_s_at	GTF3C2	2976	5.27e-03	NM_001521	NP_001512	0.94	general transcription factor IIIC, polypeptide 2, beta 110kDa
212434_at	GRPEL1	80273	0.02	NM_025196	NP_079472	0.92	GrpE-like 1, mitochondrial (E. coli)
212438_at	RY1	11017	0.04	NM_006857	NP_006848	0.91	putative nucleic acid binding protein RY-1
212449_s_at	LYPLA1	10434	0.01	NM_006330	NP_006321	0.89	lysophospholipase I
212454_x_at	HNRPDL	9987	4.37e-04	AI762552		0.88	heterogeneous nuclear ribonucleoprotein D-like
212458_at	SPRED2	200734	2.01e-03	NM_181784	NP_861449	1.29	sprouty-related, EVH1 domain containing 2
212459_x_at	SUCLG2	8801	0.03	NM_003848	NP_003839	0.86	succinate-CoA ligase, GDP-forming, beta subunit
212463_at	CD59	966	0.04	NM_000611	NP_000602	0.90	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)
212480_at	KIAA0376	23384	0.04	NM_015330	NP_056145	0.92	KIAA0376 protein
212481_s_at	TPM4	7171	7.35e-03	NM_003290	NP_003281	0.92	tropomyosin 4
212485_at	KIAA0553	23131	0.02	NM_001002909	NP_001002909	0.90	KIAA0553 protein
212486_s_at	FYN	2534	0.02	NM_002037	NP_002028	0.88	FYN oncogene related to SRC, FGR, YES
212487_at	KIAA0553	23131	0.02	NM_001002909	NP_001002909	0.86	KIAA0553 protein
212491_s_at	DNAJC8	22826	0.03	NM_014280	NP_055095	0.91	DnaJ (Hsp40) homolog, subfamily C, member 8
212502_at	C10orf22	84890	0.02	NM_032804	NP_116193	0.91	chromosome 10 open reading frame 22
212505_s_at	KIAA0892	23383	0.03	NM_015329	NP_056144	1.09	KIAA0892
212507_at	RW1	23505	8.05e-03	D87446	BAA13387	0.94	RW1 protein
212508_at	MOAP1	64112	1.49e-03	NM_022151	NP_071434	0.80	modulator of apoptosis 1
212513_s_at	USP33	23032	0.01	NM_015017	NP_055832	0.93	ubiquitin specific protease 33
212519_at	UBE2E1	7324	0.02	NM_003341	NP_003332	0.91	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
212522_at	PDE8A	5151	0.01	NM_002605	NP_002596	0.92	phosphodiesterase 8A
212526_at	SPG20	23111	0.01	NM_015087	NP_055902	0.86	spastic paraplegia 20, spartin (Troyer syndrome)
212529_at	FLJ30656	124801	0.02	NM_152344	NP_689557	0.86	hypothetical protein FLJ30656
212534_at	ZNF24	7572	8.82e-03	AU144066		0.94	zinc finger protein 24 (KOX 17)
212535_at	MEF2A	4205	0.02	AL831995		0.88	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)
212542_s_at	PHIP	55023	0.03	NM_017934	NP_060404	0.91	pleckstrin homology domain interacting protein
212543_at	AIM1	202	0.01	U83115	AAB53791	0.93	absent in melanoma 1
212547_at	FLJ35348	266655	2.86e-03	N34842		0.92	FLJ35348
212548_s_at	KIAA0826	23045	0.04	AK128452		0.93	KIAA0826
212557_at	ZNF451	26036	6.73e-04	NM_015555	NP_056370	0.92	zinc finger protein 451
212572_at	STK38L	23012	0.04	NM_015000	NP_055815	0.91	serine/threonine kinase 38 like
212584_at	AQR	9716	0.04	NM_014691	NP_055506	0.95	aquarius homolog (mouse)
212590_at	RRAS2	22800	0.04	NM_012250	NP_036382	0.83	related RAS viral (r-ras) oncogene homolog 2
212591_at	KIAA0117	23029	7.02e-03	NM_015014	NP_055829	0.89	KIAA0117 protein
212593_s_at	PDCD4	27250	0.01	NM_014456	NP_055271	0.90	programmed cell death 4 (neoplastic transformation inhibitor)
212596_s_at	HMG2L1	10042	0.02	NM_005487	NP_005478	0.93	high-mobility group protein 2-like 1
212597_s_at	HMG2L1	10042	1.54e-03	NM_005487	NP_005478	0.92	high-mobility group protein 2-like 1

212600_s_at	UQCRC2	7385	0.02	NM_003366	NP_003357	0.91	ubiquinol-cytochrome c reductase core protein II
212605_s_at	NUDT3	11165	5.07e-03	AK025759		1.19	nudix (nucleoside diphosphate linked moiety X)-type motif 3
212607_at	AKT3	10000	0.03	AK055109		0.90	v-akt murine thymoma viral oncogene homolog 3 (protein kinase
B, gamma)							
212608_s_at	NUDT3	11165	0.01	W85912		0.90	nudix (nucleoside diphosphate linked moiety X)-type motif 3
212610_at	PTPN11	5781	0.02	NM_002834	NP_002825	0.91	protein tyrosine phosphatase, non-receptor type 11
(Noonan syndrome 1)							
212616_at	CHD9	80205	3.5e-04	NM_025134	NP_079410	0.92	chromodomain helicase DNA binding protein 9
212623_at	TMEM41B	23027	6.4e-03	D26067	BAA05062	0.87	transmembrane protein 41B
212630_at	SEC6L1	11336	0.04	NM_007277	NP_009208	0.87	SEC6-like 1 (S. cerevisiae)
212633_at	KIAA0776	23376	0.01	NM_015323	NP_056138	0.86	KIAA0776
212634_at	KIAA0776	23376	1.95e-03	NM_015323	NP_056138	1.10	KIAA0776
212637_s_at	WWP1	11059	7.67e-03	NM_007013	NP_008944	0.80	WW domain containing E3 ubiquitin protein ligase 1
212638_s_at	WWP1	11059	0.03	NM_007013	NP_008944	0.87	WW domain containing E3 ubiquitin protein ligase 1
212648_at	DHX29	54505	0.04	NM_019030	NP_061903	0.89	DEAH (Asp-Glu-Ala-His) box polypeptide 29
212653_s_at	EHBP1	23301	0.02	NM_015252	NP_056067	0.83	EH domain binding protein 1
212655_at	ZCCHC14	23174	0.02	NM_015144	NP_055959	0.85	zinc finger, CCHC domain containing 14
212672_at	ATM	472	6.11e-03	U82828		0.88	ataxia telangiectasia mutated (includes complementation groups A,
C and D)							
212673_at	METAP1	23173	0.03	NM_015143	NP_055958	0.91	methionyl aminopeptidase 1
212674_s_at	DHX30	22907	0.01	NM_138615	NP_619520	0.91	DEAH (Asp-Glu-Ala-His) box polypeptide 30
212685_s_at	TBL2	26608	3.98e-03	NM_012453	NP_036585	0.89	transducin (beta)-like 2
212687_at	LIMS1	3987	0.02	AL110164		0.95	LIM and senescent cell antigen-like domains 1
212688_at	PIK3CB	5291	0.03	BC003393	AAH03393	0.93	phosphoinositide-3-kinase, catalytic, beta polypeptide
212690_at	DDHD2	23259	0.02	AB018268	BAA34445	0.86	DDHD domain containing 2
212693_at	MDN1	23195	0.01	BE670928		0.86	MDN1, midasin homolog (yeast)
212694_s_at	PCCB	5096	0.01	NM_000532	NP_000523	0.85	propionyl Coenzyme A carboxylase, beta polypeptide
212696_s_at	RNF4	6047	9.35e-03	NM_002938	NP_002929	0.93	ring finger protein 4
212699_at	SCAMP5	192683	0.02	NM_138967	NP_620417	0.92	secretory carrier membrane protein 5
212714_at	LOC113251	113251	0.04	NM_052879	NP_443111	1.10	c-Mpl binding protein
212716_s_at	EIF3S12	27335	9.32e-03	NM_013234	NP_037366	0.94	eukaryotic translation initiation factor 3, subunit 12
212721_at	SFRS12	140890	9.0e-04	NM_139168	NP_631907	0.89	splicing factor, arginine/serine-rich 12
212725_s_at	TI-227H	29793	6.4e-03	D50525		0.92	hypothetical protein TI-227H
212731_at	LOC157567	157567	0.04	NM_198401	NP_940683	0.88	hypothetical protein LOC157567
212740_at	PIK3R4	30849	0.01	NM_014602	NP_055417	0.90	phosphoinositide-3-kinase, regulatory subunit 4, p150
212743_at	RCHY1	25898	0.02	NM_015436	NP_056251	0.87	ring finger and CHY zinc finger domain containing 1
212749_s_at	RCHY1	25898	0.02	NM_015436	NP_056251	0.91	ring finger and CHY zinc finger domain containing 1
212754_s_at	KIAA1040	23041	0.02	AK092646	BAC03935	0.92	KIAA1040 protein
212781_at	RBBP6	5930	7.29e-03	NM_006910	NP_008841	0.88	retinoblastoma binding protein 6
212784_at	CIC	23152	0.01	NM_015125	NP_055940	1.18	capicua homolog (Drosophila)
212786_at	KIAA0350	23274	0.04	NM_015226	NP_056041	0.92	KIAA0350 protein
212787_at	YLPM1	56252	0.02	BC007792	AAH07792	0.91	YLP motif containing 1
212794_s_at	KIAA1033	23325	0.03	NM_015275	NP_056090	1.15	KIAA1033 protein
212796_s_at	KIAA1055	23102	5.7e-03	NM_015079	NP_055894	0.93	KIAA1055 protein
212798_s_at	ANKMY2	57037	6.34e-04	NM_020319	NP_064715	0.89	ankyrin repeat and MYND domain containing 2

212800_at	STX6	10228	0.03	AF038202		0.92	syntaxin 6
212809_at	NFATC2IP	84901	0.01	NM_032815	NP_116204	0.91	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein
212815_at	ASCC3	10973	0.01	NM_006828	NP_006819	0.92	activating signal cointegrator 1 complex subunit 3
212821_at	PLEKHG3	26030	4.66e-03	AB011171	BAA25525	1.20	pleckstrin homology domain containing, family G (with RhoGef domain) member 3
212826_s_at	SLC25A6	293	0.04	NM_001636	NP_001627	0.89	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6
212831_at	EGFL5	1955	0.04	XM_376905	XP_376905	1.12	EGF-like-domain, multiple 5
212833_at	LOC91137	91137	1.81e-04	NM_138773	NP_620128	0.96	hypothetical protein BC017169
212835_at	KIAA0157	23172	6.11e-03	NM_032182	NP_115558	0.89	KIAA0157
212842_x_at	RANBP2L1	84220	0.02	NM_005054	NP_005045	0.88	RAN binding protein 2-like 1
212857_x_at	PC4	10923	0.02	NM_006713	NP_006704	0.91	activated RNA polymerase II transcription cofactor 4
212861_at	MGC11308	84975	0.04	NM_032889	NP_116278	0.93	hypothetical protein MGC11308
212871_at	MAPKAPK5	8550	0.01	NM_003668	NP_003659	0.94	mitogen-activated protein kinase-activated protein kinase 5
212876_at	B4GALT4	8702	0.02	NM_212543	NP_997708	0.82	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4
212877_at	KNS2	3831	0.04	NM_182923	NP_891553	0.90	kinesin 2 60/70kDa
212877_at	KNS2	3831	0.04	NM_005552	NP_005543	0.90	kinesin 2 60/70kDa
212878_s_at	KNS2	3831	0.04	NM_182923	NP_891553	0.93	kinesin 2 60/70kDa
212878_s_at	KNS2	3831	0.04	NM_005552	NP_005543	0.93	kinesin 2 60/70kDa
212880_at	WDR7	23335	9.2e-03	NM_015285	NP_056100	0.91	WD repeat domain 7
212885_at	MPHOSPH10	10199	0.02	NM_005791	NP_005782	0.86	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
212893_at	ZZZ3	26009	4.31e-03	NM_015534	NP_056349	0.86	zinc finger, ZZ domain containing 3
212897_at	CDC2L6	23097	0.01	NM_015076	NP_055891	1.33	cell division cycle 2-like 6 (CDK8-like)
212905_at	CSTF2T	23283	0.02	NM_015235	NP_056050	0.88	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant
212907_at	SLC30A1	7779	0.03	AI972416		0.87	solute carrier family 30 (zinc transporter), member 1
212914_at	CBX7	23492	0.01	NM_175709	NP_783640	0.93	chromobox homolog 7
212919_at	DCP2	167227	0.02	NM_152624	NP_689837	0.89	DCP2 decapping enzyme homolog (S. cerevisiae)
212922_s_at	SMYD2	56950	0.02	NM_020197	NP_064582	0.90	SET and MYND domain containing 2
212923_s_at	C6orf145	221749	0.03	NM_183373	NP_899229	1.10	chromosome 6 open reading frame 145
212928_at	TSPYL4	23270	0.02	NM_021648	NP_067680	0.89	TSPY-like 4
212932_at	RAB3GAP	22930	3.37e-03	AK022494		0.86	RAB3 GTPase-activating protein
212933_x_at	RPL13	6137	0.04	NM_000977	NP_000968	0.89	ribosomal protein L13
212943_at	KIAA0528	9847	1.85e-03	NM_014802	NP_055617	0.88	KIAA0528 gene product
212944_at	MRPS6	64968	6.4e-03	AK024896		0.87	mitochondrial ribosomal protein S6
212959_s_at	MGC4170	79158	0.04	NM_024312	NP_077288	0.87	MGC4170 protein
212961_x_at	CXorf40	91966	0.03	NM_178124	NP_835225	0.93	chromosome X open reading frame 40
212964_at	HIC2	23119	0.02	NM_015094	NP_055909	0.90	hypermethylated in cancer 2
212967_x_at	NAP1L1	4673	1.68e-03	AK055020		0.91	nucleosome assembly protein 1-like 1
212968_at	RFNG	5986	0.04	BC050399		1.12	radical fringe homolog (Drosophila)
212971_at	CARS	833	3.78e-03	NM_139273	NP_644802	0.96	cysteinyl-tRNA synthetase

212973_at	RPIA	22934	6.66e-03	NM_144563	NP_653164	0.87	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)
212975_at	KIAA0870	22898	0.04	NM_014957	NP_055772	0.93	KIAA0870 protein
212978_at	TA-LRRP	23507	0.03	D86984	BAA13220	0.82	T-cell activation leucine repeat-rich protein
212980_at	AHSA2	130872	8.05e-03	BC050395		0.87	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)
212981_s_at	KIAA0738	9747	0.04	BF030508		0.79	KIAA0738 gene product
212987_at	FBXO9	26268	3.84e-04	NM_012347	NP_036479	0.91	F-box protein 9
213000_at	ZCWCC3	23515	7.12e-04	NM_015358	NP_056173	0.95	zinc finger, CW type with coiled-coil domain 3
213011_s_at	TPI1	7167	0.02	NM_000365	NP_000356	0.97	triosephosphate isomerase 1
213019_at	RANBP6	26953	0.02	NM_012416	NP_036548	0.90	RAN binding protein 6
213022_s_at	UTRN	7402	0.03	NM_007124	NP_009055	0.90	utrophin (homologous to dystrophin)
213026_at	APG12L	9140	0.04	NM_004707	NP_004698	0.93	APG12 autophagy 12-like (S. cerevisiae)
213027_at	SSA2	6738	0.04	AU146655		0.92	Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro)
213030_s_at	PLXNA2	5362	9.75e-03	NM_025179	NP_079455	1.16	plexin A2
213036_x_at	ATP2A3	489	0.01	NM_005173	NP_005164	1.13	ATPase, Ca++ transporting, ubiquitous
213042_s_at	ATP2A3	489	0.02	NM_005173	NP_005164	0.87	ATPase, Ca++ transporting, ubiquitous
213045_at	MAST3	23031	0.01	AB011133	BAA25487	1.13	microtubule associated serine/threonine kinase 3
213065_at	MGC23401	196441	0.02	NM_144982	NP_659419	0.95	hypothetical protein MGC23401
213077_at	YTHDC2	64848	3.37e-03	NM_022828	NP_073739	0.88	YTH domain containing 2
213080_x_at	RPL5	6125	0.02	NM_000969	NP_000960	0.90	ribosomal protein L5
213086_s_at	CSNK1A1	1452	7.35e-03	NM_001892	NP_001883	0.95	casein kinase 1, alpha 1
213093_at	PRKCA	5578	0.03	NM_002737	NP_002728	0.88	protein kinase C, alpha
213095_x_at	AIF1	199	3.37e-03	NM_004847	NP_004838	0.94	allograft inflammatory factor 1
213097_s_at	ZRF1	27000	0.02	AL832847		0.84	zuotin related factor 1
213111_at	PIP5K3	200576	0.03	NM_152671	NP_689884	0.93	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III
213111_at	PIP5K3	200576	0.03	NM_015040	NP_055855	0.93	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III
213111_at	PIP5K3	200576	0.03	NM_001002881	NP_001002881	0.93	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III
213119_at	SLC36A1	206358	3.6e-03	NM_078483	NP_510968	0.86	solute carrier family 36 (proton/amino acid symporter), member 1
213123_at	MFAP3	4238	0.02	BE222709		0.90	microfibrillar-associated protein 3
213129_s_at	GCSH	2653	0.03	NM_004483	NP_004474	0.89	glycine cleavage system protein H (aminomethyl carrier)
213135_at	TIAM1	7074	0.03	U90902		0.90	T-cell lymphoma invasion and metastasis 1
213136_at	PTPN2	5771	3.1e-03	NM_080422	NP_536347	0.93	protein tyrosine phosphatase, non-receptor type 2
213137_s_at	PTPN2	5771	1.74e-03	NM_002828	NP_002819	0.87	protein tyrosine phosphatase, non-receptor type 2
213140_s_at	SS18L1	26039	0.02	NM_198935	NP_945173	0.91	synovial sarcoma translocation gene on chromosome 18-like 1
213142_x_at	LOC54103	54103	0.01	AK026696		0.83	hypothetical protein LOC54103
213146_at	JMJD3	23135	0.04	AB002344	BAA21572	1.14	jumonji domain containing 3
213153_at	KIAA1076	23067	0.04	AB028999	BAA83028	0.94	KIAA1076 protein
213160_at	DOCK2	1794	0.03	NM_004946	NP_004937	0.96	dedicator of cytokinesis 2

213161_at	C9orf97	158427	9.61e-03	NM_139246	NP_640339	0.90	chromosome 9 open reading frame 97
213186_at	DZIP3	9666	0.04	NM_014648	NP_055463	0.88	zinc finger DAZ interacting protein 3
213203_at	SNAPC5	10302	3.04e-04	NM_006049	NP_006040	0.89	small nuclear RNA activating complex, polypeptide 5, 19kDa
213208_at	KIAA0240	23506	0.01	NM_015349	NP_056164	0.91	KIAA0240
213225_at	PPM1B	5495	0.01	NM_002706	NP_002697	0.90	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform
213227_at	PGRMC2	10424	0.04	AK094949		0.89	progesterone receptor membrane component 2
213233_s_at	KLHL9	55958	0.03	NM_018847	NP_061335	0.88	kelch-like 9 (Drosophila)
213238_at	ATP10D	57205	0.01	NM_020453	NP_065186	0.90	ATPase, Class V, type 10D
213239_at	C13orf24	10464	2.39e-03	NM_006346	NP_006337	0.85	chromosome 13 open reading frame 24
213241_at	PLXNC1	10154	0.03	AF035307		1.05	plexin C1
213243_at	COH1	157680	0.02	NM_152564	NP_689777	0.95	Cohen syndrome 1
213251_at	SMARCA5	8467	0.02	AV712064		0.88	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
213267_at	KIAA1117	23033	0.04	AL162056	CAB82395	0.91	KIAA1117
213269_at	ZNF248	57209	9.4e-04	NM_021045	NP_066383	0.86	zinc finger protein 248
213271_s_at	KIAA1117	23033	0.02	NM_015018	NP_055833	0.87	KIAA1117
213293_s_at	TRIM22	10346	0.02	NM_006074	NP_006065	0.83	tripartite motif-containing 22
213295_at	CYLD	1540	0.01	AA555096		0.93	cylindromatosis (turban tumor syndrome)
213297_at	FLJ22318	64777	0.04	AK122692		1.09	hypothetical protein FLJ22318
213300_at	KIAA0404	23130	0.03	AW168132		1.17	KIAA0404 protein
213304_at	KIAA0423	23116	0.02	NM_015091	NP_055906	0.91	KIAA0423
213305_s_at	PPP2R5C	5527	0.04	NM_002719	NP_002710	0.93	protein phosphatase 2, regulatory subunit B (B56), gamma isoform
213307_at	SHANK2	22941	0.02	NM_012309	NP_036441	1.11	SH3 and multiple ankyrin repeat domains 2
213309_at	PLCL2	23228	1.83e-03	NM_015184	NP_055999	0.92	phospholipase C-like 2
213314_at	C6orf162	57150	2.39e-03	NM_020425	NP_065158	0.86	chromosome 6 open reading frame 162
213320_at	HRMT1L3	10196	0.02	NM_005788	NP_005779	0.92	HMT1 hnRNP methyltransferase-like 3 (S. cerevisiae)
213331_s_at	NEK1	4750	0.04	NM_012224	NP_036356	0.82	NIMA (never in mitosis gene a)-related kinase 1
213334_x_at	TREX2	11219	0.01	BC008141	AAH08141	0.89	three prime repair exonuclease 2
213340_s_at	KIAA0495	57212	0.02	NM_207306	NP_997189	0.90	KIAA0495
213347_x_at	RPS4X	6191	0.03	NM_001007	NP_000998	0.91	ribosomal protein S4, X-linked
213356_x_at	HNRPA1	3178	0.02	NM_002136	NP_002127	0.94	heterogeneous nuclear ribonucleoprotein A1
213357_at	GTF2H5	404672	0.01	NM_207118	NP_997001	0.86	general transcription factor IIH, polypeptide 5
213359_at	HNRPD	3184	5.18e-03	W74620		0.90	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
213365_at	MGC16943	112479	0.03	AB040937	BAA96028	0.87	similar to RIKEN cDNA 4933424N09 gene
213366_x_at	ATP5C1	509	2.05e-03	NM_001001973	NP_001001973	0.95	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
213372_at	PAQR3	152559	0.04	NM_177453	NP_803236	0.88	progestin and adipoQ receptor family member III
213373_s_at	CASP8	841	0.01	NM_001228	NP_001219	0.88	caspase 8, apoptosis-related cysteine protease
213374_x_at	HIBCH	26275	7.02e-03	NM_014362	NP_055177	0.90	3-hydroxyisobutyryl-Coenzyme A hydrolase
213375_s_at	CG018	90634	0.04	NM_052818	NP_438169	0.90	hypothetical gene CG018
213376_at	ZBTB1	22890	0.02	BC050719	AAH50719	0.91	zinc finger and BTB domain containing 1

213379_at	CL640	27235	0.02	NM_015697	NP_056512	0.91	hypothetical protein CL640
213393_at	MGC11332	84804	1.97e-03	AI767210		0.84	hypothetical protein MGC11332
213396_s_at	AKAP10	11216	0.04	NM_007202	NP_009133	0.87	A kinase (PRKA) anchor protein 10
213399_x_at	RPN2	6185	8.42e-03	NM_002951	NP_002942	0.91	ribophorin II
213403_at	MGC11332	84804	0.02	BF223370		0.82	hypothetical protein MGC11332
213404_s_at	RHEB	6009	0.02	NM_005614	NP_005605	0.90	Ras homolog enriched in brain
213405_at	RAB22A	57403	0.01	NM_020673	NP_065724	0.93	RAB22A, member RAS oncogene family
213408_s_at	LOC220686	220686	0.01	NM_199283	NP_954977	0.86	hypothetical protein LOC220686
213410_at	C10orf137	26098	0.02	NM_015608	NP_056423	0.92	chromosome 10 open reading frame 137
213421_x_at	PRSS3	5646	0.03	NM_002771	NP_002762	1.10	protease, serine, 3 (mesotrypsin)
213453_x_at	GAPD	2597	0.03	NM_002046	NP_002037	0.95	glyceraldehyde-3-phosphate dehydrogenase
213457_at	MFHAS1	9258	5.05e-03	NM_004225	NP_004216	1.17	malignant fibrous histiocytoma amplified sequence 1
213459_at	RPL37A	6168	4.52e-03	AU155515		0.89	ribosomal protein L37a
213465_s_at	PPP1R7	5510	3.26e-03	NM_002712	NP_002703	0.91	protein phosphatase 1, regulatory subunit 7
213470_s_at	HNRPH1	3187	0.01	NM_005520	NP_005511	0.68	heterogeneous nuclear ribonucleoprotein H1 (H)
213472_at	HNRPH1	3187	0.01	BX647205		0.70	heterogeneous nuclear ribonucleoprotein H1 (H)
213480_at	VAMP4	8674	0.02	NM_201994	NP_973723	0.89	vesicle-associated membrane protein 4
213483_at	KIAA0073	23398	0.01	NM_015342	NP_056157	0.93	KIAA0073 protein
213485_s_at	ABCC10	89845	7.69e-03	NM_033450	NP_258261	0.86	ATP-binding cassette, sub-family C (CFTR/MRP),
member 10							
213491_x_at	RPN2	6185	0.03	NM_002951	NP_002942	0.93	ribophorin II
213497_at	ABTB2	25841	0.01	NM_145804	NP_665803	0.82	ankyrin repeat and BTB (POZ) domain containing 2
213500_at	MRPS22	56945	0.04	AI307760		0.86	mitochondrial ribosomal protein S22
213503_x_at	ANXA2	302	0.02	NM_001002858	NP_001002858	0.86	annexin A2
213505_s_at	SFRS14	10147	1.85e-03	NM_014884	NP_055699	0.84	splicing factor, arginine/serine-rich 14
213511_s_at	MTMR1	8776	0.01	NM_003828	NP_003819	0.92	myotubularin related protein 1
213518_at	PRKCI	5584	0.02	NM_002740	NP_002731	0.91	protein kinase C, iota
213535_s_at	UBE2I	7329	0.02	NM_003345	NP_003336	0.93	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)
213538_at	SON	6651	0.02	NM_032195	NP_115571	0.92	SON DNA binding protein
213540_at	HSD17B8	7923	7.12e-04	NM_014234	NP_055049	0.79	hydroxysteroid (17-beta) dehydrogenase 8
213548_s_at	H41	55573	0.02	NM_017548	NP_060018	0.86	hypothetical protein H41
213552_at	GLCE	26035	0.01	NM_015554	NP_056369	0.83	glucuronyl C5-epimerase
213554_s_at	H41	55573	0.04	NM_017548	NP_060018	0.90	hypothetical protein H41
213564_x_at	LDHB	3945	6.11e-03	NM_002300	NP_002291	0.89	lactate dehydrogenase B
213578_at	BMPR1A	657	0.03	NM_004329	NP_004320	1.11	bone morphogenetic protein receptor, type IA
213581_at	PDCD2	5134	0.03	NM_144781	NP_659005	0.89	programmed cell death 2
213588_x_at	RPL14	9045	0.04	NM_003973	NP_003964	0.90	ribosomal protein L14
213589_s_at	LOC146712	146712	0.04	NM_194288	NP_919264	0.90	hypothetical protein LOC146712
213604_at	TCEB3	6924	0.03	AW451236		0.89	transcription elongation factor B (SIII), polypeptide 3 (110kDa,
elongin A)							
213618_at	CENTD1	116984	0.01	NM_015230	NP_056045	0.88	centaurin, delta 1
213629_x_at	MT1F	4494	0.02	NM_005949	NP_005940	1.08	metallothionein 1F (functional)
213639_s_at	ZNF500	26048	0.01	AB011129	BAA25483	0.88	zinc finger protein 500
213652_at	PCSK5	5125	6.39e-03	AU152579		0.85	proprotein convertase subtilisin/kexin type 5
213653_at	METTL3	56339	0.04	AW069290		0.90	methyltransferase like 3

213658_at	DKFZp547K1113	374655	9.84e-05	BE858194		0.90	hypothetical protein DKFZp547K1113
213659_at	ZNF75	7626	7.02e-03	NM_007131	NP_009062	0.88	zinc finger protein 75 (D8C6)
213666_at	SEPT6	23157	6.11e-03	NM_145800	NP_665799	0.83	septin 6
213670_x_at	NSUN5	55695	4.6e-03	NM_148956	NP_683759	0.83	NOL1/NOP2/Sun domain family, member 5
213672_at	MARS	4141	0.02	AA621558		0.91	methionine-tRNA synthetase
213677_s_at	PMS1	5378	0.02	NM_000534	NP_000525	0.91	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)
213689_x_at	RPL5	6125	0.02	U66589		0.84	ribosomal protein L5
213694_at	RSBN1	54665	1.05e-03	NM_018364	NP_060834	0.83	round spermatid basic protein 1
213699_s_at	YWHAQ	10971	0.04	NM_006826	NP_006817	0.93	tyrosine 3-monooxygenase/tryptophan 5-
monooxygenase activation protein, theta polypeptide							
213703_at	LOC150759	150759	0.01	AK057596	BAB71531	0.81	hypothetical protein LOC150759
213704_at	RABGGTB	5876	0.01	NM_004582	NP_004573	0.87	Rab geranylgeranyltransferase, beta subunit
213705_at	MAT2A	4144	0.01	AW301861		1.09	methionine adenosyltransferase II, alpha
213718_at	RBM4	5936	0.01	BC021120	AAH21120	0.83	RNA binding motif protein 4
213730_x_at	TCF3	6929	0.02	NM_003200	NP_003191	0.88	transcription factor 3 (E2A immunoglobulin enhancer
binding factors E12/E47)							
213735_s_at	COX5B	1329	0.04	NM_001862	NP_001853	0.92	cytochrome c oxidase subunit Vb
213737_x_at	LOC283768	283768	1.94e-04	BC066774		0.85	hypothetical LOC283768
213738_s_at	ATP5A1	498	3.38e-03	NM_004046	NP_004037	0.93	ATP synthase, H+ transporting, mitochondrial F1
complex, alpha subunit, isoform 1, cardiac muscle							
213743_at	CCNT2	905	0.01	NM_001241	NP_001232	0.92	cyclin T2
213754_s_at	PAIP1	10605	4.56e-03	NM_006451	NP_006442	0.84	poly(A) binding protein interacting protein 1
213761_at	MDM1	56890	0.02	NM_017440	NP_059136	0.88	Mdm4, transformed 3T3 cell double minute 1, p53 binding
protein (mouse)							
213761_at	MDM1	56890	0.02	NM_020128	NP_064513	0.88	Mdm4, transformed 3T3 cell double minute 1, p53 binding
protein (mouse)							
213762_x_at	RBMX	27316	0.04	BX647131		0.92	RNA binding motif protein, X-linked
213773_x_at	NSUN5	55695	0.03	NM_148956	NP_683759	0.94	NOL1/NOP2/Sun domain family, member 5
213778_x_at	ZFP276	92822	0.01	NM_152287	NP_689500	0.91	zinc finger protein 276 homolog (mouse)
213797_at	RSAD2	91543	0.03	NM_080657	NP_542388	1.50	radical S-adenosyl methionine domain containing 2
213811_x_at	TCF3	6929	0.04	NM_003200	NP_003191	0.89	transcription factor 3 (E2A immunoglobulin enhancer
binding factors E12/E47)							
213835_x_at	GTPBP3	84705	0.02	NM_133644	NP_598399	0.89	GTP binding protein 3 (mitochondrial)
213835_x_at	GTPBP3	84705	0.02	NM_032620	NP_116009	0.89	GTP binding protein 3 (mitochondrial)
213848_at	DUSP7	1849	0.02	AI655015		0.86	dual specificity phosphatase 7
213857_s_at	CD47	961	3.66e-03	NM_001777	NP_001768	0.92	CD47 antigen (Rh-related antigen, integrin-associated
signal transducer)							
213859_x_at	SMARCA5	8467	0.02	NM_003601	NP_003592	0.89	SWI/SNF related, matrix associated, actin dependent
regulator of chromatin, subfamily a, member 5							
213860_x_at	CSNK1A1	1452	0.04	NM_001892	NP_001883	0.91	casein kinase 1, alpha 1
213864_s_at	NAP1L1	4673	0.03	NM_139207	NP_631946	0.92	nucleosome assembly protein 1-like 1
213873_at	DCBLD2	131566	0.03	D29810	BAA18909	1.13	discoidin, CUB and LCCL domain containing 2
213878_at	RECQL	5965	0.04	AI685944		0.91	RecQ protein-like (DNA helicase Q1-like)
213881_x_at	SUMO2	6613	0.02	NM_006937	NP_008868	0.93	SMT3 suppressor of mif two 3 homolog 2 (yeast)

213887_s_at	POLR2E	5434	0.03	NM_002695	NP_002686	0.93	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa
213888_s_at	T3JAM	80342	0.01	AL022398		0.87	TRAF3-interacting Jun N-terminal kinase (JNK)-activating modulator
213892_s_at	APRT	353	0.04	NM_000485	NP_000476	0.89	adenine phosphoribosyltransferase
213893_x_at	PMS2L5	5383	3.6e-03	NM_174930	NP_777590	0.87	postmeiotic segregation increased 2-like 5
213897_s_at	MRPL23	6150	0.01	NM_021134	NP_066957	0.88	mitochondrial ribosomal protein L23
213906_at	MYBL1	4603	0.04	XM_034274	XP_034274	0.84	v-myb myeloblastosis viral oncogene homolog (avian)-like 1
213936_x_at	SFTPB	6439	9.61e-03	NM_198843	NP_942140	1.14	surfactant, pulmonary-associated protein B
213937_s_at	FTSJ1	24140	0.04	NM_012280	NP_036412	0.90	FtsJ homolog 1 (E. coli)
213941_x_at	RPS7	6201	0.03	NM_001011	NP_001002	0.92	ribosomal protein S7
213957_s_at	CAP350	9857	0.02	NM_014810	NP_055625	0.89	centrosome-associated protein 350
213969_x_at	RPL29	6159	0.03	NM_000992	NP_000983	0.90	ribosomal protein L29
213986_s_at	C19orf6	91304	0.01	NM_033420	NP_219488	0.84	chromosome 19 open reading frame 6
213988_s_at	SAT	6303	0.01	NM_002970	NP_002961	0.85	spermidine/spermine N1-acetyltransferase
213995_at	ATP5S	27109	9.2e-03	NM_001003803	NP_001003803	0.85	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)
214005_at	GGCX	2677	0.03	NM_000821	NP_000812	0.94	gamma-glutamyl carboxylase
214016_s_at	SFPQ	6421	0.02	AL558875		0.89	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)
214022_s_at	IFITM1	8519	2.39e-03	NM_003641	NP_003632	0.87	interferon induced transmembrane protein 1 (9-27)
214030_at	DKFZp667G2110	131544	0.04	XM_376254	XP_376254	0.92	hypothetical protein DKFZp667G2110
214032_at	ZAP70	7535	0.01	NM_001079	NP_001070	0.85	zeta-chain (TCR) associated protein kinase 70kDa
214034_at	ARTS-1	51752	6.71e-03	NM_016442	NP_057526	1.15	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
214047_s_at	MBD4	8930	0.02	NM_003925	NP_003916	0.94	methyl-CpG binding domain protein 4
214049_x_at	CD7	924	0.02	NM_006137	NP_006128	0.86	CD7 antigen (p41)
214061_at	MGC21654	93594	8.05e-03	NM_145647	NP_663622	0.84	unknown MGC21654 product
214081_at	PLXDC1	57125	4.42e-04	NM_020405	NP_065138	0.80	plexin domain containing 1
214083_at	PPP2R5C	5527	0.02	AW772123		1.07	protein phosphatase 2, regulatory subunit B (B56), gamma isoform
214091_s_at	GPX3	2878	1.16e-03	NM_002084	NP_002075	1.39	glutathione peroxidase 3 (plasma)
214092_x_at	SFRS14	10147	0.01	NM_014884	NP_055699	0.90	splicing factor, arginine/serine-rich 14
214093_s_at	FUBP1	8880	0.02	AA156865		0.88	far upstream element (FUSE) binding protein 1
214096_s_at	SHMT2	6472	0.02	NM_005412	NP_005403	0.87	serine hydroxymethyltransferase 2 (mitochondrial)
214097_at	RPS21	6227	0.02	NM_001024	NP_001015	0.85	ribosomal protein S21
214100_x_at	NSUN5	55695	8.42e-03	NM_148956	NP_683759	0.82	NOL1/NOP2/Sun domain family, member 5
214118_x_at	PCM1	5108	7.38e-03	NM_006197	NP_006188	0.91	pericentriolar material 1
214129_at	PDE4DIP	9659	0.04	NM_014644	NP_055459	1.10	phosphodiesterase 4D interacting protein (myomegalin)
214132_at	ATP5C1	509	0.04	NM_001001973	NP_001001973	0.90	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
214141_x_at	SFRS7	6432	0.02	AK094126	BAC04292	0.90	splicing factor, arginine/serine-rich 7, 35kDa
214144_at	POLR2D	5433	0.03	NM_004805	NP_004796	0.86	polymerase (RNA) II (DNA directed) polypeptide D
214151_s_at	PIGB	9488	0.03	BC042826		0.91	phosphatidylinositol glycan, class B

214155_s_at	LOC113251	113251	1.05e-03	NM_052879	NP_443111	0.81	c-Mpl binding protein
214167_s_at	RPLP0	6175	0.03	NM_001002	NP_000993	0.90	ribosomal protein, large, P0
214186_s_at	3.8-1	352961	0.01	L29376		0.90	MHC class I mRNA fragment 3.8-1
214193_s_at	MGC29875	27042	0.03	AI770084		0.87	hypothetical protein MGC29875
214214_s_at	C1QBP	708	0.02	NM_001212	NP_001203	0.84	complement component 1, q subcomponent binding protein
214216_s_at	KIAA0217	23185	0.03	AW628686		0.87	KIAA0217
214241_at	NDUFB8	4714	0.01	NM_005004	NP_004995	0.85	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
214251_s_at	NUMA1	4926	6.27e-04	NM_006185	NP_006176	0.84	nuclear mitotic apparatus protein 1
214258_x_at	HTATIP	10524	0.04	NM_182710	NP_874369	0.96	HIV-1 Tat interacting protein, 60kDa
214259_s_at	AKR7A2	8574	0.03	NM_003689	NP_003680	0.85	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
214260_at	COPS8	10920	2.5e-04	NM_006710	NP_006701	0.69	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)
214263_x_at	POLR2C	5432	7.52e-03	NM_032940	NP_116558	0.88	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa
214268_s_at	MTMR4	9110	3.5e-04	NM_004687	NP_004678	0.93	myotubularin related protein 4
214271_x_at	RPL12	6136	0.03	AK057602		0.90	ribosomal protein L12
214274_s_at	ACAA1	30	3.17e-03	NM_001607	NP_001598	0.88	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
214280_x_at	HNRPA1	3178	0.03	BC070315	AAH70315	0.90	heterogeneous nuclear ribonucleoprotein A1
214306_at	OPA1	4976	0.01	NM_015560	NP_056375	0.83	optic atrophy 1 (autosomal dominant)
214317_x_at	RPS9	6203	0.02	NM_001013	NP_001004	0.86	ribosomal protein S9
214323_s_at	UPF3A	65110	0.01	NM_023011	NP_075387	0.87	UPF3 regulator of nonsense transcripts homolog A (yeast)
214337_at	COPA	1314	0.02	NM_004371	NP_004362	1.15	coatomer protein complex, subunit alpha
214352_s_at	KRAS	3845	0.02	NM_033360	NP_203524	1.19	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
214356_s_at	KIAA0368	23392	0.03	AB002366	BAA20823	0.87	KIAA0368
214363_s_at	MATR3	9782	0.01	NM_018834	NP_061322	0.92	matrin 3
214364_at	MGC61716	130916	4.24e-03	NM_182501	NP_872307	0.88	hypothetical protein MGC61716
214369_s_at	RASGRP2	10235	0.04	NM_005825	NP_005816	0.93	RAS guanyl releasing protein 2 (calcium and DAG-regulated)
214383_x_at	KLHDC3	116138	0.01	NM_057161	NP_476502	0.90	kelch domain containing 3
214427_at	NOL1	4839	0.01	NM_006170	NP_006161	0.89	nucleolar protein 1, 120kDa
214431_at	GMPS	8833	3.45e-04	NM_003875	NP_003866	0.78	guanine monphosphate synthetase
214437_s_at	SHMT2	6472	0.02	NM_005412	NP_005403	0.88	serine hydroxymethyltransferase 2 (mitochondrial)
214440_at	NAT1	9	0.01	NM_000662	NP_000653	0.89	N-acetyltransferase 1 (arylamine N-acetyltransferase)
214447_at	ETS1	2113	6.54e-05	NM_005238	NP_005229	0.73	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)
214453_s_at	IFI44	10561	0.03	NM_006417	NP_006408	0.48	interferon-induced protein 44
214455_at	HIST1H2BC	8347	9.2e-03	NM_003526	NP_003517	1.17	histone 1, H2bc
214467_at	GPR65	8477	0.01	NM_003608	NP_003599	0.88	G protein-coupled receptor 65
214473_x_at	PMS2L3	5387	2.35e-04	NM_005395	NP_005386	0.86	postmeiotic segregation increased 2-like 3
214474_at	PRKAB2	5565	0.04	NM_005399	NP_005390	0.91	protein kinase, AMP-activated, beta 2 non-catalytic subunit
214482_at	ZNF46	7597	0.03	NM_006977	NP_008908	0.89	zinc finger protein 46 (KUP)

214512_s_at	PC4	10923	0.02	NM_006713	NP_006704	0.92	activated RNA polymerase II transcription cofactor 4
214531_s_at	SNX1	6642	4.83e-03	NM_003099	NP_003090	0.95	sorting nexin 1
214550_s_at	TNPO3	23534	7.06e-03	NM_012470	NP_036602	0.86	transportin 3
214551_s_at	CD7	924	7.02e-03	NM_006137	NP_006128	0.83	CD7 antigen (p41)
214567_s_at	XCL2	6846	0.02	NM_003175	NP_003166	0.80	chemokine (C motif) ligand 2
214583_at	RSC1A1	6248	0.01	NM_006511	NP_006502	0.85	regulatory solute carrier protein, family 1, member 1
214585_s_at	VPS52	6293	1.45e-03	NM_080564	NP_542131	0.91	vacuolar protein sorting 52 (yeast)
214590_s_at	UBE2D1	7321	0.01	NM_003338	NP_003329	1.19	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)
214618_at	CFLAR	8837	0.04	NM_003879	NP_003870	1.13	CASP8 and FADD-like apoptosis regulator
214626_s_at	GANAB	23193	0.04	NM_198335	NP_938149	0.92	glucosidase, alpha; neutral AB
214626_s_at	GANAB	23193	0.04	NM_198334	NP_938148	0.92	glucosidase, alpha; neutral AB
214626_s_at	GANAB	23193	0.04	NM_014610	NP_055425	0.92	glucosidase, alpha; neutral AB
214665_s_at	CHP	11261	0.01	NM_007236	NP_009167	0.93	calcium binding protein P22
214683_s_at	CLK1	1195	9.61e-03	NM_004071	NP_004062	0.89	CDC-like kinase 1
214686_at	ZNF266	10781	0.03	NM_198058	NP_932175	0.90	zinc finger protein 266
214686_at	ZNF266	10781	0.03	NM_006631	NP_006622	0.90	zinc finger protein 266
214700_x_at	RIF1	55183	0.03	AK000323	0.94		RAP1 interacting factor homolog (yeast)
214706_at	ZNF200	7752	3.28e-03	NM_198087	NP_932353	0.79	zinc finger protein 200
214706_at	ZNF200	7752	3.28e-03	NM_198088	NP_932354	0.79	zinc finger protein 200
214706_at	ZNF200	7752	3.28e-03	NM_003454	NP_003445	0.79	zinc finger protein 200
214707_x_at	ALMS1	7840	0.01	NM_015120	NP_055935	1.05	Alstrom syndrome 1
214711_at	15E1.2	283459	0.04	AK094319	0.85		hypothetical protein 15E1.2
214714_at	ZNF394	84124	7.52e-03	NM_032164	NP_115540	0.85	zinc finger protein 394
214715_x_at	ZNF160	90338	9.61e-03	AK024789	1.06		zinc finger protein 160
214726_x_at	ADD1	118	0.03	NM_001119	NP_001110	1.07	adducin 1 (alpha)
214734_at	SLAC2-B	23086	3.58e-03	NM_015065	NP_055880	1.18	SLAC2-B
214735_at	PIP3-E	26034	8.95e-03	NM_015553	NP_056368	0.92	phosphoinositide-binding protein PIP3-E
214756_x_at	PMS2L1	5379	2.35e-04	AB017004	BAA74753	0.88	postmeiotic segregation increased 2-like 1
214762_at	ATP6V1G2	534	9.66e-03	NM_130463	NP_569730	1.17	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 2
214789_x_at	SRP46	10929	1.66e-03	NM_032102	NP_115285	0.86	Splicing factor, arginine/serine-rich, 46kD
214791_at	LOC93349	93349	0.02	NM_138402	NP_612411	0.89	hypothetical protein BC004921
214792_x_at	VAMP2	6844	0.03	AI955119	1.13		vesicle-associated membrane protein 2 (synaptobrevin 2)
214813_at	ZNF75	7626	0.02	NM_007131	NP_009062	0.89	zinc finger protein 75 (D8C6)
214816_x_at	MGC32020	91442	6.63e-03	NM_152266	NP_689479	1.15	hypothetical protein MGC32020
214820_at	WDR9	54014	3.45e-04	NM_033656	NP_387505	0.84	WD repeat domain 9
214844_s_at	DOK5	55816	0.01	NM_018431	NP_060901	1.18	docking protein 5
214848_at	YWHAZ	7534	6.92e-03	U79277	0.79		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
214853_s_at	SHC1	6464	0.03	NM_003029	NP_003020	0.93	SHC (Src homology 2 domain containing) transforming protein 1
214870_x_at	NPIP	9284	3.63e-03	NM_006985	NP_008916	0.78	nuclear pore complex interacting protein
214875_x_at	APLP2	334	0.01	NM_001642	NP_001633	0.93	amyloid beta (A4) precursor-like protein 2
214882_s_at	SFRS2	6427	0.01	NM_003016	NP_003007	0.89	splicing factor, arginine/serine-rich 2

214888_at	CAPN2	824	0.02	AK023851		1.12	calpain 2, (m/II) large subunit
214895_s_at	ADAM10	102	0.02	NM_001110	NP_001101	0.93	a disintegrin and metalloproteinase domain 10
214906_x_at	CG018	90634	0.01	NM_052818	NP_438169	0.89	hypothetical gene CG018
214908_s_at	TRRAP	8295	8.42e-03	NM_003496	NP_003487	0.89	transformation/transcription domain-associated protein
214909_s_at	DDAH2	23564	4.68e-03	NM_013974	NP_039268	0.83	dimethylarginine dimethylaminohydrolase 2
214911_s_at	BRD2	6046	0.03	NM_005104	NP_005095	0.89	bromodomain containing 2
214915_at	FLJ25476	149076	0.03	AK021842		1.16	FLJ25476 protein
214934_at	ATP9B	374868	0.01	NM_198531	NP_940933	0.80	ATPase, Class II, type 9B
214937_x_at	PCM1	5108	0.01	NM_006197	NP_006188	0.90	pericentriolar material 1
214945_at	NY-REN-7	285596	0.04	NM_173663	NP_775934	0.73	NY-REN-7 antigen
214949_at	LOC441347	441347	0.02	AL050136		0.93	similar to family with sequence similarity 9, member C
214959_s_at	API5	8539	0.02	NM_006595	NP_006586	0.89	apoptosis inhibitor 5
214964_at	TNRC18	27320	0.03	AA554430		1.12	trinucleotide repeat containing 18
214975_s_at	MTMR1	8776	0.01	NM_003828	NP_003819	0.86	myotubularin related protein 1
214984_at	IMAA	387254	8.84e-03	NM_199182	NP_954651	1.19	hLAT1-3TM
215000_s_at	FEZ2	9637	0.01	NM_005102	NP_005093	0.92	fasciculation and elongation protein zeta 2 (zygin II)
215009_s_at	SEC31L1	22872	0.03	U92014		0.88	SEC31-like 1 (S. cerevisiae)
215012_at	ZNF451	26036	4.73e-03	BC021712	AAH21712	0.83	zinc finger protein 451
215023_s_at	PEX1	5189	0.01	NM_000466	NP_000457	0.90	peroxisome biogenesis factor 1
215031_x_at	RNF126	55658	0.03	NM_194460	NP_919442	0.88	ring finger protein 126
215051_x_at	AIF1	199	0.03	NM_032955	NP_116573	0.96	allograft inflammatory factor 1
215068_s_at	FBXL18	80028	0.01	BC013435	AAH13435	1.16	F-box and leucine-rich repeat protein 18
215075_s_at	GRB2	2885	0.01	NM_002086	NP_002077	1.14	growth factor receptor-bound protein 2
215088_s_at	SDHC	6391	8.04e-03	NM_003001	NP_002992	0.92	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa
215091_s_at	GTF3A	2971	0.01	NM_002097	NP_002088	0.92	general transcription factor IIIA
215096_s_at	ESD	2098	2.61e-03	NM_001984	NP_001975	0.85	esterase D/formylglutathione hydrolase
215123_at	KIAA0220	283846	0.03	AL049250		0.82	PI-3-kinase-related kinase SMG-1-like
215136_s_at	EXOSC8	11340	9.2e-03	NM_181503	NP_852480	0.89	exosome component 8
215171_s_at	TIMM17A	10440	0.02	NM_006335	NP_006326	0.85	translocase of inner mitochondrial membrane 17 homolog A (yeast)
215177_s_at	ITGA6	3655	4.6e-04	NM_000210	NP_000201	0.81	integrin, alpha 6
215203_at	GOLGA4	2803	0.02	AK022389		0.83	golgi autoantigen, golgin subfamily a, 4
215204_at	SENP6	26054	0.04	AU147295		1.16	SUMO1/sentrin specific protease 6
215206_at	EXT1	2131	0.01	AK025143		1.14	exostoses (multiple) 1
215210_s_at	DLST	1743	4.6e-03	NM_001933	NP_001924	0.89	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
215227_x_at	ACP1	52	0.02	NM_177554	NP_808222	0.89	acid phosphatase 1, soluble
215228_at	NHLH2	4808	4.7e-03	NM_005599	NP_005590	1.28	nescient helix loop helix 2
215253_s_at	DSCR1	1827	0.04	NM_004414	NP_004405	0.88	Down syndrome critical region gene 1
215263_at	ZXDA	7789	0.01	NM_007156	NP_009087	0.83	zinc finger, X-linked, duplicated A
215268_at	KIAA0754	23056	0.01	AB018297	BAA34474	0.84	KIAA0754 protein
215275_at	T3JAM	80342	4.99e-04	AK126139	BAC86461	0.86	TRAF3-interacting Jun N-terminal kinase (JNK)-activating modulator
215330_at	FLJ43663	378805	0.02	AL049991		1.19	hypothetical protein FLJ43663

215338_s_at	NKTR	4820	0.04	NM_005385	NP_005376	0.91	natural killer-tumor recognition sequence
215358_x_at	ZNF37B	256112	9.09e-03	AK026980		0.85	zinc finger protein 37b (KOX 21)
215374_at	PAPOLA	10914	0.04	AK024849		1.12	poly(A) polymerase alpha
215378_at	ANKHD1	54882	0.02	AU148255		1.18	ankyrin repeat and KH domain containing 1
215383_x_at	SPG21	51324	0.01	AL137312		1.10	spastic paraplegia 21 (autosomal recessive, Mast syndrome)
215394_at	PIK3C3	5289	0.01	AU148957		1.11	phosphoinositide-3-kinase, class 3
215412_x_at	PMS2L2	5380	0.02	AB017007	BAA74756	0.91	postmeiotic segregation increased 2-like 2
215416_s_at	STOML2	30968	0.02	NM_013442	NP_038470	0.85	stomatin (EPB72)-like 2
215424_s_at	SKIIP	22938	1.77e-03	NM_012245	NP_036377	0.95	SKI interacting protein
215438_x_at	GSPT1	2935	0.04	NM_002094	NP_002085	0.89	G1 to S phase transition 1
215440_s_at	BEXL1	56271	9.63e-03	XM_043653	XP_043653	0.87	brain expressed X-linked-like 1
215451_s_at	MLLT2	4299	0.04	NM_005935	NP_005926	1.11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2
215452_x_at	SUMO4	387082	0.04	NM_001002255	NP_001002255	0.94	SMT3 suppressor of mif two 3 homolog 4 (yeast)
215457_at	ARPC1A	10552	0.01	AF070647		1.19	actin related protein 2/3 complex, subunit 1A, 41kDa
215512_at	MARCH6	10299	0.01	AK000970		0.83	membrane-associated ring finger (C3HC4) 6
215532_x_at	ZNF492	57615	0.01	AB040906	BAA95997	1.19	zinc finger protein 492
215548_s_at	SCFD1	23256	6.64e-03	NM_016106	NP_057190	0.93	sec1 family domain containing 1
215553_x_at	WDR45	11152	0.02	AK024315		1.05	WD repeat domain 45
215576_at	ULK4	54986	0.02	AU146809		1.13	unc-51-like kinase 4 (C. elegans)
215581_s_at	MCM3AP	8888	1.35e-03	NM_003906	NP_003897	0.86	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein
215596_s_at	ZNF294	26046	0.03	NM_015565	NP_056380	0.95	zinc finger protein 294
215597_x_at	MYST4	23522	0.03	AU143799		1.16	MYST histone acetyltransferase (monocytic leukemia) 4
215616_s_at	JMJD2B	23030	0.03	NM_015015	NP_055830	1.19	jumonji domain containing 2B
215639_at	SH2D3C	10044	0.01	AK000861		1.11	SH2 domain containing 3C
215667_x_at	PMS2L2	5380	1.66e-03	NM_002679	NP_002670	0.92	postmeiotic segregation increased 2-like 2
215684_s_at	ASCC2	84164	0.03	NM_032204	NP_115580	0.88	activating signal cointegrator 1 complex subunit 2
215690_x_at	GPAA1	8733	3.69e-03	NM_003801	NP_003792	0.90	GPAA1P anchor attachment protein 1 homolog (yeast)
215691_x_at	C1orf41	51668	0.02	NM_016126	NP_057210	0.85	chromosome 1 open reading frame 41
215693_x_at	DDX27	55661	0.04	AL512707		0.94	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27
215698_at	JARID1A	5927	0.01	AF007135		1.19	Jumonji, AT rich interactive domain 1A (RBBP2-like)
215707_s_at	PRNP	5621	7.69e-03	NM_000311	NP_000302	0.92	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)
215731_s_at	MPHOSPH9	10198	0.02	X98258	CAA66911	0.79	M-phase phosphoprotein 9
215735_s_at	TSC2	7249	0.01	NM_000548	NP_000539	0.88	tuberous sclerosis 2
215737_x_at	USF2	7392	0.01	NM_003367	NP_003358	1.08	upstream transcription factor 2, c-fos interacting
215739_s_at	TUBGCP3	10426	4.6e-03	NM_006322	NP_006313	0.92	tubulin, gamma complex associated protein 3
215750_at	KIAA1659	85373	0.03	AB051446	BAB33329	1.13	KIAA1659 protein
215766_at	GSTA1	2938	1.65e-03	AL096729		1.10	glutathione S-transferase A1
215772_x_at	SUCLG2	8801	0.03	NM_003848	NP_003839	0.89	succinate-CoA ligase, GDP-forming, beta subunit
215780_s_at	SET	6418	0.02	NM_003011	NP_003002	0.83	SET translocation (myeloid leukemia-associated)
215810_x_at	D6S1101	7943	3.57e-03	AL049215		1.20	Dystonia musculorum of mouse, human homolog of
215883_at	LOC401210	401210	0.03	AK022326		1.08	hypothetical gene supported by AK022326
215898_at	KIAA0998	23093	0.03	AK021879		0.91	KIAA0998

215947_s_at	FLJ14668	84908	0.04	NM_032822	NP_116211	0.89	hypothetical protein FLJ14668		
215954_s_at	C19orf29	58509	0.01	BC004262	AAH04262	0.87	chromosome 19 open reading frame 29		
215994_x_at	KIAA0676	23061	0.01	NM_198868	NP_942568	0.91	KIAA0676 protein		
215997_s_at	CUL4B	8450	0.01	NM_003588	NP_003579	0.93	cullin 4B		
216025_x_at	CYP2C9	1559	9.22e-03	M21940	AAA52159	1.12	cytochrome P450, family 2, subfamily C, polypeptide 9		
216035_x_at	TCF7L2	6934	0.02	BX648364	0.87		transcription factor 7-like 2 (T-cell specific, HMG-box)		
216044_x_at	LOC388650	388650	0.03	AK027146	0.86		hypothetical LOC388650		
216095_x_at	MTMR1	8776	3.7e-03	NM_003828	NP_003819	0.90	myotubularin related protein 1		
216111_x_at	PMS2L3	5387	3.24e-04	NM_005395	NP_005386	0.86	postmeiotic segregation increased 2-like 3		
216115_at	EVI2A	2123	1.06e-04	AK024873	1.32		ecotropic viral integration site 2A		
216153_x_at	RECK	8434	0.01	AK022897	0.84		reversion-inducing-cysteine-rich protein with kazal motifs		
216197_at	ATF7IP	55729	0.01	AK021569	1.16		activating transcription factor 7 interacting protein		
216203_at	SPTLC2	9517	9.91e-03	U15555	AAC50871	1.11	serine palmitoyltransferase, long chain base subunit 2		
216210_x_at	HRIHFB2122	11078	0.04	NM_007032	NP_008963	1.16	Tara-like protein		
216221_s_at	PUM2	23369	5.53e-03	NM_015317	NP_056132	0.94	pumilio homolog 2 (Drosophila)		
216229_x_at	HCG2P7	80867	0.02	X81001	1.07		HLA complex group 2 pseudogene 7		
216241_s_at	TCEA1	6917	0.02	NM_006756	NP_006747	0.87	transcription elongation factor A (SII), 1		
216261_at	ITGB3	3690	0.02	M25108	AAA36121	1.10	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)		
216274_s_at	SEC11L1	23478	0.03	NM_014300	NP_055115	0.96	SEC11-like 1 (S. cerevisiae)		
216304_x_at	YME1L1	10730	0.04	NM_139312	NP_647473	0.93	YME1-like 1 (S. cerevisiae)		
216305_s_at	C2orf3	6936	0.01	NM_003203	NP_003194	0.90	chromosome 2 open reading frame 3		
216306_x_at	PTBP1	5725	0.01	NM_002819	NP_002810	0.92	polypyrimidine tract binding protein 1		
216322_at	CD58	965	1.53e-03	D28586	BAA05922	1.32	CD58 antigen, (lymphocyte function-associated antigen 3)		
216341_s_at	GNRHR	2798	0.01	NM_000406	NP_000397	1.14	gonadotropin-releasing hormone receptor		
216380_x_at	CALN1	83698	0.04	AC005011	0.84		calneuron 1		
216389_s_at	WDR23	80344	4.18e-03	NM_025230	NP_079506	0.83	WD repeat domain 23		
216421_at	RPL27AP	128481	1.96e-03	AL121886	0.75		ribosomal protein L27a pseudogene		
216421_at	C20orf65	149699	1.96e-03	AL121886	0.75		chromosome 20 open reading frame 65		
216421_at	C20orf9	51098	1.96e-03	AL121886	0.75		chromosome 20 open reading frame 9		
216421_at	MYBL2	4605	1.96e-03	AL121886	0.75		v-myb myeloblastosis viral oncogene homolog (avian)-like 2		
216449_x_at	TRA1	7184	0.02	AK025862	0.85		tumor rejection antigen (gp96) 1		
216483_s_at	C19orf10	56005	2.53e-03	NM_019107	NP_061980	0.94	chromosome 19 open reading frame 10		
216515_x_at	PTMA	5757	2.84e-03	NM_002823	NP_002814	0.82	prothymosin, alpha (gene sequence 28)		
216525_x_at	LOC441263	441263	0.04	D38437	0.92		similar to PMS4 homolog mismatch repair protein - human		
216537_s_at	SIGLEC7	27036	0.02	NM_016543	NP_057627	0.91	sialic acid binding Ig-like lectin 7		
216537_s_at	SIGLEC7	27036	0.02	NM_014385	NP_055200	0.91	sialic acid binding Ig-like lectin 7		
216547_at	LOC127406	127406	2.01e-03	XM_497679	XP_497679	0.89	similar to Laminin receptor 1		
216565_x_at	LOC391020	391020	0.01	XM_497663	XP_497663	1.12	similar to Interferon-induced transmembrane protein 3 (Interferon-inducible protein 1-8U)		
216582_at	PRSS16	10279	0.02	AL021808	1.10		protease, serine, 16 (thymus)		
216582_at	POM121L2	94026	0.02	AL021808	1.10		POM121 membrane glycoprotein-like 2 (rat)		
216593_s_at	PIGC	5279	9.35e-03	NM_153747	NP_714969	0.91	phosphatidylinositol glycan, class C		
216602_s_at	FARSLA	2193	1.8e-03	NM_004461	NP_004452	0.81	phenylalanine-tRNA synthetase-like, alpha subunit		
216607_s_at	CYP51A1	1595	0.02	NM_000786	NP_000777	0.88	cytochrome P450, family 51, subfamily A, polypeptide 1		

216640_s_at	TXNDC7	10130	5.97e-03	NM_005742	NP_005733	0.85	thioredoxin domain containing 7 (protein disulfide isomerase)
216689_x_at	ARHGAP1	392	0.04	NM_004308	NP_004299	0.89	Rho GTPase activating protein 1
216713_at	CCM1	889	0.03	NM_194456	NP_919438	0.87	cerebral cavernous malformations 1
216783_at	SDFR1	27020	0.03	AK025552		1.12	stromal cell derived factor receptor 1
216809_at	CYLC1	1538	7.86e-04	Z22780	CAA80457	1.22	cylicin, basic protein of sperm head cytoskeleton 1
216843_x_at	PMS2L8	5386	5.35e-03	U38964		0.91	postmeiotic segregation increased 2-like 8
216902_s_at	RRN3	54700	8.42e-03	NM_018427	NP_060897	0.82	RRN3 RNA polymerase I transcription factor homolog (yeast)
216903_s_at	CBARA1	10367	0.04	NM_006077	NP_006068	0.94	calcium binding atopy-related autoantigen 1
216908_x_at	LOC94431	94431	5.94e-04	NM_145237	NP_660280	0.85	similar to RNA polymerase I transcription factor RRN3
216945_x_at	PASK	23178	0.04	NM_015148	NP_055963	0.87	PAS domain containing serine/threonine kinase
216976_s_at	RYK	6259	0.02	NM_001005861	NP_001005861	0.88	RYK receptor-like tyrosine kinase
216977_x_at	SNRPA1	6627	0.02	NM_003090	NP_003081	0.85	small nuclear ribonucleoprotein polypeptide A'
216988_s_at	PTP4A2	8073	0.03	NM_003479	NP_003470	0.95	protein tyrosine phosphatase type IVA, member 2
216996_s_at	KIAA0971	22868	2.05e-03	NM_014929	NP_055744	0.87	KIAA0971
217016_x_at	LOC389177	389177	0.01	AK026825		1.12	hypothetical LOC389177
217027_x_at	KPNB1	3837	0.01	NM_002265	NP_002256	1.25	karyopherin (importin) beta 1
217045_x_at	NCR2	9436	0.04	AL136967		1.07	natural cytotoxicity triggering receptor 2
217094_s_at	ITCH	83737	0.03	NM_031483	NP_113671	0.88	itchy homolog E3 ubiquitin protein ligase (mouse)
217106_x_at	HSA9761	27292	0.01	NM_014473	NP_055288	0.85	putative dimethyladenosine transferase
217122_s_at	SLC35E2	9906	0.04	NM_182838	NP_878258	0.91	solute carrier family 35, member E2
217122_s_at	SLC35E2	9906	0.04	NM_014854	NP_055669	0.91	solute carrier family 35, member E2
217140_s_at	VDAC1	7416	0.04	NM_003374	NP_003365	0.87	voltage-dependent anion channel 1
217149_x_at	TNK1	8711	0.03	AF097738		0.88	tyrosine kinase, non-receptor, 1
217168_s_at	HERPUD1	9709	0.04	NM_014685	NP_055500	0.95	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
217208_s_at	DLG1	1739	4.38e-03	NM_004087	NP_004078	0.86	discs, large homolog 1 (Drosophila)
217211_at	ACTBP9	69	0.03	D50604		0.92	actin, beta pseudogene 9
217294_s_at	ENO1	2023	0.02	U88968	AAC39935	0.93	enolase 1, (alpha)
217299_s_at	NBS1	4683	1.21e-03	NM_002485	NP_002476	1.14	Nijmegen breakage syndrome 1 (nibrin)
217301_x_at	RBBP4	5928	2.66e-03	NM_005610	NP_005601	0.87	retinoblastoma binding protein 4
217317_s_at	MN7	400322	0.01	AB002391		0.85	D15F37 (pseudogene)
217346_at	PPIAL	170536	0.01	AL021395		0.88	peptidylprolyl isomerase A (cyclophilin A)-like
217356_s_at	PGK1	5230	5.27e-03	NM_000291	NP_000282	0.95	phosphoglycerate kinase 1
217362_x_at	HLA-DRB6	3128	0.01	AF005487		0.70	major histocompatibility complex, class II, DR beta 6 (pseudogene)
217364_x_at	EIF3S1	8669	0.03	NM_003758	NP_003749	0.83	eukaryotic translation initiation factor 3, subunit 1 alpha, 35kDa
217370_x_at	FUS	2521	5.3e-04	NM_004960	NP_004951	0.83	fusion (involved in t(12;16) in malignant liposarcoma)
217408_at	MRPS18B	28973	0.03	NM_014046	NP_054765	0.89	mitochondrial ribosomal protein S18B
217485_x_at	PMS2L1	5379	9.0e-04	D38435	BAA07470	0.90	postmeiotic segregation increased 2-like 1
217491_x_at	COX7C	1350	0.02	NM_001867	NP_001858	0.88	cytochrome c oxidase subunit VIIc
217496_s_at	IDE	3416	0.04	NM_004969	NP_004960	0.88	insulin-degrading enzyme

217499_x_at	OR7E38P	389537	7.47e-03	AW874308		0.91	olfactory receptor, family 7, subfamily E, member 38 pseudogene
217508_s_at	C18orf25	147339	0.02	BX640683	CAE45812	0.86	chromosome 18 open reading frame 25
217527_s_at	NFATC2IP	84901	0.01	NM_032815	NP_116204	0.88	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein
217538_at	RUTBC1	9905	0.03	AK124883	BAC85979	0.85	RUN and TBC1 domain containing 1
217543_s_at	MBTPS1	8720	0.02	NM_003791	NP_003782	1.21	membrane-bound transcription factor protease, site 1
217547_x_at	TIZ	171392	2.61e-03	NM_138330	NP_612203	0.78	TRAF6-inhibitory zinc finger protein
217559_at	RPL10L	140801	0.01	NM_080746	NP_542784	0.82	ribosomal protein L10-like
217691_x_at	SLC16A3	9123	2.68e-04	NM_004207	NP_004198	1.17	solute carrier family 16 (monocarboxylic acid transporters), member 3
217719_at	EIF3S6IP	51386	0.04	NM_016091	NP_057175	0.96	eukaryotic translation initiation factor 3, subunit 6 interacting protein
217724_at	PAI-RBP1	26135	5.16e-03	NM_015640	NP_056455	0.92	PAI-1 mRNA-binding protein
217725_x_at	PAI-RBP1	26135	0.02	NM_015640	NP_056455	0.92	PAI-1 mRNA-binding protein
217726_at	COPZ1	22818	0.04	NM_016057	NP_057141	0.90	coatomer protein complex, subunit zeta 1
217733_s_at	TMSB10	9168	0.02	NM_021103	NP_066926	0.89	thymosin, beta 10
217736_s_at	EIF2AK1	27102	1.01e-03	NM_014413	NP_055228	0.93	eukaryotic translation initiation factor 2-alpha kinase 1
217745_s_at	MAK3	80218	0.03	NM_025146	NP_079422	0.87	Mak3 homolog (S. cerevisiae)
217746_s_at	PDCD6IP	10015	0.02	NM_013374	NP_037506	0.95	programmed cell death 6 interacting protein
217751_at	GSTK1	373156	8.92e-03	NM_015917	NP_057001	0.85	glutathione S-transferase kappa 1
217758_s_at	SMBP	56889	3.1e-03	NM_020123	NP_064508	0.93	SM-11044 binding protein
217759_at	TRIM44	54765	5.3e-03	NM_017583	NP_060053	0.86	tripartite motif-containing 44
217762_s_at	RAB31	11031	2.4e-03	NM_006868	NP_006859	1.12	RAB31, member RAS oncogene family
217763_s_at	RAB31	11031	5.98e-04	NM_006868	NP_006859	1.20	RAB31, member RAS oncogene family
217768_at	C14orf166	51637	0.02	NM_016039	NP_057123	0.94	chromosome 14 open reading frame 166
217772_s_at	MTCH2	23788	3.43e-03	NM_014342	NP_055157	0.89	mitochondrial carrier homolog 2 (C. elegans)
217775_s_at	RDH11	51109	0.02	NM_016026	NP_057110	0.87	retinol dehydrogenase 11 (all-trans and 9-cis)
217776_at	RDH11	51109	0.04	NM_016026	NP_057110	0.88	retinol dehydrogenase 11 (all-trans and 9-cis)
217779_s_at	PNRC2	55629	0.02	NM_017761	NP_060231	0.91	proline-rich nuclear receptor coactivator 2
217781_s_at	ZFP106	64397	0.01	NM_022473	NP_071918	0.89	zinc finger protein 106 homolog (mouse)
217792_at	SNX5	27131	7.79e-03	NM_014426	NP_055241	0.93	sorting nexin 5
217797_at	Ufc1	51506	9.2e-03	NM_016406	NP_057490	0.87	Ufm1-conjugating enzyme 1
217802_s_at	NUCKS	64710	0.02	NM_022731	NP_073568	0.92	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate
217804_s_at	ILF3	3609	0.01	NM_012218	NP_036350	0.87	interleukin enhancer binding factor 3, 90kDa
217805_at	ILF3	3609	5.83e-03	NM_004516	NP_004507	0.83	interleukin enhancer binding factor 3, 90kDa
217806_s_at	POLDIP2	26073	2.26e-03	NM_015584	NP_056399	0.94	polymerase (DNA-directed), delta interacting protein 2
217809_at	BZW2	28969	0.02	NM_014038	NP_054757	0.92	basic leucine zipper and W2 domains 2
217812_at	YTHDF2	51441	0.03	NM_016258	NP_057342	0.93	YTH domain family, member 2
217814_at	GK001	57003	0.01	NM_020198	NP_064583	0.90	GK001 protein
217815_at	SUPT16H	11198	0.04	NM_007192	NP_009123	0.93	suppressor of Ty 16 homolog (S. cerevisiae)
217816_s_at	PCNP	57092	0.01	NM_020357	NP_065090	0.91	PEST-containing nuclear protein
217819_at	GOLGA7	51125	0.03	NM_016099	NP_057183	0.94	golgi autoantigen, golgin subfamily a, 7

217823_s_at	UBE2J1	51465	0.01	NM_016021	NP_057105	0.82	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
217824_at	UBE2J1	51465	0.01	NM_016021	NP_057105	0.77	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
217828_at	FLJ13213	79811	9.2e-03	NM_024755	NP_079031	0.93	hypothetical protein FLJ13213
217832_at	SYNCRIP	10492	0.01	BC032643	AAH32643	0.90	synaptotagmin binding, cytoplasmic RNA interacting protein
217833_at	SYNCRIP	10492	0.03	AL520908		0.92	synaptotagmin binding, cytoplasmic RNA interacting protein
217834_s_at	SYNCRIP	10492	0.02	NM_006372	NP_006363	0.86	synaptotagmin binding, cytoplasmic RNA interacting protein
217839_at	TFG	10342	0.04	NM_006070	NP_006061	0.89	TRK-fused gene
217842_at	LUC7L2	51631	0.01	NM_016019	NP_057103	0.90	LUC7-like 2 (S. cerevisiae)
217843_s_at	MED4	29079	1.39e-03	NM_014166	NP_054885	0.86	mediator of RNA polymerase II transcription, subunit 4 homolog (yeast)
217845_x_at	HIG1	25994	0.03	NM_014056	NP_054775	0.91	likely ortholog of mouse hypoxia induced gene 1
217850_at	GNL3	26354	1.95e-03	NM_014366	NP_055181	0.87	guanine nucleotide binding protein-like 3 (nucleolar)
217852_s_at	ARL10C	55207	1.75e-03	NM_018184	NP_060654	0.95	ADP-ribosylation factor-like 10C
217854_s_at	POLR2E	5434	0.04	NM_002695	NP_002686	0.92	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa
217857_s_at	RBM8A	9939	0.02	NM_005105	NP_005096	0.95	RNA binding motif protein 8A
217858_s_at	ARMCX3	51566	2.26e-03	NM_016607	NP_057691	0.87	armadillo repeat containing, X-linked 3
217860_at	NDUFA10	4705	0.04	NM_004544	NP_004535	0.92	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa
217866_at	FLJ12529	79869	0.02	NM_024811	NP_079087	1.12	pre-mRNA cleavage factor I, 59 kDa subunit
217868_s_at	DREV1	51108	0.02	NM_016025	NP_057109	0.91	DORA reverse strand protein 1
217869_at	HSD17B12	51144	1.57e-03	NM_016142	NP_057226	0.80	hydroxysteroid (17-beta) dehydrogenase 12
217874_at	SUCLG1	8802	0.01	NM_003849	NP_003840	0.92	succinate-CoA ligase, GDP-forming, alpha subunit
217879_at	CDC27	996	0.02	NM_001256	NP_001247	0.91	cell division cycle 27
217881_s_at	CDC27	996	0.03	NM_001256	NP_001247	0.88	cell division cycle 27
217884_at	FLJ10774	55226	2.8e-03	NM_024662	NP_078938	0.87	N-acetyltransferase-like protein
217893_s_at	FLJ12666	79647	0.02	NM_024595	NP_078871	1.13	hypothetical protein FLJ12666
217895_at	FLJ20758	55037	8.42e-03	NM_017952	NP_060422	0.86	FLJ20758 protein
217900_at	FLJ10326	55699	2.16e-03	NM_018060	NP_060530	0.94	mitochondrial isoleucine tRNA synthetase
217902_s_at	HERC2	8924	0.04	NM_004667	NP_004658	0.88	hect domain and RLD 2
217907_at	MRPL18	29074	0.03	NM_014161	NP_054880	0.89	mitochondrial ribosomal protein L18
217914_at	TPCN1	53373	0.01	NM_017901	NP_060371	0.90	two pore segment channel 1
217915_s_at	C15orf15	51187	8.05e-03	NM_016304	NP_057388	0.87	chromosome 15 open reading frame 15
217917_s_at	DNCL2A	83658	0.01	NM_014183	NP_054902	0.93	dynein, cytoplasmic, light polypeptide 2A
217918_at	DNCL2A	83658	0.04	NM_014183	NP_054902	0.96	dynein, cytoplasmic, light polypeptide 2A
217919_s_at	MRPL42	28977	0.01	NM_014050	NP_054769	0.91	mitochondrial ribosomal protein L42
217922_at	MAN1A2	10905	0.01	AL157902		0.90	mannosidase, alpha, class 1A, member 2
217923_at	PEF (peflin)	23578	1.36e-03	NM_012392	NP_036524	0.92	PEF protein with a long N-terminal hydrophobic domain
217924_at	C6orf106	64771	0.01	NM_024294	NP_077270	0.87	chromosome 6 open reading frame 106
217927_at	SPCS1	28972	0.01	NM_014041	NP_054760	0.94	signal peptidase complex subunit 1 homolog (S. cerevisiae)

217930_s_at	TOLLIP	54472	0.01	NM_019009	NP_061882	0.87	toll interacting protein
217932_at	MRPS7	51081	0.03	NM_015971	NP_057055	0.89	mitochondrial ribosomal protein S7
217933_s_at	LAP3	51056	0.03	NM_015907	NP_056991	0.75	leucine aminopeptidase 3
217934_x_at	STUB1	10273	0.04	NM_005861	NP_005852	0.94	STIP1 homology and U-box containing protein 1
217936_at	ARHGAP5	394	0.01	NM_001173	NP_001164	0.86	Rho GTPase activating protein 5
217938_s_at	KCMF1	56888	0.03	NM_020122	NP_064507	0.95	potassium channel modulatory factor 1
217940_s_at	FLJ10769	55739	8.07e-03	NM_018210	NP_060680	0.87	hypothetical protein FLJ10769
217941_s_at	ERBB2IP	55914	0.02	NM_018695	NP_061165	0.91	erbb2 interacting protein
217942_at	MRPS35	60488	0.01	NM_021821	NP_068593	0.90	mitochondrial ribosomal protein S35
217945_at	BTBD1	53339	0.02	NM_025238	NP_079514	0.88	BTB (POZ) domain containing 1
217950_at	NOSIP	51070	0.04	NM_015953	NP_057037	0.88	nitric oxide synthase interacting protein
217951_s_at	PHF3	23469	0.01	NM_015153	NP_055968	0.84	PHD finger protein 3
217956_s_at	MASA	58478	6.65e-03	NM_021204	NP_067027	0.84	E-1 enzyme
217957_at	GTL3	29105	0.02	NM_013242	NP_037374	0.90	likely ortholog of mouse gene trap locus 3
217962_at	NOLA3	55505	0.02	NM_018648	NP_061118	0.94	nucleolar protein family A, member 3 (H/ACA small
nucleolar RNPs)							
217964_at	TTC19	54902	1.01e-03	NM_017775	NP_060245	0.90	tetratricopeptide repeat domain 19
217966_s_at	C1orf24	116496	7.35e-03	NM_022083	NP_071366	1.19	chromosome 1 open reading frame 24
217976_s_at	DNCLI1	51143	0.02	NM_016141	NP_057225	0.87	dynein, cytoplasmic, light intermediate polypeptide 1
217980_s_at	MRPL16	54948	0.01	NM_017840	NP_060310	0.83	mitochondrial ribosomal protein L16
217981_s_at	FXC1	26515	0.03	NM_012192	NP_036324	0.90	fracture callus 1 homolog (rat)
217982_s_at	MORF4L1	10933	0.01	NM_006791	NP_006782	0.92	mortality factor 4 like 1
217985_s_at	BAZ1A	11177	1.57e-03	NM_013448	NP_038476	1.13	bromodomain adjacent to zinc finger domain, 1A
217987_at	NS3TP1	54529	0.02	NM_019048	NP_061921	0.87	HCV NS3-transactivated protein 1
217990_at	GMPR2	51292	4.95e-03	NM_016576	NP_057660	0.91	guanosine monophosphate reductase 2
217993_s_at	MAT2B	27430	0.02	NM_013283	NP_037415	0.93	methionine adenosyltransferase II, beta
217995_at	SQRDL	58472	0.02	NM_021199	NP_067022	0.91	sulfide quinone reductase-like (yeast)
218003_s_at	FKBP3	2287	0.04	NM_002013	NP_002004	0.89	FK506 binding protein 3, 25kDa
218005_at	ZNF22	7570	0.02	NM_006963	NP_008894	0.86	zinc finger protein 22 (KOX 15)
218006_s_at	ZNF22	7570	0.01	NM_006963	NP_008894	0.88	zinc finger protein 22 (KOX 15)
218011_at	UBL5	59286	0.02	NM_024292	NP_077268	0.96	ubiquitin-like 5
218016_s_at	POLR3E	55718	0.02	NM_018119	NP_060589	0.86	polymerase (RNA) III (DNA directed) polypeptide E
(80kD)							
218017_s_at	FLJ32731	138050	2.66e-03	XM_372038	XP_372038	0.93	hypothetical protein FLJ32731
218019_s_at	PDXK	8566	0.01	NM_003681	NP_003672	1.14	pyridoxal (pyridoxine, vitamin B6) kinase
218025_s_at	PECI	10455	0.01	NM_006117	NP_006108	0.88	peroxisomal D3,D2-enoyl-CoA isomerase
218026_at	HSPC009	28958	0.01	BC002698	AAH02698	0.87	HSPC009 protein
218027_at	MRPL15	29088	0.02	NM_014175	NP_054894	0.93	mitochondrial ribosomal protein L15
218030_at	GIT1	28964	0.01	NM_014030	NP_054749	1.15	G protein-coupled receptor kinase interactor 1
218037_at	C2orf17	79137	0.01	NM_024293	NP_077269	0.93	chromosome 2 open reading frame 17
218040_at	FLJ10330	55119	0.04	NM_018061	NP_060531	0.89	sarcoma antigen NY-SAR-27
218041_x_at	SLC38A2	54407	0.02	NM_018976	NP_061849	0.95	solute carrier family 38, member 2
218047_at	OSBPL9	114883	6.85e-03	NM_024586	NP_078862	0.91	oxysterol binding protein-like 9
218049_s_at	MRPL13	28998	0.02	NM_014078	NP_054797	1.14	mitochondrial ribosomal protein L13
218050_at	Ufm1	51569	7.69e-03	NM_016617	NP_057701	0.87	ubiquitin-fold modifier 1

218052_s_at	ATP13A1	57130	1.07e-03	NM_020410	NP_065143	0.92	ATPase type 13A1
218053_at	FNBP3	55660	2.39e-03	XM_371575	XP_371575	0.90	formin binding protein 3
218055_s_at	WDR41	55255	2.42e-03	NM_018268	NP_060738	0.87	WD repeat domain 41
218059_at	LOC51123	51123	8.05e-03	NM_016096	NP_057180	0.92	HSPC038 protein
218067_s_at	FLJ10154	55082	0.02	NM_018011	NP_060481	0.89	hypothetical protein FLJ10154
218073_s_at	FLJ10407	55706	9.08e-03	NM_018087	NP_060557	0.83	hypothetical protein FLJ10407
218079_s_at	ZNF403	79893	7.69e-03	NM_024835	NP_079111	0.94	zinc finger protein 403
218082_s_at	UBP1	7342	0.01	NM_014517	NP_055332	0.88	upstream binding protein 1 (LBP-1a)
218083_at	PTGES2	80142	0.04	NM_025072	NP_079348	0.87	prostaglandin E synthase 2
218084_x_at	FXYD5	53827	0.03	NM_014164	NP_054883	0.92	FXYD domain containing ion transport regulator 5
218085_at	SNF7DC2	51510	8.67e-03	NM_016410	NP_057494	0.82	SNF7 domain containing 2
218090_s_at	WDR11	55717	6.92e-03	NM_018117	NP_060587	0.85	WD repeat domain 11
218091_at	HRB	3267	0.03	NM_004504	NP_004495	0.96	HIV-1 Rev binding protein
218093_s_at	ANKRD10	55608	0.03	NM_017664	NP_060134	0.91	ankyrin repeat domain 10
218094_s_at	C20orf35	55861	0.02	NM_018478	NP_060948	0.87	chromosome 20 open reading frame 35
218095_s_at	TPARL	55858	0.04	NM_018475	NP_060945	0.90	TPA regulated locus
218098_at	ARFGEF2	10564	6.71e-03	NM_006420	NP_006411	0.88	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
218101_s_at	NDUFC2	4718	0.04	NM_004549	NP_004540	0.92	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa
218102_at	DERA	51071	2.39e-03	NM_015954	NP_057038	0.87	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)
218107_at	WDR26	80232	0.01	NM_025160	NP_079436	0.93	WD repeat domain 26
218108_at	C14orf130	55148	0.02	NM_018108	NP_060578	0.92	chromosome 14 open reading frame 130
218109_s_at	MFSD1	64747	5.27e-03	NM_022736	NP_073573	0.93	major facilitator superfamily domain containing 1
218111_s_at	CMAS	55907	3.92e-03	NM_018686	NP_061156	0.85	cytidine monophosphate N-acetylneuraminic acid synthetase
218113_at	TMEM2	23670	0.01	NM_013390	NP_037522	0.90	transmembrane protein 2
218116_at	C9orf78	51759	0.03	NM_016520	NP_057604	0.91	chromosome 9 open reading frame 78
218118_s_at	TIMM23	10431	5.07e-03	NM_006327	NP_006318	0.91	translocase of inner mitochondrial membrane 23 homolog (yeast)
218119_at	TIMM23	10431	1.41e-03	NM_006327	NP_006318	0.92	translocase of inner mitochondrial membrane 23 homolog (yeast)
218122_s_at	SENP2	59343	0.02	NM_021627	NP_067640	0.94	SUMO1/sentrin/SMT3 specific protease 2
218124_at	RetSat	54884	0.02	NM_017750	NP_060220	0.92	all-trans-13,14-dihydroretinol saturase
218126_at	FLJ10579	55177	0.02	NM_018145	NP_060615	0.91	hypothetical protein FLJ10579
218129_s_at	NFYB	4801	0.01	NM_006166	NP_006157	0.91	nuclear transcription factor Y, beta
218140_x_at	SRPRB	58477	8.5e-04	NM_021203	NP_067026	0.89	signal recognition particle receptor, B subunit
218142_s_at	CRBN	51185	3.1e-04	NM_016302	NP_057386	0.84	cereblon
218152_at	HMG20A	10363	0.01	NM_018200	NP_060670	0.88	high-mobility group 20A
218156_s_at	FLJ10534	55720	0.01	NM_018128	NP_060598	0.84	hypothetical protein FLJ10534
218160_at	NDUFA8	4702	0.03	NM_014222	NP_055037	0.87	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa
218163_at	MCTS1	28985	0.04	NM_014060	NP_054779	0.86	malignant T cell amplified sequence 1
218165_at	FLJ11730	64769	0.02	NM_022756	NP_073593	0.89	sarcoma antigen NY-SAR-91

218167_at	LOC51321	51321	0.04	NM_016627	NP_057711	0.91	hypothetical protein LOC51321
218172_s_at	DERL1	79139	3.37e-03	NM_024295	NP_077271	0.83	Der1-like domain family, member 1
218177_at	CHMP1.5	57132	0.04	NM_020412	NP_065145	1.14	CHMP1.5 protein
218179_s_at	FLJ12716	60684	0.04	NM_021942	NP_068761	0.95	FLJ12716 protein
218185_s_at	ARMC1	55156	0.01	NM_018120	NP_060590	0.85	armadillo repeat containing 1
218188_s_at	TIMM13	26517	3.1e-03	NM_012458	NP_036590	0.84	translocase of inner mitochondrial membrane 13
homolog (yeast)							
218190_s_at	HSPC051	29796	0.03	NM_013387	NP_037519	0.96	ubiquinol-cytochrome c reductase complex (7.2 kD)
218193_s_at	GOLT1B	51026	0.04	NM_016072	NP_057156	0.87	golgi transport 1 homolog B (S. cerevisiae)
218194_at	DKFZP566E144	25996	0.02	NM_015523	NP_056338	0.90	small fragment nuclease
218197_s_at	OXR1	55074	0.03	AL833193	CAI46186	0.91	oxidation resistance 1
218203_at	ALG5	29880	0.01	NM_013338	NP_037470	0.91	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-
phosphate beta-glucosyltransferase)							
218206_x_at	SCAND1	51282	0.01	NM_016558	NP_057642	0.87	SCAN domain containing 1
218213_s_at	C11orf10	746	0.03	NM_014206	NP_055021	0.96	chromosome 11 open reading frame 10
218214_at	FLJ11773	60673	0.01	NM_021934	NP_068753	0.83	hypothetical protein FLJ11773
218217_at	SCPEP1	59342	0.02	NM_021626	NP_067639	0.91	serine carboxypeptidase 1
218220_at	C12orf10	60314	7.69e-03	NM_021640	NP_067653	0.91	chromosome 12 open reading frame 10
218224_at	PNMA1	9240	3.26e-03	NM_006029	NP_006020	0.84	paraneoplastic antigen MA1
218225_at	SITPEC	51295	0.03	NM_016581	NP_057665	0.89	likely ortholog of mouse signaling intermediate in Toll
pathway-evolutionarily conserved							
218226_s_at	NDUFB4	4710	4.82e-03	NM_004547	NP_004538	0.95	NADH dehydrogenase (ubiquinone) 1 beta
subcomplex, 4, 15kDa							
218228_s_at	TNKS2	80351	0.01	NM_025235	NP_079511	0.91	tankyrase, TRF1-interacting ankyrin-related ADP-ribose
polymerase 2							
218229_s_at	POGK	57645	0.01	NM_017542	NP_060012	0.93	pogo transposable element with KRAB domain
218233_s_at	C6orf49	29964	0.01	NM_013397	NP_037529	0.89	chromosome 6 open reading frame 49
218239_s_at	GTPBP4	23560	0.01	NM_012341	NP_036473	0.88	GTP binding protein 4
218241_at	GOLGA5	9950	0.03	NM_005113	NP_005104	0.94	golgi autoantigen, golgin subfamily a, 5
218243_at	RUFY1	80230	0.03	NM_025158	NP_079434	0.95	RUN and FYVE domain containing 1
218244_at	NOL8	55035	0.01	NM_017948	NP_060418	0.83	nucleolar protein 8
218247_s_at	RKHD2	51320	5.57e-03	NM_016626	NP_057710	0.83	ring finger and KH domain containing 2
218249_at	ZDHHC6	64429	6.95e-03	NM_022494	NP_071939	0.94	zinc finger, DHHC domain containing 6
218250_s_at	CNOT7	29883	0.01	NM_013354	NP_037486	0.94	CCR4-NOT transcription complex, subunit 7
218253_s_at	LGTN	1939	0.01	NM_006893	NP_008824	0.88	ligatin
218258_at	POLR1D	51082	9.61e-03	NM_015972	NP_057056	0.84	polymerase (RNA) I polypeptide D, 16kDa
218262_at	FLJ22318	64777	0.04	NM_022762	NP_073599	0.94	hypothetical protein FLJ22318
218263_s_at	LOC58486	58486	0.01	NM_021211	NP_067034	0.93	transposon-derived Buster1 transposase-like protein
gene							
218264_at	BCCIP	56647	0.03	NM_016567	NP_057651	0.78	BRCA2 and CDKN1A interacting protein
218265_at	SECISBP2	79048	0.03	NM_024077	NP_076982	0.91	SECIS binding protein 2
218269_at	RNASE3L	29102	6.71e-03	NM_013235	NP_037367	0.89	nuclear RNase III Drosha
218271_s_at	PSARL	55486	7.1e-04	NM_018622	NP_061092	0.90	presenilin associated, rhomboid-like
218273_s_at	PPM2C	54704	0.04	NM_018444	NP_060914	0.89	protein phosphatase 2C, magnesium-dependent, catalytic
subunit							

218281_at	MRPL48	51642	0.02	NM_016055	NP_057139	0.89	mitochondrial ribosomal protein L48
218283_at	SS18L2	51188	0.03	NM_016305	NP_057389	0.90	synovial sarcoma translocation gene on chromosome 18-like 2
218285_s_at	DHRS6	56898	2.09e-03	NM_020139	NP_064524	0.83	dehydrogenase/reductase (SDR family) member 6
218286_s_at	RNF7	9616	4.8e-03	NM_014245	NP_055060	0.91	ring finger protein 7
218287_s_at	EIF2C1	26523	0.01	NM_012199	NP_036331	0.96	eukaryotic translation initiation factor 2C, 1
218289_s_at	UBE1DC1	79876	7.89e-03	NM_024818	NP_079094	0.85	ubiquitin-activating enzyme E1-domain containing 1
218290_at	PLEKHJ1	55111	0.03	NM_018049	NP_060519	0.93	pleckstrin homology domain containing, family J member 1
218291_at	MAPBPIP	28956	0.03	NM_014017	NP_054736	0.95	mitogen-activated protein-binding protein-interacting protein
218297_at	C10orf97	80013	0.01	NM_024948	NP_079224	0.82	chromosome 10 open reading frame 97
218301_at	RNPEPL1	57140	0.03	NM_018226	NP_060696	1.06	arginyl aminopeptidase (aminopeptidase B)-like 1
218306_s_at	HERC1	8925	0.03	NM_003922	NP_003913	0.90	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1
218311_at	MAP4K3	8491	8.97e-03	NM_003618	NP_003609	0.83	mitogen-activated protein kinase kinase kinase kinase 3
218316_at	TIMM9	26520	6.31e-03	NM_012460	NP_036592	0.89	translocase of inner mitochondrial membrane 9 homolog (yeast)
218318_s_at	NLK	51701	0.04	NM_016231	NP_057315	0.90	nemo like kinase
218331_s_at	C10orf18	54906	6.11e-03	AK095469		0.88	chromosome 10 open reading frame 18
218333_at	DERL2	51009	8.67e-03	NM_016041	NP_057125	0.95	Der1-like domain family, member 2
218334_at	NIF3L1BP1	80145	0.01	NM_025075	NP_079351	0.89	Ngg1 interacting factor 3 like 1 binding protein 1
218336_at	PFDN2	5202	0.01	NM_012394	NP_036526	0.88	prefoldin 2
218343_s_at	GTF3C3	9330	0.01	NM_012086	NP_036218	0.92	general transcription factor IIIC, polypeptide 3, 102kDa
218344_s_at	RCOR3	55758	2.4e-03	NM_018254	NP_060724	0.90	REST corepressor 3
218346_s_at	SESN1	27244	3.98e-03	NM_014454	NP_055269	0.84	sestrin 1
218348_s_at	ZC3HDC7	29066	7.26e-03	NM_014153	NP_054872	0.93	zinc finger CCCH type domain containing 7
218350_s_at	GMNN	51053	0.04	NM_015895	NP_056979	0.86	geminin, DNA replication inhibitor
218351_at	COMMD8	54951	5.01e-03	NM_017845	NP_060315	0.87	COMM domain containing 8
218352_at	RCBTB1	55213	0.01	NM_018191	NP_060661	0.89	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1
218362_s_at	KIAA1008	22894	0.04	NM_014953	NP_055768	0.89	KIAA1008
218366_x_at	FLJ20859	64745	6.11e-03	NM_022734	NP_073571	0.80	FLJ20859 gene
218370_s_at	FLJ12903	64766	8.5e-04	NM_022753	NP_073590	0.91	hypothetical protein FLJ12903
218372_at	MED9	55090	3.56e-04	NM_018019	NP_060489	0.84	mediator of RNA polymerase II transcription, subunit 9 homolog (yeast)
218379_at	RBM7	10179	0.01	NM_016090	NP_057174	0.88	RNA binding motif protein 7
218386_x_at	USP16	10600	1.75e-03	NM_006447	NP_006438	0.94	ubiquitin specific protease 16
218388_at	PGLS	25796	0.01	NM_012088	NP_036220	0.94	6-phosphogluconolactonase
218391_at	EAP30	11267	2.07e-03	NM_007241	NP_009172	0.93	EAP30 subunit of ELL complex
218392_x_at	SFXN1	94081	0.03	NM_022754	NP_073591	0.84	sideroflexin 1
218393_s_at	SMU1	55234	0.03	NM_018225	NP_060695	0.87	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)
218395_at	ACTR6	64431	0.01	NM_022496	NP_071941	0.83	ARP6 actin-related protein 6 homolog (yeast)
218396_at	VPS13C	54832	0.03	NM_017684	NP_060154	0.87	vacuolar protein sorting 13C (yeast)

218398_at	MRPS30	10884	0.02	NM_016640	NP_057724	0.91	mitochondrial ribosomal protein S30
218401_s_at	ZNF281	23528	0.04	NM_012482	NP_036614	0.86	zinc finger protein 281
218403_at	HSPC132	51499	0.02	NM_016399	NP_057483	0.91	hypothetical protein HSPC132
218408_at	TIMM10	26519	1.27e-03	NM_012456	NP_036588	0.77	translocase of inner mitochondrial membrane 10
homolog (yeast)							
218422_s_at	C13orf10	64062	0.01	NM_022118	NP_071401	0.89	chromosome 13 open reading frame 10
218423_x_at	VPS54	51542	6.12e-06	NM_016516	NP_057600	0.92	vacuolar protein sorting 54 (yeast)
218426_s_at	TRIAD3	54476	0.01	NM_019011	NP_061884	1.08	TRIAD3 protein
218437_s_at	LZTFL1	54585	0.02	NM_020347	NP_065080	0.85	leucine zipper transcription factor-like 1
218440_at	MCCC1	56922	3.26e-03	NM_020166	NP_064551	0.88	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)
218446_s_at	FAM18B	51030	3.98e-03	NM_016078	NP_057162	0.84	family with sequence similarity 18, member B
218447_at	DC13	56942	0.03	NM_020188	NP_064573	0.90	DC13 protein
218452_at	SMARCAL1	50485	0.02	NM_014140	NP_054859	0.85	SWI/SNF related, matrix associated, actin dependent
regulator of chromatin, subfamily a-like 1							
218459_at	TOR3A	64222	0.02	NM_022371	NP_071766	0.87	torsin family 3, member A
218462_at	RPF1	80135	5.25e-04	NM_025065	NP_079341	0.94	RNA processing factor 1
218467_at	TNFSF5IP1	56984	0.03	NM_020232	NP_064617	0.89	tumor necrosis factor superfamily, member 5-induced
protein 1							
218471_s_at	BBS1	582	9.91e-03	NM_024649	NP_078925	0.94	Bardet-Biedl syndrome 1
218472_s_at	PELO	53918	1.71e-03	NM_015946	NP_057030	0.84	pelota homolog (Drosophila)
218478_s_at	ZCCHC8	55596	0.03	NM_017612	NP_060082	0.92	zinc finger, CCHC domain containing 8
218482_at	e(y)2	56943	0.03	NM_020189	NP_064574	0.94	e(y)2 protein
218490_s_at	ZNF302	55900	0.02	NM_018443	NP_060913	0.85	zinc finger protein 302
218491_s_at	THY28	29087	0.02	NM_014174	NP_054893	0.93	thymocyte protein thy28
218492_s_at	THAP7	80764	0.04	NM_030573	NP_085050	0.94	THAP domain containing 7
218495_at	UXT	8409	0.02	NM_004182	NP_004173	0.92	ubiquitously-expressed transcript
218497_s_at	RNASEH1	246243	0.02	NM_002936	NP_002927	0.91	ribonuclease H1
218511_s_at	PNPO	55163	0.02	NM_018129	NP_060599	0.91	pyridoxine 5'-phosphate oxidase
218512_at	WDR12	55759	4.38e-03	NM_018256	NP_060726	0.89	WD repeat domain 12
218514_at	FLJ10587	55181	9.63e-03	NM_018149	NP_060619	0.94	hypothetical protein FLJ10587
218515_at	C21orf66	94104	0.03	NM_016631	NP_057715	0.90	chromosome 21 open reading frame 66
218517_at	PHF17	79960	0.01	NM_024900	NP_079176	0.91	PHD finger protein 17
218522_s_at	BPY2IP1	55201	9.33e-03	NM_018174	NP_060644	1.14	BPY2 interacting protein 1
218524_at	E4F1	1877	0.03	NM_004424	NP_004415	0.90	E4F transcription factor 1
218526_s_at	RANGNRF	29098	0.03	NM_016492	NP_057576	0.87	RAN guanine nucleotide release factor
218528_s_at	RNF38	152006	0.02	NM_022781	NP_073618	0.93	ring finger protein 38
218534_s_at	AGGF1	55109	8.57e-03	NM_018046	NP_060516	0.93	angiogenic factor with G patch and FHA domains 1
218538_s_at	MRS2L	57380	7.02e-03	NM_020662	NP_065713	0.89	MRS2-like, magnesium homeostasis factor (S.
cerevisiae)							
218545_at	FLJ11088	55297	0.01	NM_018318	NP_060788	0.87	GGA binding partner
218549_s_at	CGI-90	51115	7.12e-04	NM_016033	NP_057117	0.90	CGI-90 protein
218552_at	ECHDC2	55268	6.4e-03	NM_018281	NP_060751	0.82	enoyl Coenzyme A hydratase domain containing 2
218555_at	ANAPC2	29882	0.01	NM_013366	NP_037498	0.86	anaphase promoting complex subunit 2
218556_at	ORMDL2	29095	0.01	NM_014182	NP_054901	0.96	ORM1-like 2 (S. cerevisiae)
218557_at	NIT2	56954	0.02	NM_020202	NP_064587	0.88	nitrilase family, member 2

218558_s_at	MRPL39	54148	0.04	NM_017446	NP_059142	0.86	mitochondrial ribosomal protein L39
218563_at	NDUFA3	4696	0.03	NM_004542	NP_004533	0.90	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa
218564_at	RFWD3	55159	0.01	BC002574	AAH02574	1.11	ring finger and WD repeat domain 3
218568_at	MULK	55750	0.04	NM_018238	NP_060708	0.90	multiple substrate lipid kinase
218570_at	KBTBD4	55709	0.02	NM_018095	NP_060565	0.90	kelch repeat and BTB (POZ) domain containing 4
218571_s_at	C14orf123	29082	5.48e-03	NM_014169	NP_054888	0.81	chromosome 14 open reading frame 123
218573_at	MAGEH1	28986	7.8e-03	NM_014061	NP_054780	1.15	melanoma antigen family H, 1
218577_at	FLJ20331	55631	8.21e-03	NM_017768	NP_060238	0.85	hypothetical protein FLJ20331
218582_at	MARCH5	54708	0.01	NM_017824	NP_060294	0.93	membrane-associated ring finger (C3HC4) 5
218583_s_at	RP42	54165	0.04	NM_020640	NP_065691	0.96	RP42 homolog
218588_s_at	C5orf3	10827	1.22e-03	NM_018691	NP_061161	0.90	chromosome 5 open reading frame 3
218589_at	P2RY5	10161	3.66e-03	NM_005767	NP_005758	0.82	purinergic receptor P2Y, G-protein coupled, 5
218593_at	RBM28	55131	5.48e-03	NM_018077	NP_060547	0.89	RNA binding motif protein 28
218594_at	FLJ10359	55127	8.69e-03	XM_375853	XP_375853	0.91	protein BAP28
218595_s_at	FLJ10359	55127	1.99e-04	XM_375853	XP_375853	0.81	protein BAP28
218597_s_at	C10orf70	55847	9.52e-03	NM_018464	NP_060934	0.92	chromosome 10 open reading frame 70
218598_at	RINT-1	60561	0.03	NM_021930	NP_068749	0.91	Rad50-interacting protein 1
218599_at	REC8L1	9985	0.03	NM_005132	NP_005123	0.88	REC8-like 1 (yeast)
218611_at	IER5	51278	0.01	NM_016545	NP_057629	0.89	immediate early response 5
218617_at	TRIT1	54802	0.02	NM_017646	NP_060116	0.90	tRNA isopentenyltransferase 1
218618_s_at	FNDC3B	64778	0.02	NM_022763	NP_073600	1.21	fibronectin type III domain containing 3B
218622_at	NUP37	79023	0.03	NM_024057	NP_076962	0.90	nucleoporin 37kDa
218628_at	CGI-116	51019	0.01	NM_016053	NP_057137	0.89	CGI-116 protein
218633_x_at	ABHD10	55347	4.68e-03	NM_018394	NP_060864	0.85	abhydrolase domain containing 10
218642_s_at	CHCHD7	79145	9.17e-03	NM_024300	NP_077276	0.88	coiled-coil-helix-coiled-coil-helix domain containing 7
218643_s_at	CRIPT	9419	0.04	NM_014171	NP_054890	1.10	postsynaptic protein CRIPT
218645_at	ZNF277	11179	8.37e-03	NM_021994	NP_068834	0.84	zinc finger protein (C2H2 type) 277
218646_at	FLJ20534	54969	0.02	NM_017867	NP_060337	0.93	hypothetical protein FLJ20534
218648_at	TORC3	64784	0.01	NM_022769	NP_073606	0.92	transducer of regulated cAMP response element-binding protein (CREB) 3
218667_at	PJA1	64219	9.56e-03	NM_022368	NP_071763	0.87	praja 1
218669_at	RAP2C	57826	0.01	NM_021183	NP_067006	0.89	RAP2C, member of RAS oncogene family
218682_s_at	SLC4A1AP	22950	0.04	NM_018158	NP_060628	0.94	solute carrier family 4 (anion exchanger), member 1, adaptor protein
218683_at	PTBP2	58155	0.02	NM_021190	NP_067013	0.86	polypyrimidine tract binding protein 2
218698_at	MMRP19	51074	0.02	NM_015957	NP_057041	0.86	likely ortholog of mouse monocyte macrophage 19
218699_at	RAB7L1	8934	0.01	NM_003929	NP_003920	0.90	RAB7, member RAS oncogene family-like 1
218708_at	NXT1	29107	0.01	NM_013248	NP_037380	0.86	NTF2-like export factor 1
218713_at	NARG2	79664	0.01	NM_024611	NP_078887	0.86	NMDA receptor regulated 2
218722_s_at	FLJ12436	79714	5.3e-04	NM_024661	NP_078937	0.82	hypothetical protein FLJ12436
218723_s_at	RGC32	28984	0.04	NM_014059	NP_054778	0.86	response gene to complement 32
218732_at	Bit1	51651	0.01	NM_016077	NP_057161	0.95	Bcl-2 inhibitor of transcription
218733_at	RNF184	55167	0.03	NM_018133	NP_060603	0.94	ring finger protein 184

218734_at	FLJ13848	79829	0.04	NM_024771	NP_079047	0.91	hypothetical protein FLJ13848
218738_s_at	RNF138	51444	3.79e-03	NM_016271	NP_057355	0.88	ring finger protein 138
218740_s_at	CDK5RAP3	80279	0.02	NM_025197	NP_079473	0.90	CDK5 regulatory subunit associated protein 3
218751_s_at	FBXW7	55294	0.03	NM_018315	NP_060785	0.86	F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila)
218754_at	FLJ23323	79707	0.03	NM_024654	NP_078930	0.91	hypothetical protein FLJ23323
218757_s_at	UPF3B	65109	0.01	NM_023010	NP_075386	0.93	UPF3 regulator of nonsense transcripts homolog B (yeast)
218761_at	RNF111	54778	0.04	NM_017610	NP_060080	0.94	ring finger protein 111
218763_at	STX18	53407	0.01	NM_016930	NP_058626	0.85	syntaxin 18
218764_at	PRKCH	5583	0.03	NM_006255	NP_006246	0.89	protein kinase C, eta
218768_at	NUP107	57122	5.57e-03	NM_020401	NP_065134	0.87	nucleoporin 107kDa
218769_s_at	ANKRA2	57763	0.01	NM_023039	NP_075526	0.86	ankyrin repeat, family A (RFXANK-like), 2
218793_s_at	SCML1	6322	0.01	NM_006746	NP_006737	0.84	sex comb on midleg-like 1 (Drosophila)
218795_at	ACP6	51205	6.24e-03	NM_016361	NP_057445	0.90	acid phosphatase 6, lysophosphatidic
218799_at	FLJ10349	54707	0.04	NM_018066	NP_060536	0.87	hypothetical protein FLJ10349
218802_at	FLJ20647	55013	2.72e-03	NM_017918	NP_060388	0.93	hypothetical protein FLJ20647
218805_at	GIMAP5	55340	8.42e-03	NM_018384	NP_060854	0.88	GTPase, IMAP family member 5
218809_at	PANK2	80025	0.01	NM_024960	NP_079236	0.94	pantothenate kinase 2 (Hallervorden-Spatz syndrome)
218817_at	SPCS3	60559	0.01	NM_021928	NP_068747	0.84	signal peptidase complex subunit 3 homolog (S. cerevisiae)
218823_s_at	KCTD9	54793	0.02	NM_017634	NP_060104	0.91	potassium channel tetramerisation domain containing 9
218827_s_at	Cep192	55125	9.3e-03	NM_018069	NP_060539	0.89	centrosomal protein 192 kDa
218830_at	RPL26L1	51121	6.41e-03	NM_016093	NP_057177	0.88	ribosomal protein L26-like 1
218836_at	RPP21	79897	0.03	NM_024839	NP_079115	0.88	ribonuclease P 21kDa subunit
218842_at	FLJ21908	79657	4.27e-04	NM_024604	NP_078880	0.84	hypothetical protein FLJ21908
218846_at	CRSP3	9439	9.33e-03	NM_004830	NP_004821	0.93	cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa
218850_s_at	LIMD1	8994	0.04	NM_014240	NP_055055	0.92	LIM domains containing 1
218854_at	SART2	29940	0.02	NM_013352	NP_037484	0.91	squamous cell carcinoma antigen recognized by T cells 2
218867_s_at	FLJ21415	79794	0.01	NM_024738	NP_079014	1.06	hypothetical protein FLJ21415
218870_at	ARHGAP15	55843	0.03	NM_018460	NP_060930	0.91	Rho GTPase activating protein 15
218873_at	FLJ20203	54856	2.11e-03	AB046826	BAB13432	0.90	hypothetical protein FLJ20203
218875_s_at	FBXO5	26271	9.77e-03	NM_012177	NP_036309	0.80	F-box protein 5
218877_s_at	C6orf75	60487	0.01	NM_021820	NP_068592	0.80	chromosome 6 open reading frame 75
218881_s_at	FOSL2	2355	5.89e-03	NM_005253	NP_005244	1.15	FOS-like antigen 2
218889_at	C10orf117	64318	0.01	NM_022451	NP_071896	0.86	chromosome 10 open reading frame 117
218904_s_at	C9orf40	55071	0.02	NM_017998	NP_060468	0.86	chromosome 9 open reading frame 40
218909_at	RPS6KC1	26750	6.39e-03	NM_012424	NP_036556	0.86	ribosomal protein S6 kinase, 52kDa, polypeptide 1
218917_s_at	ARID1A	8289	5.11e-03	NM_018450	NP_060920	0.95	AT rich interactive domain 1A (SWI- like)
218918_at	MAN1C1	57134	0.02	NM_020379	NP_065112	0.88	mannosidase, alpha, class 1C, member 1
218919_at	FLJ14007	79752	2.91e-03	NM_024699	NP_078975	0.86	hypothetical protein FLJ14007
218923_at	CTBS	1486	0.04	BC024007	AAH24007	1.07	chitobiase, di-N-acetyl-
218927_s_at	CHST12	55501	0.01	NM_018641	NP_061111	0.82	carbohydrate (chondroitin 4) sulfotransferase 12
218929_at	CARF	55602	4.38e-03	NM_017632	NP_060102	0.89	collaborates/cooperates with ARF (alternate reading frame) protein
218932_at	FLJ20729	54680	0.01	NM_017953	NP_060423	0.87	hypothetical protein FLJ20729

218941_at	FBXW2	26190	7.69e-03	NM_012164	NP_036296	0.94	F-box and WD-40 domain protein 2
218955_at	BRF2	55290	9.33e-03	NM_018310	NP_060780	1.07	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like
218962_s_at	FLJ13576	64418	0.01	NM_022484	NP_071929	0.94	hypothetical protein FLJ13576
218967_s_at	PTER	9317	0.01	NM_030664	NP_109589	0.90	phosphotriesterase related
218968_s_at	ZFP64	55734	0.04	NM_018197	NP_060667	0.88	zinc finger protein 64 homolog (mouse)
218970_s_at	CUTC	51076	0.01	NM_015960	NP_057044	0.95	cutC copper transporter homolog (E.coli)
218972_at	TTC17	55761	6.34e-04	NM_018259	NP_060729	0.90	tetratricopeptide repeat domain 17
218973_at	EFTUD1	79631	0.01	NM_024580	NP_078856	0.90	elongation factor Tu GTP binding domain containing 1
218982_s_at	MRPS17	51373	0.01	NM_015969	NP_057053	0.87	mitochondrial ribosomal protein S17
218986_s_at	FLJ20035	55601	4.31e-03	NM_017631	NP_060101	0.59	hypothetical protein FLJ20035
218989_x_at	SLC30A5	64924	0.02	NM_022902	NP_075053	0.88	solute carrier family 30 (zinc transporter), member 5
218993_at	RNMTL1	55178	0.03	NM_018146	NP_060616	0.87	RNA methyltransferase like 1
218998_at	FLJ20457	54942	0.01	NM_017832	NP_060302	0.89	hypothetical protein FLJ20457
218999_at	FLJ11000	55281	0.01	NM_018295	NP_060765	1.17	hypothetical protein FLJ11000
219001_s_at	WDR32	79269	0.04	NM_024345	NP_077321	1.12	WD repeat domain 32
219002_at	FLJ21901	79675	0.03	NM_024622	NP_078898	0.88	hypothetical protein FLJ21901
219006_at	C6orf66	29078	0.04	NM_014165	NP_054884	0.85	chromosome 6 open reading frame 66
219007_at	NUP43	348995	0.01	NM_024647	NP_078923	0.89	nucleoporin 43kDa
219008_at	FLJ21820	60526	0.03	NM_021925	NP_068744	0.90	hypothetical protein FLJ21820
219009_at	C14orf93	60686	0.02	NM_021944	NP_068763	0.91	chromosome 14 open reading frame 93
219012_s_at	C11orf30	56946	0.03	NM_020193	NP_064578	1.12	chromosome 11 open reading frame 30
219014_at	PLAC8	51316	4.47e-04	NM_016619	NP_057703	0.91	placenta-specific 8
219015_s_at	GLT28D1	55849	0.02	NM_018466	NP_060936	0.93	glycosyltransferase 28 domain containing 1
219022_at	FLJ12448	64897	0.01	NM_022895	NP_075046	0.90	hypothetical protein FLJ12448
219023_at	C4orf16	55435	0.03	NM_018569	NP_061039	0.92	chromosome 4 open reading frame 16
219024_at	PLEKHA1	59338	0.03	NM_021622	NP_067635	0.85	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1
219030_at	CGI-121	51002	0.04	NM_016058	NP_057142	0.92	CGI-121 protein
219033_at	PARP8	79668	0.03	NM_024615	NP_078891	0.91	poly (ADP-ribose) polymerase family, member 8
219035_s_at	RNF34	80196	2.26e-03	NM_025126	NP_079402	0.94	ring finger protein 34
219043_s_at	PDCL3	79031	0.01	NM_024065	NP_076970	0.91	phosducin-like 3
219045_at	RHOF	54509	0.01	NM_019034	NP_061907	0.87	ras homolog gene family, member F (in filopodia)
219055_at	FLJ10379	55133	0.02	NM_018079	NP_060549	0.86	hypothetical protein FLJ10379
219063_at	C1orf35	79169	9.66e-03	NM_024319	NP_077295	0.87	chromosome 1 open reading frame 35
219067_s_at	C10orf86	54780	0.02	NM_017615	NP_060085	0.90	chromosome 10 open reading frame 86
219081_at	ANKHD1	54882	5.83e-03	NM_024668	NP_078944	0.89	ankyrin repeat and KH domain containing 1
219086_at	C14orf131	55778	0.03	NM_018335	NP_060805	1.10	chromosome 14 open reading frame 131
219093_at	FLJ20701	55022	1.27e-03	NM_017933	NP_060403	0.71	hypothetical protein FLJ20701
219099_at	C12orf5	57103	3.65e-03	NM_020375	NP_065108	0.92	chromosome 12 open reading frame 5
219100_at	OBFC1	79991	0.02	NM_024928	NP_079204	0.90	oligonucleotide/oligosaccharide-binding fold containing 1
219109_at	SPAG16	79582	0.02	NM_024532	NP_078808	0.86	sperm associated antigen 16
219111_s_at	DDX54	79039	0.01	NM_024072	NP_076977	0.91	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54
219112_at	RAPGEF6	51735	0.04	NM_016340	NP_057424	0.89	Rap guanine nucleotide exchange factor (GEF) 6
219117_s_at	FKBP11	51303	0.02	NM_016594	NP_057678	0.87	FK506 binding protein 11, 19 kDa

219118_at	FKBP11	51303	8.8e-03	NM_016594	NP_057678	0.83	FK506 binding protein 11, 19 kDa
219119_at	LSM8	51691	2.46e-03	NM_016200	NP_057284	0.91	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)
219122_s_at	ICF45	54974	0.03	NM_017872	NP_060342	0.89	interphase cyctoplasmic foci protein 45
219123_at	ZNF232	7775	0.02	NM_014519	NP_055334	0.87	zinc finger protein 232
219126_at	PHF10	55274	0.02	NM_018288	NP_060758	0.92	PHD finger protein 10
219137_s_at	C2orf33	56947	0.04	NM_020194	NP_064579	0.90	chromosome 2 open reading frame 33
219147_s_at	C9orf95	54981	7.69e-03	NM_017881	NP_060351	0.88	chromosome 9 open reading frame 95
219151_s_at	RABL2B	11158	0.01	NM_007081	NP_009012	0.84	RAB, member of RAS oncogene family-like 2B
219156_at	SYNJ2BP	55333	0.04	NM_018373	NP_060843	0.88	synaptojanin 2 binding protein
219161_s_at	CKLF	51192	0.02	NM_016951	NP_058647	0.91	chemokine-like factor
219166_at	C14orf104	55172	0.03	NM_018139	NP_060609	0.84	chromosome 14 open reading frame 104
219169_s_at	TFB1M	51106	0.02	NM_016020	NP_057104	0.91	transcription factor B1, mitochondrial
219178_at	QTRTD1	79691	0.02	NM_024638	NP_078914	0.90	queuine tRNA-ribosyltransferase domain containing 1
219185_at	SIRT5	23408	0.01	NM_012241	NP_036373	0.90	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)
219189_at	FBXL6	26233	8.91e-03	NM_024555	NP_078831	0.90	F-box and leucine-rich repeat protein 6
219192_at	UBAP2	55833	0.02	NM_018449	NP_060919	0.87	ubiquitin associated protein 2
219200_at	MGC5297	79072	9.61e-03	NM_024091	NP_076996	0.87	hypothetical protein MGC5297
219202_at	RHBDL6	79651	0.02	NM_024599	NP_078875	0.83	rhomboid, veinlet-like 6 (Drosophila)
219209_at	IFIH1	64135	0.01	NM_022168	NP_071451	0.70	interferon induced with helicase C domain 1
219212_at	HSPA14	51182	9.33e-03	NM_016299	NP_057383	0.87	heat shock 70kDa protein 14
219216_at	ETAA16	54465	0.02	NM_019002	NP_061875	0.90	ETAA16 protein
219220_x_at	MRPS22	56945	0.01	NM_020191	NP_064576	0.95	mitochondrial ribosomal protein S22
219227_at	FLJ14166	79616	0.03	NM_024565	NP_078841	1.16	hypothetical protein FLJ14166
219235_s_at	PHACTR4	65979	0.03	NM_023923	NP_076412	0.90	phosphatase and actin regulator 4
219236_at	PAQR6	79957	0.03	NM_024897	NP_079173	0.87	progestin and adipoQ receptor family member VI
219243_at	GIMAP4	55303	2.01e-03	NM_018326	NP_060796	0.93	GTPase, IMAP family member 4
219244_s_at	MRPL46	26589	1.02e-03	NM_022163	NP_071446	0.87	mitochondrial ribosomal protein L46
219246_s_at	FLJ13491	79676	2.22e-03	NM_024623	NP_078899	0.84	hypothetical protein FLJ13491
219256_s_at	SH3TC1	54436	0.04	NM_018986	NP_061859	0.87	SH3 domain and tetratricopeptide repeats 1
219259_at	SEMA4A	64218	0.02	NM_022367	NP_071762	0.88	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A
219260_s_at	DERP6	23587	8.68e-03	NM_015362	NP_056177	0.85	S-phase 2 protein
219266_at	ZNF350	59348	0.04	NM_021632	NP_067645	0.88	zinc finger protein 350
219275_at	PDCD5	9141	8.05e-03	NM_004708	NP_004699	0.83	programmed cell death 5
219276_x_at	C9orf82	79886	0.01	NM_024828	NP_079104	0.89	chromosome 9 open reading frame 82
219279_at	DOCK10	55619	9.2e-03	AK000227	BAA91022	0.83	dedicator of cytokinesis 10
219281_at	MSRA	4482	0.03	NM_012331	NP_036463	1.12	methionine sulfoxide reductase A
219282_s_at	TRPV2	51393	0.03	NM_016113	NP_057197	0.93	transient receptor potential cation channel, subfamily V, member 2
219289_at	FLJ20718	55027	4.82e-04	NM_017939	NP_060409	0.87	hypothetical protein FLJ20718
219290_x_at	DAPP1	27071	0.01	NM_014395	NP_055210	1.08	dual adaptor of phosphotyrosine and 3-phosphoinositides
219291_at	MDS009	56986	0.03	NM_020234	NP_064619	0.84	x 009 protein
219293_s_at	PTD004	29789	0.01	NM_013341	NP_037473	0.87	GTP-binding protein PTD004

219296_at	ZDHHC13	54503	0.01	NM_019028	NP_061901	0.89	zinc finger, DHHC domain containing 13
219317_at	POLI	11201	6.92e-03	NM_007195	NP_009126	0.84	polymerase (DNA directed) iota
219329_s_at	C2orf28	51374	0.03	NM_016085	NP_057169	0.90	chromosome 2 open reading frame 28
219342_at	CAS1	64921	0.02	NM_022900	NP_075051	0.85	O-acetyltransferase
219343_at	CDC37L1	55664	0.01	NM_017913	NP_060383	0.92	cell division cycle 37 homolog (S. cerevisiae)-like 1
219345_at	CGI-143	51027	0.03	NM_016074	NP_057158	0.88	CGI-143 protein
219351_at	TRAPPC2	6399	5.83e-03	NM_014563	NP_055378	0.90	trafficking protein particle complex 2
219353_at	NHLRC2	374354	0.03	BX647663		0.83	NHL repeat containing 2
219356_s_at	SNF7DC2	51510	0.01	NM_016410	NP_057494	0.84	SNF7 domain containing 2
219359_at	FLJ22635	80162	0.03	NM_025092	NP_079368	0.86	hypothetical protein FLJ22635
219362_at	MAK10	60560	0.01	NM_024635	NP_078911	0.89	MAK10 homolog, amino-acid N-acetyltransferase
subunit, (S. cerevisiae)							
219368_at	NAP1L2	4674	0.04	NM_021963	NP_068798	0.85	nucleosome assembly protein 1-like 2
219373_at	DPM3	54344	0.03	NM_018973	NP_061846	0.92	dolichyl-phosphate mannosyltransferase polypeptide 3
219375_at	CEPT1	10390	0.02	NM_006090	NP_006081	0.81	choline/ethanolamine phosphotransferase 1
219378_at	NARG1L	79612	2.4e-03	NM_024561	NP_078837	0.83	NMDA receptor regulated 1-like
219394_at	PGS1	9489	0.04	NM_024419	NP_077733	0.91	phosphatidylglycerophosphate synthase
219399_at	LIN7C	55327	0.01	NM_018362	NP_060832	0.83	lin-7 homolog C (C. elegans)
219402_s_at	DERL1	79139	0.01	NM_024295	NP_077271	0.93	Der1-like domain family, member 1
219403_s_at	HPSE	10855	0.04	NM_006665	NP_006656	0.82	heparanase
219409_at	SNIP1	79753	9.53e-04	NM_024700	NP_078976	0.93	Smad nuclear interacting protein
219421_at	OSRF	23548	0.03	NM_012382	NP_036514	0.89	osmosis responsive factor
219428_s_at	PXMP4	11264	0.01	NM_007238	NP_009169	0.95	peroxisomal membrane protein 4, 24kDa
219433_at	BCOR	54880	0.01	NM_017745	NP_060215	0.84	BCL6 co-repressor
219439_at	C1GALT1	56913	0.03	NM_020156	NP_064541	0.84	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-
beta-galactosyltransferase, 1							
219443_at	C20orf13	55617	0.02	NM_017714	NP_060184	0.91	chromosome 20 open reading frame 13
219446_at	hSyn	55188	2.16e-03	NM_018157	NP_060627	0.91	brain synembryn
219459_at	POLR3B	55703	0.03	NM_018082	NP_060552	0.90	polymerase (RNA) III (DNA directed) polypeptide B
219470_x_at	CCNJ	54619	0.03	NM_019084	NP_061957	0.84	cyclin J
219471_at	C13orf18	80183	0.02	NM_025113	NP_079389	1.23	chromosome 13 open reading frame 18
219473_at	GDAP2	54834	0.01	NM_017686	NP_060156	0.91	ganglioside induced differentiation associated protein 2
219481_at	TTC13	79573	0.03	NM_024525	NP_078801	0.86	tetratricopeptide repeat domain 13
219484_at	HCFC2	29915	6.71e-03	NM_013320	NP_037452	0.87	host cell factor C2
219485_s_at	PSMD10	5716	0.01	NM_002814	NP_002805	0.90	proteasome (prosome, macropain) 26S subunit, non-
ATPase, 10							
219487_at	FLJ23560	79738	0.03	NM_024685	NP_078961	0.83	hypothetical protein FLJ23560
219495_s_at	ZNF180	7733	0.01	NM_013256	NP_037388	0.92	zinc finger protein 180 (HHZ168)
219504_s_at	FLJ13150	79871	0.01	NM_024813	NP_079089	0.87	hypothetical protein FLJ13150
219512_at	C20orf172	79980	0.02	NM_024918	NP_079194	1.17	chromosome 20 open reading frame 172
219528_s_at	BCL11B	64919	0.03	NM_022898	NP_075049	0.89	B-cell CLL/lymphoma 11B (zinc finger protein)
219529_at	CLIC3	9022	0.04	NM_004669	NP_004660	0.76	chloride intracellular channel 3
219543_at	MAWBP	64081	8.57e-03	NM_022129	NP_071412	0.91	MAWD binding protein
219544_at	FLJ22624	79866	5.82e-04	NM_024808	NP_079084	0.82	FLJ22624 protein

219547_at	COX15	1355	0.04	NM_004376	NP_004367	0.93	COX15 homolog, cytochrome c oxidase assembly protein (yeast)
219563_at	C14orf139	79686	8.05e-03	NM_024633	NP_078909	0.93	chromosome 14 open reading frame 139
219571_s_at	ZNF12	7559	0.02	NM_006956	NP_008887	0.91	zinc finger protein 12 (KOX 3)
219575_s_at	PDF	64146	8.33e-03	NM_022341	NP_071736	0.88	peptide deformylase-like protein
219581_at	SEN2L	80746	0.02	NM_025265	NP_079541	0.83	likely homolog of yeast SEN2
219594_at	NINJ2	4815	9.02e-03	NM_016533	NP_057617	0.87	ninjurin 2
219598_s_at	RWDD1	51389	2.8e-03	NM_016104	NP_057188	0.87	RWD domain containing 1
219600_s_at	C21orf4	757	6.4e-03	NM_006134	NP_006125	0.85	chromosome 21 open reading frame 4
219624_at	BAG4	9530	0.03	NM_004874	NP_004865	0.91	BCL2-associated athanogene 4
219627_at	FLJ12700	79970	0.04	NM_024910	NP_079186	0.93	hypothetical protein FLJ12700
219628_at	WIG1	64393	0.02	NM_022470	NP_071915	1.14	p53 target zinc finger protein
219629_at	C22orf8	55007	0.01	NM_017911	NP_060381	0.64	chromosome 22 open reading frame 8
219639_x_at	PARP6	56965	0.03	NM_020213	NP_064598	0.93	poly (ADP-ribose) polymerase family, member 6
219649_at	ALG6	29929	4.51e-03	NM_013339	NP_037471	0.93	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3-glucosyltransferase)
219653_at	C20orf40	149986	9.37e-03	AF165185	AAD46654	0.85	chromosome 20 open reading frame 40
219666_at	MS4A6A	64231	0.02	NM_022349	NP_071744	0.93	membrane-spanning 4-domains, subfamily A, member 6A
219673_at	C6orf61	54844	6.41e-03	AK000177	BAA90991	0.88	chromosome 6 open reading frame 61
219690_at	FLJ22573	79713	0.04	NM_024660	NP_078936	0.91	hypothetical protein FLJ22573
219694_at	FLJ11127	54491	0.01	NM_019018	NP_061891	0.95	hypothetical protein FLJ11127
219696_at	FLJ20054	54530	0.03	NM_019049	NP_061922	0.84	hypothetical protein FLJ20054
219698_s_at	METTL4	64863	0.04	NM_022840	NP_073751	0.94	methyltransferase like 4
219700_at	PLXDC1	57125	1.91e-03	NM_020405	NP_065138	0.77	plexin domain containing 1
219701_at	TMOD2	29767	6.85e-03	NM_014548	NP_055363	0.79	tropomodulin 2 (neuronal)
219731_at	FLJ34077	404033	0.04	BC003519		0.92	weakly similar to zinc finger protein 195
219734_at	SIDT1	54847	2.95e-03	NM_017699	NP_060169	0.80	SID1 transmembrane family, member 1
219767_s_at	CRYZL1	9946	4.27e-04	NM_005111	NP_005102	0.91	crystallin, zeta (quinone reductase)-like 1
219774_at	FLJ10996	54520	0.02	NM_019044	NP_061917	0.90	hypothetical protein FLJ10996
219777_at	GIMAP6	474344	7.78e-03	NM_024711	NP_078987	0.82	GTPase, IMAP family member 6
219806_s_at	FN5	56935	0.04	NM_020179	NP_064564	0.93	FN5 protein
219818_s_at	GPATC1	55094	0.03	NM_018025	NP_060495	0.86	G patch domain containing 1
219819_s_at	MRPS28	28957	0.03	NM_014018	NP_054737	0.94	mitochondrial ribosomal protein S28
219822_at	MTRF1	9617	2.8e-03	NM_004294	NP_004285	0.84	mitochondrial translational release factor 1
219843_at	IPP	3652	0.01	NM_005897	NP_005888	0.87	intracisternal A particle-promoted polypeptide
219869_s_at	SLC39A8	64116	3.79e-03	NM_022154	NP_071437	0.84	solute carrier family 39 (zinc transporter), member 8
219870_at	ATF7IP2	80063	0.02	NM_024997	NP_079273	0.84	activating transcription factor 7 interacting protein 2
219883_at	KCNK4	50801	0.04	NM_016611	NP_057695	1.10	potassium channel, subfamily K, member 4
219910_at	HYPE	11153	0.04	NM_007076	NP_009007	1.07	Huntingtin interacting protein E
219913_s_at	CRNKL1	51340	0.03	NM_016652	NP_057736	0.92	Crn, crooked neck-like 1 (Drosophila)
219929_s_at	ZFYVE21	79038	5.89e-03	NM_024071	NP_076976	0.93	zinc finger, FYVE domain containing 21
219933_at	GLRX2	51022	0.03	NM_016066	NP_057150	0.90	glutaredoxin 2
219957_at	RUFY2	55680	0.01	NM_017987	NP_060457	1.14	RUN and FYVE domain containing 2
219980_at	FLJ21106	80167	5.81e-03	NM_025097	NP_079373	1.12	hypothetical protein FLJ21106

220001_at	PADI4	23569	0.03	NM_012387	NP_036519	1.23	peptidyl arginine deiminase, type IV
220019_s_at	ZNF224	7767	0.01	NM_013398	NP_037530	0.92	zinc finger protein 224
220044_x_at	CROP	51747	0.01	NM_016424	NP_057508	0.93	cisplatin resistance-associated overexpressed protein
220046_s_at	CCNL1	57018	0.01	NM_020307	NP_064703	0.90	cyclin L1
220083_x_at	UCHL5	51377	5.93e-03	BC025369	AAH25369	0.85	ubiquitin carboxyl-terminal hydrolase L5
220094_s_at	C6orf79	63933	0.03	NM_022102	NP_071385	0.90	chromosome 6 open reading frame 79
220097_s_at	FLJ20255	54868	0.02	NM_017728	NP_060198	1.12	hypothetical protein FLJ20255
220113_x_at	POLR1B	84172	0.03	NM_019014	NP_061887	1.09	polymerase (RNA) I polypeptide B, 128kDa
220122_at	MCTP1	79772	0.04	NM_024717	NP_078993	1.14	multiple C2-domains with two transmembrane regions 1
220127_s_at	FBXL12	54850	0.01	NM_017703	NP_060173	0.95	F-box and leucine-rich repeat protein 12
220132_s_at	CLEC2D	29121	5.31e-03	NM_013269	NP_037401	0.83	C-type lectin superfamily 2, member D
220143_x_at	LUC7L	55692	0.04	NM_018032	NP_060502	0.89	LUC7-like (S. cerevisiae)
220147_s_at	C12orf14	58516	0.04	NM_021238	NP_067061	0.93	chromosome 12 open reading frame 14
220167_s_at	TP53TG3	24150	2.42e-03	NM_015369	NP_056184	1.16	TP53TG3 protein
220173_at	C14orf45	80127	0.04	NM_025057	NP_079333	1.05	chromosome 14 open reading frame 45
220175_s_at	CBWD1	55871	2.19e-03	NM_018491	NP_060961	0.86	COBW domain containing 1
220195_at	MBD5	55777	0.04	NM_018328	NP_060798	1.09	methyl-CpG binding domain protein 5
220219_s_at	LOC474170	474170	0.01	NM_001006607	NP_001006608	0.91	c114 SLIT-like testicular protein
220232_at	SCD4	79966	5.31e-03	NM_024906	NP_079182	1.12	stearoyl-CoA desaturase 4
220242_x_at	FLJ10891	55762	5.95e-03	NM_018260	NP_060730	1.18	hypothetical protein FLJ10891
220244_at	LOH3CR2A	29931	0.04	NM_013343	NP_037475	1.16	loss of heterozygosity, 3, chromosomal region 2, gene
A							
220252_x_at	CXorf21	80231	0.01	NM_025159	NP_079435	1.14	chromosome X open reading frame 21
220288_at	MYO15A	51168	0.03	NM_016239	NP_057323	1.15	myosin XVA
220307_at	CD244	51744	0.03	NM_016382	NP_057466	0.91	CD244 natural killer cell receptor 2B4
220330_s_at	SAMSN1	64092	0.04	NM_022136	NP_071419	0.91	SAM domain, SH3 domain and nuclear localisation
signals, 1							
220355_s_at	PB1	55193	0.02	NM_018165	NP_060635	0.92	polybromo 1
220370_s_at	USP36	57602	0.04	NM_025090	NP_079366	0.85	ubiquitin specific protease 36
220399_at	FLJ22639	79854	6.53e-03	NM_024796	NP_079072	0.86	hypothetical protein FLJ22639
220404_at	GPR97	222487	0.03	NM_170776	NP_740746	1.21	G protein-coupled receptor 97
220446_s_at	CHST4	10164	8.28e-03	NM_005769	NP_005760	1.14	carbohydrate (N-acetylglucosamine 6-O)
sulfotransferase 4							
220477_s_at	C20orf30	29058	0.01	NM_014145	NP_054864	0.93	chromosome 20 open reading frame 30
220485_s_at	SIRPB2	55423	0.04	NM_018556	NP_061026	0.87	signal-regulatory protein beta 2
220495_s_at	C5orf14	79770	0.02	NM_024715	NP_078991	0.87	chromosome 5 open reading frame 14
220526_s_at	MRPL20	55052	4.65e-03	NM_017971	NP_060441	0.85	mitochondrial ribosomal protein L20
220547_s_at	FAM35A	54537	0.01	NM_019054	NP_061927	0.91	family with sequence similarity 35, member A
220590_at	MDS028	55846	0.02	NM_018463	NP_060933	0.86	uncharacterized hematopoietic stem/progenitor cells
protein MDS028							
220597_s_at	ARL6IP4	51329	0.04	NM_018694	NP_061164	0.91	ADP-ribosylation-like factor 6 interacting protein 4
220642_x_at	GPR89	51463	1.65e-03	NM_016334	NP_057418	0.85	G protein-coupled receptor 89
220647_s_at	E2IG2	51287	0.04	NM_016565	NP_057649	0.91	E2IG2 protein
220710_at	C15orf28	80035	0.04	AK021784	BAB13894	1.12	chromosome 15 open reading frame 28
220741_s_at	PPA2	27068	1.99e-04	NM_006903	NP_008834	0.92	inorganic pyrophosphatase 2

220742_s_at	NGLY1	55768	0.01	NM_018297	NP_060767	0.95	N-glycanase 1
220753_s_at	CRYL1	51084	1.83e-03	NM_015974	NP_057058	0.88	crystallin, lambda 1
220755_s_at	C6orf48	50854	0.02	NM_016947	NP_058643	0.88	chromosome 6 open reading frame 48
220760_x_at	FLJ14345	79788	0.01	NM_024733	NP_079009	0.92	hypothetical protein FLJ14345
220761_s_at	TAOK3	51347	5.48e-03	NM_016281	NP_057365	0.89	TAO kinase 3
220776_at	KCNJ14	3770	0.02	NM_013348	NP_037480	1.17	potassium inwardly-rectifying channel, subfamily J, member 14
220788_s_at	RNF31	55072	0.04	NM_017999	NP_060469	0.89	ring finger protein 31
220796_x_at	SLC35E1	79939	1.19e-03	NM_024881	NP_079157	1.11	solute carrier family 35, member E1
220890_s_at	DDX47	51202	1.53e-03	NM_016355	NP_057439	0.88	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47
220924_s_at	SLC38A2	54407	0.02	NM_018976	NP_061849	0.95	solute carrier family 38, member 2
220925_at	MAK10	60560	0.04	NM_024635	NP_078911	0.87	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)
220933_s_at	ZCCHC6	79670	0.04	NM_024617	NP_078893	0.90	zinc finger, CCHC domain containing 6
220937_s_at	ST6GALNAC4	27090	2.66e-03	NM_014403	NP_055218	0.89	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4
220940_at	KIAA1641	57730	5.83e-03	NM_020970	NP_066021	0.84	KIAA1641
220947_s_at	DKFZP434P1750	26000	0.02	NM_015527	NP_056342	1.09	DKFZP434P1750 protein
220948_s_at	ATP1A1	476	0.04	NM_000701	NP_000692	0.92	ATPase, Na+/K+ transporting, alpha 1 polypeptide
220954_s_at	PILRB	29990	0.01	NM_013440	NP_038468	0.87	paired immunoglobin-like type 2 receptor beta
220957_at	CTAGE1	64693	0.03	NM_022663	NP_073154	1.14	cutaneous T-cell lymphoma-associated antigen 1
220966_x_at	ARPC5L	81873	0.01	NM_030978	NP_112240	0.88	actin related protein 2/3 complex, subunit 5-like
220992_s_at	C1orf25	81627	2.8e-03	NM_030934	NP_112196	0.82	chromosome 1 open reading frame 25
220998_s_at	UNC93B1	81622	0.02	NM_030930	NP_112192	1.17	unc-93 homolog B1 (C. elegans)
221002_s_at	TM4SF14	81619	0.04	NM_030927	NP_112189	0.93	transmembrane 4 superfamily member 14
221007_s_at	FIP1L1	81608	8.81e-03	NM_030917	NP_112179	0.94	FIP1 like 1 (S. cerevisiae)
221011_s_at	LBH	81606	0.02	NM_030915	NP_112177	0.86	likely ortholog of mouse limb-bud and heart gene
221012_s_at	TRIM8	81603	0.03	NM_030912	NP_112174	1.08	tripartite motif-containing 8
221027_s_at	PLA2G12A	81579	0.02	NM_030821	NP_110448	0.85	phospholipase A2, group XIIA
221036_s_at	APH1B	83464	0.03	NM_031301	NP_112591	0.93	anterior pharynx defective 1 homolog B (C. elegans)
221078_s_at	KIAA1212	55704	0.01	NM_018084	NP_060554	0.91	KIAA1212
221081_s_at	FLJ22457	79961	1.57e-03	NM_024901	NP_079177	0.83	hypothetical protein FLJ22457
221082_s_at	NDRG3	57446	0.02	NM_022477	NP_071922	1.13	NDRG family member 3
221087_s_at	APOL3	80833	0.04	NM_014349	NP_055164	0.85	apolipoprotein L, 3
221090_s_at	FLJ10826	55239	0.03	NM_018233	NP_060703	1.08	hypothetical protein FLJ10826
221158_at	C21orf66	94104	0.01	NM_013329	NP_037461	0.91	chromosome 21 open reading frame 66
221169_s_at	HRH4	59340	0.02	NM_021624	NP_067637	1.15	histamine receptor H4
221193_s_at	ZCCHC10	54819	3.1e-03	NM_017665	NP_060135	0.83	zinc finger, CCHC domain containing 10
221194_s_at	LOC51136	51136	0.03	NM_016125	NP_057209	0.90	PTD016 protein
221196_x_at	CXorf53	79184	0.01	NM_024332	NP_077308	0.92	chromosome X open reading frame 53
221207_s_at	NBEA	26960	0.04	NM_015678	NP_056493	1.14	neurobeachin
221213_s_at	SUHW4	54816	0.01	NM_017661	NP_060131	0.93	suppressor of hairy wing homolog 4 (Drosophila)
221214_s_at	NELF	26012	0.01	NM_015537	NP_056352	0.87	nasal embryonic LHRH factor
221218_s_at	TPK1	27010	0.04	NM_022445	NP_071890	0.88	thiamin pyrophosphokinase 1
221219_s_at	KLHDC4	54758	0.04	NM_017566	NP_060036	0.81	kelch domain containing 4

221230_s_at	ARID4B	51742	0.02	NM_016374	NP_057458	0.95	AT rich interactive domain 4B (RBP1- like)
221234_s_at	BACH2	60468	0.02	NM_021813	NP_068585	0.85	BTB and CNC homology 1, basic leucine zipper transcription factor 2
221247_s_at	WBSCR16	81554	0.03	NM_030798	NP_110425	0.87	Williams-Beuren syndrome chromosome region 16
221260_s_at	C12orf22	81566	1.55e-03	NM_030809	NP_110436	0.88	chromosome 12 open reading frame 22
221268_s_at	SGPP1	81537	0.03	NM_030791	NP_110418	0.90	sphingosine-1-phosphate phosphatase 1
221311_x_at	DJ122O8.2	57226	0.02	NM_020466	NP_065199	0.93	hypothetical protein dJ122O8.2
221381_s_at	MORF4	10934	0.02	NM_006792	NP_006783	0.89	mortality factor 4
221425_s_at	HBLD2	81689	0.02	NM_030940	NP_112202	0.89	HESB like domain containing 2
221428_s_at	TBL1XR1	79718	0.01	NM_024665	NP_078941	0.89	transducin (beta)-like 1X-linked receptor 1
221430_s_at	RNF146	81847	2.86e-03	NM_030963	NP_112225	0.91	ring finger protein 146
221434_s_at	C14orf156	81892	0.01	NM_031210	NP_112487	0.93	chromosome 14 open reading frame 156
221472_at	TDE1	10955	3.1e-03	NM_006811	NP_006802	0.93	tumor differentially expressed 1
221476_s_at	RPL15	6138	0.02	NM_002948	NP_002939	0.94	ribosomal protein L15
221481_x_at	HNRPD	3184	0.01	NM_001003810	NP_001003810	0.92	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
221488_s_at	C6orf82	51596	0.03	NM_015921	NP_057005	0.86	chromosome 6 open reading frame 82
221492_s_at	APG3L	64422	0.01	NM_022488	NP_071933	0.90	APG3 autophagy 3-like (S. cerevisiae)
221493_at	TSPYL1	7259	4.31e-03	BC048969	AAH48969	0.88	TSPY-like 1
221500_s_at	STX16	8675	0.04	NM_001001433	NP_001001433	0.95	syntaxin 16
221501_x_at	LOC339047	339047	0.02	AF229069	AAF82267	0.79	hypothetical protein LOC339047
221502_at	KPNA3	3839	0.03	NM_002267	NP_002258	0.89	karyopherin alpha 3 (importin alpha 4)
221505_at	ANP32E	81611	0.01	NM_030920	NP_112182	0.86	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
221509_at	DENR	8562	0.03	NM_003677	NP_003668	0.93	density-regulated protein
221510_s_at	GLS	2744	0.02	AF158555	AAD47056	0.86	glutaminase
221514_at	UTP14A	10813	0.02	NM_006649	NP_006640	0.89	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)
221531_at	REC14	80349	0.04	NM_025234	NP_079510	0.88	recombination protein REC14
221537_at	PLXNA1	5361	0.01	NM_032242	NP_115618	0.87	plexin A1
221539_at	EIF4EBP1	1978	0.03	NM_004095	NP_004086	1.14	eukaryotic translation initiation factor 4E binding protein 1
221555_x_at	CDC14B	8555	0.01	NM_003671	NP_003662	1.14	CDC14 cell division cycle 14 homolog B (S. cerevisiae)
221558_s_at	LEF1	51176	0.01	NM_016269	NP_057353	0.81	lymphoid enhancer-binding factor 1
221564_at	HRMT1L1	3275	0.03	AL109794	CAB52454	0.95	HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae)
221570_s_at	HSPC133	29081	0.02	NM_014168	NP_054887	0.91	HSPC133 protein
221575_at	SCLY	51540	0.03	NM_016510	NP_057594	0.91	selenocysteine lyase
221580_s_at	MGC5306	79101	3.79e-03	NM_024116	NP_077021	0.91	hypothetical protein MGC5306
221582_at	HIST3H2A	92815	0.02	NM_033445	NP_254280	0.85	histone 3, H2a
221593_s_at	RPL31	6160	3.1e-03	BC001663		0.88	ribosomal protein L31
221596_s_at	DKFZP564O0523	84060	3.79e-03	NM_032120	NP_115496	1.13	hypothetical protein DKFZp564O0523
221600_s_at	PTD015	28971	0.03	NM_024684	NP_078960	0.93	PTD015 protein
221602_s_at	TOSO	9214	0.04	NM_005449	NP_005440	0.87	regulator of Fas-induced apoptosis
221614_s_at	RPH3AL	9501	0.02	NM_006987	NP_008918	0.85	rabphilin 3A-like (without C2 domains)

221618_s_at	TAF9L	51616	0.03	NM_015975	NP_057059	0.85	TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa
221619_s_at	MTCH1	23787	0.03	NM_014341	NP_055156	0.95	mitochondrial carrier homolog 1 (C. elegans)
221620_s_at	MGC4825	79135	1.05e-03	NM_024122	NP_077027	0.83	hypothetical protein MGC4825
221622_s_at	HT007	55863	0.03	NM_018480	NP_060950	0.92	uncharacterized hypothalamus protein HT007
221645_s_at	ZNF83	55769	8.05e-03	NM_018300	NP_060770	0.80	zinc finger protein 83 (HPF1)
221646_s_at	ZDHHC11	79844	0.01	NM_024786	NP_079062	0.83	zinc finger, DHHC domain containing 11
221648_s_at	PNAS-4	51029	5.31e-03	AK025651		0.84	CGI-146 protein
221652_s_at	C12orf11	55726	2.95e-03	NM_018164	NP_060634	0.81	chromosome 12 open reading frame 11
221653_x_at	APOL2	23780	7.54e-03	NM_030882	NP_112092	1.14	apolipoprotein L, 2
221658_s_at	IL21R	50615	5.51e-03	NM_021798	NP_068570	0.81	interleukin 21 receptor
221664_s_at	F11R	50848	0.04	NM_016946	NP_058642	0.88	F11 receptor
221685_s_at	FLJ20364	54908	0.04	NM_017785	NP_060255	0.83	hypothetical protein FLJ20364
221688_s_at	C15orf12	55272	0.01	NM_018285	NP_060755	0.86	chromosome 15 open reading frame 12
221691_x_at	NPM1	4869	0.03	NM_199185	NP_954654	0.89	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
221691_x_at	NPM1	4869	0.03	NM_002520	NP_002511	0.89	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
221692_s_at	MRPL34	64981	0.02	NM_023937	NP_076426	0.86	mitochondrial ribosomal protein L34
221699_s_at	DDX50	79009	3.45e-03	NM_024045	NP_076950	0.91	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50
221711_s_at	HSPC142	29086	0.01	NM_014173	NP_054892	0.89	HSPC142 protein
221712_s_at	FLJ10439	54663	9.05e-03	NM_018093	NP_060563	0.84	hypothetical protein FLJ10439
221718_s_at	AKAP13	11214	0.04	NM_006738	NP_006729	0.92	A kinase (PRKA) anchor protein 13
221724_s_at	CLEC4A	50856	0.02	NM_016184	NP_057268	0.91	C-type lectin domain family 4, member A
221726_at	RPL22	6146	0.02	NM_000983	NP_000974	0.87	ribosomal protein L22
221727_at	PC4	10923	0.02	NM_006713	NP_006704	0.90	activated RNA polymerase II transcription cofactor 4
221736_at	KIAA1219	57148	0.01	AB033045	BAA86533	0.88	KIAA1219 protein
221743_at	CUGBP1	10658	0.04	AK054655		0.91	CUG triplet repeat, RNA binding protein 1
221744_at	HAN11	10238	0.02	NM_005828	NP_005819	0.89	WD-repeat protein
221751_at	PANK3	79646	0.01	AL565516		0.86	pantothenate kinase 3
221754_s_at	CORO1B	57175	0.04	NM_020441	NP_065174	1.16	coronin, actin binding protein, 1B
221756_at	MGC17330	113791	0.02	NM_052880	NP_443112	0.83	HGFL gene
221757_at	MGC17330	113791	0.01	NM_052880	NP_443112	0.86	HGFL gene
221761_at	ADSS	159	5.31e-03	NM_001126	NP_001117	0.92	adenylosuccinate synthase
221766_s_at	FAM46A	55603	6.05e-04	NM_017633	NP_060103	0.83	family with sequence similarity 46, member A
221767_x_at	HDLBP	3069	0.02	AA515560		0.93	high density lipoprotein binding protein (vigilin)
221768_at	SFPQ	6421	0.02	AV705803		0.90	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)
221771_s_at	HSMPP8	54737	9.61e-03	NM_017520	NP_059990	0.85	M-phase phosphoprotein, mpp8
221773_at	ELK3	2004	0.03	AW575374		0.88	ELK3, ETS-domain protein (SRF accessory protein 2)
221775_x_at	RPL22	6146	0.03	NM_000983	NP_000974	0.92	ribosomal protein L22
221781_s_at	DNAJC10	54431	0.03	NM_018981	NP_061854	0.86	DnaJ (Hsp40) homolog, subfamily C, member 10
221782_at	DNAJC10	54431	0.03	NM_018981	NP_061854	0.93	DnaJ (Hsp40) homolog, subfamily C, member 10
221787_at	PHF10	55274	3.45e-04	BC051700		0.89	PHD finger protein 10
221804_s_at	FAM45A	404636	7.69e-03	NM_207009	NP_996892	1.16	family with sequence similarity 45, member A
221808_at	RAB9A	9367	5.16e-03	NM_004251	NP_004242	0.93	RAB9A, member RAS oncogene family
221826_at	LOC90806	90806	0.01	NM_144567	NP_653168	0.89	similar to RIKEN cDNA 2610307I21

221829_s_at	TNPO1	3842	0.03	NM_002270	NP_002261	0.92	transportin 1
221847_at	LOC440123	440123	3.79e-03	XM_498557	XP_498557	0.84	LOC440123
221858_at	TBC1D12	23232	2.5e-03	XM_051081	XP_051081	0.90	TBC1 domain family, member 12
221860_at	HNRPL	3191	7.69e-03	AL044078		0.81	heterogeneous nuclear ribonucleoprotein L
221878_at	LOC388969	388969	0.03	BF110411		0.92	hypothetical LOC388969
221891_x_at	HSPA8	3312	0.02	NM_006597	NP_006588	0.90	heat shock 70kDa protein 8
221903_s_at	CYLD	1540	0.04	NM_015247	NP_056062	0.90	cylindromatosis (turban tumor syndrome)
221918_at	PCTK2	5128	4.27e-04	NM_002595	NP_002586	0.84	PCTAIRE protein kinase 2
221919_at	HNRPA1	3178	3.5e-03	BC070315	AAH70315	0.88	heterogeneous nuclear ribonucleoprotein A1
221931_s_at	SEH1L	81929	5.13e-03	NM_031216	NP_112493	0.90	SEH1-like (S. cerevisiae)
221937_at	AP1GBP1	11276	8.91e-04	AI472320		0.90	AP1 gamma subunit binding protein 1
221952_x_at	KIAA1393	57570	0.03	NM_020810	NP_065861	0.93	KIAA1393
221962_s_at	UBE2H	7328	0.02	NM_003344	NP_003335	0.87	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
221965_at	MPHOSPH9	10198	4.83e-03	X98258	CAA66911	0.85	M-phase phosphoprotein 9
221970_s_at	DKFZP586L0724	25926	1.33e-03	NM_015462	NP_056277	0.86	DKFZP586L0724 protein
221973_at	LOC150759	150759	0.01	AI983904		0.82	hypothetical protein LOC150759
221984_s_at	C2orf17	79137	0.03	NM_024293	NP_077269	0.86	chromosome 2 open reading frame 17
221989_at	RPL10	6134	0.04	AK027197	BAB15688	0.90	ribosomal protein L10
222010_at	TCP1	6950	1.33e-03	NM_030752	NP_110379	0.89	t-complex 1
222011_s_at	TCP1	6950	0.01	NM_030752	NP_110379	0.88	t-complex 1
222021_x_at	SDHA	6389	0.03	NM_004168	NP_004159	0.93	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
222023_at	AKAP13	11214	0.04	AK022014	BAB13953	1.11	A kinase (PRKA) anchor protein 13
222035_s_at	PAPOLA	10914	0.02	NM_032632	NP_116021	0.93	poly(A) polymerase alpha
222040_at	HNRPA1	3178	0.01	BC070315	AAH70315	0.89	heterogeneous nuclear ribonucleoprotein A1
222061_at	CD58	965	4.93e-03	AA700015		0.86	CD58 antigen, (lymphocyte function-associated antigen 3)
222062_at	IL27RA	9466	0.03	NM_004843	NP_004834	0.83	interleukin 27 receptor, alpha
222064_s_at	MGC2744	80755	0.02	NM_025267	NP_079543	0.86	hypothetical protein MGC2744
222099_s_at	C19orf13	26065	2.76e-05	NM_015578	NP_056393	0.79	chromosome 19 open reading frame 13
222108_at	AMIGO2	347902	3.79e-03	NM_181847	NP_862830	0.82	amphoterin induced gene 2
222115_x_at	N-PAC	84656	0.04	NM_032569	NP_115958	0.88	cytokine-like nuclear factor n-pac
222122_s_at	THOC2	57187	3.43e-03	NM_020449	NP_065182	0.86	THO complex 2
222127_s_at	SEC3L1	55763	9.08e-03	NM_018261	NP_060731	0.95	SEC3-like 1 (S. cerevisiae)
222132_s_at	MULK	55750	0.01	NM_018238	NP_060708	0.85	multiple substrate lipid kinase
222136_x_at	ZNF43	7594	0.01	AK022905		0.86	zinc finger protein 43 (HTF6)
222140_s_at	GPR89	51463	0.04	NM_016334	NP_057418	0.91	G protein-coupled receptor 89
222142_at	CYLD	1540	1.48e-04	AK024212		0.79	cylindromatosis (turban tumor syndrome)
222143_s_at	FLJ22405	64419	0.02	NM_022485	NP_071930	0.95	hypothetical protein FLJ22405
222145_at	LOC441749	441749	0.01	AK027225		1.18	similar to Group X secretory phospholipase A2 precursor (Phosphatidylcholine 2-acylhydrolase GX) (GX sPLA2) (sPLA2-X)
222146_s_at	TCF4	6925	0.01	NM_003199	NP_003190	0.88	transcription factor 4
222147_s_at	ACTR5	79913	8.58e-03	AL133519		0.89	ARP5 actin-related protein 5 homolog (yeast)
222147_s_at	SLC32A1	140679	8.58e-03	AL133519		0.89	solute carrier family 32 (GABA vesicular transporter), member 1

222149_x_at	LOC283768	283768	5.59e-03	AL137398		0.82	hypothetical LOC283768
222150_s_at	LOC54103	54103	0.02	AK026747		0.85	hypothetical protein LOC54103
222152_at	LOC391733	391733	4.19e-03	AK024175		0.88	similar to Microneme antigen
222156_x_at	CCPG1	9236	0.04	NM_020739	NP_065790	0.91	cell cycle progression 1
222156_x_at	CCPG1	9236	0.04	NM_004748	NP_004739	0.91	cell cycle progression 1
222159_at	PLXNA2	5362	6.89e-03	AK023058		1.14	plexin A2
222164_at	FGFR1	2260	0.03	AU145411		0.88	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
222182_s_at	CNOT2	4848	3.58e-03	NM_014515	NP_055330	0.84	CCR4-NOT transcription complex, subunit 2
222186_at	ZA20D3	54469	0.04	AL109684		1.14	zinc finger, A20 domain containing 3
222203_s_at	RDH14	57665	0.01	NM_020905	NP_065956	0.86	retinol dehydrogenase 14 (all-trans and 9-cis)
222217_s_at	SLC27A3	11000	0.01	NM_024330	NP_077306	0.86	solute carrier family 27 (fatty acid transporter), member 3
222230_s_at	ACTR10	55860	0.03	NM_018477	NP_060947	0.95	actin-related protein 10 homolog (S. cerevisiae)
222231_s_at	PRO1855	55379	0.04	NM_018509	NP_060979	0.97	hypothetical protein PRO1855
222239_s_at	DDX26	26512	0.03	NM_012141	NP_036273	0.89	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26
222285_at	IGHD	3495	9.59e-03	AK128658		1.22	immunoglobulin heavy constant delta
222286_at	SNAPC3	6619	0.04	NM_003084	NP_003075	0.89	small nuclear RNA activating complex, polypeptide 3, 50kDa
222307_at	LOC282997	282997	0.02	AK093606		0.90	hypothetical protein LOC282997
222310_at	SFRS15	57466	0.01	AK057840		1.17	splicing factor, arginine/serine-rich 15
222311_s_at	SFRS15	57466	3.91e-04	NM_020706	NP_065757	0.86	splicing factor, arginine/serine-rich 15
222380_s_at	LOC391733	391733	0.03	AI907083		0.89	similar to Microneme antigen
222385_x_at	SEC61A1	29927	1.05e-03	NM_013336	NP_037468	0.90	Sec61 alpha 1 subunit (S. cerevisiae)
222387_s_at	VPS35	55737	0.01	NM_018206	NP_060676	0.84	vacuolar protein sorting 35 (yeast)
222391_at	TMEM30A	55754	0.01	NM_018247	NP_060717	0.93	transmembrane protein 30A
222393_s_at	MAK3	80218	0.01	NM_025146	NP_079422	0.91	Mak3 homolog (S. cerevisiae)
222395_s_at	FLJ13855	65264	0.02	NM_023079	NP_075567	0.94	hypothetical protein FLJ13855
222398_s_at	U5-116KD	9343	8.05e-03	NM_004247	NP_004238	0.92	U5 snRNP-specific protein, 116 kD
222399_s_at	SMBP	56889	9.73e-03	NM_020123	NP_064508	0.91	SM-11044 binding protein
222402_at	C13orf12	51371	0.01	NM_015932	NP_057016	0.83	chromosome 13 open reading frame 12
222403_at	MTCH2	23788	0.03	NM_014342	NP_055157	0.89	mitochondrial carrier homolog 2 (C. elegans)
222410_s_at	SNX6	58533	0.04	NM_021249	NP_067072	0.93	sorting nexin 6
222412_s_at	SSR3	6747	0.04	NM_007107	NP_009038	0.84	signal sequence receptor, gamma (translocon-associated protein gamma)
222417_s_at	SNX5	27131	0.01	NM_152227	NP_689413	0.83	sorting nexin 5
222423_at	NDFIP1	80762	7.42e-05	AK075495	BAC11652	0.93	Nedd4 family interacting protein 1
222426_at	MAPKAP1	79109	0.01	NM_024117	NP_077022	0.85	mitogen-activated protein kinase associated protein 1
222427_s_at	LARS	51520	7.35e-03	NM_020117	NP_064502	0.88	leucyl-tRNA synthetase
222428_s_at	LARS	51520	0.01	NM_020117	NP_064502	0.86	leucyl-tRNA synthetase
222430_s_at	YTHDF2	51441	8.8e-03	NM_016258	NP_057342	0.89	YTH domain family, member 2
222431_at	SPIN	10927	2.95e-03	AL136719	CAB66653	0.89	spindlin
222441_x_at	C20orf45	51012	0.01	NM_016045	NP_057129	0.92	chromosome 20 open reading frame 45
222442_s_at	ARL10C	55207	0.01	NM_018184	NP_060654	0.94	ADP-ribosylation factor-like 10C
222443_s_at	RBM8A	9939	5.93e-03	NM_005105	NP_005096	0.88	RNA binding motif protein 8A

222444_at	ARMCX3	51566	0.01	NM_016607	NP_057691	0.90	armadillo repeat containing, X-linked 3
222465_at	C15orf15	51187	0.01	NM_016304	NP_057388	0.86	chromosome 15 open reading frame 15
222467_s_at	C11orf23	55291	0.03	NM_018312	NP_060782	0.95	chromosome 11 open reading frame 23
222473_s_at	ERBB2IP	55914	0.01	NM_018695	NP_061165	0.91	erbb2 interacting protein
222474_s_at	TOMM22 homolog (yeast)	56993	0.04	NM_020243	NP_064628	0.87	translocase of outer mitochondrial membrane 22
222480_at	UBE2Q	55585	0.02	NM_017582	NP_060052	0.91	ubiquitin-conjugating enzyme E2Q (putative)
222481_at	FXC1	26515	0.04	NM_012192	NP_036324	0.91	fracture callus 1 homolog (rat)
222487_s_at	RPS27L	51065	0.01	BC003667	AAH03667	0.88	ribosomal protein S27-like
222488_s_at	DCTN4	51164	0.04	NM_016221	NP_057305	0.94	dynactin 4 (p62)
222493_s_at	TEX27	60685	0.03	NM_021943	NP_068762	0.91	testis expressed sequence 27
222498_at	AZI2	64343	0.01	BX648471		0.88	5-azacytidine induced 2
222502_s_at	Ufm1	51569	0.04	NM_016617	NP_057701	0.85	ubiquitin-fold modifier 1
222503_s_at	WDR41	55255	0.02	NM_018268	NP_060738	0.90	WD repeat domain 41
222507_s_at	C11orf15	56674	7.02e-03	NM_020644	NP_065695	0.87	chromosome 11 open reading frame 15
222508_s_at	FLJ10154	55082	0.01	NM_018011	NP_060481	0.85	hypothetical protein FLJ10154
222524_s_at	ASB6	140459	1.97e-03	NM_017873	NP_060343	0.90	ankyrin repeat and SOCS box-containing 6
222526_at	p66alpha	54815	9.2e-03	AK024670		0.86	p66 alpha
222529_at	MSCP	51312	1.01e-03	NM_016612	NP_057696	1.26	mitochondrial solute carrier protein
222529_at	MSCP	51312	1.01e-03	NM_018579	NP_061049	1.26	mitochondrial solute carrier protein
222530_s_at	MKKS	8195	0.03	NM_018848	NP_061336	0.91	McKusick-Kaufman syndrome
222532_at	SRPRB	58477	9.24e-03	NM_021203	NP_067026	0.88	signal recognition particle receptor, B subunit
222533_at	CRBN	51185	0.01	NM_016302	NP_057386	0.96	cereblon
222538_s_at	APPL leucine zipper motif 1	26060	0.01	NM_012096	NP_036228	0.87	adaptor protein containing pH domain, PTB domain and
222559_s_at	P15RS	55197	0.03	NM_018170	NP_060640	0.92	hypothetical protein FLJ10656
222562_s_at	TNKS2 ribose polymerase 2	80351	6.41e-03	NM_025235	NP_079511	0.93	tankyrase, TRF1-interacting ankyrin-related ADP-
222564_at	POGK	57645	0.02	AB040946	BAA96037	0.88	pogo transposable element with KRAB domain
222568_at	UGCGL1	56886	0.04	AK023240		1.18	UDP-glucose ceramide glucosyltransferase-like 1
222569_at	UGCGL1	56886	0.01	AK023240		0.95	UDP-glucose ceramide glucosyltransferase-like 1
222578_s_at	UBE1DC1	79876	0.01	NM_024818	NP_079094	0.89	ubiquitin-activating enzyme E1-domain containing 1
222579_at	UBE1DC1	79876	1.75e-03	NM_024818	NP_079094	0.91	ubiquitin-activating enzyme E1-domain containing 1
222580_at	ZNF644	84146	0.04	NM_201269	NP_958357	0.89	zinc finger protein 644
222582_at	PRKAG2 subunit	51422	4.68e-03	AF087875	AAK00413	0.84	protein kinase, AMP-activated, gamma 2 non-catalytic
222584_at	FLJ10504	55154	0.04	NM_018116	NP_060586	0.88	misato
222586_s_at	OSBPL11	114885	0.04	NM_022776	NP_073613	1.17	oxysterol binding protein-like 11
222587_s_at	GALNT7 acetylgalactosaminyltransferase 7 (GalNAc-T7)	51809	0.04	NM_017423	NP_059119	1.06	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-
222590_s_at	NLK	51701	0.01	NM_016231	NP_057315	0.90	nemo like kinase
222592_s_at	ACSL5	51703	0.03	NM_016234	NP_057318	0.90	acyl-CoA synthetase long-chain family member 5
222600_s_at	FLJ10808	55236	0.01	NM_018227	NP_060697	0.92	hypothetical protein FLJ10808
222601_at	FLJ10808	55236	9.85e-03	NM_018227	NP_060697	0.85	hypothetical protein FLJ10808
222602_at	FLJ10808	55236	0.01	NM_018227	NP_060697	0.92	hypothetical protein FLJ10808

222604_at	GTF3C3	9330	4.34e-03	AL137453	CAB70745	0.89	general transcription factor IIIC, polypeptide 3, 102kDa
222607_s_at	KIAA1008	22894	0.01	NM_014953	NP_055768	0.94	KIAA1008
222609_s_at	EXOSC1	51013	0.04	NM_016046	NP_057130	0.90	exosome component 1
222611_s_at	PSPC1	55269	6.71e-03	NM_018282	NP_060752	0.90	paraspeckle component 1
222618_at	LOC401500	401500	0.01	AI611315		0.92	hypothetical gene supported by AL512690
222622_at	LOC283871	283871	0.03	BC035985		0.91	hypothetical protein LOC283871
222623_s_at	ZNF639	51193	0.02	NM_016331	NP_057415	0.86	zinc finger protein 639
222629_at	REV1L	51455	0.03	NM_016316	NP_057400	0.85	REV1-like (yeast)
222638_s_at	C6orf35	55836	0.01	NM_018452	NP_060922	0.87	chromosome 6 open reading frame 35
222649_at	XPO4	64328	0.03	NM_022459	NP_071904	0.89	exportin 4
222656_at	FLJ11011	55284	0.03	NM_001001481	NP_001001481	0.89	hypothetical protein FLJ11011
222661_at	AGGF1	55109	1.85e-03	NM_018046	NP_060516	0.87	angiogenic factor with G patch and FHA domains 1
222663_at	RIOK2	55781	4.39e-03	AK001697	BAA91844	0.88	RIO kinase 2 (yeast)
222668_at	KCTD15	79047	0.01	NM_024076	NP_076981	0.83	potassium channel tetramerisation domain containing 15
222669_s_at	SBDS	51119	0.01	NM_016038	NP_057122	0.87	Shwachman-Bodian-Diamond syndrome
222673_x_at	LOC159090	159090	7.35e-03	NM_145284	NP_660327	0.92	similar to hypothetical protein MGC17347
222674_at	C9orf114	51490	8.62e-03	AL110193		0.87	chromosome 9 open reading frame 114
222681_at	MDS010	56983	0.03	NM_152305	NP_689518	0.91	x 010 protein
222681_at	MDS010	56983	0.03	NM_020231	NP_064616	0.91	x 010 protein
222682_s_at	C5orf3	10827	0.02	NM_018691	NP_061161	0.91	chromosome 5 open reading frame 3
222683_at	RNF20	56254	0.04	NM_019592	NP_062538	0.96	ring finger protein 20
222685_at	FAM29A	54801	0.02	NM_017645	NP_060115	0.83	family with sequence similarity 29, member A
222688_at	PHCA	55331	0.03	NM_018367	NP_060837	0.88	phytoceramidase, alkaline
222689_at	PHCA	55331	7.93e-03	NM_018367	NP_060837	0.88	phytoceramidase, alkaline
222691_at	SLC35B3	51000	0.01	NM_015948	NP_057032	0.88	solute carrier family 35, member B3
222692_s_at	FNDC3B	64778	0.04	NM_022763	NP_073600	0.97	fibronectin type III domain containing 3B
222697_s_at	ABHD10	55347	4.73e-04	NM_018394	NP_060864	0.94	abhydrolase domain containing 10
222701_s_at	CHCHD7	79145	6.71e-03	NM_024300	NP_077276	0.92	coiled-coil-helix-coiled-coil-helix domain containing 7
222702_x_at	CRIPT	9419	8.42e-03	NM_014171	NP_054890	1.12	postsynaptic protein CRIPT
222706_at	FLJ20291	54883	0.01	NM_017748	NP_060218	0.94	hypothetical protein FLJ20291
222713_s_at	FANCF	2188	0.03	NM_022725	NP_073562	0.89	Fanconi anemia, complementation group F
222715_s_at	AP1GBP1	11276	0.01	NM_007247	NP_009178	0.85	AP1 gamma subunit binding protein 1
222728_s_at	MGC5306	79101	0.01	NM_024116	NP_077021	0.89	hypothetical protein MGC5306
222729_at	FBXW7	55294	0.04	NM_033632	NP_361014	1.09	F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila)
222732_at	TRIM39	56658	0.02	NM_021253	NP_067076	0.92	tripartite motif-containing 39
222740_at	ATAD2	29028	0.04	NM_014109	NP_054828	0.87	ATPase family, AAA domain containing 2
222752_s_at	FLJ10874	55248	1.45e-03	NM_018252	NP_060722	0.84	hypothetical protein FLJ10874
222754_at	TRNT1	51095	4.83e-03	NM_182916	NP_886552	0.86	tRNA nucleotidyl transferase, CCA-adding, 1
222754_at	TRNT1	51095	4.83e-03	NM_016000	NP_057084	0.86	tRNA nucleotidyl transferase, CCA-adding, 1
222757_s_at	ZAK	51776	2.53e-03	NM_133646	NP_598407	1.14	sterile alpha motif and leucine zipper containing kinase AZK
222757_s_at	ZAK	51776	2.53e-03	NM_016653	NP_057737	1.14	sterile alpha motif and leucine zipper containing kinase AZK

222759_at	SUV420H1	51111	0.04	NM_016028	NP_057112	0.91	suppressor of variegation 4-20 homolog 1 (Drosophila)
222765_x_at	C20orf6	51575	0.01	NM_016649	NP_057733	0.83	chromosome 20 open reading frame 6
222775_s_at	MRPL35	51318	9.04e-03	NM_016622	NP_057706	0.87	mitochondrial ribosomal protein L35
222777_s_at	WHSC1	7468	0.02	NM_007331	NP_015627	0.88	Wolf-Hirschhorn syndrome candidate 1
222779_s_at	HSA277841	55421	0.03	NM_018553	NP_061023	0.94	ELG protein
222781_s_at	C9orf40	55071	0.04	NM_017998	NP_060468	0.84	chromosome 9 open reading frame 40
222788_s_at	RSBN1	54665	0.03	NM_018364	NP_060834	0.85	round spermatid basic protein 1
222793_at	DDX58	23586	0.01	NM_014314	NP_055129	0.75	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
222794_x_at	PAPD1	55149	0.04	NM_018109	NP_060579	0.86	PAP associated domain containing 1
222804_x_at	WDR32	79269	0.01	NM_024345	NP_077321	0.92	WD repeat domain 32
222806_s_at	C11orf30	56946	0.03	NM_020193	NP_064578	0.91	chromosome 11 open reading frame 30
222816_s_at	ZCCHC2	54877	0.03	NM_017742	NP_060212	1.27	zinc finger, CCHC domain containing 2
222820_at	TNRC6C	57690	9.53e-04	AK000022	BAA90890	0.83	trinucleotide repeat containing 6C
222824_at	NUDT5	11164	0.03	AW237290		0.89	nudix (nucleoside diphosphate linked moiety X)-type motif 5
222832_s_at	C2orf33	56947	0.01	NM_020194	NP_064579	0.93	chromosome 2 open reading frame 33
222835_at	FLJ13710	79875	0.03	BG163478		1.06	hypothetical protein FLJ13710
222837_s_at	NARG1	80155	0.04	NM_057175	NP_476516	0.86	NMDA receptor regulated 1
222838_at	SLAMF7	57823	0.02	NM_021181	NP_067004	0.83	SLAM family member 7
222846_at	RAB8B	51762	0.02	AB038995	BAA92249	0.91	RAB8B, member RAS oncogene family
222849_s_at	SCRN3	79634	6.08e-03	NM_024583	NP_078859	0.94	secernin 3
222850_s_at	FLJ14281	79982	0.02	NM_024920	NP_079196	0.95	hypothetical protein FLJ14281
222851_at	ZNF654	55279	0.04	NM_018293	NP_060763	0.93	zinc finger protein 654
222868_s_at	IL18BP	10068	4.02e-03	NM_173042	NP_766630	0.92	interleukin 18 binding protein
222872_x_at	FLJ22833	64859	5.31e-03	NM_022837	NP_073748	1.10	hypothetical protein FLJ22833
222874_s_at	CLN8	2055	0.03	NM_018941	NP_061764	0.85	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive
with mental retardation)							
222883_at	FLJ12439	65260	0.03	NM_023077	NP_075565	0.85	hypothetical protein FLJ12439
222889_at	DCLRE1B	64858	0.04	NM_022836	NP_073747	0.86	DNA cross-link repair 1B (PSO2 homolog, S.
cerevisiae)							
222893_s_at	FLJ13150	79871	0.02	NM_024813	NP_079089	0.90	hypothetical protein FLJ13150
222903_s_at	CPEB1	64506	0.02	NM_030594	NP_085097	1.16	cytoplasmic polyadenylation element binding protein 1
222907_x_at	C21orf4	757	0.04	NM_006134	NP_006125	0.90	chromosome 21 open reading frame 4
222913_at	KLF3	51274	0.03	NM_016531	NP_057615	0.91	Kruppel-like factor 3 (basic)
222955_s_at	FAM45A	404636	6.71e-03	NM_207009	NP_996892	1.19	family with sequence similarity 45, member A
222978_at	SURF4	6836	6.11e-03	NM_033161	NP_149351	0.88	surfeit 4
222979_s_at	SURF4	6836	5.4e-03	NM_033161	NP_149351	0.93	surfeit 4
222980_at	RAB10	10890	0.03	NM_016131	NP_057215	0.96	RAB10, member RAS oncogene family
222981_s_at	RAB10	10890	0.03	NM_016131	NP_057215	0.88	RAB10, member RAS oncogene family
222982_x_at	SLC38A2	54407	0.01	NM_018976	NP_061849	0.90	solute carrier family 38, member 2
222985_at	YWHAG	7532	0.01	NM_012479	NP_036611	0.87	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
activation protein, gamma polypeptide							
222989_s_at	UBQLN1	29979	0.01	NM_013438	NP_038466	0.81	ubiquilin 1
222993_at	MRPL37	51253	6.92e-03	NM_016491	NP_057575	0.84	mitochondrial ribosomal protein L37
222997_s_at	MRPS21	54460	0.04	NM_031901	NP_114107	0.90	mitochondrial ribosomal protein S21
222999_s_at	CCNL2	81669	0.03	NM_030937	NP_112199	0.89	cyclin L2

223001_at	DC2	58505	0.01	NM_021227	NP_067050	0.91	DC2 protein
223002_s_at	XRN2	22803	8.32e-03	NM_012255	NP_036387	0.92	5'-3' exoribonuclease 2
223004_s_at	C3orf1	51300	0.01	NM_016589	NP_057673	0.93	chromosome 3 open reading frame 1
223010_s_at	OCIAD1	54940	0.02	NM_017830	NP_060300	0.94	OCIA domain containing 1
223011_s_at	OCIAD1	54940	5.83e-03	NM_017830	NP_060300	0.94	OCIA domain containing 1
223013_at	TBL1XR1	79718	0.03	AF267864	AAG44733	0.95	transducin (beta)-like 1X-linked receptor 1
223016_x_at	ZNF265	9406	0.02	NM_203350	NP_976225	0.91	zinc finger protein 265
223020_at	CRR9	81037	0.02	NM_030782	NP_110409	0.90	cisplatin resistance related protein CRR9p
223021_x_at	C6orf55	51534	0.01	NM_016485	NP_057569	0.92	chromosome 6 open reading frame 55
223022_s_at	C6orf55	51534	0.01	NM_016485	NP_057569	0.89	chromosome 6 open reading frame 55
223023_at	BET1L	51272	0.01	NM_016526	NP_057610	0.92	blocked early in transport 1 homolog (S. cerevisiae) like
223026_s_at	VPS29	51699	5.82e-04	NM_016226	NP_057310	0.95	vacuolar protein sorting 29 (yeast)
223032_x_at	PX19	27166	0.01	NM_013237	NP_037369	0.95	px19-like protein
223036_at	FARSLB	10056	0.03	NM_005687	NP_005678	1.11	phenylalanine-tRNA synthetase-like, beta subunit
223040_at	NAT5	51126	0.04	NM_016100	NP_057184	0.89	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae)
223041_at	CD99L2	83692	5.78e-03	NM_134446	NP_604395	0.90	CD99 antigen-like 2
223041_at	CD99L2	83692	5.78e-03	NM_134445	NP_604394	0.90	CD99 antigen-like 2
223041_at	CD99L2	83692	5.78e-03	NM_031462	NP_113650	0.90	CD99 antigen-like 2
223042_s_at	FUNDC2	65991	3.98e-03	NM_023934	NP_076423	0.93	FUN14 domain containing 2
223053_x_at	HSPC182	29101	0.02	NM_014188	NP_054907	0.92	HSPC182 protein
223057_s_at	XPO5	57510	3.55e-03	NM_020750	NP_065801	0.93	exportin 5
223066_at	SNAPAP	23557	0.01	NM_012437	NP_036569	0.92	SNAP-associated protein
223069_s_at	EML4	27436	6.11e-03	NM_019063	NP_061936	0.91	echinoderm microtubule associated protein like 4
223071_at	IER3IP1	51124	8.05e-03	NM_016097	NP_057181	0.86	immediate early response 3 interacting protein 1
223076_s_at	NSUN2	54888	0.04	NM_017755	NP_060225	0.83	NOL1/NOP2/Sun domain family, member 2
223079_s_at	GLS	2744	0.01	AF158555	AAD47056	0.89	glutaminase
223080_at	GLS	2744	0.04	AK025021	0.89	glutaminase	
223085_at	RNF19	25897	0.03	NM_183419	NP_904355	0.89	ring finger protein 19
223086_x_at	MRPL51	51258	8.42e-03	NM_016497	NP_057581	0.92	mitochondrial ribosomal protein L51
223087_at	ECHDC1	55862	0.04	NM_018479	NP_060949	0.89	enoyl Coenzyme A hydratase domain containing 1
223088_x_at	ECHDC1	55862	3.37e-03	NM_018479	NP_060949	0.91	enoyl Coenzyme A hydratase domain containing 1
223090_x_at	VEZATIN	55591	0.03	NM_017599	NP_060069	0.84	transmembrane protein vezatin
223092_at	ANKH	56172	0.01	NM_054027	NP_473368	0.85	ankylosis, progressive homolog (mouse)
223096_at	NOP5/NOP58	51602	2.28e-03	NM_015934	NP_057018	0.85	nucleolar protein NOP5/NOP58
223098_s_at	LONP	83752	0.01	NM_031490	NP_113678	0.88	peroxisomal lon protease
223101_s_at	ARPC5L	81873	0.03	NM_030978	NP_112240	0.90	actin related protein 2/3 complex, subunit 5-like
223107_s_at	PSID	51538	0.04	NM_016505	NP_057589	0.84	putative S1 RNA binding domain protein
223112_s_at	NDUFB10	4716	0.04	NM_004548	NP_004539	0.92	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa
223114_at	MGC4767	84274	0.02	BC004916	AAH04916	0.88	hypothetical protein MGC4767
223117_s_at	USP47	55031	9.61e-03	AK074076	BAB84902	0.89	ubiquitin specific protease 47
223118_s_at	USP47	55031	0.04	AK074076	BAB84902	0.90	ubiquitin specific protease 47
223130_s_at	MYLIP	29116	7.16e-03	NM_013262	NP_037394	0.89	myosin regulatory light chain interacting protein
223133_at	TMEM14B	81853	0.01	NM_030969	NP_112231	0.87	transmembrane protein 14B
223134_at	BBX	56987	0.02	NM_020235	NP_064620	0.88	bobby sox homolog (Drosophila)

223140_s_at	DHX36	170506	0.01	NM_020865	NP_065916	0.95	DEAH (Asp-Glu-Ala-His) box polypeptide 36
223154_at	MRPL1	65008	0.02	NM_020236	NP_064621	0.84	mitochondrial ribosomal protein L1
223155_at	HDHD2	84064	0.02	NM_032124	NP_115500	0.90	haloacid dehalogenase-like hydrolase domain containing 2
223156_at	MRPS23	51649	0.01	NM_016070	NP_057154	0.84	mitochondrial ribosomal protein S23
223161_at	LCHN	57189	0.02	AB032973	BAA86461	0.88	LCHN protein
223162_s_at	LCHN	57189	1.19e-03	AF116707	AAF71127	0.89	LCHN protein
223163_s_at	ZC3HC1	51530	0.03	NM_016478	NP_057562	0.92	zinc finger, C3HC type 1
223164_at	CCM2	83605	5.07e-03	NM_031443	NP_113631	0.88	cerebral cavernous malformation 2
223175_s_at	FEM1A	55527	0.02	NM_018708	NP_061178	0.87	fem-1 homolog a (C.elegans)
223181_at	C18orf55	29090	9.92e-03	NM_014177	NP_054896	0.80	chromosome 18 open reading frame 55
223182_s_at	AGPAT3	56894	0.01	AK074300	BAB85042	1.18	1-acylglycerol-3-phosphate O-acyltransferase 3
223187_s_at	ORMDL1	94101	2.4e-03	NM_016467	NP_057551	0.89	ORM1-like 1 (S. cerevisiae)
223191_at	C14orf112	51241	0.02	NM_016468	NP_057552	0.88	chromosome 14 open reading frame 112
223199_at	MKNK2	2872	0.03	NM_199054	NP_951009	1.15	MAP kinase interacting serine/threonine kinase 2
223199_at	MKNK2	2872	0.03	NM_017572	NP_060042	1.15	MAP kinase interacting serine/threonine kinase 2
223200_s_at	FLJ11301	55341	0.02	NM_018385	NP_060855	0.83	hypothetical protein FLJ11301
223203_at	TMEM29	29057	0.04	NM_014138	NP_054857	0.93	transmembrane protein 29
223205_s_at	L3MBTL2	83746	2.6e-03	NM_031488	NP_113676	0.87	l(3)mbt-like 2 (Drosophila)
223208_at	KCTD10	83892	0.03	NM_031954	NP_114160	0.90	potassium channel tetramerisation domain containing 10
223209_s_at	SELS	55829	0.03	NM_018445	NP_060915	0.92	selenoprotein S
223211_at	HPCL2	26061	0.02	BC001627	AAH01627	0.90	2-hydroxyphytanoyl-CoA lyase
223213_s_at	ZHX1	11244	9.27e-03	NM_007222	NP_009153	0.86	zinc fingers and homeoboxes 1
223214_s_at	ZHX1	11244	0.01	NM_007222	NP_009153	0.82	zinc fingers and homeoboxes 1
223215_s_at	C14orf100	51528	0.01	NM_016475	NP_057559	0.96	chromosome 14 open reading frame 100
223222_at	SLC25A19	60386	0.03	NM_021734	NP_068380	0.90	solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19
223223_at	ARV1	64801	0.02	NM_022786	NP_073623	0.88	ARV1 homolog (yeast)
223226_x_at	SSBP4	170463	0.02	NM_032627	NP_116016	0.92	single stranded DNA binding protein 4
223227_at	BBS2	583	0.03	NM_031885	NP_114091	0.87	Bardet-Biedl syndrome 2
223230_at	FLJ14936	84950	6.4e-03	NM_032864	NP_116253	0.89	hypothetical protein FLJ14936
223230_at	FLJ14936	84950	6.4e-03	NM_032284	NP_115660	0.89	hypothetical protein FLJ14936
223242_s_at	ET	79157	0.04	NM_024311	NP_077287	0.93	hypothetical protein ET
223244_s_at	DAP13	55967	7.7e-03	NM_018838	NP_061326	0.83	13kDa differentiation-associated protein
223247_at	MGC5309	84246	0.02	NM_032286	NP_115662	0.86	hypothetical protein MGC5309
223251_s_at	ANKRD10	55608	0.03	BC001727	AAH01727	0.90	ankyrin repeat domain 10
223259_at	ORMDL3	94103	0.02	NM_139280	NP_644809	0.85	ORM1-like 3 (S. cerevisiae)
223262_s_at	FGFR1OP2	26127	3.1e-03	NM_015633	NP_056448	0.81	FGFR1 oncogene partner 2
223269_at	POLR3GL	84265	5.32e-03	NM_032305	NP_115681	0.92	polymerase (RNA) III (DNA directed) polypeptide G (32kD) like
223271_s_at	HSPC129	51496	4.31e-03	NM_016396	NP_057480	0.88	hypothetical protein HSPC129
223273_at	C14orf142	84520	2.97e-03	NM_032490	NP_115879	0.85	chromosome 14 open reading frame 142
223275_at	HRMT1L6	55170	0.01	NM_018137	NP_060607	0.87	HMT1 hnRNP methyltransferase-like 6 (S. cerevisiae)
223277_at	FLJ20211	54859	0.04	BC000623	AAH00623	0.90	hypothetical protein FLJ20211
223282_at	SDCCAG33	10194	0.04	NM_005786	NP_005777	0.88	serologically defined colon cancer antigen 33
223288_at	USP38	84640	0.03	NM_032557	NP_115946	0.89	ubiquitin specific protease 38

223297_at	MGC4268	83607	0.04	NM_031445	NP_113633	0.93	hypothetical protein MGC4268
223298_s_at	NT5C3	51251	0.02	NM_016489	NP_057573	0.78	5'-nucleotidase, cytosolic III
223299_at	SEC11L3	90701	0.02	NM_033280	NP_150596	0.90	SEC11-like 3 (S. cerevisiae)
223302_s_at	ZNF655	79027	0.04	NM_024061	NP_076966	0.91	zinc finger protein 655
223306_at	EBPL	84650	0.03	NM_032565	NP_115954	0.90	emopamil binding protein-like
223309_x_at	IPLA2(GAMMA)	50640	0.02	NM_015723	NP_056538	0.94	intracellular membrane-associated calcium-independent phospholipase A2 gamma
223314_at	TM4SF14	81619	2.84e-05	AK025157		0.91	transmembrane 4 superfamily member 14
223320_s_at	ABCB10	23456	0.01	NM_012089	NP_036221	0.88	ATP-binding cassette, sub-family B (MDR/TAP), member 10
223324_s_at	TRPM7	54822	0.01	NM_017672	NP_060142	0.89	transient receptor potential cation channel, subfamily M, member 7
223329_x_at	SUGT1	10910	0.02	NM_006704	NP_006695	0.92	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)
223330_s_at	SUGT1	10910	0.02	NM_006704	NP_006695	0.87	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)
223331_s_at	DDX20	11218	4.83e-03	NM_007204	NP_009135	0.90	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20
223337_at	SDCCAG10	10283	4.77e-03	NM_005869	NP_005860	0.87	serologically defined colon cancer antigen 10
223354_x_at	C2orf33	56947	6.71e-03	NM_020194	NP_064579	0.87	chromosome 2 open reading frame 33
223358_s_at	PDE7A	5150	0.02	AW269834		0.90	phosphodiesterase 7A
223361_at	C6orf115	58527	5.93e-03	AF116682	AAF71102	0.83	chromosome 6 open reading frame 115
223369_at	AD-003	28989	0.01	NM_014064	NP_054783	0.92	AD-003 protein
223380_s_at	LATS2	26524	0.04	NM_014572	NP_055387	1.20	LATS, large tumor suppressor, homolog 2 (Drosophila)
223386_at	FLJ21103	79607	8.05e-03	NM_024556	NP_078832	0.88	hypothetical protein FLJ21103
223391_at	SGPP1	81537	7.69e-03	NM_030791	NP_110418	0.87	sphingosine-1-phosphate phosphatase 1
223394_at	SERTAD1	29950	0.01	NM_013376	NP_037508	1.11	SERTA domain containing 1
223396_at	C7orf35	85025	0.02	NM_032936	NP_116325	0.95	chromosome 7 open reading frame 35
223401_at	MDS006	56985	0.04	NM_020233	NP_064618	1.07	x 006 protein
223403_s_at	POLR1B	84172	0.01	NM_019014	NP_061887	0.83	polymerase (RNA) I polypeptide B, 128kDa
223406_x_at	NIP30	80011	0.01	AF212249	AAK14932	0.94	NEFA-interacting nuclear protein NIP30
223411_at	AD023	57409	0.03	NM_020679	NP_065730	0.87	AD023 protein
223412_at	KBTBD7	84078	0.04	NM_032138	NP_115514	1.16	kelch repeat and BTB (POZ) domain containing 7
223413_s_at	LYAR	55646	1.85e-03	NM_017816	NP_060286	0.83	hypothetical protein FLJ20425
223416_at	SF3B14	51639	0.03	NM_016047	NP_057131	0.97	splicing factor 3B, 14 kDa subunit
223418_x_at	DKFZP566D1346	81573	0.01	NM_030816	NP_110443	0.85	hypothetical protein DKFZp566D1346
223421_at	CYHR1	50626	4.9e-03	NM_032687	NP_116076	0.85	cysteine and histidine rich 1
223422_s_at	ARHGAP24	83478	0.04	NM_031305	NP_112595	1.12	Rho GTPase activating protein 24
223425_at	RAVER1	125950	6.92e-03	NM_133452	NP_597709	1.10	RAVER1
223431_at	CNO	55330	0.03	NM_018366	NP_060836	0.88	cappuccino
223433_at	C7orf36	57002	0.03	NM_020192	NP_064577	0.85	chromosome 7 open reading frame 36
223440_at	Lin10	80262	0.03	NM_025187	NP_079463	0.94	lin-10 protein homolog
223443_s_at	FLJ32065	201283	0.02	NM_153032	NP_694577	0.88	hypothetical protein FLJ32065
223446_s_at	DTNBP1	84062	0.03	NM_032122	NP_115498	0.85	dystrobrevin binding protein 1
223450_s_at	COG3	83548	0.02	NM_031431	NP_113619	0.91	component of oligomeric golgi complex 3
223455_at	MGC10854	84260	0.02	NM_032300	NP_115676	0.92	hypothetical protein MGC10854
223459_s_at	FLJ20519	54964	0.03	NM_017860	NP_060330	1.11	hypothetical protein FLJ20519
223461_at	TBC1D7	51256	0.02	NM_016495	NP_057579	0.89	TBC1 domain family, member 7

223469_at	MGC10812	83542	0.04	BC004942	AAH04942	0.88	hypothetical protein MGC10812
223470_at	PIGM	93183	0.03	NM_145167	NP_660150	0.89	phosphatidylinositol glycan, class M
223474_at	C14orf4	64207	0.04	NM_024496	NP_078772	0.92	chromosome 14 open reading frame 4
223480_s_at	MRPL47	57129	8.05e-03	NM_020409	NP_065142	0.90	mitochondrial ribosomal protein L47
223490_s_at	EXOSC3	51010	0.02	NM_016042	NP_057126	0.86	exosome component 3
223501_at	TNFSF13B	10673	0.04	NM_006573	NP_006564	1.13	tumor necrosis factor (ligand) superfamily, member 13b
223502_s_at	TNFSF13B	10673	6.71e-03	NM_006573	NP_006564	1.19	tumor necrosis factor (ligand) superfamily, member 13b
223506_at	ZC3HDC8	84524	0.04	NM_032494	NP_115883	0.88	zinc finger CCCH type domain containing 8
223515_s_at	COQ3	51805	0.04	NM_017421	NP_059117	0.83	coenzyme Q3 homolog, methyltransferase (yeast)
223516_s_at	C6orf49	29964	0.02	NM_013397	NP_037529	0.91	chromosome 6 open reading frame 49
223527_s_at	CDADC1	81602	0.04	NM_030911	NP_112173	0.90	cytidine and dCMP deaminase domain containing 1
223528_s_at	FLJ20859	64745	2.02e-03	NM_022734	NP_073571	0.82	FLJ20859 gene
223531_x_at	GPR89	51463	0.03	NM_016334	NP_057418	0.84	G protein-coupled receptor 89
223533_at	FAD158	84230	7.76e-03	NM_032270	NP_115646	0.89	factor for adipocyte differentiation 158
223547_at	C14orf100	51528	0.02	NM_016475	NP_057559	1.12	chromosome 14 open reading frame 100
223552_at	LRRC4	64101	0.01	NM_022143	NP_071426	1.20	leucine rich repeat containing 4
223555_at	FLJ20203	54856	0.02	NM_032292	NP_115668	0.91	hypothetical protein FLJ20203
223590_at	DKFZp434I1610	90592	0.02	AL136732	CAB66666	0.92	hypothetical protein DKFZp434I1610
223591_at	RNF135	84282	9.63e-03	NM_032322	NP_115698	0.92	ring finger protein 135
223592_s_at	RNF135	84282	2.67e-03	NM_032322	NP_115698	0.93	ring finger protein 135
223602_at	USP30	84749	9.35e-03	NM_032663	NP_116052	0.91	ubiquitin specific protease 30
223606_x_at	KIAA1704	55425	0.02	AF245045	AAG44482	0.90	KIAA1704
223611_s_at	LNX	84708	0.01	NM_032622	NP_116011	1.24	ligand of numb-protein X
223615_at	ABI3	51225	0.04	NM_016428	NP_057512	0.87	ABI gene family, member 3
223626_x_at	FAM14A	83982	0.01	NM_032036	NP_114425	0.90	family with sequence similarity 14, member A
223637_s_at	DKFZP566M1046	84067	0.03	NM_032127	NP_115503	0.91	hypothetical protein DKFZp566M1046
223639_s_at	ZNRD1	30834	5.57e-03	NM_170783	NP_740753	0.89	zinc ribbon domain containing, 1
223640_at	HCST	10870	2.8e-03	NM_014266	NP_055081	0.86	hematopoietic cell signal transducer
223649_s_at	CGI-69	51629	0.04	NM_016016	NP_057100	0.90	CGI-69 protein
223675_s_at	VEZATIN	55591	0.02	NM_017599	NP_060069	0.83	transmembrane protein vezatin
223686_at	TPK1	27010	0.03	NM_022445	NP_071890	0.90	thiamin pyrophosphokinase 1
223701_s_at	USP47	55031	0.02	NM_017944	NP_060414	0.90	ubiquitin specific protease 47
223705_s_at	DKFZp761C169	65056	0.01	NM_022913	NP_075064	0.92	vasculin
223716_s_at	ZNF265	9406	0.03	NM_203350	NP_976225	0.91	zinc finger protein 265
223728_at	MGC16385	92806	0.04	NM_145039	NP_659476	0.93	hypothetical protein MGC16385
223735_at	ARL6	84100	8.65e-03	NM_032146	NP_115522	0.80	ADP-ribosylation factor-like 6
223740_at	C6orf59	79992	0.03	NM_024929	NP_079205	1.21	chromosome 6 open reading frame 59
223741_s_at	TTYH2	94015	7.69e-04	NM_032646	NP_116035	0.75	tweety homolog 2 (Drosophila)
223751_x_at	TLR10	81793	2.53e-03	NM_030956	NP_112218	1.17	toll-like receptor 10
223776_x_at	TINF2	26277	0.03	BC005030	AAH05030	0.96	TERF1 (TRF1)-interacting nuclear factor 2
223803_s_at	ZCCHC10	54819	0.01	NM_017665	NP_060135	0.91	zinc finger, CCHC domain containing 10
223814_at	TRNT1	51095	0.02	BC005184	AAH05184	0.86	tRNA nucleotidyl transferase, CCA-adding, 1
223824_at	C10orf59	55328	0.03	BC005364	AAH05364	0.91	chromosome 10 open reading frame 59
223835_x_at	OTP	23440	0.03	NM_032109	NP_115485	1.16	orthopedia homolog (Drosophila)

223887_at	GPR132	29933	0.04	NM_013345	NP_037477	0.91	G protein-coupled receptor 132
223894_s_at	FTS	64400	0.02	NM_022476	NP_071921	0.91	fused toes homolog (mouse)
223944_at	NALP12	91662	0.01	NM_144687	NP_653288	1.20	NACHT, leucine rich repeat and PYD containing 12
223944_at	NALP12	91662	0.01	NM_033297	NP_150639	1.20	NACHT, leucine rich repeat and PYD containing 12
223983_s_at	C19orf12	83636	0.01	NM_031448	NP_113636	0.88	chromosome 19 open reading frame 12
223988_x_at	FLJ20859	64745	3.98e-03	NM_022734	NP_073571	0.79	FLJ20859 gene
223996_s_at	MRPL30	51263	0.01	NM_145212	NP_660213	0.90	mitochondrial ribosomal protein L30
224025_s_at	APG7L	10533	0.04	NM_006395	NP_006386	0.88	APG7 autophagy 7-like (S. cerevisiae)
224035_s_at	BCL2L13	23786	7.84e-03	NM_015367	NP_056182	0.88	BCL2-like 13 (apoptosis facilitator)
224042_at	UPB1	51733	0.02	AF163312	AAF06735	1.13	ureidopropionase, beta
224044_at	RHOT1	55288	0.01	NM_018307	NP_060777	1.38	ras homolog gene family, member T1
224046_s_at	PDE7A	5150	5.06e-03	NM_002603	NP_002594	0.88	phosphodiesterase 7A
224058_s_at	LOC158160	158160	9.96e-03	NM_182829	NP_878249	0.72	hypothetical protein LOC158160
224060_s_at	CGI-30	51611	0.01	NM_015958	NP_057042	0.88	CGI-30 protein
224068_x_at	RBM22	55696	5.86e-04	NM_018047	NP_060517	0.94	RNA binding motif protein 22
224124_at	ZRANB3	84083	0.02	NM_032143	NP_115519	1.09	zinc finger, RAN-binding domain containing 3
224129_s_at	LOC84661	84661	0.02	NM_032574	NP_115963	0.93	dpy-30-like protein
224132_at	MGC13008	84772	0.01	BC005072	AAH05072	0.88	hypothetical protein MGC13008
224148_at	FYB	2533	0.03	AF116653	AAF71073	0.89	FYN binding protein (FYB-120/130)
224175_s_at	TRIM34	53840	7.27e-04	NM_021616	NP_067629	0.83	tripartite motif-containing 34
224187_x_at	HSPA8	3312	0.03	NM_006597	NP_006588	0.90	heat shock 70kDa protein 8
224196_x_at	CGI-30	51611	0.01	NM_015958	NP_057042	0.91	CGI-30 protein
224206_x_at	MYNN	55892	9.29e-03	NM_018657	NP_061127	0.97	myoneurin
224221_s_at	VAV3	10451	0.03	NM_006113	NP_006104	0.92	vav 3 oncogene
224232_s_at	PX19	27166	5.84e-03	NM_013237	NP_037369	0.86	px19-like protein
224281_s_at	NEUGRIN	51335	0.01	NM_016645	NP_057729	0.89	mesenchymal stem cell protein DSC92
224316_at	KCTD9	54793	5.83e-03	AF130091	AAG35517	1.10	potassium channel tetramerisation domain containing 9
224318_s_at	FLJ10081	55683	6.11e-03	NM_017991	NP_060461	0.92	hypothetical protein FLJ10081
224326_s_at	PCGF6	84108	0.01	NM_032154	NP_115530	0.91	polycomb group ring finger 6
224330_s_at	MRPL27	51264	0.03	NM_016504	NP_057588	0.91	mitochondrial ribosomal protein L27
224331_s_at	MRPL36	64979	0.01	NM_032479	NP_115868	0.90	mitochondrial ribosomal protein L36
224334_s_at	MRPL51	51258	0.01	NM_016497	NP_057581	0.90	mitochondrial ribosomal protein L51
224352_s_at	CFL2	1073	0.01	NM_021914	NP_068733	0.85	cofilin 2 (muscle)
224364_s_at	PPIL3	53938	0.01	NM_032472	NP_115861	0.88	peptidylprolyl isomerase (cyclophilin)-like 3
224366_s_at	REPS1	85021	0.01	NM_031922	NP_114128	0.91	RALBP1 associated Eps domain containing 1
224368_s_at	NDRG3	57446	1.24e-03	NM_032013	NP_114402	1.15	NDRG family member 3
224391_s_at	CSE-C	54414	3.6e-03	NM_170601	NP_733746	0.87	cytosolic sialic acid 9-O-acetylesterase homolog
224395_s_at	RNF7	9616	0.02	NM_014245	NP_055060	0.90	ring finger protein 7
224407_s_at	MST4	51765	0.01	NM_016542	NP_057626	0.85	Mst3 and SOK1-related kinase
224413_s_at	BLP1	83877	0.01	NM_078473	NP_510882	0.90	BBP-like protein 1
224416_s_at	MED28	80306	5.48e-03	NM_025205	NP_079481	0.86	mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)
224427_s_at	PAPOLG	64895	0.01	NM_022894	NP_075045	0.92	poly(A) polymerase gamma
224434_s_at	MGC4238	84292	2.31e-03	NM_032332	NP_115708	0.91	mitogen-activated protein kinase organizer 1
224436_s_at	NIPSNAP3A	25934	0.01	NM_015469	NP_056284	0.86	nipsnap homolog 3A (C. elegans)

224437_s_at	C6orf55	51534	8.05e-03	NM_016485	NP_057569	0.90	chromosome 6 open reading frame 55
224439_x_at	RNF7	9616	0.02	NM_014245	NP_055060	0.95	ring finger protein 7
224445_s_at	ZFYVE21	79038	0.01	NM_024071	NP_076976	0.89	zinc finger, FYVE domain containing 21
224446_at	MGC14817	84298	2.28e-03	NM_032338	NP_115714	0.87	hypothetical protein MGC14817
224448_s_at	C6orf125	84300	0.01	NM_032340	NP_115716	0.83	chromosome 6 open reading frame 125
224452_s_at	MGC12966	84792	0.03	NM_032706	NP_116095	0.88	hypothetical protein MGC12966
224479_s_at	MRPL45	84311	1.21e-04	NM_032351	NP_115727	0.93	mitochondrial ribosomal protein L45
224481_s_at	HECTD1	25831	0.04	NM_015382	NP_056197	0.93	HECT domain containing 1
224492_s_at	ZNF627	199692	0.01	NM_145295	NP_660338	0.91	zinc finger protein 627
224502_s_at	KIAA1191	57179	0.03	NM_020444	NP_065177	0.88	KIAA1191 protein
224518_s_at	ZNF559	84527	0.03	NM_032497	NP_115886	0.89	zinc finger protein 559
224524_s_at	ASB3	51130	0.01	NM_016115	NP_057199	0.90	ankyrin repeat and SOCS box-containing 3
224558_s_at	MALAT1	378938	8.8e-03	BX538238		0.94	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)
224561_s_at	MORF4L1	10933	0.01	NM_006791	NP_006782	0.95	mortality factor 4 like 1
224574_at	MGC49942	124944	0.04	NM_174893	NP_777553	0.94	hypothetical protein MGC49942
224575_at	C3orf10	55845	0.02	NM_018462	NP_060932	0.95	chromosome 3 open reading frame 10
224578_at	TD-60	55920	0.02	NM_018715	NP_061185	0.88	RCC1-like
224579_at	SLC38A1	81539	0.01	BF247552		0.85	solute carrier family 38, member 1
224584_at	C20orf30	29058	1.33e-03	NM_014145	NP_054864	0.94	chromosome 20 open reading frame 30
224586_x_at	PC4	10923	0.03	NM_006713	NP_006704	0.91	activated RNA polymerase II transcription cofactor 4
224593_at	ZFOC1	144348	0.04	NM_152437	NP_689650	0.89	zinc finger protein ZFOC1
224598_at	MGAT4B	11282	0.02	NM_014275	NP_055090	0.89	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme B
224599_at	CGGBP1	8545	2.78e-04	NM_003663	NP_003654	0.86	CGG triplet repeat binding protein 1
224600_at	CGGBP1	8545	5.48e-03	NM_003663	NP_003654	0.94	CGG triplet repeat binding protein 1
224607_s_at	SRP68	6730	0.02	NM_014230	NP_055045	0.90	signal recognition particle 68kDa
224608_s_at	MGC10540	84313	0.01	NM_032353	NP_115729	0.92	hypothetical protein MGC10540
224610_at	RNU22	9304	7.02e-03	AL530869		0.82	RNA, U22 small nucleolar
224616_at	DNCLI2	1783	0.03	NM_006141	NP_006132	0.87	dynein, cytoplasmic, light intermediate polypeptide 2
224624_at	LRRC8	56262	1.13e-03	NM_019594	NP_062540	0.84	leucine rich repeat containing 8
224626_at	SLC35A4	113829	0.04	NM_080670	NP_542401	0.93	solute carrier family 35, member A4
224635_s_at	BIRC6	57448	0.01	AK023848	BAB14700	0.92	baculoviral IAP repeat-containing 6 (apollon)
224636_at	ZFP91	80829	0.03	NM_053023	NP_444251	0.93	zinc finger protein 91 homolog (mouse)
224638_at	SPPL3	121665	4.19e-03	NM_139015	NP_620584	1.24	signal peptide peptidase 3
224641_at	FYTTD1	84248	7.35e-03	NM_032288	NP_115664	0.93	forty-two-three domain containing 1
224642_at	FYTTD1	84248	0.01	NM_032288	NP_115664	0.92	forty-two-three domain containing 1
224643_at	LOC133619	133619	8.8e-03	NM_130809	NP_570721	0.94	hypothetical protein MGC12103
224645_at	EIF4EBP2	1979	8.05e-03	BG106477		0.90	eukaryotic translation initiation factor 4E binding protein 2
224648_at	DKFZp761C169	65056	0.03	AK024807	BAB15013	0.92	vasculin
224651_at	C10orf9	219771	0.04	NM_181698	NP_859049	0.94	chromosome 10 open reading frame 9
224651_at	C10orf9	219771	0.04	NM_145012	NP_659449	0.94	chromosome 10 open reading frame 9
224652_at	C10orf9	219771	1.54e-03	NM_145012	NP_659449	0.90	chromosome 10 open reading frame 9
224652_at	C10orf9	219771	1.54e-03	NM_181698	NP_859049	0.90	chromosome 10 open reading frame 9
224653_at	EIF4EBP2	1979	0.03	U88989		0.91	eukaryotic translation initiation factor 4E binding protein 2

224654_at	ZNF596	169270	6.71e-03	AK093442	BAC04166	0.94	zinc finger protein 596
224655_at	AK3L1	50808	5.83e-03	NM_016282	NP_057366	0.86	adenylate kinase 3 like 1
224656_s_at	MTPN	136319	0.02	NM_145808	NP_665807	0.93	myotrophin
224660_at	MGC14156	84992	0.02	NM_032906	NP_116295	0.91	hypothetical protein MGC14156
224661_at	MGC14156	84992	0.01	NM_032906	NP_116295	1.28	hypothetical protein MGC14156
224664_at	C10orf104	119504	0.04	NM_173473	NP_775744	0.93	chromosome 10 open reading frame 104
224669_at	C20orf35	55861	0.03	NM_018478	NP_060948	0.95	chromosome 20 open reading frame 35
224669_at	C20orf35	55861	0.03	NM_033542	NP_291020	0.95	chromosome 20 open reading frame 35
224670_at	C20orf35	55861	0.01	NM_018478	NP_060948	0.89	chromosome 20 open reading frame 35
224670_at	C20orf35	55861	0.01	NM_033542	NP_291020	0.89	chromosome 20 open reading frame 35
224675_at	MESDC2	23184	0.01	AK026606		0.91	mesoderm development candidate 2
224677_x_at	C11orf31	280636	0.04	NM_170746	NP_734467	0.89	chromosome 11 open reading frame 31
224679_at	MESDC2	23184	0.04	D42039	BAA07640	0.85	mesoderm development candidate 2
224680_at containing 4	TMED4	222068	0.03	NM_182547	NP_872353	0.86	transmembrane emp24 protein transport domain
224687_at	ANKIB1	54467	0.02	AB037807	BAA92624	0.87	ankyrin repeat and IBR domain containing 1
224688_at	FLJ10099	55069	0.01	BE962299		0.90	hypothetical protein FLJ10099
224690_at	C20orf108	116151	8.8e-03	NM_080821	NP_543011	0.87	chromosome 20 open reading frame 108
224691_at	UHMK1	127933	3.6e-03	BE622897		0.90	U2AF homology motif (UHM) kinase 1
224698_at	CHR2SYT	57488	5.83e-03	NM_020728	NP_065779	0.82	chr2 synaptotagmin
224699_s_at	CHR2SYT	57488	1.57e-03	NM_020728	NP_065779	0.83	chr2 synaptotagmin
224714_at phosphoprotein	MKI67IP	84365	0.02	NM_032390	NP_115766	0.90	MKI67 (FHA domain) interacting nucleolar
224716_at	SLC35B2	347734	0.01	NM_178148	NP_835361	0.92	solute carrier family 35, member B2
224717_s_at	MGC2747	79086	5.48e-03	NM_024104	NP_077009	0.93	hypothetical protein MGC2747
224720_at	MIB1	57534	2.91e-03	NM_020774	NP_065825	0.93	mindbomb homolog 1 (Drosophila)
224729_s_at factor 1	ATPAF1	64756	6.89e-03	NM_022745	NP_073582	0.94	ATP synthase mitochondrial F1 complex assembly
224736_at	CCAR1	55749	4.6e-03	NM_018237	NP_060707	0.88	cell division cycle and apoptosis regulator 1
224740_at	LOC441075	441075	4.73e-04	BE613001		0.96	LOC441075
224743_at	IMPA3	54928	3.98e-03	AK090988	BAC03563	0.91	myo-inositol monophosphatase A3
224744_at	IMPA3	54928	0.01	AK090988	BAC03563	0.89	myo-inositol monophosphatase A3
224747_at	LOC92912	92912	0.01	NM_173469	NP_775740	0.91	hypothetical protein LOC92912
224759_s_at	MGC17943	90488	0.02	NM_152261	NP_689474	0.84	hypothetical protein MGC17943
224776_at	DKFZp586M1819	137964	4.83e-03	BC051377	AAH51377	0.90	putative lysophosphatidic acid acyltransferase
224779_s_at	FLJ22875	84191	6.85e-03	NM_032231	NP_115607	0.96	hypothetical protein FLJ22875
224784_at Drosophila); translocated to, 6	MLLT6	4302	0.01	AK092893		0.86	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,
224786_at	SCOC	60592	6.02e-03	NM_032547	NP_115936	0.85	short coiled-coil protein
224787_s_at	RAB18	22931	0.04	NM_021252	NP_067075	0.96	RAB18, member RAS oncogene family
224788_at	ARF6	382	0.02	AV700721		0.88	ADP-ribosylation factor 6
224798_s_at	C15orf17	57184	0.04	NM_020447	NP_065180	0.91	chromosome 15 open reading frame 17
224809_x_at	TINF2	26277	0.01	AK023166	BAB14440	0.95	TERF1 (TRF1)-interacting nuclear factor 2
224815_at	COMMD7	149951	0.04	NM_053041	NP_444269	0.90	COMM domain containing 7
224819_at	TCEAL8	90843	4.73e-04	NM_153333	NP_699164	0.83	transcription elongation factor A (SII)-like 8

224821_at	MGC15429	84836	0.01	NM_032750	NP_116139	0.86	hypothetical protein MGC15429
224826_at	KIAA1434	56261	0.02	NM_019593	NP_062539	0.93	hypothetical protein KIAA1434
224833_at	ETS1	2113	0.01	NM_005238	NP_005229	0.88	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)
224834_at	DC-UbP	92181	0.04	BF243404		1.10	dendritic cell-derived ubiquitin-like protein
224835_at	KIAA1434	56261	0.04	AL109935		0.94	hypothetical protein KIAA1434
224836_at	TP53INP2	58476	0.03	NM_021202	NP_067025	1.25	tumor protein p53 inducible nuclear protein 2
224841_x_at	GAS5	60674	0.03	BC038733		0.89	growth arrest-specific 5
224842_at	SMG1	23049	0.02	AK025794		0.91	PI-3-kinase-related kinase SMG-1
224844_at	KIAA1458	57606	0.02	XM_044434	XP_044434	0.92	KIAA1458 protein
224847_at	CDK6	1021	8.05e-03	NM_001259	NP_001250	0.86	cyclin-dependent kinase 6
224849_at	TTC17	55761	4.18e-03	AK023161	BAB14438	0.87	tetratricopeptide repeat domain 17
224850_at	ATAD1	84896	0.01	NM_032810	NP_116199	0.90	ATPase family, AAA domain containing 1
224852_at	TTC17	55761	0.01	NM_018259	NP_060729	0.87	tetratricopeptide repeat domain 17
224860_at	C9orf123	90871	0.02	AL137489	CAB70768	0.86	chromosome 9 open reading frame 123
224862_at	GNAQ	2776	0.02	BF969428		1.09	guanine nucleotide binding protein (G protein), q polypeptide
224863_at	GNAQ	2776	0.01	BF477658		1.14	guanine nucleotide binding protein (G protein), q polypeptide
224865_at	MLSTD2	84188	0.02	NM_032228	NP_115604	0.92	male sterility domain containing 2
224867_at (2C514)	LOC440574	440574	0.03	AK094318		0.95	similar to protein of fungal metazoan origin like (11.1 kD)
224871_at	LOC127262	127262	0.02	NM_182752	NP_877429	0.92	hypothetical protein LOC127262
224878_at	UBPH	56061	0.01	AK124139		0.92	similar to ubiquitin binding protein
224879_at	C9orf123	90871	0.02	XM_372075	XP_372075	0.93	chromosome 9 open reading frame 123
224880_at related)	RALA	5898	0.01	NM_005402	NP_005393	0.90	v-ral simian leukemia viral oncogene homolog A (ras
224881_at	VKORC1L1	154807	0.04	AL137548		0.92	vitamin K epoxide reductase complex, subunit 1-like 1
224883_at	PLDN	26258	0.03	NM_012388	NP_036520	0.87	pallidin homolog (mouse)
224887_at subunit	GNPTG	84572	0.02	NM_032520	NP_115909	0.89	N-acetylglucosamine-1-phosphotransferase, gamma
224889_at	FOXO3A	2309	0.01	AK024103		1.23	forkhead box O3A
224893_at	DKFZP564J0863	25923	0.02	BX648468		0.93	DKFZP564J0863 protein
224899_s_at	DKFZp564K142	84061	5.93e-03	NM_032121	NP_115497	0.93	implantation-associated protein
224900_at	ANKFY1	51479	0.04	NM_016376	NP_057460	0.88	ankyrin repeat and FYVE domain containing 1
224905_at	WDR26	80232	0.01	NM_025160	NP_079436	0.89	WD repeat domain 26
224914_s_at	CIP29	84324	0.03	NM_033082	NP_149073	0.91	cytokine induced protein 29 kDa
224916_at	LOC340061	340061	7.02e-03	NM_198282	NP_938023	0.91	hypothetical protein LOC340061
224921_at	SCAMP2	10066	0.04	AK096376		0.91	secretory carrier membrane protein 2
224932_at	C22orf16	400916	0.01	NM_213720	NP_998885	0.85	chromosome 22 open reading frame 16
224935_at	EIF2S3	1968	0.01	BG165815		0.90	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa
224936_at 52kDa	EIF2S3	1968	0.04	NM_001415	NP_001406	0.93	eukaryotic translation initiation factor 2, subunit 3 gamma,
224938_at	182-FIP	57532	0.01	AW007746		0.96	82-kD FMRP Interacting Protein
224943_at	BTBD7	55727	0.02	BX538231	CAD98074	0.91	BTB (POZ) domain containing 7
224946_s_at	MGC12981	84317	0.03	NM_032357	NP_115733	0.92	hypothetical protein MGC12981
224948_at	MRPS24	64951	0.02	NM_032014	NP_114403	0.96	mitochondrial ribosomal protein S24
224959_at	SLC26A2	1836	0.01	NM_000112	NP_000103	0.90	solute carrier family 26 (sulfate transporter), member 2

224960_at	SCYL2	55681	0.02	NM_017988	NP_060458	0.92	SCY1-like 2 (S. cerevisiae)
224965_at	GNG2	54331	0.02	NM_053064	NP_444292	1.20	guanine nucleotide binding protein (G protein), gamma 2
224968_at	MGC15407	112942	0.03	NM_080667	NP_542398	0.81	similar to RIKEN cDNA 4931428D14 gene
224969_at	ATXN7L3	56970	0.03	AL390158	CAB99093	0.95	ataxin 7-like 3
224971_at	MRPL30	51263	0.01	NM_145212	NP_660213	0.90	mitochondrial ribosomal protein L30
224973_at	FAM46A	55603	0.04	AF350451	AAM53071	0.81	family with sequence similarity 46, member A
224974_at	SDS3	64426	0.03	NM_022491	NP_071936	0.89	likely ortholog of mouse Sds3
224981_at	LOC124446	124446	0.04	BC017488	AAH17488	0.95	hypothetical protein BC017488
224984_at	NFAT5	10725	9.91e-03	NM_138714	NP_619728	0.92	nuclear factor of activated T-cells 5, tonicity-responsive
224991_at	CMIP	80790	0.01	NM_198390	NP_938204	1.12	c-Maf-inducing protein
224993_at	LOC56930	56930	0.01	BC063667		0.92	hypothetical protein from EUROIMAGE 1669387
225002_s_at	SUMF2	25870	0.02	NM_015411	NP_056226	0.86	sulfatase modifying factor 2
225006_x_at	TH1L	51497	0.03	NM_198976	NP_945327	0.91	TH1-like (Drosophila)
225012_at	HDLBP	3069	0.03	BE378479		0.91	high density lipoprotein binding protein (vigilin)
225017_at	CCDC14	64770	0.01	NM_022757	NP_073594	0.89	coiled-coil domain containing 14
225029_at	LOC550643	550643	0.04	BX537532		0.88	hypothetical protein LOC550643
225030_at	FAM44B	91272	0.03	NM_138369	NP_612378	0.92	family with sequence similarity 44, member B
225036_at	C9orf105	401505	0.01	NM_001001790	NP_001001790	0.88	chromosome 9 open reading frame 105
225037_at	SLC35C2	51006	0.01	NM_173179	NP_775271	0.89	solute carrier family 35, member C2
225039_at	RPE	6120	0.04	NM_199229	NP_954699	0.87	ribulose-5-phosphate-3-epimerase
225040_s_at	RPE	6120	0.03	NM_199229	NP_954699	0.84	ribulose-5-phosphate-3-epimerase
225042_s_at	C12orf22	81566	0.02	NM_030809	NP_110436	0.88	chromosome 12 open reading frame 22
225045_at	KIAA1212	55704	0.02	NM_018084	NP_060554	0.89	KIAA1212
225048_at	PHF10	55274	0.03	AJ420510		0.86	PHD finger protein 10
225050_at	ZNF512	84450	1.07e-03	NM_032434	NP_115810	0.89	zinc finger protein 512
225052_at	MGC14327	94107	8.05e-03	NM_053045	NP_444273	0.91	hypothetical protein MGC14327
225053_at	CNOT7	29883	0.01	NM_013354	NP_037486	0.87	CCR4-NOT transcription complex, subunit 7
225055_at	LOC440460	440460	4.18e-03	AV735241		0.85	LOC440460
225058_at	GPR108	56927	5.48e-03	AL365404	CAB96950	0.90	G protein-coupled receptor 108
225064_at	RABEP1	9135	8.21e-04	NM_004703	NP_004694	0.88	rabaptin, RAB GTPase binding effector protein 1
225068_at	KLHL12	59349	9.6e-04	NM_021633	NP_067646	0.92	kelch-like 12 (Drosophila)
225069_at	PCYT1A	5130	1.24e-03	BF063382		0.88	phosphate cytidylyltransferase 1, choline, alpha isoform
225070_at	C6orf68	116150	2.95e-03	BF112132		0.85	chromosome 6 open reading frame 68
225071_at	C6orf68	116150	3.19e-03	NM_138459	NP_612468	0.91	chromosome 6 open reading frame 68
225074_at	RAB2B	84932	1.33e-03	NM_032846	NP_116235	0.86	RAB2B, member RAS oncogene family
225083_at	C6orf51	112495	0.03	NM_138408	NP_612417	0.89	chromosome 6 open reading frame 51
225086_at	FLJ38426	283742	3.02e-03	BF679966		0.79	hypothetical protein FLJ38426
225088_at	FLJ31153	123811	1.31e-03	NM_144600	NP_653201	0.82	hypothetical protein FLJ31153
225092_at	RABEP1	9135	0.03	NM_004703	NP_004694	0.90	rabaptin, RAB GTPase binding effector protein 1
225093_at	UTRN	7402	1.27e-03	AK023675		0.83	utrophin (homologous to dystrophin)
225097_at	HIPK2	28996	9.91e-03	BF594155		0.93	homeodomain interacting protein kinase 2
225099_at	FBXO45	200933	0.04	XM_117294	XP_117294	0.91	F-box protein 45
225100_at	FBXO45	200933	0.02	XM_117294	XP_117294	0.92	F-box protein 45
225101_s_at	SNX14	57231	2.01e-03	NM_153816	NP_722523	0.92	sorting nexin 14
225106_s_at	FLJ10826	55239	0.03	NM_018233	NP_060703	0.90	hypothetical protein FLJ10826

225107_at	HNRPA2B1	3181	1.13e-03	AI963008		0.90		heterogeneous nuclear ribonucleoprotein A2/B1
225110_at	FLJ10826	55239	0.04	NM_018233	NP_060703	0.93		hypothetical protein FLJ10826
225114_at	AGPS	8540	0.01	AA127674		0.85		alkylglycerone phosphate synthase
225115_at	HIPK2	28996	0.03	BF529628		1.14		homeodomain interacting protein kinase 2
225119_at	C20orf178	128866	0.02	NM_176812	NP_789782	0.78		chromosome 20 open reading frame 178
225125_at	TMEM32	93380	0.03	NM_173470	NP_775741	0.94		transmembrane protein 32
225129_at	CPNE2	221184	5.93e-03	NM_152727	NP_689940	1.25		copine II
225134_at	FLJ14800	84926	0.01	NM_032840	NP_116229	0.87		hypothetical protein FLJ14800
225137_at	NFATC3	4775	0.02	NM_173165	NP_775188	0.92		nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3
225138_at	ZRANB1	54764	0.02	BC048281	AAH48281	0.93		zinc finger, RAN-binding domain containing 1
225142_at	KIAA1718	80853	0.04	XM_376680	XP_376680	0.93		KIAA1718 protein
225148_at	MGC52010	91582	0.03	NM_194326	NP_919307	0.95		hypothetical protein MGC52010
225152_at	ZNF622	90441	5.93e-03	NM_033414	NP_219482	0.92		zinc finger protein 622
225153_at	GFM1	85476	1.95e-03	NM_024996	NP_079272	0.86		G elongation factor, mitochondrial 1
225156_at	MGC4549	84337	0.01	NM_032377	NP_115753	0.91		hypothetical protein MGC4549
225158_at	GFM1	85476	0.02	NM_024996	NP_079272	0.83		G elongation factor, mitochondrial 1
225160_x_at	CPM	1368	0.04	AI952357		0.86		carboxypeptidase M
225169_at	MGC16733	92105	0.02	NM_033547	NP_291025	0.93		hypothetical gene MGC16733 similar to CG12113
225170_at	WDR5	11091	0.01	AK024484	BAB15774	0.85		WD repeat domain 5
225171_at	ARHGAP18	93663	0.02	NM_033515	NP_277050	0.89		Rho GTPase activating protein 18
225174_at	DNAJC10	54431	0.04	NM_018981	NP_061854	0.92		DnaJ (Hsp40) homolog, subfamily C, member 10
225179_at	HIP2	3093	1.59e-04	AA161140		0.93		huntingtin interacting protein 2
225180_at	TTC14	151613	5.83e-03	NM_133462	NP_597719	0.88		tetratricopeptide repeat domain 14
225182_at	C21orf4	757	0.02	NM_006134	NP_006125	0.87		chromosome 21 open reading frame 4
225190_x_at	RPL35A	6165	0.02	NM_000996	NP_000987	0.88		ribosomal protein L35a
225192_at	C10orf46	143384	0.01	AA044726		0.92		chromosome 10 open reading frame 46
225194_at	PLRG1	5356	0.01	NM_002669	NP_002660	0.90		pleiotropic regulator 1 (PRL1 homolog, Arabidopsis)
225196_s_at	MRPS26	64949	0.04	NM_030811	NP_110438	0.91		mitochondrial ribosomal protein S26
225201_s_at	MRPL14	64928	0.01	NM_032111	NP_115487	0.86		mitochondrial ribosomal protein L14
225210_s_at	MGC2560	83640	0.01	NM_031452	NP_113640	0.91		hypothetical LOC83640
225213_at	TA-PP2C	160760	0.03	AW300598		0.95		T-cell activation protein phosphatase 2C
225215_s_at	MTRF1L	54516	0.03	NM_019041	NP_061914	0.88		mitochondrial translational release factor 1-like
225221_at	ZKSCAN1	7586	0.03	AA195485		0.91		zinc finger with KRAB and SCAN domains 1
225222_at	HIAT1	64645	0.01	NM_033055	NP_149044	0.95		hippocampus abundant transcript 1
225226_at	FAM40A	85369	0.02	NM_033088	NP_149079	0.94		family with sequence similarity 40, member A
225229_at	AF5Q31	27125	2.49e-04	AK126818		0.83		ALL1 fused gene from 5q31
225230_at	MGC54289	128338	0.04	NM_178454	NP_848549	0.93		hypothetical protein MGC54289
225235_at	TM4SF17	26262	0.02	NM_012171	NP_036303	0.87		transmembrane 4 superfamily member 17
225237_s_at	MSI2	124540	0.01	NM_138962	NP_620412	0.89		musashi homolog 2 (Drosophila)
225246_at	STIM2	57620	7.69e-03	NM_020860	NP_065911	0.89		stromal interaction molecule 2
225253_s_at	FLJ12760	339175	0.03	NM_181725	NP_859076	0.93		hypothetical protein FLJ12760
225253_s_at	FLJ12760	339175	0.03	NM_001005372	NP_001005372	0.93		hypothetical protein FLJ12760
225260_s_at	MRPL32	64983	0.01	NM_031903	NP_114109	0.91		mitochondrial ribosomal protein L32
225261_x_at	TH1L	51497	0.03	NM_198976	NP_945327	0.88		TH1-like (Drosophila)

225264_at	RARSL	57038	1.01e-03	NM_020320	NP_064716	0.87	arginyl-tRNA synthetase-like
225266_at	ZNF652	22834	7.96e-03	AA526904		0.91	zinc finger protein 652
225268_at	KPNA4	3840	0.02	NM_002268	NP_002259	0.91	karyopherin alpha 4 (importin alpha 3)
225269_s_at	C2orf12	192137	0.01	AL117617		0.93	chromosome 2 open reading frame 12
225279_s_at	LOC285338	285338	1.11e-03	AK092546		0.87	hypothetical protein LOC285338
225281_at	C3orf17	25871	2.39e-03	NM_015412	NP_056227	0.85	chromosome 3 open reading frame 17
225284_at	LOC144871	144871	4.18e-03	AK024941		1.11	hypothetical protein LOC144871
225294_s_at	TRAPPC1	58485	0.02	NM_021210	NP_067033	0.93	trafficking protein particle complex 1
225295_at	SLC39A10	57181	5.93e-03	AB033091	BAA86579	0.81	solute carrier family 39 (zinc transporter), member 10
225296_at	ZNF317	57693	0.01	AB046808	BAB13414	0.88	zinc finger protein 317
225302_at	TXNDC10	54495	7.12e-04	NM_019022	NP_061895	0.88	thioredoxin domain containing 10
225310_at	RBMX	27316	6.11e-03	BX647131		0.90	RNA binding motif protein, X-linked
225313_at	C20orf177	63939	7.35e-03	NM_022106	NP_071389	0.94	chromosome 20 open reading frame 177
225321_s_at	PILRB	29990	0.03	NM_013440	NP_038468	0.86	paired immunoglobin-like type 2 receptor beta
225324_at	MCM8	84515	0.04	AL035461		0.88	MCM8 minichromosome maintenance deficient 8 (S. cerevisiae)
225324_at	CHGB	1114	0.04	AL035461		0.88	chromogranin B (secretogranin 1)
225324_at	C20orf155	54675	0.04	AL035461		0.88	chromosome 20 open reading frame 155
225324_at	CGI-09	51605	0.04	AL035461		0.88	CGI-09 protein
225325_at	FLJ20160	54842	0.04	NM_017694	NP_060164	0.92	FLJ20160 protein
225331_at	C3orf6	152137	7.47e-03	NM_174908	NP_777568	0.92	chromosome 3 open reading frame 6
225332_at	KRTAP4-7	85287	3.1e-03	BF674064		0.87	keratin associated protein 4-7
225334_at	C10orf32	119032	7.38e-03	NM_144591	NP_653192	0.90	chromosome 10 open reading frame 32
225337_at	ABHD2	11057	0.03	AI346910		0.87	abhydrolase domain containing 2
225341_at	LOC80298	80298	7.6e-03	NM_025198	NP_079474	0.87	transcription termination factor-like protein
225344_at	NCOA7	135112	0.03	NM_181782	NP_861447	0.86	nuclear receptor coactivator 7
225346_at	LOC80298	80298	0.04	NM_025198	NP_079474	0.90	transcription termination factor-like protein
225352_at	TLOC1	7095	0.03	BX648539		0.93	translocation protein 1
225354_s_at	SH3BGRL2	83699	0.03	NM_031469	NP_113657	1.17	SH3 domain binding glutamic acid-rich protein like 2
225358_at	TIM14	131118	0.01	NM_145261	NP_660304	0.91	homolog of yeast TIM14
225360_at	PP2447	80305	0.03	NM_025204	NP_079480	1.12	hypothetical protein PP2447
225361_x_at	LOC159090	159090	0.01	NM_145284	NP_660327	0.86	similar to hypothetical protein MGC17347
225365_at	FLJ25952	253832	0.04	AK090979		0.88	DHHC-containing protein 20
225368_at	HIPK2	28996	0.01	BF218115		0.92	homeodomain interacting protein kinase 2
225371_at	GLE1L	2733	4.55e-04	NM_001003722	NP_001003722	0.91	GLE1 RNA export mediator-like (yeast)
225374_at	C17orf32	147007	0.02	NM_152464	NP_689677	0.93	chromosome 17 open reading frame 32
225375_at	C17orf32	147007	0.03	NM_152464	NP_689677	0.92	chromosome 17 open reading frame 32
225376_at	C20orf11	54994	0.04	NM_017896	NP_060366	0.91	chromosome 20 open reading frame 11
225383_at	ZNF275	10838	0.02	AL833683		0.91	zinc finger protein 275
225384_at	DOCK7	85440	0.03	NM_033407	NP_212132	0.88	dedicator of cytokinesis 7
225386_s_at	HNRPLL	92906	0.01	NM_138394	NP_612403	0.87	heterogeneous nuclear ribonucleoprotein L-like
225391_at	LOC93622	93622	0.02	NM_138699	NP_619644	0.87	hypothetical protein BC006130
225393_at	P66beta	57459	0.01	NM_020699	NP_065750	1.09	transcription repressor p66 beta component of the MeCP1 complex
225397_at	MGC20481	90416	0.03	NM_052849	NP_443081	0.89	hypothetical protein MGC20481
225399_at	C1orf19	116461	0.04	NM_052965	NP_443197	0.87	chromosome 1 open reading frame 19

225401_at	MGC31963	112770	0.02	NM_144580	NP_653181	0.90	kidney predominant protein NCU-G1
225411_at	FLJ14681	84910	4.43e-03	NM_032824	NP_116213	0.83	hypothetical protein FLJ14681
225416_at	RNF12	51132	0.04	N58188		0.94	ring finger protein 12
225422_at	CDC26	246184	1.83e-03	NM_139286	NP_644815	0.91	cell division cycle 26
225427_s_at	APOA1BP	128240	0.03	NM_144772	NP_658985	0.90	apolipoprotein A-I binding protein
225432_s_at	CSRP2BP	57325	0.02	NM_020536	NP_065397	0.91	CSRP2 binding protein
225433_at	GTF2A1	2957	0.02	AU144104		0.92	general transcription factor IIA, 1, 19/37kDa
225439_at	NUDCD1	84955	0.04	NM_032869	NP_116258	0.87	NudC domain containing 1
225447_at	GPD2	2820	7.7e-03	AA613031		0.89	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
225448_at	NAPG	8774	0.03	AL519376		0.90	N-ethylmaleimide-sensitive factor attachment protein, gamma
225451_at	GRIPAP1	56850	0.03	NM_020137	NP_064522	0.91	GRIP1 associated protein 1
225455_at	STAF42	117143	0.04	NM_053053	NP_444281	0.88	SPT3-associated factor 42
225457_s_at	DKFZP564I1171	25845	0.04	AK023178		0.87	DKFZP564I1171 protein
225458_at	DKFZP564I1171	25845	4.38e-03	AK023178		0.85	DKFZP564I1171 protein
225460_at	SEC22L3	9117	0.03	NM_004206	NP_004197	0.93	SEC22 vesicle trafficking protein-like 3 (S. cerevisiae)
225463_x_at	GPR89	51463	0.03	NM_016334	NP_057418	0.89	G protein-coupled receptor 89
225469_at	LOC144363	144363	0.04	NM_001001660	NP_001001660	0.87	hypothetical protein LOC144363
225470_at	NUP35	129401	9.06e-03	NM_138285	NP_612142	0.87	nucleoporin 35kDa
225477_s_at	MRPS25	64432	9.63e-03	AL138444		0.94	mitochondrial ribosomal protein S25
225483_at	MGC10485	112936	2.16e-03	BC007799		0.90	hypothetical protein MGC10485
225490_at	ARID2	196528	0.01	BX648152		0.89	AT rich interactive domain 2 (ARID, RFX-like)
225498_at	C20orf178	128866	0.04	NM_176812	NP_789782	0.94	chromosome 20 open reading frame 178
225501_at	PHF6	84295	4.02e-03	NM_032335	NP_115711	0.77	PHD finger protein 6
225501_at	PHF6	84295	4.02e-03	NM_032458	NP_115834	0.77	PHD finger protein 6
225508_at	KIAA1468	57614	6.35e-03	NM_020854	NP_065905	0.93	KIAA1468
225509_at	LOC56757	56757	0.03	AL833381		0.91	hypothetical protein LOC56757
225522_at	LOC388957	388957	3.43e-03	AW628987		0.88	similar to BMP2 inducible kinase
225523_at	MRPL53	116540	3.49e-03	NM_053050	NP_444278	0.93	mitochondrial ribosomal protein L53
225526_at	MKLN1	4289	0.02	NM_013255	NP_037387	0.93	muskelin 1, intracellular mediator containing kelch motifs
225528_at	IPO8	10526	0.03	NM_006390	NP_006381	0.95	importin 8
225529_at	CENTB5	116983	0.01	BC047001	AAH47001	0.89	centaurin, beta 5
225533_at	PHF19	26147	0.04	AL117477	CAB55950	0.81	PHD finger protein 19
225534_at	LOC114926	114926	0.04	NM_138436	NP_612445	0.93	hypothetical protein BC013035
225538_at	ZCCHC9	84240	8.02e-04	NM_032280	NP_115656	0.89	zinc finger, CCHC domain containing 9
225541_at	LOC200916	200916	0.01	BC049823		0.85	similar to ribosomal protein L22
225550_at	FLJ32001	163882	7.33e-03	NM_152609	NP_689822	0.84	hypothetical protein FLJ32001
225551_at	FLJ32001	163882	0.01	NM_152609	NP_689822	0.87	hypothetical protein FLJ32001
225554_s_at	ANAPC7	51434	0.04	AY007104		0.91	anaphase promoting complex subunit 7
225558_at	GIT2	9815	0.04	NM_057169	NP_476510	0.95	G protein-coupled receptor kinase interactor 2
225561_at	SELT	51714	0.04	NM_016275	NP_057359	0.87	selenoprotein T
225565_at	CREB1	1385	7.69e-03	AA769455		1.19	cAMP responsive element binding protein 1
225573_at	FLJ12592	84129	8.42e-03	NM_032169	NP_115545	0.85	putative acyl-CoA dehydrogenase
225574_at	MGC10198	201965	3.37e-03	NM_152682	NP_689895	0.90	hypothetical protein MGC10198
225578_at	LOC440145	440145	0.03	XM_495961	XP_495961	0.90	similar to RIKEN cDNA 2410129H14
225579_at	C2orf22	130814	0.01	NM_152391	NP_689604	0.90	chromosome 2 open reading frame 22

225580_at	MRPL50	54534	0.02	NM_019051	NP_061924	0.84	mitochondrial ribosomal protein L50
225586_at	C9orf112	92715	5.36e-03	NM_138778	NP_620133	0.84	chromosome 9 open reading frame 112
225591_at	FBXO25	26260	0.02	NM_183421	NP_904357	0.92	F-box protein 25
225593_at	LSM10	84967	0.02	NM_032881	NP_116270	0.95	LSM10, U7 small nuclear RNA associated
225602_at	C9orf19	152007	0.03	NM_022343	NP_071738	0.94	chromosome 9 open reading frame 19
225609_at	GSR	2936	0.01	BC035691		0.89	glutathione reductase
225610_at	UHRF2	115426	0.04	NM_152306	NP_689519	0.91	ubiquitin-like, containing PHD and RING finger domains, 2
225618_at	ARHGAP27	201176	0.04	NM_199282	NP_954976	1.07	Rho GTPase activating protein 27
225621_at	ALG2	85365	7.86e-04	NM_033087	NP_149078	0.92	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)
225623_at	KIAA1737	85457	0.02	NM_033426	NP_219494	0.93	KIAA1737
225626_at	PAG	55824	0.02	NM_018440	NP_060910	0.88	phosphoprotein associated with glycosphingolipid-enriched microdomains
225629_s_at	ZBTB4	57659	0.02	NM_020899	NP_065950	0.87	zinc finger and BTB domain containing 4
225631_at	KIAA1706	80820	0.01	NM_030636	NP_085139	1.15	KIAA1706 protein
225635_s_at	LOC401504	401504	6.11e-03	XM_379634	XP_379634	0.84	hypothetical gene supported by AK091718
225641_at	MEF2D	4209	0.02	NM_005920	NP_005911	0.88	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D)
225642_at	MGC20419	112970	0.03	NM_138417	NP_612426	0.84	hypothetical protein BC012173
225643_at	C14orf32	93487	0.04	AI261542		0.92	chromosome 14 open reading frame 32
225644_at	FLJ33814	150275	0.01	NM_173510	NP_775781	0.87	hypothetical protein FLJ33814
225656_at	EFHC1	114327	0.03	AI564473		1.13	EF-hand domain (C-terminal) containing 1
225657_at	LOC152217	152217	0.02	BE563042		0.91	hypothetical protein BC007882
225663_at	ACBD5	91452	0.03	AB082527	BAC02705	0.95	acyl-Coenzyme A binding domain containing 5
225666_at	FLJ14624	84899	6.41e-03	NM_032813	NP_116202	0.86	hypothetical protein FLJ14624
225676_s_at	DKFZP564O0463	25879	6.24e-03	NM_015420	NP_056235	0.89	DKFZP564O0463 protein
225679_at	C14orf35	122830	0.03	AA534210		0.89	chromosome 14 open reading frame 35
225685_at	CDC42EP3	10602	0.03	AI801777		0.89	CDC42 effector protein (Rho GTPase binding) 3
225690_at	CRK7	51755	0.03	NM_016507	NP_057591	0.92	CDC2-related protein kinase 7
225694_at	CRK7	51755	0.02	NM_016507	NP_057591	0.95	CDC2-related protein kinase 7
225698_at	TIGA1	114915	2.95e-03	NM_053000	NP_443726	0.87	TIGA1
225702_at	FLJ14825	84933	0.01	NM_032847	NP_116236	0.86	hypothetical protein FLJ14825
225704_at	KIAA1545	57666	4.42e-04	AB046765	BAB13371	0.86	KIAA1545 protein
225707_at	ARL6IP6	151188	6.04e-03	NM_152522	NP_689735	0.86	ADP-ribosylation-like factor 6 interacting protein 6
225717_at	KIAA1715	80856	9.2e-03	NM_030650	NP_085153	0.84	KIAA1715
225724_at	FLJ31306	379025	0.02	BC034618	AAH34618	0.95	hypothetical protein FLJ31306
225732_at	KLHDC5	57542	9.2e-03	AU146850		0.85	kelch domain containing 5
225734_at	FBXO22	26263	8.67e-03	NM_147188	NP_671717	0.91	F-box protein 22
225739_at	RAB11FIP4	84440	0.01	NM_032932	NP_116321	0.90	RAB11 family interacting protein 4 (class II)
225741_at	THUMPD3	25917	0.02	NM_015453	NP_056268	0.87	THUMP domain containing 3
225746_at	RAB11FIP4	84440	0.03	NM_032932	NP_116321	0.80	RAB11 family interacting protein 4 (class II)
225748_at	C6orf93	84946	7.78e-03	NM_032860	NP_116249	0.86	chromosome 6 open reading frame 93
225749_at	LOC283951	283951	0.01	BE889319		0.89	hypothetical protein LOC283951
225751_at	RBM17	84991	0.02	NM_032905	NP_116294	0.87	RNA binding motif protein 17

225754_at	AP1G1	164	1.49e-03	NM_001128	NP_001119	0.89	adaptor-related protein complex 1, gamma 1 subunit
225760_at	KIAA1915	114803	0.02	AB067502	BAB67808	0.92	KIAA1915 protein
225761_at	PAPD4	167153	3.37e-03	NM_173797	NP_776158	0.89	PAP associated domain containing 4
225764_at	ETV6	2120	9.61e-03	NM_001987	NP_001978	1.11	ets variant gene 6 (TEL oncogene)
225765_at	TNPO1	3842	0.04	AA527296		0.91	transportin 1
225771_at	AP1G1	164	0.01	NM_001128	NP_001119	0.93	adaptor-related protein complex 1, gamma 1 subunit
225783_at	NCE2	140739	0.02	NM_080678	NP_542409	0.87	NEDD8-conjugating enzyme
225793_at	LIX1L	128077	0.01	AK128733		0.91	Lix1 homolog (mouse) like
225808_at	LOC124512	124512	8.8e-03	BC045819	AAH45819	0.89	hypothetical protein LOC124512
225813_at	MNAB	54542	0.03	AA524361		0.92	membrane associated DNA binding protein
225814_at	XRN1	54464	0.01	NM_019001	NP_061874	0.85	5'-3' exoribonuclease 1
225819_at	TBRG1	84897	0.02	NM_032811	NP_116200	0.93	transforming growth factor beta regulator 1
225823_at	QIL1	125988	0.03	NM_205767	NP_991330	0.92	QIL1 protein
225834_at	MGC57827	389835	0.01	NM_207418	NP_997301	0.89	Similar to RIKEN cDNA 2700049P18 gene
225837_at	MGC13204	83695	1.57e-03	NM_031465	NP_113653	0.81	hypothetical protein MGC13204
225841_at	FLJ30525	113802	7.35e-03	NM_144584	NP_653185	0.92	hypothetical protein FLJ30525
225852_at	ANKRD17	26057	1.75e-03	NM_032217	NP_115593	0.88	ankyrin repeat domain 17
225855_at	EPB41L5	57669	4.59e-03	NM_020909	NP_065960	1.20	erythrocyte membrane protein band 4.1 like 5
225864_at	NSE2	157638	0.03	NM_174911	NP_777571	0.80	breast cancer membrane protein 101
225866_at	BXDC1	84154	3.32e-03	NM_032194	NP_115570	0.88	brix domain containing 1
225872_at	SLC35F5	80255	0.03	NM_025181	NP_079457	0.91	solute carrier family 35, member F5
225882_at	SLC35B4	84912	1.62e-03	NM_032826	NP_116215	0.83	solute carrier family 35, member B4
225884_s_at	ZNF336	64412	0.01	NM_022482	NP_071927	0.92	zinc finger protein 336
225885_at	EEA1	8411	4.18e-03	AI336848		0.88	early endosome antigen 1, 162kD
225886_at	DDX5	1655	4.83e-03	AA156797		0.84	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5
225887_at	C13orf23	80209	5.06e-03	NM_025138	NP_079414	0.87	chromosome 13 open reading frame 23
225896_at	M-RIP	23164	0.04	AI656836		0.85	myosin phosphatase-Rho interacting protein
225903_at	CDC91L1	128869	0.03	NM_080476	NP_536724	0.86	CDC91 cell division cycle 91-like 1 (S. cerevisiae)
225908_at	LOC285148	285148	0.02	BC039709		0.94	hypothetical protein LOC285148
225932_s_at	HNRPA2B1	3181	0.01	AI375753		0.94	heterogeneous nuclear ribonucleoprotein A2/B1
225933_at	LOC339229	339229	0.01	BF115231		0.85	hypothetical protein LOC339229
225945_at	ZNF655	79027	3.79e-03	NM_138494	NP_612503	0.87	zinc finger protein 655
225947_at	MYOHD1	80179	9.43e-03	NM_025109	NP_079385	0.93	myosin head domain containing 1
225948_at	C14orf153	84334	0.01	NM_032374	NP_115750	0.92	chromosome 14 open reading frame 153
225949_at	NRBP2	340371	7.01e-04	NM_178564	NP_848659	0.88	nuclear receptor binding protein 2
225951_s_at	LOC440309	440309	5.93e-03	AV756026		0.91	LOC440309
225956_at	LOC153222	153222	0.04	NM_153607	NP_705835	1.10	adult retina protein
225957_at	LOC153222	153222	0.03	NM_153607	NP_705835	1.09	adult retina protein
225969_at	MGC15677	84964	0.01	NM_198867	NP_942567	0.85	hypothetical protein MGC15677
225970_at	DDHD1	80821	0.02	NM_030637	NP_085140	0.80	DDHD domain containing 1
225974_at	DKFZp762C1112	169200	0.04	AK123958		0.86	hypothetical protein DKFZp762C1112
225976_at	MGC23908	91408	8.55e-03	AL568049		0.93	similar to transcription factor BTF3
225984_at	PRKAA1	5562	0.03	NM_006251	NP_006242	0.87	protein kinase, AMP-activated, alpha 1 catalytic subunit
225985_at	PRKAA1	5562	0.01	NM_006251	NP_006242	0.96	protein kinase, AMP-activated, alpha 1 catalytic subunit
225988_at	HERC4	26091	0.04	NM_015601	NP_056416	0.93	hect domain and RLD 4

225989_at	HERC4	26091	0.01	AB046813	BAB13419	0.85	hect domain and RLD 4
225994_at	CPSF2	53981	0.01	NM_017437	NP_059133	0.86	cleavage and polyadenylation specific factor 2, 100kDa
226007_at	HBLD1	122961	1.13e-03	NM_194279	NP_919255	0.90	HESB like domain containing 1
226012_at	ANKRD11	29123	0.03	NM_013275	NP_037407	0.92	ankyrin repeat domain 11
226015_at	ZNF12	7559	3.6e-03	NM_006956	NP_008887	0.92	zinc finger protein 12 (KOX 3)
226016_at	CD47	961	6.16e-03	NM_001777	NP_001768	0.86	CD47 antigen (Rh-related antigen, integrin-associated
signal transducer)							
226018_at	Ells1	222166	0.03	NM_152793	NP_690006	1.14	hypothetical protein Ells1
226026_at	DIRC2	84925	0.04	NM_032839	NP_116228	0.92	disrupted in renal carcinoma 2
226030_at	ACADSB	36	0.02	NM_001609	NP_001600	0.87	acyl-Coenzyme A dehydrogenase, short/branched chain
226031_at	FLJ20097	55610	0.04	AB058764	BAB47490	0.91	hypothetical protein FLJ20097
226032_at	CASP2	835	0.01	NM_001224	NP_001215	0.91	caspase 2, apoptosis-related cysteine protease (neural
precursor cell expressed, developmentally down-regulated 2)							
226037_s_at	TAF9L	51616	0.02	NM_015975	NP_057059	0.90	TAF9-like RNA polymerase II, TATA box binding
protein (TBP)-associated factor, 31kDa							
226039_at	MGAT4A	11320	3.43e-03	AW006441		0.89	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-
acetylglucosaminyltransferase, isoenzyme A							
226046_at	MAPK8	5599	2.23e-03	AL137667		0.86	mitogen-activated protein kinase 8
226050_at	C13orf11	55002	0.02	NM_017905	NP_060375	0.93	chromosome 13 open reading frame 11
226053_at	MAP2K7	5609	1.53e-03	NM_145185	NP_660186	1.16	mitogen-activated protein kinase kinase 7
226054_at	BRD4	23476	0.01	NM_058243	NP_490597	1.15	bromodomain containing 4
226055_at	ARRDC2	27106	0.02	NM_015683	NP_056498	0.86	arrestin domain containing 2
226062_x_at	FLJ11280	55793	0.02	AB037811	BAA92628	1.08	hypothetical protein FLJ11280
226063_at	VAV2	7410	1.85e-03	NM_003371	NP_003362	0.91	vav 2 oncogene
226066_at	MITF	4286	0.02	NM_198159	NP_937802	0.84	microphthalmia-associated transcription factor
226071_at	TSRC1	54507	0.02	NM_019032	NP_061905	1.17	thrombospondin repeat containing 1
226073_at	LOC219854	219854	4.36e-03	AK091324		0.92	hypothetical protein LOC219854
226074_at	FLJ32332	132160	4.51e-03	NM_144641	NP_653242	0.90	likely ortholog of mouse protein phosphatase 2C eta
226087_at	LZIC	84328	9.35e-03	NM_032368	NP_115744	0.90	leucine zipper and CTNNBIP1 domain containing
226092_at	MPP5	64398	0.01	NM_022474	NP_071919	0.92	membrane protein, palmitoylated 5 (MAGUK p55
subfamily member 5)							
226098_at	KIAA1374	57560	0.04	NM_020800	NP_065851	0.91	KIAA1374 protein
226117_at	TIFA	92610	0.04	NM_052864	NP_443096	0.82	TRAF-interacting protein with a forkhead-associated
domain							
226121_at	MGC23280	147015	0.02	NM_144683	NP_653284	1.16	hypothetical protein MGC23280
226128_at	FLJ32421	148362	0.01	N73682		0.91	hypothetical protein FLJ32421
226143_at	RAI1	10743	0.04	NM_030665	NP_109590	0.87	retinoic acid induced 1
226144_at	TCEB3BP1	57455	0.03	NM_020695	NP_065746	1.15	transcription elongation factor B polypeptide 3 binding
protein 1							
226151_x_at	CRYZL1	9946	2.48e-03	NM_005111	NP_005102	0.87	crystallin, zeta (quinone reductase)-like 1
226154_at	DNM1L	10059	1.13e-03	AL043631		0.90	dynamin 1-like
226157_at	TFDP2	7029	0.03	AI569747		0.87	transcription factor Dp-2 (E2F dimerization partner 2)
226163_at	ZBTB9	221504	2.78e-04	NM_152735	NP_689948	1.12	zinc finger and BTB domain containing 9
226165_at	LOC401466	401466	0.03	XM_376783	XP_376783	0.89	hypothetical gene supported by BC055092
226171_at	FLJ20209	57245	0.03	BF111925		0.94	hypothetical protein FLJ20209

226175_at	MGC29649	283237	0.02	NM_173810	NP_776171	0.93	hypothetical protein MGC29649
226183_at	GSK3B	2932	0.01	AW139538	0.88		glycogen synthase kinase 3 beta
226199_at	MGC23937	139596	0.03	NM_145052	NP_659489	0.91	hypothetical protein MGC23937 similar to CG4798
226206_at	MAFK	7975	0.01	AK056767	BAB71276	0.87	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)
226207_at	FLJ39378	353116	0.04	NM_178314	NP_847884	1.16	hypothetical protein FLJ39378
226218_at	IL7R	3575	7.96e-03	BE217880	0.86		interleukin 7 receptor
226222_at	KIAA1432	57589	0.02	AB037853	BAA92670	0.88	KIAA1432
226224_at	FOXK2	3607	3.52e-03	AK098140	0.85		forkhead box K2
226236_at	LOC388789	388789	6.83e-05	XM_373908	XP_373908	0.90	hypothetical gene supported by AF147354
226238_at	MCEE	84693	0.02	NM_032601	NP_115990	0.90	methylmalonyl CoA epimerase
226243_at	LOC391356	391356	0.02	BF590958	0.94		similar to CG14903-PA
226247_at	PLEKHA1	59338	0.01	NM_001001974	NP_001001974	0.84	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1
226249_at	LOC401548	401548	0.01	AK126644	0.92		similar to RIKEN cDNA 4732481H14
226251_at	ASXL2	55252	0.01	BX648218	0.87		additional sex combs like 2 (Drosophila)
226254_s_at	KIAA1430	57587	0.04	AB037851	BAA92668	0.83	KIAA1430
226255_at	ZBTB33	10009	4.18e-03	NM_006777	NP_006768	0.89	zinc finger and BTB domain containing 33
226257_x_at	MRPS22	56945	2.39e-03	NM_020191	NP_064576	0.93	mitochondrial ribosomal protein S22
226261_at	ZNRF2	223082	0.01	NM_147128	NP_667339	0.89	zinc and ring finger 2
226268_at	RAB21	23011	0.01	BC009109	AAH09109	0.90	RAB21, member RAS oncogene family
226276_at	MGC23909	153339	0.02	NM_174909	NP_777569	0.93	hypothetical protein MGC23909
226278_at	DKFZp313A2432	258010	7.6e-03	AL833119	0.79		hypothetical protein DKFZp313A2432
226283_at	WDR51B	282809	0.03	NM_172240	NP_758440	0.91	WD repeat domain 51B
226300_at	MED19	219541	0.02	NM_153450	NP_703151	0.89	mediator of RNA polymerase II transcription, subunit 19 homolog (yeast)
226312_at	AVO3	253260	0.03	AB082530	BAC02708	0.90	likely ortholog of mouse TORC2-specific protein AVO3 (S. cerevisiae)
226314_at	D4ST1	113189	0.01	NM_130468	NP_569735	1.08	dermatan 4 sulfotransferase 1
226315_at	MGC20398	91603	0.02	NM_052857	NP_443089	0.92	hypothetical protein MGC20398
226316_at	C13orf10	64062	0.02	BF592957	0.84		chromosome 13 open reading frame 10
226318_at	TBRG1	84897	0.02	AK074594	BAC11080	0.91	transforming growth factor beta regulator 1
226319_s_at	THOC4	10189	0.02	NM_005782	NP_005773	0.78	THO complex 4
226320_at	THOC4	10189	0.01	NM_005782	NP_005773	0.86	THO complex 4
226321_at	LOC116068	116068	5.93e-03	XM_371760	XP_371760	0.90	hypothetical protein LOC116068
226323_at	MGC20398	91603	0.03	NM_052857	NP_443089	0.87	hypothetical protein MGC20398
226326_at	PCGF5	84333	3.7e-03	AK055625	0.81		polycomb group ring finger 5
226329_s_at	LOC129531	129531	0.02	NM_138798	NP_620153	0.89	hypothetical protein BC018453
226334_s_at	AHSA2	130872	0.03	NM_152392	NP_689605	0.90	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)
226345_at	ARL8	221079	8.05e-03	AW270158	0.86		ADP-ribosylation factor-like 8
226351_at	NSUN4	387338	0.02	NM_199044	NP_950245	0.90	NOL1/NOP2/Sun domain family, member 4
226353_at	SPPL2A	84888	8.57e-03	NM_032802	NP_116191	0.93	putative intramembrane cleaving protease
226361_at	TMEM42	131616	0.04	NM_144638	NP_653239	0.91	transmembrane protein 42
226362_at	LOC153561	153561	0.03	AI198515	0.92		hypothetical protein LOC153561

226366_at	SHPRH	257218	0.01	NM_173082	NP_775105	0.82	SNF2 histone linker PHD RING helicase
226376_at	ZC3HDC5	85451	1.92e-04	XM_036115	XP_036115	0.82	zinc finger CCCH type domain containing 5
226385_s_at	C7orf30	115416	0.02	NM_138446	NP_612455	0.91	chromosome 7 open reading frame 30
226386_at	C7orf30	115416	0.02	NM_138446	NP_612455	0.94	chromosome 7 open reading frame 30
226391_at	NDUFB2	4708	0.03	AW271788		0.92	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa
226398_s_at	C10orf4	118924	3.69e-03	NM_145246	NP_660289	0.83	chromosome 10 open reading frame 4
226399_at	FLJ14281	79982	0.01	AL121021		0.93	hypothetical protein FLJ14281
226404_at	RNPC2	9584	6.44e-04	NM_184234	NP_909122	0.82	RNA-binding region (RNP1, RRM) containing 2
226406_at	C18orf25	147339	2.16e-03	BX640683	CAE45812	0.86	chromosome 18 open reading frame 25
226409_at	TBC1D20	128637	0.02	AK095110		0.91	TBC1 domain family, member 20
226421_at	LOC286505	286505	1.37e-03	BC051895		0.88	hypothetical protein LOC286505
226425_at	RSNL2	79745	0.01	NM_024692	NP_078968	0.85	restin-like 2
226437_at	LOC90522	90522	0.03	NM_033557	NP_291035	0.91	similar to putative transmembrane protein; homolog of yeast Golgi membrane protein Yif1p (Yip1p-interacting factor)
226438_at	SNTB1	6641	0.02	AK025100		0.87	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)
226444_at	SLC39A10	57181	0.01	AI700476		0.82	solute carrier family 39 (zinc transporter), member 10
226459_at	PIK3AP1	118788	0.04	NM_152309	NP_689522	0.87	phosphoinositide-3-kinase adaptor protein 1
226466_s_at	MGC29729	92002	2.61e-03	NM_152274	NP_689487	0.92	hypothetical protein MGC29729
226474_at	NOD27	84166	0.04	AK025212		0.88	nucleotide-binding oligomerization domains 27
226476_s_at	VprBP	9730	0.03	NM_014703	NP_055518	0.86	Vpr-binding protein
226501_at	LOC63929	63929	0.03	BX648018		0.92	hypothetical protein LOC63929
226508_at	PHC3	80012	0.04	AI042019		0.90	polyhomeotic like 3 (Drosophila)
226515_at	LOC133957	133957	4.15e-03	NM_145265	NP_660308	0.84	similar to RIKEN cDNA 0610011N22
226518_at	KCTD10	83892	0.04	NM_031954	NP_114160	0.89	potassium channel tetramerisation domain containing 10
226524_at	MGC26717	285237	1.77e-04	NM_173824	NP_776185	0.83	hypothetical protein MGC26717
226528_at	MTX3	345778	0.01	BX647596	CAI46098	0.89	metaxin 3
226529_at	FLJ11273	54664	0.02	NM_018374	NP_060844	0.89	hypothetical protein FLJ11273
226538_at	MAN2A1	4124	5.06e-03	AL833486		0.90	mannosidase, alpha, class 2A, member 1
226541_at	FBXO30	84085	0.04	NM_032145	NP_115521	0.90	F-box protein 30
226558_at	LOC441057	441057	7.91e-03	XM_498989	XP_498989	0.66	hypothetical gene supported by AK096952; AK126241; BC068588
226559_at	IER5L	389792	4.07e-03	NM_203434	NP_982258	1.18	immediate early response 5-like
226561_at	LOC285086	285086	0.04	BX648387		0.94	hypothetical protein LOC285086
226572_at	SOCS7	30837	0.04	AL045666		0.89	suppressor of cytokine signaling 7
226583_at	FLJ40142	400073	0.04	NM_207435	NP_997318	0.94	FLJ40142 protein
226584_s_at	C20orf55	83541	0.01	NM_031424	NP_113612	0.86	chromosome 20 open reading frame 55
226608_at	LOC388272	388272	4.31e-03	NM_001001436	NP_001001436	0.86	similar to RIKEN cDNA 4921524J17
226629_at	SLC43A2	124935	0.02	NM_152346	NP_689559	1.10	solute carrier family 43, member 2
226631_at	LOC399818	399818	5.25e-04	NM_212554	NP_997719	0.89	similar to CG9643-PA
226633_at	RAB8B	51762	0.02	AI807023		0.90	RAB8B, member RAS oncogene family
226642_s_at	NUDCD2	134492	0.01	NM_145266	NP_660309	0.92	NudC domain containing 2
226660_at	RPS6KB1	6198	0.02	AK091503		0.91	ribosomal protein S6 kinase, 70kDa, polypeptide 1
226662_at	STX17	55014	8.89e-03	AW085575		0.88	syntaxin 17

226665_at	AHSA2	130872	6.71e-03	AK092505		0.77	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)
226682_at	LOC283666	283666	7.02e-03	BC033285		0.86	hypothetical protein LOC283666
226684_at	C14orf103	55102	6.06e-03	AI217906		0.92	chromosome 14 open reading frame 103
226692_at	SERF2	10169	0.01	AI092931		0.92	small EDRK-rich factor 2
226702_at	LOC129607	129607	0.03	BC016969	AAH16969	0.54	hypothetical protein LOC129607
226714_at	FLJ10211	55095	0.01	BC054518	AAH54518	1.24	hypothetical protein FLJ10211
226727_at	LOC284106	284106	4.84e-05	AK097047		0.81	hypothetical protein LOC284106
226734_at	EIF4E2	9470	6.4e-03	AW242220		0.94	eukaryotic translation initiation factor 4E member 2
226739_at	KIAA1991	254225	0.03	XM_495886	XP_495886	1.09	hypothetical protein KIAA1991
226740_x_at	LOC200030	200030	0.04	NM_183372	NP_899228	0.94	hypothetical protein LOC200030
226745_at	CYP4V2	285440	0.02	NM_207352	NP_997235	0.85	cytochrome P450, family 4, subfamily V, polypeptide 2
226747_at	KIAA1344	57544	8.05e-03	AB037765	BAA92582	0.86	KIAA1344
226748_at	MGC35274	256586	4.53e-03	NM_153374	NP_699205	0.84	hypothetical protein MGC35274
226749_at	MRPS9	64965	6.16e-05	NM_182640	NP_872578	0.83	mitochondrial ribosomal protein S9
226753_at	MGC33371	143684	6.11e-03	NM_144664	NP_653265	0.92	hypothetical protein MGC33371
226757_at	IFIT2	3433	0.01	NM_001547	NP_001538	1.18	interferon-induced protein with tetratricopeptide repeats 2
226758_at	LUC7L2	51631	1.57e-03	BC041001		0.92	LUC7-like 2 (S. cerevisiae)
226771_at	ATP8B2	57198	8.8e-03	AB032963	BAA86451	0.80	ATPase, Class I, type 8B, member 2
226782_at	SLC25A30	253512	0.02	AK094133		0.86	solute carrier family 25, member 30
226785_at	ATP11C	286410	0.04	NM_173694	NP_775965	0.88	ATPase, Class VI, type 11C
226801_s_at	FLJ12806	64853	0.01	AF131838		0.91	hypothetical protein FLJ12806
226808_at	KIAA0543	23145	0.03	AW771007		0.86	KIAA0543 protein
226816_s_at	KIAA1143	57456	0.04	AB032969	BAA86457	0.91	KIAA1143 protein
226818_at	MPEG1	219972	0.01	AK074166	BAB84992	0.91	macrophage expressed gene 1
226823_at	PHACTR4	65979	0.02	NM_023923	NP_076412	0.90	phosphatase and actin regulator 4
226825_s_at	TPARL	55858	0.03	NM_018475	NP_060945	0.91	TPA regulated locus
226826_at	LSM11	134353	5.82e-04	AU152993		0.89	LSM11, U7 small nuclear RNA associated
226835_s_at	LOC441951	441951	0.01	BC062222		0.91	similar to RPE-spondin
226848_at	NR2C2	7182	0.01	AI571166		0.85	nuclear receptor subfamily 2, group C, member 2
226862_at	MBD1	4152	0.03	NM_015846	NP_056671	0.91	methyl-CpG binding domain protein 1
226866_at	ESCO1	114799	0.02	NM_052911	NP_443143	0.93	establishment of cohesion 1 homolog 1 (S. cerevisiae)
226876_at	MGC45871	359845	4.73e-04	AF085987		1.40	hypothetical protein MGC45871
226880_at	NUCKS	64710	0.01	AF306939		0.85	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate
226881_at	GRPEL2	134266	0.01	NM_152407	NP_689620	0.81	GrpE-like 2, mitochondrial (E. coli)
226886_at	GFPT1	2673	0.01	AF131846		0.88	glutamine-fructose-6-phosphate transaminase 1
226888_at	CSNK1G1	53944	0.04	BG104860		0.93	casein kinase 1, gamma 1
226896_at	CHCHD1	118487	0.02	NM_203298	NP_976043	0.93	coiled-coil-helix-coiled-coil-helix domain containing 1
226897_s_at	ZC3HDC7	29066	0.01	NM_014153	NP_054872	0.90	zinc finger CCCH type domain containing 7
226910_at	COMMD2	51122	9.61e-03	AW008502		0.88	COMM domain containing 2
226914_at	ARPC5L	81873	9.2e-03	AU158936		0.85	actin related protein 2/3 complex, subunit 5-like
226915_s_at	ARPC5L	81873	0.02	NM_030978	NP_112240	0.84	actin related protein 2/3 complex, subunit 5-like
226921_at	UBR1	197131	8.05e-03	AV715153		0.90	ubiquitin protein ligase E3 component n-recognin 1
226924_at	LOC400657	400657	0.02	BC036588		0.90	hypothetical gene supported by BC036588

226934_at	CPSF6	11052	0.03	AU149663		0.85	cleavage and polyadenylation specific factor 6, 68kDa
226935_s_at	CRR9	81037	8.55e-04	NM_030782	NP_110409	0.84	cisplatin resistance related protein CRR9p
226936_at	C6orf173	387103	9.4e-03	BC039556		0.91	chromosome 6 open reading frame 173
226936_at	LOC503503	503503	9.4e-03	BC039556		0.91	hypothetical LOC503503
226947_at	C6orf216	375513	1.46e-04	NM_206910	NP_996793	0.81	chromosome 6 open reading frame 216
226952_at	EAF1	85403	0.01	NM_033083	NP_149074	0.93	ELL associated factor 1
226962_at	FRBZ1	360023	0.04	BC043426		0.85	FRBZ1 protein
226963_at	MGC23908	91408	5.57e-03	AI380378		0.95	similar to transcription factor BTF3
226965_at	FLJ34969	201627	0.01	NM_152678	NP_689891	0.91	hypothetical protein FLJ34969
226968_at	KIF1B	23095	0.02	NM_183416	NP_904325	1.12	kinesin family member 1B
226975_at	RNP	55599	0.02	NM_017619	NP_060089	0.89	U11/U12 snRNP 65K
226979_at	MAP3K2	10746	0.01	AI125541		1.13	mitogen-activated protein kinase kinase kinase 2
226990_at	M11S1	4076	0.02	AI798775		0.92	membrane component, chromosome 11, surface marker 1
226991_at	NFATC2	4773	0.02	AA489681		0.86	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2
226993_at	TRIP12	9320	0.02	AA973551		0.94	thyroid hormone receptor interactor 12
226994_at	DNAJA2	10294	0.03	NM_005880	NP_005871	0.88	DnaJ (Hsp40) homolog, subfamily A, member 2
227000_at	Ells1	222166	0.03	NM_152793	NP_690006	1.17	hypothetical protein Ells1
227014_at	LOC57168	57168	0.04	NM_020437	NP_065170	0.87	similar to aspartate beta hydroxylase (ASPH)
227018_at	DPP8	54878	0.01	NM_130434	NP_569118	0.92	dipeptidylpeptidase 8
227020_at	YPEL2	388403	0.01	AK096866		0.95	yippee-like 2 (Drosophila)
227022_at	GNPDA2	132789	0.01	NM_138335	NP_612208	0.86	glucosamine-6-phosphate deaminase 2
227026_at	HSMPP8	54737	0.03	AK056785	BAB71284	0.92	M-phase phosphoprotein, mpp8
227033_at	GRP58	2923	1.16e-03	NM_005313	NP_005304	0.84	glucose regulated protein, 58kDa
227064_at	MGC15396	91369	0.01	AV712687		0.89	hypothetical protein MGC15396
227066_at	MOBKL2C	148932	8.42e-03	NM_145279	NP_660322	0.92	MOB1, Mps One Binder kinase activator-like 2C (yeast)
227077_at	ZNF286	57335	0.01	AK055651		0.87	zinc finger protein 286
227085_at	H2AFV	94239	0.02	AK025785		0.93	H2A histone family, member V
227087_at	INPP4A	3631	0.04	AA126419		0.90	inositol polyphosphate-4-phosphatase, type I, 107kDa
227113_at	ADHFE1	137872	3.26e-03	NM_144650	NP_653251	0.84	alcohol dehydrogenase, iron containing, 1
227132_at	LOC51123	51123	4.15e-03	NM_016096	NP_057180	0.86	HSPC038 protein
227133_at	CXorf39	139231	0.02	BE856541		0.89	chromosome X open reading frame 39
227138_at	CRTAP	10491	0.04	NM_006371	NP_006362	1.12	cartilage associated protein
227139_s_at	HPS3	84343	7.02e-03	NM_032383	NP_115759	0.94	Hermansky-Pudlak syndrome 3
227149_at	TNRC6C	57690	0.02	NM_018996	NP_061869	0.89	trinucleotide repeat containing 6C
227156_at	TNRC8	27325	5.23e-03	AK025872		0.83	trinucleotide repeat containing 8
227161_at	C7orf3	64434	0.02	XM_374590	XP_374590	0.88	chromosome 7 open reading frame 3
227172_at	LOC89894	89894	0.02	NM_138341	NP_612350	0.90	hypothetical protein BC000282
227178_at	CUGBP2	10659	7.38e-03	AI652861		0.90	CUG triplet repeat, RNA binding protein 2
227181_at	LOC348801	348801	2.52e-03	AK056320		1.11	hypothetical protein LOC348801
227182_at	SUSD3	203328	0.03	NM_145006	NP_659443	0.87	sushi domain containing 3
227195_at	ZNF503	84858	0.03	NM_032772	NP_116161	0.92	zinc finger protein 503
227207_x_at	ZNF213	7760	0.01	NM_004220	NP_004211	0.90	zinc finger protein 213
227208_at	DLNB14	338657	7.02e-03	NM_198489	NP_940891	0.91	similar to DLNB14

227210_at	SFMBT2	57713	9.53e-04	T65020		0.83	Scm-like with four mbt domains 2
227214_at	GOPC	57120	0.01	NM_020399	NP_065132	0.88	golgi associated PDZ and coiled-coil motif containing
227215_at	GOPC	57120	0.04	NM_020399	NP_065132	0.91	golgi associated PDZ and coiled-coil motif containing
227239_at	DRCTNNB1A	84668	0.04	BX640757	CAE45864	0.92	down-regulated by Ctnnb1, a
227261_at	KLF12	11278	0.02	NM_007249	NP_009180	0.86	Kruppel-like factor 12
227266_s_at	FYB	2533	0.02	NM_199335	NP_955367	0.90	FYN binding protein (FYB-120/130)
227266_s_at	FYB	2533	0.02	NM_001465	NP_001456	0.90	FYN binding protein (FYB-120/130)
227267_at	FLJ35779	134359	0.04	NM_152408	NP_689621	0.90	hypothetical protein FLJ35779
227268_at	LOC51136	51136	0.01	NM_016125	NP_057209	0.87	PTD016 protein
227270_at	LOC285550	285550	0.03	BC048993		0.95	hypothetical protein LOC285550
227280_s_at	FLJ40432	151195	9.63e-03	AK026922		0.88	hypothetical protein FLJ40432
227291_s_at	LOC388962	388962	6.48e-03	NM_212552	NP_997717	0.83	similar to RIKEN 1810056O20
227294_at	LOC115509	115509	0.01	AL834299	CAH56363	0.93	hypothetical protein BC014000
227304_at	SHMT1	6470	7.16e-03	N25727		0.91	serine hydroxymethyltransferase 1 (soluble)
227322_s_at	BCCIP	56647	0.01	NM_078468	NP_510868	0.91	BRCA2 and CDKN1A interacting protein
227344_at	ZNFN1A1	10320	0.02	AI439886		0.85	zinc finger protein, subfamily 1A, 1 (Ikaros)
227345_at	TNFRSF10D	8793	0.01	NM_003840	NP_003831	0.86	tumor necrosis factor receptor superfamily, member
10d, decoy with truncated death domain							
227346_at	ZNFN1A1	10320	0.02	AI741188		0.92	zinc finger protein, subfamily 1A, 1 (Ikaros)
227351_at	LOC146174	146174	0.03	BC045557		0.82	hypothetical protein LOC146174
227354_at	FLJ37858	441357	0.03	AK095177	BAC04494	0.90	FLJ37858 protein
227363_s_at	NOC4	10328	0.04	NM_006067	NP_006058	0.90	neighbor of COX4
227373_at	LOC146517	146517	5.61e-03	BX537575		0.93	hypothetical protein LOC146517
227375_at	DKFZP566D1346	81573	2.84e-03	AA152232		0.83	hypothetical protein DKFZp566D1346
227379_at	OACT1	154141	0.02	XM_371801	XP_371801	0.90	O-acyltransferase (membrane bound) domain containing 1
227395_at	MGC10233	219899	0.03	BE672045		0.89	catastrophin
227402_s_at	MGC14595	84294	0.03	NM_032334	NP_115710	0.89	hypothetical protein MGC14595
227418_at	KIAA1826	84437	0.03	AI808746		0.89	KIAA1826 protein
227435_at	KIAA2018	205717	0.03	BX537728	CAD97821	0.89	similar to K06A9.1b.p
227442_at	FLJ38991	285521	0.03	NM_173827	NP_776188	0.90	hypothetical protein FLJ38991
227445_at	LOC115509	115509	0.01	NM_138447	NP_612456	0.85	hypothetical protein BC014000
227447_at	SKIV2L2	23517	0.03	NM_015360	NP_056175	0.93	superkiller viralicidic activity 2-like 2 (S. cerevisiae)
227450_at	FLJ32115	121506	8.57e-03	NM_152321	NP_689534	0.92	hypothetical protein FLJ32115
227470_at	ZNF553	197407	0.02	AI870369		1.07	zinc finger protein 553
227485_at	DDX26B	203522	8.42e-03	NM_182540	NP_872346	0.92	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B
227502_at	MULK	55750	1.21e-03	AV649579		0.88	multiple substrate lipid kinase
227504_s_at	KIAA1276	27146	0.03	N64630		0.89	KIAA1276 protein
227505_at	KIAA1276	27146	0.02	N64630		0.89	KIAA1276 protein
227517_s_at	GAS5	60674	2.16e-03	BC038733		0.80	growth arrest-specific 5
227539_at	GNA13	10672	6.35e-03	AW298099		0.91	guanine nucleotide binding protein (G protein), alpha 13
227560_at	SFXN2	118980	3.64e-03	NM_178858	NP_849189	0.85	sideroflexin 2
227569_at	LNX2	222484	8.48e-03	NM_153371	NP_699202	0.80	ligand of numb-protein X 2
227575_s_at	C14orf102	55051	0.03	NM_017970	NP_060440	0.91	chromosome 14 open reading frame 102
227580_s_at	DKFZP434B0335	25851	0.01	AL117495	CAB55961	0.92	DKFZP434B0335 protein
227594_at	ZNF258	9204	0.01	AB037774	BAA92591	0.91	zinc finger protein 258

227607_at	AMSH-LP	57559	0.03	NM_020799	NP_065850	0.87	associated molecule with the SH3 domain of STAM (AMSH) like protein
227608_at	YY1AP1	55249	7.28e-04	AA225118		0.93	YY1 associated protein 1
227616_at	BCL9L	283149	0.04	NM_182557	NP_872363	1.13	B-cell CLL/lymphoma 9-like
227622_at	PCF11	51585	5.57e-03	AF086097		0.86	pre-mRNA cleavage complex II protein Pcf11
227625_s_at	STUB1	10273	0.03	NM_005861	NP_005852	0.92	STIP1 homology and U-box containing protein 1
227626_at	C6orf33	85315	0.02	NM_133367	NP_588608	0.86	chromosome 6 open reading frame 33
227627_at	SGKL	23678	7.02e-03	NM_013257	NP_037389	0.90	serum/glucocorticoid regulated kinase-like
227630_at	PPP2R5E	5529	0.01	AW274445		0.87	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
227638_at	KIAA1632	57724	9.63e-03	BC036911	AAH36911	0.93	KIAA1632
227639_at	PIGK	10026	2.61e-03	BX648473		0.86	phosphatidylinositol glycan, class K
227658_s_at	PLEKHA3	65977	0.03	NM_019091	NP_061964	0.89	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3
227668_at	FLJ31528	146705	0.03	NM_144679	NP_653280	0.92	hypothetical protein FLJ31528
227670_at	ZNF75A	7627	0.04	NM_153028	NP_694573	0.84	zinc finger protein 75a
227678_at	KUB3	91419	0.03	NM_033276	NP_150592	0.88	Ku70-binding protein 3
227686_at	MGC15763	92106	0.02	NM_138381	NP_612390	0.82	hypothetical protein BC008322
227689_at	ZNF227	7770	8.55e-05	NM_182490	NP_872296	0.92	zinc finger protein 227
227693_at	WDR20	91833	0.02	NM_181291	NP_851808	0.93	WD repeat domain 20
227712_at	DJ122O8.2	57226	0.01	NM_020466	NP_065199	0.90	hypothetical protein dJ122O8.2
227724_at	LOC439987	439987	0.04	XM_498488	XP_498488	0.84	LOC439987
227741_at	PTPLB	201562	1.26e-03	NM_198402	NP_940684	0.84	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b
227751_at	PDCD5	9141	5.03e-03	AI817145		0.92	programmed cell death 5
227754_at	USP54	159195	0.02	AK127081	BAC86817	0.86	ubiquitin specific protease 54
227796_at	ZFP62	92379	0.03	NM_152283	NP_689496	0.91	zinc finger protein 62 homolog (mouse)
227837_at	FLJ20309	54891	0.02	BF057711		0.92	hypothetical protein FLJ20309
227844_at	FMNL3	91010	1.25e-03	NM_175736	NP_783863	0.85	formin-like 3
227855_at	FLJ10357	55701	0.01	NM_018071	NP_060541	1.17	hypothetical protein FLJ10357
227859_at	RBJ	51277	8.63e-03	NM_016544	NP_057628	0.81	Ras-associated protein Rap1
227867_at	LOC129293	129293	4.6e-03	BC051789	AAH51789	0.77	hypothetical protein LOC129293
227873_at	C5orf14	79770	0.04	BX538131	CAD98032	0.90	chromosome 5 open reading frame 14
227905_s_at	AZI2	64343	7.38e-03	NM_022461	NP_071906	0.81	5-azacytidine induced 2
227916_x_at	EXOSC3	51010	4.36e-03	NM_016042	NP_057126	0.94	exosome component 3
227920_at	KIAA1553	57673	0.02	XM_166320	XP_166320	1.10	KIAA1553
227925_at	LOC399972	399972	8.24e-03	AK096370		1.14	hypothetical gene supported by AK096370
227946_at	OSBPL7	114881	8.69e-03	NM_145798	NP_665741	0.87	oxysterol binding protein-like 7
227960_s_at	FAHD1	81889	0.04	NM_031208	NP_112485	0.88	fumarylacetoacetate hydrolase domain containing 1
227965_at	APC2	10297	0.01	BE262551		0.81	adenomatosis polyposis coli 2
227968_at	FLJ34283	347862	0.04	NM_182612	NP_872418	0.90	hypothetical protein FLJ34283
227973_at	FLJ38973	205327	0.04	NM_153689	NP_710156	0.89	hypothetical protein FLJ38973
227979_at	RBM30	83759	0.01	AU152162		0.90	RNA binding motif protein 30
227981_at	CYB561D1	284613	0.02	NM_182580	NP_872386	0.95	cytochrome b-561 domain containing 1
227982_at	SLA/LP	51091	0.03	AI806592		0.86	soluble liver antigen/liver pancreas antigen

227984_at	FLJ12681	64788	0.04	BE464483		0.76	hypothetical protein FLJ12681
227993_at	METAP2	10988	8.67e-04	BC016008	AAH16008	0.87	methionyl aminopeptidase 2
227994_x_at	C20orf149	79144	0.04	NM_024299	NP_077275	0.83	chromosome 20 open reading frame 149
228009_x_at	ZNRD1	30834	0.01	NM_014596	NP_055411	0.95	zinc ribbon domain containing, 1
228019_s_at	MRPS18C	51023	4.16e-03	NM_016067	NP_057151	0.94	mitochondrial ribosomal protein S18C
228023_x_at	AMY2B	280	9.71e-03	AK095605		0.92	amylase, alpha 2B; pancreatic
228041_at	AASDH	132949	0.02	NM_181806	NP_861522	0.93	2-aminoadipic 6-semialdehyde dehydrogenase
228047_at	RPL30	6156	5.96e-03	AI815001		0.77	ribosomal protein L30
228050_at	FLJ12787	84135	0.01	NM_032175	NP_115551	0.86	Src-associated protein SAW
228071_at	GIMAP7	168537	0.03	NM_153236	NP_694968	0.88	GTPase, IMAP family member 7
228083_at	CACNA2D4	93589	4.86e-03	NM_172364	NP_758952	0.79	calcium channel, voltage-dependent, alpha 2/delta subunit 4
228089_x_at	LOC374395	374395	0.02	NM_199337	NP_955369	0.91	similar to RIKEN cDNA 1810059G22
228095_at	PHF14	9678	0.01	AA608749		0.83	PHD finger protein 14
228106_at	FLJ20280	54876	0.03	NM_017741	NP_060211	0.88	hypothetical protein FLJ20280
228109_at	RASGRF2	5924	0.02	AI912976		0.87	Ras protein-specific guanine nucleotide-releasing factor 2
228120_at	EIF2C1	26523	0.04	AW136032		0.93	eukaryotic translation initiation factor 2C, 1
228135_at	C1orf52	148423	0.02	NM_198077	NP_932343	0.91	chromosome 1 open reading frame 52
228152_s_at	FLJ31033	91351	0.03	AK023743		1.22	hypothetical protein FLJ31033
228164_at	AP4E1	23431	0.01	BE964704		0.84	adaptor-related protein complex 4, epsilon 1 subunit
228167_at	KLHL6	89857	0.01	NM_130446	NP_569713	0.93	kelch-like 6 (Drosophila)
228183_s_at	RIP	84268	0.04	NM_032308	NP_115684	0.92	RPA interacting protein
228185_at	ZNF25	219749	4.31e-03	NM_145011	NP_659448	0.82	zinc finger protein 25 (KOX 19)
228200_at	LOC441383	441383	0.02	BF110363		0.93	hypothetical gene supported by AF086559; BC065734
228217_s_at	LOC389362	389362	0.01	AK126623		0.83	hypothetical LOC389362
228234_at	TICAM2	353376	0.03	NM_021649	NP_067681	0.90	toll-like receptor adaptor molecule 2
228238_at	GAS5	60674	5.57e-03	BC038733		0.89	growth arrest-specific 5
228248_at	AVO3	253260	0.02	AB082530	BAC02708	1.19	likely ortholog of mouse TORC2-specific protein AVO3 (S. cerevisiae)
228268_at	FMO2	2327	2.22e-04	AI758223		1.21	flavin containing monooxygenase 2
228271_at	SND1	27044	0.01	AW001186		1.13	staphylococcal nuclease domain containing 1
228282_at	MGC33302	256471	7.69e-03	AW611550		0.91	hypothetical protein MGC33302
228284_at	TLE1	7088	0.02	NM_005077	NP_005068	0.88	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
228287_at	ING5	84289	0.01	NM_032329	NP_115705	0.86	inhibitor of growth family, member 5
228298_at	MGC16044	91523	1.75e-03	NM_138371	NP_612380	0.80	hypothetical protein MGC16044
228305_at	ZNF565	147929	7.53e-04	NM_152477	NP_689690	0.90	zinc finger protein 565
228306_at	HSPC163	29097	0.02	T87074		0.92	HSPC163 protein
228324_at	C9orf41	138199	5.41e-03	BX647386		0.84	chromosome 9 open reading frame 41
228330_at	C6orf113	221302	0.03	NM_145062	NP_659499	0.93	chromosome 6 open reading frame 113
228331_at	C11orf31	280636	3.5e-03	BC064570	AAH64570	0.87	chromosome 11 open reading frame 31
228332_s_at	C11orf31	280636	0.02	NM_170746	NP_734467	0.86	chromosome 11 open reading frame 31
228334_x_at	KIAA1712	80817	0.01	AB051499	BAB21803	0.92	KIAA1712
228341_at	NUDT16	131870	4.68e-03	AI809108		0.90	nudix (nucleoside diphosphate linked moiety X)-type motif 16

228348_at	WINS1	55180	8.05e-03	NM_018148	NP_060618	0.88	WINS1 protein with Drosophila Lines (Lin) homologous domain
228353_x_at	STS-1	84959	7.19e-03	NM_032873	NP_116262	0.90	Cbl-interacting protein Sts-1
228355_s_at	LOC91942	91942	0.01	NM_174889	NP_777549	0.87	hypothetical protein LOC91942
228357_at	ZC3HDC5	85451	0.02	BE966979		0.91	zinc finger CCCH type domain containing 5
228365_at	CPNE8	144402	0.02	NM_153634	NP_705898	0.93	copine VIII
228376_at	GGTA1	2681	0.03	AF378122		0.82	glycoprotein, alpha-galactosyltransferase 1
228381_at	ATF7IP2	80063	0.03	AV716964		0.90	activating transcription factor 7 interacting protein 2
228385_at	DKFZP564B1023	83479	0.01	BC041801	AAH41801	0.86	hypothetical protein DKFZp564B1023
228386_s_at	DKFZP564B1023	83479	0.04	NM_031306	NP_112596	0.95	hypothetical protein DKFZp564B1023
228402_at	ZBED3	84327	0.02	NM_032367	NP_115743	1.10	zinc finger, BED domain containing 3
228408_s_at	SDAD1	55153	3.98e-03	NM_018115	NP_060585	0.90	SDA1 domain containing 1
228426_at	CLEC2D	29121	0.02	NM_013269	NP_037401	0.82	C-type lectin superfamily 2, member D
228439_at	MGC20410	116071	0.04	NM_138456	NP_612465	1.25	hypothetical protein BC012330
228452_at	C17orf39	79018	0.02	NM_024052	NP_076957	0.87	chromosome 17 open reading frame 39
228453_at	LOC284267	284267	0.03	AK094080		0.92	hypothetical protein LOC284267
228456_s_at	LOC149832	149832	0.02	AK123831		0.91	hypothetical protein LOC149832
228482_at	FLJ36674	284040	9.04e-03	NM_173622	NP_775893	0.84	hypothetical protein FLJ36674
228506_at	C10orf86	54780	0.02	NM_017615	NP_060085	0.89	chromosome 10 open reading frame 86
228512_at	FLJ20758	55037	3.45e-03	NM_017952	NP_060422	0.76	FLJ20758 protein
228520_s_at	APLP2	334	0.03	AA022510		1.12	amyloid beta (A4) precursor-like protein 2
228531_at	SAMD9	54809	6.92e-03	NM_017654	NP_060124	0.75	sterile alpha motif domain containing 9
228536_at	LOC90826	90826	0.02	NM_138364	NP_612373	0.92	hypothetical protein BC004337
228544_s_at	CSRP2BP	57325	0.04	NM_020536	NP_065397	0.83	CSRP2 binding protein
228566_at	P15RS	55197	0.02	AA778694		0.93	hypothetical protein FLJ10656
228569_at	PAPOLA	10914	0.04	NM_032632	NP_116021	0.94	poly(A) polymerase alpha
228574_at	DKFZp762A217	160335	0.02	AI862551		0.88	hypothetical protein DKFZp762A217
228583_at	C14orf46	91750	0.03	AK055422		0.89	chromosome 14 open reading frame 46
228612_at	LOC399933	399933	0.01	AI571730		0.92	hypothetical LOC399933
228613_at	RAB11FIP3	9727	0.01	BF183535		0.85	RAB11 family interacting protein 3 (class II)
228619_x_at	MGC3794	261726	2.88e-03	AI694231		0.73	putative MAPK activating protein
228641_at	CARD8	22900	0.04	BF338389		0.93	caspase recruitment domain family, member 8
228648_at	LRG1	116844	0.02	NM_052972	NP_443204	1.18	leucine-rich alpha-2-glycoprotein 1
228652_at	FLJ38288	284309	0.03	NM_173632	NP_775903	0.91	hypothetical protein FLJ38288
228670_at	TEP1	7011	0.02	BX640983	CAE45993	0.92	telomerase-associated protein 1
228715_at	ZCCHC12	170261	6.53e-03	NM_173798	NP_776159	1.19	zinc finger, CCHC domain containing 12
228722_at	HRMT1L1	3275	0.01	AK095641		0.85	HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae)
228725_x_at	HRMT1L1	3275	7.35e-03	NM_206962	NP_996845	0.89	HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae)
228745_at	FLJ13611	80006	0.02	AI376997		0.85	hypothetical protein FLJ13611
228752_at	CXorf10	93949	0.01	AK021694		0.87	chromosome X open reading frame 10
228758_at	LOC389185	389185	0.04	AW264036		1.12	hypothetical LOC389185
228762_at	LFNG	3955	0.01	AK096284		0.82	lunatic fringe homolog (Drosophila)
228769_at	HKR2	342945	0.03	NM_181846	NP_862829	0.92	GLI-Kruppel family member HKR2
228791_at	MGC61550	348110	0.03	BF434655		0.83	hypothetical protein MGC61550
228801_at	ORMDL1	94101	2.16e-03	AB064959	BAC11710	0.93	ORM1-like 1 (S. cerevisiae)

228805_at	FLJ44216	375484	0.04	NM_198567	NP_940969	0.90	FLJ44216 protein
228839_s_at	LOC439994	439994	0.04	XM_498491	XP_498491	0.86	hypothetical gene supported by AF064843; AK025716
228841_at	LOC90624	90624	0.03	AW299250		0.86	hypothetical protein LOC90624
228851_s_at	ENSA	2029	0.03	NM_207042	NP_996925	0.89	endosulfine alpha
228852_at	ENSA	2029	0.04	NM_207168	NP_997051	1.11	endosulfine alpha
228859_at	LOC91431	91431	0.03	NM_138698	NP_619643	0.83	prematurely terminated mRNA decay factor-like
228866_at	ANKRD11	29123	0.02	BF514864		1.11	ankyrin repeat domain 11
228956_at	UGT8	7368	2.48e-03	N22272		1.16	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)
228960_at	NARG2	79664	0.03	AL833122	CAH56202	0.89	NMDA receptor regulated 2
228961_at	FLJ35954	166968	0.03	NM_152622	NP_689835	0.81	hypothetical protein FLJ35954
228970_at	ARCH	339487	8.8e-03	NM_178547	NP_848642	0.90	archease
228974_at	MGC48625	342926	0.03	AI816281		0.78	hypothetical protein MGC48625
228990_at	LOC85028	85028	0.02	AK092096		0.86	PNAS-123
228991_at	CDC2L5	8621	0.01	BF707423		0.88	cell division cycle 2-like 5 (cholinesterase-related cell division controller)
228993_s_at	LOC92482	92482	0.01	XM_378250	XP_378250	0.83	hypothetical protein LOC92482
228999_at	CHD2	1106	3.96e-03	NM_001271	NP_001262	0.87	chromodomain helicase DNA binding protein 2
229017_s_at	RIPK5	25778	9.33e-03	NM_015375	NP_056190	1.10	receptor interacting protein kinase 5
229035_s_at	KLHDC4	54758	0.04	AK001742		0.90	kelch domain containing 4
229054_at	FLJ39779	400223	0.04	NM_207442	NP_997325	1.10	FLJ39779 protein
229069_at	CIP29	84324	0.01	NM_033082	NP_149073	0.91	cytokine induced protein 29 kDa
229086_at	LOC148898	148898	5.73e-04	NM_138479	NP_612488	1.21	hypothetical protein BC007899
229141_at	WDR33	55339	0.02	AK123510		0.91	WD repeat domain 33
229145_at	C10orf104	119504	0.02	NM_173473	NP_775744	0.90	chromosome 10 open reading frame 104
229146_at	C7orf31	136895	3.79e-03	NM_138811	NP_620166	0.90	chromosome 7 open reading frame 31
229156_s_at	LOC441301	441301	0.03	AI949265		0.86	LOC441301
229181_s_at	C15orf25	55142	0.02	NM_018097	NP_060567	0.89	chromosome 15 open reading frame 25
229184_at	CCNT2	905	0.04	AW293353		0.88	cyclin T2
229194_at	PCGF5	84333	5.78e-03	NM_032373	NP_115749	0.80	polycomb group ring finger 5
229217_at	SP3	6670	0.03	NM_003111	NP_003102	0.88	Sp3 transcription factor
229246_at	SFRS1	6426	0.04	AI803504		0.89	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
229253_at	CTMP	117145	0.02	NM_053055	NP_444283	0.85	C-terminal modulator protein
229257_at	KIAA1856	84629	0.03	AI625045		1.13	KIAA1856 protein
229266_at	LOC284033	284033	3.49e-03	AK095052		1.17	hypothetical protein LOC284033
229344_x_at	KIAA1238	57494	0.04	BC033793	AAH33793	0.91	KIAA1238 protein
229350_x_at	PARP10	84875	0.03	NM_032789	NP_116178	0.88	poly (ADP-ribose) polymerase family, member 10
229353_s_at	NUCKS	64710	0.04	NM_022731	NP_073568	0.83	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate
229367_s_at	GIMAP6	474344	2.16e-03	NM_024711	NP_078987	0.88	GTPase, IMAP family member 6
229394_s_at	GRLF1	2909	0.04	AI275597		0.89	glucocorticoid receptor DNA binding factor 1
229414_at	PITPNC1	26207	0.04	AK094724		0.90	phosphatidylinositol transfer protein, cytoplasmic 1
229431_at	RFXAP	5994	0.01	NM_000538	NP_000529	0.87	regulatory factor X-associated protein
229433_at	C13orf10	64062	0.01	AU144571		0.89	chromosome 13 open reading frame 10

229436_x_at	CXorf53	79184	1.75e-03	NM_024332	NP_077308	0.88	chromosome X open reading frame 53
229452_at	LOC92162	92162	4.85e-04	NM_203411	NP_981956	1.32	similar to RIKEN cDNA 2600017H02
229509_at	MGC33302	256471	0.04	NM_152778	NP_689991	0.91	hypothetical protein MGC33302
229519_at	FXR1	8087	0.04	NM_005087	NP_005078	0.92	fragile X mental retardation, autosomal homolog 1
229520_s_at	C14orf118	55668	0.01	AB032978	BAA86466	1.13	chromosome 14 open reading frame 118
229540_at	RBPSUH	3516	0.03	NM_005349	NP_005340	1.11	recombining binding protein suppressor of hairless
(Drosophila)							
229607_at	BTBD2	55643	0.02	AW302587		1.11	BTB (POZ) domain containing 2
229614_at	LOC162967	162967	0.01	AK095630		0.80	hypothetical protein LOC162967
229625_at	GBP5	115362	0.01	BG545653		0.61	guanylate binding protein 5
229632_s_at	FLJ10569	55174	0.01	NM_018142	NP_060612	0.89	hypothetical protein FLJ10569
229640_x_at	LOC440128	440128	0.03	AW439242		0.90	similar to hypothetical protein, MGC:7199
229650_s_at	MGC2747	79086	7.9e-03	AK025602		0.94	hypothetical protein MGC2747
229664_at	MAPK8	5599	0.04	AI379407		1.06	mitogen-activated protein kinase 8
229666_s_at	CSTF3	1479	9.33e-03	NM_001326	NP_001317	0.85	cleavage stimulation factor, 3' pre-RNA, subunit 3,
77kDa							
229685_at	TBC1D14	57533	2.62e-03	AI743207		0.86	TBC1 domain family, member 14
229694_at	WDR11	55717	0.03	AK124522	BAC85874	0.91	WD repeat domain 11
229736_at	MGC30208	255043	0.04	NM_173804	NP_776165	1.12	hypothetical protein MGC30208
229742_at	LOC145853	145853	0.04	XM_096885	XP_096885	0.90	hypothetical LOC145853
229804_x_at	CBWD1	55871	0.01	NM_018491	NP_060961	0.80	COBW domain containing 1
229813_x_at	DAZAP1	26528	0.01	NM_170711	NP_733829	0.87	DAZ associated protein 1
229845_at	MAPKAP1	79109	0.02	AY524430	AAS90840	0.89	mitogen-activated protein kinase associated protein 1
229862_x_at	ZNF499	84878	0.01	NM_032792	NP_116181	0.90	zinc finger protein 499
229891_x_at	KIAA1704	55425	0.04	AB051491	BAB21795	0.86	KIAA1704
229892_at	FLJ33915	347918	0.02	AK090610		0.86	hypothetical protein FLJ33915
229897_at	FLJ31295	121274	0.03	BF195808		1.18	hypothetical protein FLJ31295
229946_at	LOC389039	389039	0.03	XM_371561	XP_371561	0.87	similar to CDNA sequence BC043098
229966_at	EWSR1	2130	0.02	BX648769		0.88	Ewing sarcoma breakpoint region 1
229980_s_at	SNX5	27131	0.01	NM_152227	NP_689413	0.85	sorting nexin 5
229981_at	SNX5	27131	0.01	AL832967		0.87	sorting nexin 5
229983_at	TIGD2	166815	6.82e-03	NM_145715	NP_663761	0.88	tigger transposable element derived 2
230027_s_at	MRPL43	84545	0.01	NM_032112	NP_115488	0.86	mitochondrial ribosomal protein L43
230032_at	OSGEPL1	64172	0.01	AK055441	BAB70923	0.86	O-sialoglycoprotein endopeptidase-like 1
230078_at	RAPGEF6	51735	0.01	AI640834		0.93	Rap guanine nucleotide exchange factor (GEF) 6
230086_at	FNBP1	23048	9.4e-03	NM_015033	NP_055848	1.26	formin binding protein 1
230148_at	USP34	9736	4.39e-03	AI831431		0.83	ubiquitin specific protease 34
230179_at	LOC285812	285812	0.02	AK127555		0.80	hypothetical protein LOC285812
230192_at	RFP2	10206	0.01	NM_005798	NP_005789	0.85	ret finger protein 2
230205_at	ZNF561	93134	0.01	NM_152289	NP_689502	0.88	zinc finger protein 561
230261_at	ST8SIA4	7903	0.02	NM_005668	NP_005659	1.10	ST8 alpha-N-acetyl-neuraminide alpha-2,8-
sialyltransferase 4							
230292_at	CHC1L	1102	0.01	AA868809		0.89	chromosome condensation 1-like
230322_at	NFAM1	150372	0.01	NM_145912	NP_666017	1.11	NFAT activating protein with ITAM motif 1
230326_s_at	HSPC138	51501	8.54e-03	NM_016401	NP_057485	0.86	hypothetical protein HSPC138

230337_at	SOS1	6654	0.01	NM_005633	NP_005624	0.85	son of sevenless homolog 1 (Drosophila)
230363_s_at	INPP5F	22876	6.04e-03	NM_014937	NP_055752	0.81	inositol polyphosphate-5-phosphatase F
230395_at	DREV1	51108	0.02	AI536637		0.83	DORA reverse strand protein 1
230421_at	LOC345462	345462	0.02	XM_293828	XP_293828	0.89	similar to hypothetical protein 9630041N07
230448_at	MGC15523	124565	0.04	AK093037	BAC04027	1.10	hypothetical protein MGC15523
230452_at	LOC400999	400999	0.04	XM_379123	XP_379123	0.88	hypothetical gene supported by AK124342
230469_at	PLEKHK1	219790	9.13e-03	NM_145307	NP_660350	0.59	pleckstrin homology domain containing, family K member 1
230556_at	FLJ25059	196294	0.01	NM_144981	NP_659418	0.81	hypothetical protein FLJ25059
230561_s_at	FLJ23861	151050	0.03	NM_152519	NP_689732	0.86	hypothetical protein FLJ23861
230563_at	RASGEF1A	221002	0.03	NM_145313	NP_660356	0.87	RasGEF domain family, member 1A
230666_at	HOXA11S	221883	0.02	AA622837		0.85	homeo box A11, antisense
230707_at	SORL1	6653	0.04	NM_003105	NP_003096	1.15	sortilin-related receptor, L(DLR class) A repeats-containing
230815_at	LOC389765	389765	0.04	AK124523		0.91	similar to KIF27C
230884_s_at	SPG7	6687	6.71e-03	NM_003119	NP_003110	0.83	spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)
230885_at	SPG7	6687	5.57e-03	NM_003119	NP_003110	0.84	spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)
230888_at	HSPC049	29062	0.01	AW300278		0.91	HSPC049 protein
231012_at	TMEM20	159371	0.02	BC047102		0.92	transmembrane protein 20
231043_at	LOC200373	200373	0.03	XM_114222	XP_114222	1.08	similar to hypothetical protein
231045_x_at	C11orf31	280636	0.03	NM_170746	NP_734467	0.84	chromosome 11 open reading frame 31
231057_at	MTMR2	8898	0.03	AU144266		0.89	myotubularin related protein 2
231121_at	HPS3	84343	0.01	AK055245		0.84	Hermansky-Pudlak syndrome 3
231283_at	MGAT4A	11320	6.9e-03	AW271609		0.86	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme A
231288_at	KIAA1509	440193	1.73e-03	XM_496003	XP_496003	0.81	KIAA1509
231577_s_at	GBP1	2633	0.03	NM_002053	NP_002044	1.17	guanylate binding protein 1, interferon-inducible, 67kDa
231713_s_at	STATIP1	55250	0.03	NM_018255	NP_060725	0.90	signal transducer and activator of transcription 3 interacting protein 1
231764_at	CHRAC1	54108	0.03	NM_017444	NP_059140	0.91	chromatin accessibility complex 1
231809_x_at	PDCD7	10081	3.1e-03	NM_005707	NP_005698	0.89	programmed cell death 7
231821_x_at	LOC401149	401149	1.19e-03	AK024248		1.27	hypothetical gene supported by AK024248; AL137733
231870_s_at	NMD3	51068	0.04	BG291007		0.90	NMD3 homolog (S. cerevisiae)
231873_at	BMPR2	659	3.27e-03	NM_001204	NP_001195	0.86	bone morphogenetic protein receptor, type II (serine/threonine kinase)
231878_at	MVP	9961	0.02	AK026112		0.89	major vault protein
231894_at	SARS	6301	0.02	AU147785		0.89	seryl-tRNA synthetase
231896_s_at	DENR	8562	9.08e-03	NM_003677	NP_003668	0.93	density-regulated protein
231907_at	ABL2	27	1.27e-03	AK025877		1.17	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)
231917_at	GFM2	84340	4.18e-03	NM_170681	NP_733781	0.89	G elongation factor, mitochondrial 2
231921_at	FLJ13096	80067	0.02	AK021599		0.87	hypothetical protein FLJ13096
231926_at	EPS15L1	58513	0.04	AK023744		0.93	epidermal growth factor receptor pathway substrate 15-like 1
231927_at	ATF6	22926	0.03	BF671883		0.93	activating transcription factor 6

231948_s_at	NCE2	140739	0.01	NM_080678	NP_542409	0.86	NEDD8-conjugating enzyme
231954_at	DKFZP434I0714	54553	6.78e-03	AL137273	CAB70671	0.91	hypothetical protein DKFZP434I0714
231959_at	C14orf46	91750	0.02	AK023979		1.11	chromosome 14 open reading frame 46
231976_at	WINS1	55180	0.01	NM_018148	NP_060618	0.89	WINS1 protein with Drosophila Lines (Lin) homologous domain
232000_at	C9orf52	158219	4.6e-03	AW001030		0.79	chromosome 9 open reading frame 52
232001_at	LOC439949	439949	0.01	XM_498474	XP_498474	0.76	hypothetical gene supported by AY007155
232008_s_at	BBX	56987	0.02	NM_020235	NP_064620	0.92	bobby sox homolog (Drosophila)
232009_at	EMR2	30817	0.04	NM_013447	NP_038475	1.12	egf-like module containing, mucin-like, hormone receptor-like 2
232020_at	SMURF2	64750	0.02	AU157259		1.17	SMAD specific E3 ubiquitin protein ligase 2
232024_at	GIMAP2	26157	3.22e-03	NM_015660	NP_056475	0.84	GTPase, IMAP family member 2
232030_at	KIAA1632	57724	0.04	NM_020964	NP_066015	0.91	KIAA1632
232032_x_at	Cab45	51150	0.02	NM_016547	NP_057631	0.89	calcium binding protein Cab45 precursor
232032_x_at	Cab45	51150	0.02	NM_016176	NP_057260	0.89	calcium binding protein Cab45 precursor
232033_at	USP37	57695	0.01	NM_020935	NP_065986	0.82	ubiquitin specific protease 37
232034_at	LOC203274	203274	0.01	AL117607		1.20	hypothetical protein LOC203274
232048_at	MGC33371	143684	0.01	NM_144664	NP_653265	0.86	hypothetical protein MGC33371
232058_at	ACTN4	81	0.03	AU158358		1.14	actinin, alpha 4
232093_at	LOC147650	147650	0.02	NM_207324	NP_997207	0.83	hypothetical protein LOC147650
232094_at	C15orf29	79768	6.29e-03	AU144048		1.24	chromosome 15 open reading frame 29
232145_at	LOC388969	388969	0.03	BC057834		1.10	hypothetical LOC388969
232169_x_at	NDUFS8	4728	0.01	AK002110		1.11	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
232171_x_at	KLHDC4	54758	0.03	AK001742		0.91	kelch domain containing 4
232179_at	LOC158863	158863	0.01	AL110203		1.29	hypothetical protein LOC158863
232182_at	LOC286272	286272	0.04	AK093004		0.81	hypothetical protein LOC286272
232183_at	SERAC1	84947	8.8e-03	NM_032861	NP_116250	0.84	serine active site containing 1
232215_x_at	FLJ11029	55771	0.01	AK000296	BAA91064	1.07	hypothetical protein FLJ11029
232219_x_at	USP21	27005	0.01	NM_012475	NP_036607	0.90	ubiquitin specific protease 21
232253_at	LOC441108	441108	0.03	AL564637		1.18	hypothetical gene supported by AK128882
232307_at	THRAP2	23389	0.03	AK021554		1.23	thyroid hormone receptor associated protein 2
232312_at	C11orf23	55291	0.03	AB046778	BAB13384	0.88	chromosome 11 open reading frame 23
232363_at	PSIP1	11168	0.02	AK024516		0.90	PC4 and SFRS1 interacting protein 1
232422_at	LOC87769	87769	0.03	BC001077	AAH01077	0.83	hypothetical protein BC004360
232432_s_at	SLC30A5	64924	0.02	NM_022902	NP_075053	0.94	solute carrier family 30 (zinc transporter), member 5
232432_s_at	SLC30A5	64924	0.02	NM_024055	NP_076960	0.94	solute carrier family 30 (zinc transporter), member 5
232471_at	MYO1E	4643	0.03	BE143535		1.14	myosin IE
232524_x_at	ANAPC4	29945	9.53e-04	NM_013367	NP_037499	0.84	anaphase promoting complex subunit 4
232551_at	BRD4	23476	0.04	AA521443		1.14	bromodomain containing 4
232587_at	EML4	27436	9.86e-03	AK021782		1.18	echinoderm microtubule associated protein like 4
232591_s_at	TMEM30A	55754	0.01	NM_018247	NP_060717	0.92	transmembrane protein 30A
232594_at	LOC440498	440498	8.61e-03	AK001829		0.87	hypothetical gene supported by AK001829
232595_at	KIAA0232	9778	0.03	AK023294		1.12	KIAA0232 gene product
232610_at	PARP14	54625	0.02	AB033094	BAA86582	1.08	poly (ADP-ribose) polymerase family, member 14

232645_at	LOC153684	153684	0.03	AK002146		0.90	hypothetical protein LOC153684
232648_at	PSMA3	5684	0.01	NM_002788	NP_002779	1.15	proteasome (prosome, macropain) subunit, alpha type, 3
232661_s_at	DKFZP564O0523	84060	0.01	NM_032120	NP_115496	0.88	hypothetical protein DKFZp564O0523
232676_x_at	MYEF2	50804	0.04	NM_016132	NP_057216	0.89	myelin expression factor 2
232680_at	PWWP1	154150	0.01	NM_138574	NP_612641	1.12	PWWP domain containing 1
232683_s_at	PARP6	56965	0.03	NM_020213	NP_064598	0.91	poly (ADP-ribose) polymerase family, member 6
232683_s_at	PARP6	56965	0.03	NM_020214	NP_064599	0.91	poly (ADP-ribose) polymerase family, member 6
232685_at	ETV6	2120	6.4e-03	AK025217		1.16	ets variant gene 6 (TEL oncogene)
232695_at	C6orf102	221458	0.01	NM_145027	NP_659464	1.16	chromosome 6 open reading frame 102
232710_at	LOC441258	441258	0.01	AK021477		1.14	similar to Williams Beuren syndrome chromosome region 19
232725_s_at	MS4A6A	64231	0.04	NM_152852	NP_690591	0.87	membrane-spanning 4-domains, subfamily A, member 6A
232726_at	MAML3	55534	0.03	AK024956		1.22	mastermind-like 3 (Drosophila)
232791_at	RFX3	5991	0.02	AL157466		1.22	regulatory factor X, 3 (influences HLA class II expression)
232829_at	OR52K3P	390035	0.03	AF143328	AAD33911	0.86	olfactory receptor, family 52, subfamily K, member 3 pseudogene
232835_at	JARID2	3720	0.03	AA533080		0.86	Jumonji, AT rich interactive domain 2
232837_at	KIF13A	63971	0.04	AJ291579	CAC20443	0.89	kinesin family member 13A
232843_s_at	DOCK8	81704	0.03	NM_203447	NP_982272	0.90	dedicator of cytokinesis 8
232849_at	LOC149692	149692	0.02	AK023614		1.19	hypothetical protein LOC149692
232865_at	AF5Q31	27125	7.69e-03	AF161355		0.91	ALL1 fused gene from 5q31
232902_s_at	RARSL	57038	0.04	NM_020320	NP_064716	0.93	arginyl-tRNA synthetase-like
232922_s_at	C20orf59	63910	0.02	NM_022082	NP_071365	0.92	chromosome 20 open reading frame 59
232964_at	WBSCR19	285955	0.04	NM_175064	NP_778234	1.13	Williams Beuren syndrome chromosome region 19
232980_at	C6orf209	55788	0.04	AU146081		1.15	chromosome 6 open reading frame 209
233007_at	XRCC5	7520	0.04	AU147192		1.14	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa)
233011_at	ANXA1	301	0.02	AU155094		0.86	annexin A1
233013_x_at	RPL7L1	285855	5.25e-03	BC058020	AAH58020	1.19	ribosomal protein L7-like 1
233081_at	C5orf18	7905	0.04	AV712346		1.16	chromosome 5 open reading frame 18
233101_at	MTMR9	66036	0.03	AK022071		0.90	myotubularin related protein 9
233167_at	SELO	83642	0.01	NM_031454	NP_113642	0.89	selenoprotein O
233185_at	ITGBL1	9358	0.04	AF339819		1.09	integrin, beta-like 1 (with EGF-like repeat domains)
233202_at	CNTNAP3	79937	0.02	AB051501	BAB21805	1.20	contactin associated protein-like 3
233208_x_at	CPSF2	53981	0.03	NM_017437	NP_059133	0.90	cleavage and polyadenylation specific factor 2, 100kDa
233226_at	PTPN9	5780	0.03	AL360201		1.09	protein tyrosine phosphatase, non-receptor type 9
233230_s_at	KIAA1458	57606	0.01	XM_044434	XP_044434	0.91	KIAA1458 protein
233268_s_at	CHURC1	91612	0.04	NM_145165	NP_660148	0.92	churchill domain containing 1
233292_s_at	ANKHD1	54882	1.41e-03	NM_017747	NP_060217	0.88	ankyrin repeat and KH domain containing 1
233302_at	BCL11B	64919	6.11e-03	AU146285		0.81	B-cell CLL/lymphoma 11B (zinc finger protein)
233321_x_at	LOC90834	90834	0.03	BC001742	AAH01742	1.11	hypothetical protein BC001742
233341_s_at	POLR1B	84172	0.04	NM_019014	NP_061887	0.90	polymerase (RNA) I polypeptide B, 128kDa
233350_s_at	TEX264	51368	0.02	NM_015926	NP_057010	0.85	testis expressed sequence 264
233393_at	MSRA	4482	4.07e-03	AU146871		1.29	methionine sulfoxide reductase A
233421_s_at	NUP133	55746	0.03	NM_018230	NP_060700	0.86	nucleoporin 133kDa

233469_at	psiTPTE22	387590	0.04	AK001299		1.11	TPTE pseudogene
233500_x_at	CLEC2D	29121	4.6e-03	NM_001004419	NP_001004419	0.78	C-type lectin superfamily 2, member D
233510_s_at	PARVG	64098	0.04	NM_022141	NP_071424	0.93	parvin, gamma
233595_at	USP34	9736	0.03	AK024341		0.88	ubiquitin specific protease 34
233632_s_at	XRN1	54464	2.95e-03	NM_019001	NP_061874	0.92	5'-3' exoribonuclease 1
233637_at	WDR42A	50717	0.02	AK022091		1.15	WD repeat domain 42A
233638_s_at	FLJ20277	55624	0.01	NM_017739	NP_060209	0.88	O-linked mannose beta1,2-N-acetylglucosaminyltransferase
233647_s_at	CDADC1	81602	1.95e-03	NM_030911	NP_112173	0.84	cytidine and dCMP deaminase domain containing 1
233656_s_at	VPS54	51542	0.01	NM_016516	NP_057600	0.90	vacuolar protein sorting 54 (yeast)
233657_at	OPN5	221391	4.76e-04	NM_181744	NP_859528	1.14	opsin 5
233674_at	FOXO3A	2309	0.03	AK026286		1.20	forkhead box O3A
233678_at	TCF12	6938	0.01	AL442094		0.89	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)
233690_at	C21orf96	80215	0.04	AK026743		1.11	chromosome 21 open reading frame 96
233700_at	PPP1R12B	4660	0.02	AK025291		1.19	protein phosphatase 1, regulatory (inhibitor) subunit 12B
233775_x_at	LOC388509	388509	8.42e-03	AK023304		1.09	similar to hypothetical protein FLJ38281
233807_at	ASB7	140460	0.01	AK000966		0.90	ankyrin repeat and SOCS box-containing 7
233841_s_at	SDS3	64426	0.02	NM_022491	NP_071936	0.94	likely ortholog of mouse Sds3
233864_s_at	VPS35	55737	0.01	NM_018206	NP_060676	0.89	vacuolar protein sorting 35 (yeast)
233881_s_at	TOLLIP	54472	1.82e-05	NM_019009	NP_061882	0.82	toll interacting protein
233893_s_at	KIAA1530	57654	0.02	AB040963	BAA96054	0.93	KIAA1530 protein
233936_s_at	ZNF403	79893	4.8e-03	NM_024835	NP_079111	0.85	zinc finger protein 403
234030_at	MYCPBP	10260	1.29e-03	AF090925		1.25	c-myc promoter binding protein
234072_at	SEMA4A	64218	1.94e-04	AK022416		1.21	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A
234081_at	SETBP1	26040	0.02	AU146742		1.21	SET binding protein 1
234140_s_at	STIM2	57620	0.01	NM_020860	NP_065911	0.91	stromal interaction molecule 2
234148_at	LRRC5	55144	0.02	AK025238		1.14	leucine rich repeat containing 5
234156_at	MICAL2	9645	0.02	AK026905		1.20	microtubule associated monoxygenase, calponin and LIM domain containing 2
234165_at	PTGDR	5729	0.02	NM_000953	NP_000944	0.79	prostaglandin D2 receptor (DP)
234295_at	DBR1	51163	0.01	AK000116	BAA90954	0.86	debranching enzyme homolog 1 (S. cerevisiae)
234304_s_at	IPO11	51194	2.23e-04	NM_016338	NP_057422	0.80	importin 11
234305_s_at	MLZE	56169	0.04	NM_031415	NP_113603	1.09	melanoma-derived leucine zipper, extra-nuclear factor
234306_s_at	SLAMF7	57823	0.01	NM_021181	NP_067004	0.85	SLAM family member 7
234311_s_at	LOC85865	85865	0.01	NM_033107	NP_149098	0.90	hypothetical protein BC004923
234344_at	RAP2C	57826	0.04	AF093744		0.81	RAP2C, member of RAS oncogene family
234401_at	TRAJ55	28700	0.02	AE000661		1.18	T cell receptor alpha joining 55
234401_at	TRDV3	28516	0.02	AE000661		1.18	T cell receptor delta variable 3
234401_at	TRAJ46	28709	0.02	AE000661		1.18	T cell receptor alpha joining 46
234401_at	TRAJ50	28705	0.02	AE000661		1.18	T cell receptor alpha joining 50
234401_at	TRAV38-1	28644	0.02	AE000661		1.18	T cell receptor alpha variable 38-1
234401_at	TRAV39	28642	0.02	AE000661		1.18	T cell receptor alpha variable 39
234401_at	TRAJ54	28701	0.02	AE000661		1.18	T cell receptor alpha joining 54

234401_at	TRDJ3	28520	0.02	AE000661		1.18	T cell receptor delta joining 3
234401_at	TRDJ1	28522	0.02	AE000661		1.18	T cell receptor delta joining 1
234401_at	TRAV41	28640	0.02	AE000661		1.18	T cell receptor alpha variable 41
234401_at	TRAV40	28641	0.02	AE000661		1.18	T cell receptor alpha variable 40
234401_at	TRAJ52	28703	0.02	AE000661		1.18	T cell receptor alpha joining 52
234401_at	TRDD3	28523	0.02	AE000661		1.18	T cell receptor delta diversity 3
234401_at	TRAJ56	28699	0.02	AE000661		1.18	T cell receptor alpha joining 56
234401_at	TRAJ51	28704	0.02	AE000661		1.18	T cell receptor alpha joining 51
234401_at	TRAV37	28645	0.02	AE000661		1.18	T cell receptor alpha variable 37
234401_at	TRDC	28526	0.02	AE000661		1.18	T cell receptor delta constant
234401_at	TRAJ59	28696	0.02	AE000661		1.18	T cell receptor alpha joining 59
234401_at	TRAJ60	28695	0.02	AE000661		1.18	T cell receptor alpha joining 60
234401_at	TRDD2	28524	0.02	AE000661		1.18	T cell receptor delta diversity 2
234401_at	TRAJ61	28694	0.02	AE000661		1.18	T cell receptor alpha joining 61
234401_at	TRDD1	28525	0.02	AE000661		1.18	T cell receptor delta diversity 1
234401_at	TRAJ57	28698	0.02	AE000661		1.18	T cell receptor alpha joining 57
234401_at	TRDV2	28517	0.02	AE000661		1.18	T cell receptor delta variable 2
234401_at	TRAJ53	28702	0.02	AE000661		1.18	T cell receptor alpha joining 53
234401_at	TRDJ4	28519	0.02	AE000661		1.18	T cell receptor delta joining 4
234401_at	TRAJ47	28708	0.02	AE000661		1.18	T cell receptor alpha joining 47
234401_at	TRAJ48	28707	0.02	AE000661		1.18	T cell receptor alpha joining 48
234401_at	TRAJ58	28697	0.02	AE000661		1.18	T cell receptor alpha joining 58
234401_at	TRAJ49	28706	0.02	AE000661		1.18	T cell receptor alpha joining 49
234401_at	TRDJ2	28521	0.02	AE000661		1.18	T cell receptor delta joining 2
234401_at	TRAV38-2DV8	28643	0.02	AE000661		1.18	T cell receptor alpha variable 38-2/delta variable 8
234471_s_at	NCOA5	57727	3.1e-03	NM_020967	NP_066018	0.87	nuclear receptor coactivator 5
234486_at	OR51B2	79345	8.57e-03	NM_033180	NP_149420	1.16	olfactory receptor, family 51, subfamily B, member 2
234624_at	HHLA2	11148	0.02	AK026893		1.18	HERV-H LTR-associating 2
234710_s_at	PARP6	56965	2.53e-03	NM_020214	NP_064599	0.89	poly (ADP-ribose) polymerase family, member 6
234710_s_at	PARP6	56965	2.53e-03	NM_020213	NP_064598	0.89	poly (ADP-ribose) polymerase family, member 6
234726_s_at	FLJ13576	64418	8.02e-04	NM_022484	NP_071929	0.86	hypothetical protein FLJ13576
234734_s_at	TNRC6A	27327	0.04	NM_020847	NP_065898	0.85	trinucleotide repeat containing 6A
234734_s_at	TNRC6A	27327	0.04	NM_014494	NP_055309	0.85	trinucleotide repeat containing 6A
234915_s_at	DENR	8562	3.81e-04	NM_003677	NP_003668	0.85	density-regulated protein
234952_s_at	KIAA1542	57661	0.02	BC004950	AAH04950	0.90	CTD-binding SR-like protein rA9
234975_at	GSPT1	2935	0.02	BE544748		0.86	G1 to S phase transition 1
234981_x_at	LOC134147	134147	0.01	NM_138809	NP_620164	1.11	similar to mouse 2310016A09Rik gene
234984_at	NEDD1	121441	0.01	NM_152905	NP_690869	0.85	neural precursor cell expressed, developmentally down-regulated 1
235003_at	UHMK1	127933	5.48e-03	NM_175866	NP_787062	0.84	U2AF homology motif (UHM) kinase 1
235022_at	C18orf19	125228	0.01	NM_152352	NP_689565	0.83	chromosome 18 open reading frame 19
235023_at	VPS13C	54832	0.01	AA828371		0.87	vacuolar protein sorting 13C (yeast)
235024_at	PHF17	79960	6.4e-03	NM_024900	NP_079176	0.88	PHD finger protein 17
235025_at	C14orf150	112840	0.01	NM_080666	NP_542397	0.81	chromosome 14 open reading frame 150
235051_at	C3orf6	152137	0.03	AK093660		0.88	chromosome 3 open reading frame 6

235053_at	COX11	1353	0.01	AI077461	0.86	COX11 homolog, cytochrome c oxidase assembly protein (yeast)
235057_at	ITCH	83737	1.71e-03	NM_031483	NP_113671	0.68	itchy homolog E3 ubiquitin protein ligase (mouse)
235060_at	KIAA0220	283846	0.03	BC051311	0.87	PI-3-kinase-related kinase SMG-1-like
235085_at	DKFZp761P0423	157285	0.01	XM_291277	XP_291277	0.79	hypothetical protein DKFZp761P0423
235096_at	LOC123169	123169	0.03	NM_138792	NP_620147	0.87	senescence downregulated leo1-like
235103_at	MAN2A1	4124	2.16e-03	AL833486	0.89	mannosidase, alpha, class 2A, member 1
235113_at	PPIL5	122769	0.01	NM_152329	NP_689542	0.90	peptidylprolyl isomerase (cyclophilin)-like 5
235170_at	ZNF92	168374	0.04	NM_152626	NP_689839	0.86	zinc finger protein 92 (HTF12)
235170_at	ZNF92	168374	0.04	NM_007139	NP_009070	0.86	zinc finger protein 92 (HTF12)
235173_at	LOC401093	401093	5.46e-03	XM_379228	XP_379228	1.14	hypothetical LOC401093
235195_at	FBXW2	26190	8.05e-03	BG109988	0.91	F-box and WD-40 domain protein 2
235204_at	COX15	1355	0.02	BF878343	0.89	COX15 homolog, cytochrome c oxidase assembly protein (yeast)
235210_s_at	RPESP	157869	0.04	NM_153225	NP_694957	1.16	RPE-spondin
235230_at	PHLDB2	90102	3.26e-03	AW170015	0.84	pleckstrin homology-like domain, family B, member 2
235241_at	FLJ90709	153129	0.02	NM_173514	NP_775785	0.86	hypothetical protein FLJ90709
235306_at	GIMAP8	155038	1.28e-03	NM_175571	NP_783161	0.90	GTPase, IMAP family member 8
235308_at	ZBTB20	26137	0.01	AW499525	0.89	zinc finger and BTB domain containing 20
235310_at	GCET2	257144	0.01	NM_152785	NP_689998	1.22	germinal center expressed transcript 2
235327_x_at	UBXD4	165324	0.04	NM_181713	NP_859064	1.09	UBX domain containing 4
235331_x_at	PCGF5	84333	0.01	NM_032373	NP_115749	0.76	polycomb group ring finger 5
235346_at	FUNDC1	139341	0.04	NM_173794	NP_776155	0.89	FUN14 domain containing 1
235369_at	C14orf28	122525	0.01	AK126985	1.20	chromosome 14 open reading frame 28
235384_at	LOC390916	390916	0.02	XM_372723	XP_372723	0.89	similar to RP2 protein, testosterone-regulated - ricefield mouse (Mus caroli)
235389_at	PHF20	51230	2.11e-04	AK054597	0.83	PHD finger protein 20
235444_at	FOXP1	27086	0.02	BX647682	0.84	forkhead box P1
235458_at	HAVCR2	84868	6.56e-03	NM_032782	NP_116171	0.77	hepatitis A virus cellular receptor 2
235478_at	DCLRE1C	64421	0.04	BC022254	AAH22254	0.90	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)
235479_at	CPEB2	132864	0.01	NM_182646	NP_872587	1.12	cytoplasmic polyadenylation element binding protein 2
235484_at	PTAR1	375743	8.57e-03	AL832683	0.90	protein prenyltransferase alpha subunit repeat containing 1
235533_at	LOC90639	90639	0.03	AW021673	1.06	hypothetical protein LOC90639
235535_x_at	FRG1	2483	0.04	NM_004477	NP_004468	0.76	FSHD region gene 1
235552_at	KIAA1627	57721	0.02	NM_020961	NP_066012	0.86	KIAA1627 protein
235564_at	ZNF117	7670	0.01	BF107006	0.79	zinc finger protein 117 (HPF9)
235610_at	LOC91801	91801	0.01	AI590659	0.75	hypothetical protein BC015183
235675_at	DHFRL1	200895	0.03	NM_176815	NP_789785	0.76	dihydrofolate reductase-like 1
235687_at	ZNF626	199777	0.03	AA908777	0.74	zinc finger protein 626
235690_at	ZNF594	84622	0.03	XM_290737	XP_290737	0.85	zinc finger protein 594
235729_at	ZNF514	84874	0.02	NM_032788	NP_116177	0.87	zinc finger protein 514
235802_at	C14orf175	122618	4.27e-04	NM_138790	NP_620145	0.80	chromosome 14 open reading frame 175
235823_at	LOC197322	197322	0.02	AI763000	0.91	hypothetical protein LOC197322
236006_s_at	AKAP10	11216	0.01	NM_007202	NP_009133	0.89	A kinase (PRKA) anchor protein 10
236007_at	AKAP10	11216	0.01	NM_007202	NP_009133	0.88	A kinase (PRKA) anchor protein 10
236016_at	SMARCE1	6605	5.89e-03	AI702962	0.81	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1

236043_at	LOC92482	92482	0.02	AA213437		1.15	hypothetical protein LOC92482
236046_at	FLJ44896	401166	0.01	AK126844	BAC86718	0.79	FLJ44896 protein
236059_at	FLJ23342	79684	4.07e-03	AW168168		1.16	hypothetical protein FLJ23342
236079_at	DKFZp667E0512	202025	9.35e-03	AL713660		0.88	hypothetical protein DKFZp667E0512
236094_at	TCF7L2	6934	0.02	BF696202		1.24	transcription factor 7-like 2 (T-cell specific, HMG-box)
236133_x_at	ZNF539	399655	5.96e-03	NM_203282	NP_975011	0.84	zinc finger protein 539
236165_at	MSL3L1	10943	6.16e-03	NM_078629	NP_523353	0.86	male-specific lethal 3-like 1 (Drosophila)
236217_at	SLC31A1	1317	0.03	BC061924	AAH61924	1.18	solute carrier family 31 (copper transporters), member 1
236239_at	XPNPEP1	7511	0.03	BX537682	CAH18706	0.88	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
236240_at	FLJ21106	80167	0.03	BC058898		0.88	hypothetical protein FLJ21106
236243_at	ZCCHC6	79670	0.03	AW070776		1.11	zinc finger, CCHC domain containing 6
236247_at	NSUN4	387338	5.12e-03	NM_199044	NP_950245	0.89	NOL1/NOP2/Sun domain family, member 4
236248_x_at	MGC21874	93624	0.02	AK126966		0.89	transcriptional adaptor 2 (ADA2 homolog, yeast)-beta
236259_at	STK4	6789	0.04	NM_006282	NP_006273	1.15	serine/threonine kinase 4
236261_at	OSBPL6	114880	9.25e-03	AI949389		1.30	oxysterol binding protein-like 6
236274_at	EIF3S9	8662	0.04	NM_003751	NP_003742	0.87	eukaryotic translation initiation factor 3, subunit 9 eta,
116kDa							
236436_at	LOC283130	283130	0.02	NM_182556	NP_872362	0.88	hypothetical protein LOC283130
236476_at	MTCP1	4515	0.01	AW779983		0.81	mature T-cell proliferation 1
236554_x_at	EVER2	147138	2.11e-03	NM_152468	NP_689681	0.82	epidermodysplasia verruciformis 2
236562_at	ZNF439	90594	0.02	NM_152262	NP_689475	0.85	zinc finger protein 439
236613_at	RBM25	58517	0.01	AL832314		0.89	RNA binding motif protein 25
236621_at	RPS27	6232	0.01	NM_001030	NP_001021	1.14	ribosomal protein S27 (metallopanstimulin 1)
236645_at	HBP1	26959	0.03	AI689935		1.16	HMG-box transcription factor 1
236649_at	MDS009	56986	0.03	NM_020234	NP_064619	0.90	x 009 protein
236782_at	SAMD3	154075	0.02	AK091351	BAC03644	0.85	sterile alpha motif domain containing 3
236808_at	FGFR1OP2	26127	0.04	AA947475		1.20	FGFR1 oncogene partner 2
236826_at	C9orf52	158219	0.03	H83092		0.88	chromosome 9 open reading frame 52
236924_at	GLMN	11146	0.01	AA814383		0.83	glomulin, FKBP associated protein
236941_at	MGC50372	253143	0.01	NM_173566	NP_775837	1.11	hypothetical protein MGC50372
236966_at	ARMC8	25852	6.38e-04	AK128702		0.84	armadillo repeat containing 8
236999_at	KIAA0073	23398	0.03	AA767131		1.17	KIAA0073 protein
237640_at	C14orf138	79609	1.9e-03	NM_024558	NP_078834	1.34	chromosome 14 open reading frame 138
237702_at	DRB1	129831	0.02	AW451271		1.23	developmentally regulated RNA-binding protein 1
237725_x_at	SMC5L1	23137	0.01	NM_015110	NP_055925	0.80	SMC5 structural maintenance of chromosomes 5-like 1
(yeast)							
237745_at	TGFB1I4	8848	0.02	BC036219		1.16	transforming growth factor beta 1 induced transcript 4
237759_at	CD48	962	9.61e-03	BC030224	AAH30224	0.83	CD48 antigen (B-cell membrane protein)
237884_x_at	TRPM7	54822	0.03	NM_017672	NP_060142	1.17	transient receptor potential cation channel, subfamily M,
member 7							
238004_at	PGBD2	267002	0.04	NM_170725	NP_733843	0.88	piggyBac transposable element derived 2
238010_at	LOC339448	339448	4.62e-03	NM_207356	NP_997239	0.78	hypothetical protein LOC339448
238013_at	PLEKHA2	59339	0.02	BF347859		0.88	pleckstrin homology domain containing, family A
(phosphoinositide binding specific) member 2							
238058_at	LOC150381	150381	0.01	BC036832		0.91	hypothetical protein LOC150381

238066_at	RBP7	116362	3.6e-03	NM_052960	NP_443192	0.88	retinol binding protein 7, cellular
238324_at	p66alpha	54815	0.01	NM_017660	NP_060130	0.83	p66 alpha
238327_at	ECGF1	1890	0.01	S72487		0.80	endothelial cell growth factor 1 (platelet-derived)
238421_at	MNAB	54542	0.03	N86386		0.90	membrane associated DNA binding protein
238434_at	SHMT1	6470	0.01	AW207575		0.93	serine hydroxymethyltransferase 1 (soluble)
238438_at	CNOT6L	246175	0.04	R67226		0.85	CCR4-NOT transcription complex, subunit 6-like
238451_at	MPP7	143098	0.04	AL832380		1.15	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)
238510_at	LOC124411	124411	0.03	NM_001004300	NP_001004300	0.88	hypothetical protein LOC124411
238519_at	RSC1A1	6248	0.04	AF147408		0.90	regulatory solute carrier protein, family 1, member 1
238523_at	C16orf44	79786	8.05e-03	AK074056	BAB84882	0.84	chromosome 16 open reading frame 44
238547_at	FLJ32384	124790	0.03	NM_144608	NP_653209	1.12	hypothetical protein MGC39389
238562_at	MGC14595	84294	0.04	NM_032334	NP_115710	0.91	hypothetical protein MGC14595
238581_at	GBP5	115362	0.03	BG271923		0.66	guanylate binding protein 5
238609_at	DKFZp727G131	221786	0.01	NM_145111	NP_659802	0.85	hypothetical protein DKFZp727G131
238662_at	MGC14798	89978	1.78e-04	NM_080650	NP_542381	0.81	similar to RIKEN cDNA 5730421E18 gene
238686_at	FBXO3	26273	0.04	AA130258		0.91	F-box protein 3
238760_at	YARS	8565	0.04	NM_003680	NP_003671	0.87	tyrosyl-tRNA synthetase
238783_at	MGC33214	153396	0.02	NM_153354	NP_699185	1.12	hypothetical protein MGC33214
238791_at	ZNF100	163227	0.01	NM_173531	NP_775802	1.19	zinc finger protein 100
238800_s_at	ZCCHC6	79670	0.04	AA776496		1.10	zinc finger, CCHC domain containing 6
238811_at	ATP11B	23200	0.04	XM_087254	XP_087254	0.88	ATPase, Class VI, type 11B
238819_at	ZNF347	84671	0.02	NM_032584	NP_115973	0.86	zinc finger protein 347
238851_at	ANKRD13	88455	0.02	NM_033121	NP_149112	1.16	ankyrin repeat domain 13
238856_s_at	PANK2	80025	0.01	BG108346		0.91	pantothenate kinase 2 (Hallervorden-Spatz syndrome)
238974_at	FLJ38973	205327	0.02	NM_153689	NP_710156	0.92	hypothetical protein FLJ38973
239035_at	MTHFR	4524	0.04	BC011614		0.89	5,10-methylenetetrahydrofolate reductase (NADPH)
239067_s_at	PANX2	56666	0.01	NM_052839	NP_443071	1.18	pannexin 2
239071_at	RBBP4	5928	1.15e-03	AI972451		0.85	retinoblastoma binding protein 4
239077_at	GALNACT-2	55454	0.03	NM_018590	NP_061060	0.91	chondroitin sulfate GalNAcT-2
239081_at	LOC440064	440064	0.01	XM_498525	XP_498525	0.84	LOC440064
239147_at	DKFZp313G1735	153642	0.01	NM_198150	NP_937793	1.27	hypothetical protein DKFZp313G1735
239197_s_at	EZH1	2145	0.01	NM_001991	NP_001982	1.06	enhancer of zeste homolog 1 (Drosophila)
239198_at	EZH1	2145	5.82e-04	NM_001991	NP_001982	1.21	enhancer of zeste homolog 1 (Drosophila)
239212_at	C6orf93	84946	0.03	NM_032860	NP_116249	0.87	chromosome 6 open reading frame 93
239232_at	MSI2	124540	2.41e-03	AA521410		1.17	musashi homolog 2 (Drosophila)
239233_at	KIAA1212	55704	0.03	BX537985	CAD97945	0.86	KIAA1212
239242_at	SLC25A5	292	0.02	AI807887		1.10	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
239279_at	LOC440702	440702	9.81e-03	AI862518		1.24	LOC440702
239283_at	TMED5	50999	0.03	NM_016040	NP_057124	0.90	transmembrane emp24 protein transport domain containing 5
239314_at	LOC387921	387921	4.85e-03	XM_370722	XP_370722	0.89	similar to RIKEN cDNA 8030451K01
239342_at	DGKZ	8525	0.01	AK124693	BAC85927	1.19	diacylglycerol kinase, zeta 104kDa
239413_at	Cep152	22995	0.02	BX648822		0.84	KIAA0912 protein

239533_at	GPR155	151556	0.03	AK096665	BAC04835	1.21	G protein-coupled receptor 155
239556_at	PDE5A	8654	0.01	AW873604		0.86	phosphodiesterase 5A, cGMP-specific
239635_at	MGC15912	84972	0.04	NM_032886	NP_116275	0.90	hypothetical protein MGC15912
239660_at	KIAA1272	57186	0.02	XM_046600	XP_046600	1.25	KIAA1272 protein
239740_at	ETV6	2120	0.04	NM_001987	NP_001978	1.16	ets variant gene 6 (TEL oncogene)
239771_at	TIP120A	55832	0.04	AK027783	BAB55365	0.87	TBP-interacting protein
239792_at	LOC440288	440288	0.03	XM_496075	XP_496075	0.87	similar to FLJ16518 protein
239824_s_at	MGC10744	84314	3.96e-03	NM_032354	NP_115730	0.89	hypothetical protein MGC10744
239917_at	KIAA0804	23355	0.03	R07848		1.17	KIAA0804 protein
240265_at	T3JAM	80342	0.04	AK126139	BAC86461	0.81	TRAF3-interacting Jun N-terminal kinase (JNK)-activating modulator
240288_at	KCNRG	283518	6.61e-03	NM_173605	NP_775876	1.20	potassium channel regulator
240288_at	KCNRG	283518	6.61e-03	NM_199464	NP_955751	1.20	potassium channel regulator
240359_at	C20orf71	128861	0.02	NM_178466	NP_848561	1.11	chromosome 20 open reading frame 71
240565_at	ZFP28	140612	8.57e-03	BC028416	AAH28416	1.18	zinc finger protein 28 homolog (mouse)
240572_s_at	LOC374443	374443	0.03	AK096274		0.91	CLR pseudogene
240703_s_at	HERC1	8925	2.81e-03	NM_003922	NP_003913	0.86	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1
240801_at	C21orf37	54076	0.03	NM_001005521	NP_001005521	1.20	chromosome 21 open reading frame 37
240890_at	LOC440066	440066	0.01	XM_495897	XP_495897	0.88	similar to Caspase-4 precursor (CASP-4) (ICH-2 protease) (TX protease) (ICE(rel)-II)
241018_at	C1orf8	9528	6.16e-03	BF446758		0.88	chromosome 1 open reading frame 8
241262_at	FLJ10504	55154	0.04	AW270170		0.88	misato
241345_at	ZNF265	9406	0.03	BX538141		0.88	zinc finger protein 265
241534_at	ATP8B1	5205	0.03	AW469777		0.83	ATPase, Class I, type 8B, member 1
241683_at	HECTD1	25831	8.65e-03	NM_015382	NP_056197	0.80	HECT domain containing 1
241871_at	CAMK4	814	0.02	AL833368		0.83	calcium/calmodulin-dependent protein kinase IV
241907_at	GPC3	2719	0.03	H63988		1.12	glypican 3
241955_at	HECTD1	25831	0.04	NM_015382	NP_056197	0.90	HECT domain containing 1
242052_at	BICD1	636	6.48e-03	AW979272		0.84	bicaudal D homolog 1 (Drosophila)
242091_at	LOC124411	124411	5.65e-03	AL832197		1.20	hypothetical protein LOC124411
242214_at	RPS27A	6233	0.04	NM_002954	NP_002945	0.92	ribosomal protein S27a
242229_at	NAPE-PLD	222236	0.01	BC037350		0.87	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D
242263_at	TMED5	50999	3.26e-03	BE620297		0.85	transmembrane emp24 protein transport domain containing 5
242268_at	CUGBP2	10659	0.02	BE157991		1.15	CUG triplet repeat, RNA binding protein 2
242293_at	ING3	54556	0.01	NM_019071	NP_061944	0.87	inhibitor of growth family, member 3
242297_at	RREB1	6239	0.04	BX647723		1.07	ras responsive element binding protein 1
242304_at	PYM	84305	0.01	BC009627	AAH09627	0.92	PYM protein
242320_at	FOXO3A	2309	0.04	AI435586		1.14	forkhead box O3A
242336_at	GSK3B	2932	8.57e-03	R51305		0.89	glycogen synthase kinase 3 beta
242349_at	HECTD1	25831	0.03	NM_015382	NP_056197	0.91	HECT domain containing 1
242408_at	STYX	6815	3.62e-03	NM_145251	NP_660294	0.76	serine/threonine/tyrosine interacting protein
242451_x_at	INO80	54617	6.25e-03	BX640651	CAE45796	1.20	homolog of yeast INO80

242456_at	MRE11A	4361	0.04	NM_005591	NP_005582	0.93	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
242463_x_at	ZNF600	162966	5.07e-03	NM_198457	NP_940859	0.74	zinc finger protein 600
242507_at	KIAA0794	26043	0.01	AI375101		1.19	KIAA0794 protein
242520_s_at	MGC33556	339541	0.03	NM_001004307	NP_001004307	0.88	hypothetical LOC339541
242550_at	EIF3S9	8662	0.03	AA628539		0.83	eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa
242633_x_at	ZNF75A	7627	0.02	AA829635		0.87	zinc finger protein 75a
242706_s_at	CRSP3	9439	0.01	NM_004830	NP_004821	0.90	cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa
242734_x_at	GALT	2592	2.56e-03	NM_147131	NP_667342	0.83	galactose-1-phosphate uridylyltransferase
242791_at	FBXO3	26273	0.04	H92965		0.83	F-box protein 3
242875_at	PSEN1	5663	0.01	AI659439		1.16	presenilin 1 (Alzheimer disease 3)
242907_at	GBP2	2634	0.04	AL832451	CAD89925	1.13	guanylate binding protein 2, interferon-inducible
243009_at	MGC16733	92105	0.01	AW513654		0.84	hypothetical gene MGC16733 similar to CG12113
243100_at	NT5C1B	93034	0.03	NM_001002006	NP_001002006	1.10	5'-nucleotidase, cytosolic IB
243303_at	ECHDC1	55862	0.03	AA811657		1.09	enoyl Coenzyme A hydratase domain containing 1
243304_at	LOC286109	286109	0.03	AK092172		1.13	hypothetical protein LOC286109
243413_at	FLJ30990	150737	0.03	NM_152517	NP_689730	1.17	hypothetical protein FLJ30990
243524_at	SLC30A7	148867	0.04	AI571719		1.07	solute carrier family 30 (zinc transporter), member 7
243667_at	AP1GBP1	11276	0.03	AW977986		1.18	AP1 gamma subunit binding protein 1
243735_at	STATIP1	55250	0.02	N58363		0.89	signal transducer and activator of transcription 3 interacting protein 1
243916_x_at	MGC10067	134510	0.04	NM_145049	NP_659486	0.89	hypothetical protein MGC10067
243927_x_at	DKFZP434I116	25962	0.02	NM_015496	NP_056311	0.77	DKFZP434I116 protein
244010_at	MLL3	58508	0.04	AI057455		1.18	myeloid/lymphoid or mixed-lineage leukemia 3
244103_at	FLJ35382	163859	0.01	NM_152608	NP_689821	0.87	hypothetical protein FLJ35382
244154_at	DDHD1	80821	0.01	AI751130		1.08	DDHD domain containing 1
244235_at	IVNS1ABP	10625	0.01	NM_006469	NP_006460	0.86	influenza virus NS1A binding protein
244251_at	LCP2	3937	7.42e-03	BF363430		0.88	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)
244310_at	LOC440283	440283	0.02	AW973410		1.13	LOC440283
244396_at	G3BP	10146	0.03	NM_005754	NP_005745	0.83	Ras-GTPase-activating protein SH3-domain-binding protein
244495_x_at	C18orf45	85019	0.02	NM_032933	NP_116322	1.09	chromosome 18 open reading frame 45
244517_x_at	RNF146	81847	0.04	AW070573		0.86	ring finger protein 146
244547_at	FLJ25006	124923	9.61e-03	AW081561		1.15	hypothetical protein FLJ25006
244563_at	FLJ21924	79832	0.01	AK055185		0.90	hypothetical protein FLJ21924
244631_at	LOC389834	389834	0.02	AK123403		0.86	hypothetical gene supported by AK123403
244659_at	TRIP12	9320	9.61e-03	AL120025		1.12	thyroid hormone receptor interactor 12
244691_at	FLJ10707	55209	0.04	AB051544	BAB21848	0.85	hypothetical protein FLJ10707
244728_at	LOC130063	130063	0.01	XM_059396	XP_059396	1.11	hypothetical gene LOC130063
244752_at	LOC220929	220929	0.03	NM_182755	NP_877432	1.10	hypothetical protein LOC220929
244777_at	DCP2	167227	0.01	BC068042		1.22	DCP2 decapping enzyme homolog (S. cerevisiae)
244784_at	DHX57	90957	0.04	NM_144995	NP_659432	0.91	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57
244828_x_at	LOC92345	92345	0.02	NM_138386	NP_612395	0.86	hypothetical protein BC008207
31799_at	MRPS22	56945	2.75e-03	AF070618		0.85	mitochondrial ribosomal protein S22

32088_at	BLZF1	8548	0.02	U79751	AAB63110	0.86	basic leucine zipper nuclear factor 1 (JEM-1)
32091_at	KIAA0446	9673	0.03	NM_014655	NP_055470	1.08	KIAA0446 gene product
33148_at	ZFR	51663	0.04	NM_016107	NP_057191	0.89	zinc finger RNA binding protein
33323_r_at	SFN	2810	1.39e-03	NM_006142	NP_006133	1.15	stratifin
33494_at	ETFDH	2110	0.01	NM_004453	NP_004444	0.91	electron-transferring-flavoprotein dehydrogenase
34406_at	PACS2	23241	5.12e-03	AB011174	BAA25528	0.89	phosphofurin acidic cluster sorting protein 2
34449_at	CASP2	835	0.04	NM_001224	NP_001215	0.81	caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2)
34478_at	RAB11B	9230	0.03	NM_004218	NP_004209	1.27	RAB11B, member RAS oncogene family
35150_at	CD40	958	9.91e-03	NM_001250	NP_001241	1.09	CD40 antigen (TNF receptor superfamily member 5)
35626_at	SGSH	6448	4.3e-03	NM_000199	NP_000190	0.92	N-sulfoglucosamine sulfohydrolase (sulfamidase)
36030_at	HOM-TES-103	25900	4.23e-03	NM_015438	NP_056253	0.93	HOM-TES-103 tumor antigen-like
37152_at	PPARD	5467	0.01	NM_006238	NP_006229	0.87	peroxisome proliferative activated receptor, delta
37170_at	BMP2K	55589	0.01	AB015331	BAA34790	1.17	BMP2 inducible kinase
37425_g_at	CCHCR1	54535	0.02	NM_019052	NP_061925	0.87	coiled-coil alpha-helical rod protein 1
37433_at	PIAS2	9063	2.29e-03	NM_173206	NP_775298	0.89	protein inhibitor of activated STAT, 2
37590_g_at	DKFZp547K1113	374655	3.26e-03	AL109698		0.92	hypothetical protein DKFZp547K1113
37943_at	ZFYVE26	23503	0.02	NM_015346	NP_056161	0.90	zinc finger, FYVE domain containing 26
38069_at	CLCN7	1186	0.04	NM_001287	NP_001278	0.94	chloride channel 7
38398_at	MADD	8567	0.02	NM_130470	NP_569826	0.88	MAP-kinase activating death domain
38766_at	SRCAP	10847	0.03	NM_006662	NP_006653	1.09	Snf2-related CBP activator protein
39318_at	TCL1A	8115	0.04	NM_021966	NP_068801	1.21	T-cell leukemia/lymphoma 1A
39582_at	CYLD	1540	0.02	AL050166		0.90	cylindromatosis (turban tumor syndrome)
39729_at	PRDX2	7001	0.03	NM_005809	NP_005800	0.91	peroxiredoxin 2
39817_s_at	C6orf108	10591	8.44e-04	NM_006443	NP_006434	0.94	chromosome 6 open reading frame 108
40016_g_at	MAST4	23227	0.02	AB002301	BAA20762	0.82	microtubule associated serine/threonine kinase family member 4
40149_at	SH2B	25970	5.83e-03	NM_015503	NP_056318	0.88	SH2-B homolog
41220_at	SEPT9	10801	0.03	NM_006640	NP_006631	0.90	septin 9
41329_at	PACE-1	57147	6.41e-03	NM_020423	NP_065156	0.91	ezrin-binding partner PACE-1
43977_at	FLJ20422	54929	0.01	NM_017814	NP_060284	0.92	hypothetical protein FLJ20422
44120_at	ADCK2	90956	0.01	NM_052853	NP_443085	0.89	aarF domain containing kinase 2
44790_s_at	C13orf18	80183	0.01	NM_025113	NP_079389	1.30	chromosome 13 open reading frame 18
46665_at	SEMA4C	54910	0.01	NM_017789	NP_060259	0.83	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C
47083_at	C7orf26	79034	0.03	NM_024067	NP_076972	0.92	chromosome 7 open reading frame 26
47105_at	FLJ20399	54920	0.03	NM_017803	NP_060273	0.90	hypothetical protein FLJ20399
47560_at	LPHN1	22859	0.03	AK022001	BAB13950	0.89	latrophilin 1
47608_at	TJP4	93643	0.02	NM_080604	NP_542171	0.91	tight junction protein 4 (peripheral)
49485_at	PRDM4	11108	0.02	NM_012406	NP_036538	0.88	PR domain containing 4
50314_i_at	C20orf27	54976	0.03	NM_017874	NP_060344	0.80	chromosome 20 open reading frame 27
51176_at	CRSP8	9442	8.81e-03	NM_004269	NP_004260	0.86	cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa
52078_at	DKFZP564D0478	84065	0.03	NM_032125	NP_115501	0.92	hypothetical protein DKFZp564D0478
52159_at	HEMK1	51409	0.02	NM_016173	NP_057257	0.87	HemK methyltransferase family member 1

52285_f_at	C18orf9	79959	0.01	NM_024899	NP_079175	0.84			chromosome 18 open reading frame 9
52940_at	SIGIRR	59307	0.03	NM_021805	NP_068577	0.90			single Ig IL-1R-related molecule
53071_s_at	FLJ22222	79701	0.04	NM_175902	NP_787098	0.86			hypothetical protein FLJ22222
53071_s_at	FLJ22222	79701	0.04	NM_024648	NP_078924	0.86			hypothetical protein FLJ22222
53202_at	C7orf25	79020	0.02	NM_024054	NP_076959	1.16			chromosome 7 open reading frame 25
53987_at	RANBP10	57610	2.66e-03	NM_020850	NP_065901	0.88			RAN binding protein 10
54037_at	HPS4	89781	0.02	NM_022081	NP_071364	0.85			Hermansky-Pudlak syndrome 4
54632_at	THADA	63892	0.04	NM_198554	NP_940956	0.92			thyroid adenoma associated
54632_at	THADA	63892	0.04	NM_022065	NP_071348	0.92			thyroid adenoma associated
55616_at	PERLD1	93210	0.02	NM_033419	NP_219487	0.92			per1-like domain containing 1
55872_at	KIAA1196	57473	0.01	NM_020713	NP_065764	0.81			KIAA1196 protein
56197_at	PLSCR3	57048	0.01	NM_020360	NP_065093	0.92			phospholipid scramblase 3
57163_at	ELOVL1	64834	0.02	NM_022821	NP_073732	0.94			elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1
57532_at	DVL2	1856	0.01	NM_004422	NP_004413	0.90			dishevelled, dsh homolog 2 (Drosophila)
57540_at	RBKS	64080	0.03	NM_022128	NP_071411	1.13			ribokinase
57715_at	FAM26B	51063	0.04	NM_015916	NP_057000	1.07			family with sequence similarity 26, member B
58308_at	TRIM62	55223	0.04	NM_018207	NP_060677	0.92			tripartite motif-containing 62
59433_at	LOC286434	286434	0.04	AK000470		1.13			hypothetical protein LOC286434
64064_at	GIMAP5	55340	1.95e-03	NM_018384	NP_060854	0.87			GTPase, IMAP family member 5
64418_at	AP1GBP1	11276	0.01	AI472320		0.92			AP1 gamma subunit binding protein 1
64438_at	FLJ22222	79701	0.01	NM_175902	NP_787098	0.86			hypothetical protein FLJ22222
64438_at	FLJ22222	79701	0.01	NM_024648	NP_078924	0.86			hypothetical protein FLJ22222
64440_at	IL17RC	84818	0.01	NM_153461	NP_703191	0.90			interleukin 17 receptor C
64899_at	LPPR2	64748	0.02	NM_022737	NP_073574	1.19			lipid phosphate phosphatase-related protein type 2
65133_i_at	HMGA1L4	83444	0.02	NM_031288	NP_112578	0.90			high mobility group AT-hook 1-like 4
65493_at	ABC1	63897	5.28e-03	NM_022070	NP_071353	0.91			amplified in breast cancer 1
65588_at	LOC388796	388796	0.01	XM_373914	XP_373914	0.85			hypothetical LOC388796
65630_at	LOC283232	283232	0.02	NM_174940	NP_777600	0.89			hypothetical protein LOC283232
65770_at	RHOT2	89941	0.02	NM_138769	NP_620124	0.88			ras homolog gene family, member T2
71933_at	WNT6	7475	0.02	NM_006522	NP_006513	1.10			wingless-type MMTV integration site family, member 6
78495_at	DKFZp762P2111	55537	0.03	AK022976		0.90			hypothetical protein DKFZp762P2111
79005_at	SLC35E1	79939	2.8e-03	NM_024881	NP_079157	0.91			solute carrier family 35, member E1
89476_r_at	NPEPL1	79716	0.02	NM_024663	NP_078939	0.92			aminopeptidase-like 1
90265_at	CENTA1	11033	0.04	NM_006869	NP_006860	1.07			centaurin, alpha 1
AFFX-HUMISGF3A/M97935STAT1 1, 91kDa		6772	0.04	NM_007315	NP_009330	0.84			signal transducer and activator of transcription
AFFX-HUMISGF3A/M97935STAT1 1, 91kDa		6772	0.04	NM_007315	NP_009330	0.74			signal transducer and activator of transcription

Table 11

AffySpotID	FoldChange	p value	CV (HRiskPolyp)	CV (LowRiskPolyp)	GeneID	GeneSymbol	RNAAccess'nNo.	GeneDescription
1294_at	1.12	0.01	0.17	0.18	7318	UBE1L	NM_003335	ubiquitin-activating enzyme E1-like
1552279_a_at	0.92	0.01	0.14	0.13	113235	MGC9564	AK074161	similar to RIKEN cDNA 1110002C08 gene
1552291_at	1.16	0.02	0.26	0.24	54965	PIGX	NM_017861	phosphatidylinositol glycan, class X
1552320_a_at	1.21	8.76e-03	0.30	0.45	85478	NYD-SP28	NM_033124	NYD-SP28 protein
1552426_a_at	1.14	7.93e-03	0.20	0.17	80213	BLP2	NM_078474	BBP-like protein 2
1552660_a_at	0.85	6.37e-03	0.26	0.19	55322	FLJ11193	NM_018356	hypothetical protein FLJ11193
1552664_at	1.13	0.01	0.20	0.20	201163	FLCN	NM_144997	folliculin
1552921_a_at	0.89	0.04	0.25	0.21	63979	FIGNL1	NM_022116	fidgetin-like 1
1552930_at	1.13	0.01	0.21	0.21	79258	MELL1	NM_033467	mel transforming oncogene-like 1
1553214_a_at	1.97	2.34e-04	0.55	0.51	221016	CCDC7	NM_145023	coiled-coil domain containing 7
1553417_at	0.87	0.03	0.24	0.24	283171	FLJ39058	NM_173580	hypothetical protein FLJ39058
1553581_s_at	1.12	0.02	0.21	0.18	285672	FLJ36754	NM_173829	hypothetical protein FLJ36754
1553647_at	0.87	8.25e-03	0.24	0.18	124359	CDYL2	NM_152342	chromodomain protein, Y-like 2
1553749_at	0.85	0.02	0.35	0.27	143684	MGC33371	NM_144664	hypothetical protein MGC33371
1553978_at	1.09	7.93e-03	0.12	0.15	4207	MEF2B	BC010931	MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)
1554038_at	1.11	0.02	0.20	0.17	55132	FLJ10378	BC030516	FLJ10378 protein
1554080_at	1.15	8.3e-03	0.21	0.19	9125	RQCD1	BC007102	RCD1 required for cell differentiation1 homolog (S. pombe)
1554096_a_at	1.29	0.03	0.41	0.32	92454	MGC20460	NM_053043	hypothetical protein MGC20460
1554116_s_at	1.13	0.04	0.21	0.32	57097	PARP11	BC031073	poly (ADP-ribose) polymerase family, member 11
1554149_at	1.10	0.01	0.17	0.15	56650	C3orf4	NM_019895	chromosome 3 open reading frame 4
1554253_a_at	0.87	0.01	0.21	0.22	204219	LASS3	NM_178842	LAG1 longevity assurance homolog 3 (S. cerevisiae)
1554428_s_at	1.07	0.03	0.11	0.17	57555	NLGN2	NM_020795	neuroligin 2
1554472_a_at	1.14	0.02	0.25	0.27	51105	PHF20L1	NM_198513	PHD finger protein 20-like 1
1554545_at	0.84	0.01	0.38	0.24	403314	MGC26594	NM_203454	hypothetical protein MGC26594
1554553_s_at	1.06	0.04	0.13	0.12	90522	LOC90522	NM_033557	similar to putative transmembrane protein; homolog of yeast Golgi membrane protein Yi
1554772_at	0.77	2.08e-04	0.27	0.23	124989	FLJ40342	NM_152347	hypothetical protein FLJ40342
1555001_at	0.88	0.04	0.34	0.23	132141	IQCF1	BC034228	IQ motif containing F1
1555105_a_at	1.21	3.19e-03	0.25	0.33	57708	MI-ER1	NM_020948	mesoderm induction early response 1
1555124_at	1.13	0.03	0.25	0.18	285048	MGC40574	BC032412	hypothetical protein MGC40574
1555248_a_at	0.87	0.04	0.37	0.25	65267	WNK3	NM_020922	WNK lysine deficient protein kinase 3
1555392_at	1.27	0.01	0.33	0.45	26136	TES	AY143171	testis derived transcript (3 LIM domains)
1555514_a_at	0.91	0.04	0.19	0.18	9063	PIAS2	NM_173206	protein inhibitor of activated STAT, 2
1555730_a_at	1.08	0.01	0.15	0.11	1072	CFL1	NM_005507	cofilin 1 (non-muscle)
1555762_s_at	1.15	0.02	0.24	0.31	64783	RBM15	NM_022768	RNA binding motif protein 15

1555764_s_at	1.15	0.03	0.32	0.37	26519	TIMM10	NM_012456	translocase of inner mitochondrial membrane 10 homolog (yeast)
1555843_at	0.89	4.04e-03	0.14	0.14	4670	HNRPM	AL713781	heterogeneous nuclear ribonucleoprotein M
1555858_at	0.85	3.06e-04	0.17	0.16	440944	LOC440944	CA430188	hypothetical gene supported by AK128398
1555860_x_at	0.90	0.03	0.20	0.18	440944	LOC440944	CA430188	hypothetical gene supported by AK128398
1555886_at	1.22	1.95e-04	0.18	0.24	57107	C6orf210	BC029491	chromosome 6 open reading frame 210
1555889_a_at	0.91	6.88e-03	0.13	0.13	10491	CRTAP	NM_006371	cartilage associated protein
1555897_at	0.89	0.04	0.21	0.19	23028	AOF2	AK094536	amine oxidase (flavin containing) domain 2
1555913_at	1.10	0.03	0.19	0.18	54856	FLJ20203	NM_032292	hypothetical protein FLJ20203
1555961_a_at	1.09	0.03	0.16	0.18	3094	HINT1	NM_005340	histidine triad nucleotide binding protein 1
1555978_s_at	0.88	0.03	0.22	0.21	440476	LOC440476	AW467415	LOC440476
1556026_at	1.14	0.04	0.29	0.25	3423	IDS	AI692623	iduronate 2-sulfatase (Hunter syndrome)
1556049_at	1.13	0.01	0.18	0.23	57142	RTN4	AK093785	reticulon 4
1556067_a_at	1.18	0.01	0.28	0.28	23135	JMJD3	AB002344	jumonji domain containing 3
1556176_at	0.89	0.04	0.24	0.21	129685	TBN	BU618741	taube nuss homolog (mouse)
1556283_s_at	0.92	0.04	0.17	0.14	26127	FGFR1OP2	NM_015633	FGFR1 oncogene partner 2
1556891_at	0.85	0.03	0.27	0.29	114815	SORCS1	BE328250	sortilin-related VPS10 domain containing receptor 1
1557190_at	0.89	0.03	0.27	0.20	442658	LOC442658	T88880	similar to CGI-150 protein
1557504_at	1.21	0.02	0.31	0.30	6729	SRP54	AI076351	signal recognition particle 54kDa
1557522_x_at	1.13	0.04	0.24	0.25	10904	BLCAP	AA653638	bladder cancer associated protein
1557811_a_at	0.83	0.02	0.31	0.35	5579	PRKCB1	AF085827	protein kinase C, beta 1
1558277_at	1.17	0.01	0.26	0.27	283337	LOC283337	AK091946	hypothetical protein LOC283337
1558392_at	1.18	0.01	0.25	0.22	23224	SYNE2	NM_015180	spectrin repeat containing, nuclear envelope 2
1558641_at	1.15	0.04	0.28	0.15	202051	LOC202051	AK098740	hypothetical protein LOC202051
1558678_s_at	1.13	0.01	0.26	0.15	378938	MALAT1	BC018448	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)
1558747_at	1.20	0.01	0.29	0.29	23347	KIAA0650	XM_113962	KIAA0650 protein
1558759_s_at	0.87	4.43e-03	0.20	0.17	23122	CLASP2	AB014527	cytoplasmic linker associated protein 2
1558783_at	1.13	0.01	0.17	0.24	9589	WTAP	AK024805	Wilms tumor 1 associated protein
1558854_a_at	1.26	8.42e-03	0.36	0.34	124989	FLJ40342	BG616498	hypothetical protein FLJ40342
1559034_at	1.17	0.02	0.27	0.26	284759	PTPNS1L3	AK095499	protein tyrosine phosphatase, non-receptor type substrate 1-like 3
1559399_s_at	1.27	4.56e-04	0.26	0.22	54819	ZCCHC10	BC015986	zinc finger, CCHC domain containing 10
1559584_a_at	1.11	1.04e-03	0.11	0.14	283897	FLJ35681	NM_175900	hypothetical protein FLJ35681
1559862_at	1.28	7.54e-03	0.36	0.47	1314	COPA	BC037941	coatomer protein complex, subunit alpha
1560306_at	1.20	0.03	0.41	0.31	85464	SSH2	AF086010	slingshot homolog 2 (Drosophila)
1560493_a_at	0.87	0.04	0.27	0.25	53336	CPXCR1	NM_033048	CPX chromosome region, candidate 1
1560525_at	0.87	0.04	0.25	0.27	134541	LOC134541	BC029472	similar to Ten-m2
1560587_s_at	1.13	5.17e-03	0.18	0.17	25824	PRDX5	NM_012094	peroxiredoxin 5

1560661_x_at	1.24	0.01	0.37	0.37	150759	LOC150759	AL832439	hypothetical protein LOC150759
1560662_s_at	1.19	0.02	0.30	0.26	339005	LOC339005	BC044610	hypothetical protein LOC339005
1561286_a_at	1.22	9.5e-03	0.34	0.37	23181	C21orf106	NM_206890	chromosome 21 open reading frame 106
1561442_at	0.84	0.02	0.38	0.29	283585	LOC283585	BC034577	hypothetical protein LOC283585
1561518_at	1.13	7.61e-03	0.18	0.19	283914	LOC283914	BC038774	hypothetical protein LOC283914
1561749_at	1.08	0.04	0.16	0.21	84820	MGC13098	AF086498	hypothetical protein MGC13098
1561883_at	0.87	0.03	0.25	0.25	9628	RGS6	AF075115	regulator of G-protein signalling 6
1562256_at	0.83	0.03	0.28	0.34	22861	NALP1	AL832400	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1
1562257_x_at	0.84	0.01	0.22	0.27	22861	NALP1	AL832400	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1
1562364_at	1.40	1.6e-03	0.41	0.52	387751	GVIN1	AL833700	GTPase, very large interferon inducible 1
1562458_at	0.87	0.02	0.29	0.22	55284	FLJ11011	AL833723	hypothetical protein FLJ11011
1562612_at	1.19	4.53e-03	0.26	0.17	4200	ME2	BC020933	malic enzyme 2, NAD(+)-dependent, mitochondrial
1562619_at	0.85	0.02	0.29	0.26	347736	TXNDC6	NM_178130	thioredoxin domain containing 6
1562898_at	1.31	4.61e-04	0.32	0.26	23250	ATP11A	AL713719	ATPase, Class VI, type 11A
1563498_s_at	1.22	6.52e-03	0.30	0.30	283130	LOC283130	AK090434	hypothetical protein LOC283130
1563975_at	1.21	0.01	0.33	0.31	55819	RNF130	AL831873	ring finger protein 130
1564010_at	0.87	0.02	0.26	0.22	831	CAST	AK026822	calpastatin
1564344_at	1.16	5.06e-03	0.17	0.29	374868	ATP9B	AK097757	ATPase, Class II, type 9B
1567107_s_at	1.17	0.03	0.29	0.23	7171	TPM4	NM_003290	tropomyosin 4
1568592_at	1.09	0.04	0.18	0.24	400368	LOC400368	XM_378511	hypothetical gene supported by BC031266
1568943_at	1.12	0.01	0.16	0.22	3635	INPP5D	BC027960	inositol polyphosphate-5-phosphatase, 145kDa
1569077_x_at	0.90	0.03	0.16	0.22	162962	FLJ16287	BE791720	FLJ16287 protein
1569091_at	0.84	0.02	0.27	0.25	7750	ZNF198	BC039458	zinc finger protein 198
1569190_at	1.13	0.01	0.20	0.31	132320	FLJ30655	BC064428	hypothetical protein FLJ30655
1569294_at	1.18	6.2e-03	0.25	0.18	149603	LOC149603	BC015435	hypothetical protein LOC149603
1569464_at	0.88	0.03	0.18	0.22	8496	PPFIBP1	NM_003622	PTPRF interacting protein, binding protein 1 (liprin beta 1)
1570007_at	0.91	0.03	0.19	0.16	84230	FAD158	NM_032270	factor for adipocyte differentiation 158
1570394_at	1.12	0.02	0.20	0.33	54464	XRN1	BC048104	5'-3' exoribonuclease 1
1570523_s_at	0.85	0.01	0.32	0.18	83734	APG10L	NM_031482	APG10 autophagy 10-like (S. cerevisiae)
200019_s_at	1.08	0.01	0.13	0.15	2197	FAU	NM_001997	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox deri
200021_at	1.09	0.03	0.20	0.10	1072	CFL1	NM_005507	cofilin 1 (non-muscle)
200037_s_at	1.10	0.02	0.17	0.15	11335	CBX3	NM_016587	chromobox homolog 3 (HP1 gamma homolog, Drosophila)
200044_at	1.08	0.03	0.17	0.15	8683	SFRS9	NM_003769	splicing factor, arginine/serine-rich 9
200047_s_at	1.09	0.01	0.13	0.16	7528	YY1	NM_003403	YY1 transcription factor
200048_s_at	1.05	0.04	0.11	0.13	10899	JTB	NM_006694	jumping translocation breakpoint
200051_at	1.13	3.18e-03	0.16	0.17	9092	SART1	NM_005146	squamous cell carcinoma antigen recognised by T cells

200055_at	1.13	1.47e-03	0.16	0.14	6881	TAF10	NM_006284	TAF10 RNA polymerase II, TATA box
binding protein (TBP)-associated factor, 30kDa								
200075_s_at	1.08	0.02	0.14	0.13	2987	GUK1	NM_000858	guanylate kinase 1
200076_s_at	1.11	2.89e-03	0.15	0.15	79036	MGC2749	NM_024069	hypothetical protein MGC2749
200078_s_at	1.12	4.89e-03	0.15	0.21	533	ATP6V0B	NM_004047	ATPase, H+ transporting, lysosomal
21kDa, V0 subunit c"								
200083_at	1.10	8.8e-03	0.16	0.14	23326	USP22	XM_042698	ubiquitin specific protease 22
200085_s_at	1.12	7.34e-03	0.17	0.16	6923	TCEB2	NM_007108	transcription elongation factor B (SIII),
polypeptide 2 (18kDa, elongin B)								
200097_s_at	1.08	0.01	0.14	0.13	3190	HNRPK	NM_002140	heterogeneous nuclear ribonucleoprotein K
200593_s_at	1.07	0.02	0.13	0.11	3192	HNRPU	NM_031844	heterogeneous nuclear ribonucleoprotein U
(scaffold attachment factor A)								
200594_x_at	1.08	0.01	0.13	0.12	3192	HNRPU	NM_004501	heterogeneous nuclear ribonucleoprotein
U (scaffold attachment factor A)								
200600_at	1.07	0.02	0.13	0.11	4478	MSN	NM_002444	moesin
200601_at	1.14	0.04	0.24	0.17	81	ACTN4	NM_004924	actinin, alpha 4
200603_at	1.11	1.51e-03	0.11	0.16	5573	PRKAR1A	NM_002734	protein kinase, cAMP-dependent,
regulatory, type I, alpha (tissue specific extinguish								
200608_s_at	1.08	0.03	0.14	0.16	5885	RAD21	NM_006265	RAD21 homolog (S. pombe)
200609_s_at	1.09	3.52e-03	0.11	0.13	9948	WDR1	NM_017491	WD repeat domain 1
200622_x_at	1.13	1.87e-03	0.16	0.16	808	CALM3	NM_005184	calmodulin 3 (phosphorylase kinase,
delta)								
200623_s_at	1.14	0.04	0.30	0.25	808	CALM3	NM_005184	calmodulin 3 (phosphorylase kinase, delta)
200633_at	1.06	0.04	0.13	0.10	7314	UBB	NM_018955	ubiquitin B
200634_at	1.08	0.04	0.20	0.11	5216	PFN1	NM_005022	profilin 1
200655_s_at	1.08	0.01	0.13	0.15	801	CALM1	NM_006888	calmodulin 1 (phosphorylase kinase, delta)
200660_at	1.09	0.03	0.17	0.14	6282	S100A11	NM_005620	S100 calcium binding protein A11
(calgizzarin)								
200665_s_at	1.44	0.01	0.69	0.57	6678	SPARC	NM_003118	secreted protein, acidic, cysteine-rich
(osteonectin)								
200679_x_at	1.08	0.03	0.15	0.15	3146	HMGB1	NM_002128	high-mobility group box 1
200696_s_at	1.11	0.01	0.19	0.13	2934	GSN	NM_000177	gelsolin (amyloidosis, Finnish type)
200711_s_at	1.08	6.11e-03	0.12	0.11	6500	SKP1A	NM_006930	S-phase kinase-associated protein 1A
(p19A)								
200718_s_at	1.05	0.03	0.10	0.10	6500	SKP1A	NM_006930	S-phase kinase-associated protein 1A
(p19A)								
200719_at	0.91	0.04	0.16	0.16	6500	SKP1A	NM_006930	S-phase kinase-associated protein 1A (p19A)
200733_s_at	1.10	0.03	0.18	0.29	7803	PTP4A1	NM_003463	protein tyrosine phosphatase type IVA,
member 1								
200746_s_at	1.06	0.02	0.11	0.12	2782	GNB1	NM_002074	guanine nucleotide binding protein (G
protein), beta polypeptide 1								
200761_s_at	1.08	0.01	0.13	0.13	10550	ARL6IP5	NM_006407	ADP-ribosylation-like factor 6 interacting
protein 5								
200790_at	1.15	0.02	0.27	0.22	4953	ODC1	NM_002539	ornithine decarboxylase 1
200794_x_at	1.06	0.04	0.12	0.10	9802	DAZAP2	NM_014764	DAZ associated protein 2

200797_s_at	1.07	0.03	0.15	0.11	4170	MCL1	NM_021960	myeloid cell leukemia sequence 1 (BCL2-related)
200805_at	1.08	0.03	0.15	0.14	10960	LMAN2	NM_006816	lectin, mannose-binding 2
200810_s_at	1.09	0.02	0.16	0.16	1153	CIRBP	NM_001280	cold inducible RNA binding protein
200814_at	1.10	0.04	0.20	0.17	5720	PSME1	NM_006263	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
200816_s_at	1.09	0.03	0.15	0.15	5048	PAFAH1B1	NM_000430	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa
200846_s_at	1.12	5.46e-04	0.13	0.13	5499	PPP1CA	NM_002708	protein phosphatase 1, catalytic subunit, alpha isoform
200847_s_at	1.08	5.69e-03	0.09	0.14	51669	MGC8721	NM_016127	hypothetical protein MGC8721
200849_s_at	1.14	0.02	0.27	0.23	10768	AHCYL1	NM_006621	S-adenosylhomocysteine hydrolase-like 1
200882_s_at	1.09	0.04	0.17	0.17	5710	PSMD4	NM_002810	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
200886_s_at	1.11	5.58e-04	0.11	0.12	5223	PGAM1	NM_002629	phosphoglycerate mutase 1 (brain)
200887_s_at	1.14	0.01	0.24	0.33	6772	STAT1	NM_007315	signal transducer and activator of transcription 1, 91kDa
200904_at	1.10	1.42e-03	0.13	0.12	3133	HLA-E	X56841	major histocompatibility complex, class I, E
200905_x_at	1.10	0.02	0.22	0.13	3133	HLA-E	NM_005516	major histocompatibility complex, class I, E
200911_s_at	1.08	4.87e-03	0.10	0.15	6867	TACC1	NM_006283	transforming, acidic coiled-coil containing protein 1
200921_s_at	1.07	0.02	0.13	0.13	694	BTG1	NM_001731	B-cell translocation gene 1, anti-proliferative
200925_at	1.09	4.07e-03	0.12	0.14	1337	COX6A1	NM_004373	cytochrome c oxidase subunit VIa polypeptide 1
200953_s_at	1.13	0.04	0.24	0.24	894	CCND2	NM_001759	cyclin D2
200958_s_at	1.10	6.72e-03	0.16	0.12	6386	SDCBP	NM_005625	syndecan binding protein (syntenin)
200963_x_at	1.08	0.03	0.16	0.13	6160	RPL31	NM_000993	ribosomal protein L31
200964_at	1.15	5.05e-03	0.21	0.18	7317	UBE1	NM_003334	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)
200966_x_at	1.09	3.16e-03	0.11	0.13	226	ALDOA	NM_000034	aldolase A, fructose-bisphosphate
200989_at	1.08	0.01	0.14	0.16	3091	HIF1A	NM_001530	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription facto
201024_x_at	1.15	0.01	0.24	0.22	9669	EIF5B	NM_015904	eukaryotic translation initiation factor 5B
201031_s_at	1.16	0.01	0.22	0.20	3187	HNRPH1	NM_005520	heterogeneous nuclear ribonucleoprotein H1 (H)
201082_s_at	1.15	0.02	0.25	0.24	1639	DCTN1	NM_004082	dynactin 1 (p150, glued homolog, Drosophila)
201083_s_at	1.14	0.04	0.25	0.23	9774	BCLAF1	NM_014739	BCL2-associated transcription factor 1
201087_at	1.15	7.93e-03	0.20	0.22	5829	PXN	NM_002859	paxillin
201094_at	1.10	0.03	0.24	0.13	6235	RPS29	NM_001032	ribosomal protein S29
201099_at	1.06	0.02	0.09	0.14	8239	USP9X	AA824386	ubiquitin specific protease 9, X-linked (fat facets-like, Drosophila)
201152_s_at	1.08	0.02	0.14	0.13	4154	MBNL1	NM_021038	muscleblind-like (Drosophila)
201153_s_at	1.10	6.45e-03	0.14	0.14	4154	MBNL1	NM_021038	muscleblind-like (Drosophila)

201181_at	1.12	0.01	0.16	0.24	2773	GNAI3	NM_006496	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide
201183_s_at	1.13	7.84e-03	0.20	0.15	1108	CHD4	NM_001273	chromodomain helicase DNA binding protein 4
201210_at	1.06	0.03	0.11	0.13	1654	DDX3X	NM_001356	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
201219_at	1.11	0.02	0.18	0.20	1488	CTBP2	NM_001329	C-terminal binding protein 2
201223_s_at	1.13	2.75e-03	0.14	0.21	5887	RAD23B	NM_002874	RAD23 homolog B (S. cerevisiae)
201234_at	1.14	1.92e-03	0.17	0.13	3611	ILK	NM_004517	integrin-linked kinase
201237_at	1.12	0.02	0.20	0.25	830	CAPZA2	NM_006136	capping protein (actin filament) muscle Z-line, alpha 2
201253_s_at	1.08	0.03	0.16	0.17	10423	CDIPT	NM_006319	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase
201271_s_at	1.14	4.84e-04	0.15	0.12	22913	RALY	NM_016732	RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow)
201276_at	1.07	0.02	0.13	0.13	5869	RAB5B	NM_002868	RAB5B, member RAS oncogene family
201288_at	1.07	0.04	0.16	0.10	397	ARHGDIB	NM_001175	Rho GDP dissociation inhibitor (GDI) beta
201296_s_at	1.08	0.01	0.12	0.16	26118	WSB1	NM_015626	WD repeat and SOCS box-containing 1
201318_s_at	1.10	2.98e-03	0.12	0.13	10627	MRCL3	NM_006471	myosin regulatory light chain MRCL3
201344_at	1.09	0.02	0.18	0.14	7322	UBE2D2	NM_003339	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)
201353_s_at	1.18	0.01	0.32	0.27	11176	BAZ2A	NM_013449	bromodomain adjacent to zinc finger domain, 2A
201354_s_at	1.19	6.01e-03	0.25	0.22	11176	BAZ2A	NM_013449	bromodomain adjacent to zinc finger domain, 2A
201362_at	1.11	0.01	0.15	0.18	10625	IVNS1ABP	NM_006469	influenza virus NS1A binding protein
201368_at	1.06	0.03	0.10	0.12	678	ZFP36L2	NM_006887	zinc finger protein 36, C3H type-like 2
201388_at	1.12	0.01	0.19	0.18	5709	PSMD3	NM_002809	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3
201390_s_at	1.07	0.03	0.13	0.12	1460	CSNK2B	NM_001320	casein kinase 2, beta polypeptide
201400_at	1.10	1.67e-03	0.12	0.14	5691	PSMB3	NM_002795	proteasome (prosome, macropain) subunit, beta type, 3
201407_s_at	1.14	0.02	0.25	0.22	5500	PPP1CB	NM_002709	protein phosphatase 1, catalytic subunit, beta isoform
201410_at	1.06	0.04	0.11	0.13	55041	PLEKHB2	AI983043	pleckstrin homology domain containing, family B (evectins) member 2
201436_at	1.21	3.92e-03	0.27	0.29	1977	EIF4E	NM_001968	eukaryotic translation initiation factor 4E
201441_at	1.10	0.01	0.17	0.15	1340	COX6B1	NM_001863	cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)
201463_s_at	1.08	8.99e-03	0.12	0.14	6888	TALDO1	NM_006755	transaldolase 1
201494_at	1.06	0.03	0.09	0.14	5547	PRCP	NM_005040	prolylcarboxypeptidase (angiotensinase C)
201513_at	1.11	0.04	0.21	0.17	7247	TSN	NM_004622	translin
201526_at	1.09	0.02	0.15	0.16	381	ARF5	NM_001662	ADP-ribosylation factor 5
201541_s_at	1.09	0.03	0.16	0.18	10467	ZNHIT1	NM_006349	zinc finger, HIT domain containing 1
201553_s_at	1.07	0.02	0.13	0.10	3916	LAMP1	NM_005561	lysosomal-associated membrane protein 1

201557_at	1.15	3.96e-03	0.22	0.19	6844	VAMP2	NM_014232	vesicle-associated membrane protein 2 (synaptobrevin 2)
201558_at	1.08	0.03	0.14	0.15	8480	RAE1	NM_003610	RAE1 RNA export 1 homolog (S. pombe)
201561_s_at	1.09	0.03	0.17	0.17	22883	CLSTN1	NM_014944	calsyntenin 1
201565_s_at	1.11	0.04	0.20	0.17	3398	ID2	NM_002166	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
201568_at	1.10	0.01	0.17	0.15	27089	QP-C	NM_014402	low molecular mass ubiquinone-binding protein (9.5kD)
201575_at	1.08	0.02	0.14	0.14	22938	SKIIP	NM_012245	SKI interacting protein
201588_at	1.06	0.03	0.11	0.12	9352	TXNL1	NM_004786	thioredoxin-like 1
201597_at	1.10	0.02	0.17	0.16	1347	COX7A2	NM_001865	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
201603_at	1.10	5.31e-03	0.11	0.19	4659	PPP1R12A	NM_002480	protein phosphatase 1, regulatory (inhibitor) subunit 12A
201612_at	1.10	0.04	0.20	0.21	223	ALDH9A1	NM_000696	aldehyde dehydrogenase 9 family, member A1
201626_at	1.11	0.03	0.20	0.23	3638	INSIG1	NM_005542	insulin induced gene 1
201631_s_at	1.21	9.42e-03	0.29	0.26	8870	IER3	NM_003897	immediate early response 3
201642_at	1.08	0.01	0.11	0.16	3460	IFNGR2	NM_005534	interferon gamma receptor 2 (interferon gamma transducer 1)
201646_at	0.88	0.02	0.23	0.22	950	SCARB2	NM_005506	scavenger receptor class B, member 2
201661_s_at	1.12	0.01	0.17	0.21	2181	ACSL3	NM_004457	acyl-CoA synthetase long-chain family member 3
201669_s_at	1.10	0.03	0.18	0.22	4082	MARCKS	NM_002356	myristoylated alanine-rich protein kinase C substrate
201685_s_at	1.13	3.83e-03	0.16	0.21	9878	C14orf92	NM_014828	chromosome 14 open reading frame 92
201686_x_at	0.91	0.02	0.18	0.15	8539	API5	NM_006595	apoptosis inhibitor 5
201702_s_at	1.17	4.1e-03	0.18	0.31	5514	PPP1R10	NM_002714	protein phosphatase 1, regulatory subunit 10
201708_s_at	0.91	0.02	0.19	0.14	8508	NIPSNAP1	NM_003634	nipsnap homolog 1 (C. elegans)
201715_s_at	1.11	0.04	0.21	0.17	22985	ACIN1	NM_014977	apoptotic chromatin condensation inducer 1
201723_s_at	1.07	0.02	0.13	0.13	2589	GALNT1	NM_020474	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (G
201748_s_at	1.08	0.01	0.13	0.10	6294	SAFB	NM_002967	scaffold attachment factor B
201754_at	1.10	0.04	0.19	0.21	1345	COX6C	NM_004374	cytochrome c oxidase subunit VIc
201760_s_at	1.10	0.03	0.18	0.19	55884	WSB2	NM_018639	WD repeat and SOCS box-containing 2
201780_s_at	1.10	0.01	0.14	0.19	11342	RNF13	NM_007282	ring finger protein 13
201788_at	1.18	2.67e-03	0.21	0.19	11325	DDX42	NM_007372	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42
201794_s_at	1.11	0.04	0.23	0.23	9887	C1orf16	NM_014837	chromosome 1 open reading frame 16
201795_at	1.12	8.96e-03	0.16	0.20	3930	LBR	NM_002296	lamin B receptor
201831_s_at	0.91	0.02	0.19	0.12	8615	VDP	NM_003715	vesicle docking protein p115
201834_at	1.12	0.01	0.19	0.18	5564	PRKAB1	NM_006253	protein kinase, AMP-activated, beta 1 non-catalytic subunit

201840_at	1.10	0.03	0.20	0.17	4738	NEDD8	NM_006156	neural precursor cell expressed, developmentally down-regulated 8
201845_s_at	1.10	6.82e-03	0.14	0.18	23429	RYBP	AB029551	RING1 and YY1 binding protein
201857_at	1.10	0.01	0.15	0.15	51663	ZFR	NM_016107	zinc finger RNA binding protein
201859_at	1.11	0.02	0.24	0.12	5552	PRG1	NM_002727	proteoglycan 1, secretory granule
201871_s_at	1.13	0.01	0.23	0.15	51035	LOC51035	NM_015853	ORF
201883_s_at	1.48	9.74e-03	0.75	0.29	2683	B4GALT1	NM_001497	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1
201899_s_at	1.06	0.02	0.10	0.14	7319	UBE2A	NM_003336	ubiquitin-conjugating enzyme E2A (RAD6 homolog)
201924_at	1.12	0.01	0.18	0.25	4299	MLLT2	NM_005935	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); transloca
201933_at	1.14	8.52e-03	0.20	0.20	5119	PCOLN3	NM_002768	procollagen (type III) N-endopeptidase
201935_s_at	1.11	0.04	0.20	0.20	8672	EIF4G3	NM_003760	eukaryotic translation initiation factor 4 gamma, 3
201936_s_at	1.17	0.03	0.27	0.22	8672	EIF4G3	NM_003760	eukaryotic translation initiation factor 4 gamma, 3
201949_x_at	1.13	0.04	0.27	0.19	832	CAPZB	AL572341	capping protein (actin filament) muscle Z-line, beta
201968_s_at	1.10	8.08e-03	0.16	0.15	5236	PGM1	NM_002633	phosphoglucomutase 1
201971_s_at	0.85	0.02	0.32	0.23	523	ATP6V1A	NM_001690	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A
201972_at	1.09	0.01	0.12	0.18	523	ATP6V1A	NM_001690	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A
201996_s_at	1.18	0.03	0.32	0.34	23013	SPEN	NM_015001	spen homolog, transcriptional regulator (Drosophila)
201997_s_at	1.08	0.02	0.13	0.15	23013	SPEN	NM_015001	spen homolog, transcriptional regulator (Drosophila)
201999_s_at	1.07	0.02	0.12	0.20	6993	TCTEL1	NM_006519	t-complex-associated-testis-expressed 1-like 1
202009_at	1.08	0.04	0.15	0.16	11344	PTK9L	NM_007284	PTK9L protein tyrosine kinase 9-like (A6-related protein)
202027_at	1.13	0.02	0.23	0.18	25829	C22orf5	NM_012264	chromosome 22 open reading frame 5
202031_s_at	1.08	0.03	0.16	0.18	26100	WIPI-2	NM_015610	WIPI49-like protein 2
202034_x_at	1.09	0.04	0.18	0.18	9821	RB1CC1	NM_014781	RB1-inducible coiled-coil 1
202062_s_at	0.87	0.04	0.29	0.28	6400	SEL1L	NM_005065	sel-1 suppressor of lin-12-like (C. elegans)
202071_at	1.12	0.02	0.20	0.30	6385	SDC4	NM_002999	syndecan 4 (amphiglycan, ryudocan)
202090_s_at	1.08	9.08e-03	0.12	0.11	10975	UQCR	NM_006830	ubiquinol-cytochrome c reductase, 6.4kDa subunit
202096_s_at	1.10	0.04	0.21	0.18	706	BZRP	NM_000714	benzodiazapine receptor (peripheral)
202106_at	1.13	0.01	0.20	0.19	2802	GOLGA3	NM_005895	golgi autoantigen, golgin subfamily a, 3
202110_at	1.11	6.35e-03	0.16	0.17	1349	COX7B	NM_001866	cytochrome c oxidase subunit VIIb
202121_s_at	1.08	0.03	0.15	0.15	27243	BC-2	NM_014453	putative breast adenocarcinoma marker (32kD)

202149_at	1.10	0.01	0.12	0.23	4739	NEDD9	NM_182966	neural precursor cell expressed,
developmentally down-regulated 9								
202149_at	1.10	0.01	0.12	0.23	4739	NEDD9	NM_006403	neural precursor cell expressed,
developmentally down-regulated 9								
202154_x_at	1.30	3.16e-04	0.30	0.33	10381	TUBB3	NM_006086	tubulin, beta 3
202157_s_at	1.06	0.03	0.12	0.11	10659	CUGBP2	NM_006561	CUG triplet repeat, RNA binding protein
2								
202158_s_at	1.09	8.32e-03	0.12	0.16	10659	CUGBP2	NM_006561	CUG triplet repeat, RNA binding
protein 2								
202174_s_at	1.09	0.04	0.17	0.25	5108	PCM1	NM_006197	pericentriolar material 1
202181_at	1.09	9.04e-03	0.12	0.15	9766	KIAA0247	NM_014734	KIAA0247
202205_at	1.07	0.04	0.15	0.16	7408	VASP	NM_003370	vasodilator-stimulated phosphoprotein
202225_at	1.06	0.04	0.10	0.15	1398	CRK	AW612311	v-crk sarcoma virus CT10 oncogene homolog
(avian)								
202228_s_at	1.06	0.03	0.10	0.16	27020	SDFR1	NM_017455	stromal cell derived factor receptor 1
202243_s_at	1.09	0.02	0.17	0.15	5692	PSMB4	NM_002796	proteasome (prosome, macropain) subunit,
beta type, 4								
202244_at	1.09	0.01	0.12	0.16	5692	PSMB4	NM_002796	proteasome (prosome, macropain) subunit,
beta type, 4								
202255_s_at	1.13	5.79e-03	0.17	0.21	26037	SIPA1L1	NM_015556	signal-induced proliferation-associated 1
like 1								
202256_at	1.09	0.02	0.16	0.18	10421	CD2BP2	AB033004	CD2 antigen (cytoplasmic tail) binding
protein 2								
202257_s_at	1.14	0.01	0.20	0.23	10421	CD2BP2	NM_006110	CD2 antigen (cytoplasmic tail) binding
protein 2								
202258_s_at	1.10	2.5e-03	0.12	0.16	10443	PFAAP5	NM_014887	phosphonoformate immuno-associated
protein 5								
202298_at	1.25	1.45e-03	0.27	0.29	4694	NDUFA1	NM_004541	NADH dehydrogenase (ubiquinone) 1
alpha subcomplex, 1, 7.5kDa								
202300_at	1.07	0.02	0.12	0.10	10542	HBXIP	NM_006402	hepatitis B virus x interacting protein
202321_at	1.11	0.03	0.20	0.18	9453	GGPS1	NM_004837	geranylgeranyl diphosphate synthase 1
202329_at	1.10	1.52e-03	0.11	0.12	1445	CSK	NM_004383	c-src tyrosine kinase
202337_at	1.14	6.38e-04	0.15	0.15	11243	PMF1	NM_007221	polyamine-modulated factor 1
202343_x_at	1.07	0.03	0.14	0.14	1329	COX5B	NM_001862	cytochrome c oxidase subunit Vb
202371_at	0.88	5.55e-03	0.19	0.16	79921	TCEAL4	NM_024863	transcription elongation factor A (SII)-
like 4								
202384_s_at	1.08	0.04	0.16	0.21	6949	TCOF1	NM_000356	Treacher Collins-Franceschetti syndrome 1
202388_at	1.09	0.02	0.19	0.14	5997	RGS2	NM_002923	regulator of G-protein signalling 2, 24kDa
202425_x_at	1.12	0.02	0.20	0.17	5530	PPP3CA	NM_000944	protein phosphatase 3 (formerly 2B),
catalytic subunit, alpha isoform (calcineurin A								
202443_x_at	1.07	0.02	0.11	0.16	4853	NOTCH2	NM_024408	Notch homolog 2 (Drosophila)
202488_s_at	0.88	0.02	0.23	0.21	5349	FXYD3	NM_005971	FXYD domain containing ion transport
regulator 3								
202499_s_at	1.12	0.03	0.23	0.24	6515	SLC2A3	NM_006931	solute carrier family 2 (facilitated glucose
transporter), member 3								

202520_s_at	0.92	0.03	0.16	0.13	4292	MLH1	NM_000249	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
202531_at	1.14	9.86e-03	0.21	0.23	3659	IRF1	NM_002198	interferon regulatory factor 1
202534_x_at	1.08	0.02	0.14	0.15	1719	DHFR	NM_000791	dihydrofolate reductase
202540_s_at	1.10	0.01	0.16	0.20	3156	HMGCR	NM_000859	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
202550_s_at	1.08	0.01	0.12	0.15	9217	VAPB	NM_004738	VAMP (vesicle-associated membrane protein)-associated protein B and C
202551_s_at	1.12	0.04	0.26	0.32	51232	CRIM1	NM_016441	cysteine-rich motor neuron 1
202566_s_at	1.10	0.02	0.16	0.26	6840	SVIL	NM_003174	supervillin
202569_s_at	1.08	0.02	0.13	0.19	4140	MARK3	NM_002376	MAP/microtubule affinity-regulating kinase 3
202573_at	1.14	0.02	0.23	0.20	1455	CSNK1G2	NM_001319	casein kinase 1, gamma 2
202592_at	1.09	0.05	0.20	0.15	2647	BLOC1S1	NM_001487	biogenesis of lysosome-related organelles complex-1, subunit 1
202607_at	1.21	0.01	0.35	0.33	3340	NDST1	NM_001543	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1
202614_at	1.12	0.01	0.19	0.19	10463	SLC30A9	NM_006345	solute carrier family 30 (zinc transporter), member 9
202618_s_at	1.10	0.01	0.16	0.15	4204	MECP2	NM_004992	methyl CpG binding protein 2 (Rett syndrome)
202623_at	1.07	0.03	0.13	0.12	55837	C14orf11	NM_018453	chromosome 14 open reading frame 11
202636_at	1.10	5.01e-03	0.11	0.19	7844	RNF103	NM_005667	ring finger protein 103
202640_s_at	1.13	0.04	0.25	0.25	8498	RANBP3	NM_003624	RAN binding protein 3
202643_s_at	1.15	0.02	0.27	0.21	7128	TNFAIP3	NM_006290	tumor necrosis factor, alpha-induced protein 3
202644_s_at	1.12	0.02	0.23	0.16	7128	TNFAIP3	NM_006290	tumor necrosis factor, alpha-induced protein 3
202653_s_at	1.11	6.56e-03	0.15	0.22	64844	MARCH7	NM_022826	membrane-associated ring finger (C3HC4) 7
202660_at	1.14	3.56e-03	0.16	0.26	3709	ITPR2	NM_002223	inositol 1,4,5-triphosphate receptor, type 2
202664_at	1.11	1.63e-04	0.10	0.12	7456	WASPIP	NM_003387	Wiskott-Aldrich syndrome protein interacting protein
202673_at	1.10	0.04	0.19	0.19	8813	DPM1	NM_003859	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
202704_at	1.12	0.03	0.23	0.22	10140	TOB1	NM_005749	transducer of ERBB2, 1
202724_s_at	1.11	0.01	0.19	0.14	2308	FOXO1A	NM_002015	forkhead box O1A (rhabdomyosarcoma)
202725_at	1.19	0.03	0.37	0.29	5430	POLR2A	NM_000937	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa
202727_s_at	1.06	0.04	0.11	0.16	3459	IFNGR1	NM_000416	interferon gamma receptor 1
202729_s_at	1.23	0.03	0.46	0.24	4052	LTBP1	NM_000627	latent transforming growth factor beta binding protein 1
202748_at	1.13	0.02	0.20	0.25	2634	GBP2	NM_004120	guanylate binding protein 2, interferon-inducible
202764_at	1.12	9.12e-04	0.14	0.16	6786	STIM1	NM_003156	stromal interaction molecule 1

202769_at	1.16	1.96e-03	0.17	0.26	901	CCNG2	AW134535	cyclin G2
202772_at	1.10	2.76e-03	0.13	0.13	3155	HMGCL	NM_000191	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)
202778_s_at	1.09	0.02	0.15	0.19	7750	ZNF198	NM_003453	zinc finger protein 198
202782_s_at	1.11	5.56e-03	0.15	0.17	51763	SKIP	NM_016532	skeletal muscle and kidney enriched inositol phosphatase
202789_at	1.12	0.04	0.23	0.26	5335	PLCG1	NM_002660	phospholipase C, gamma 1
202802_at	1.12	0.01	0.18	0.24	1725	DHPS	NM_001930	deoxyhypusine synthase
202808_at	1.07	0.03	0.14	0.13	54838	C10orf26	AK000161	chromosome 10 open reading frame 26
202833_s_at	1.07	0.02	0.12	0.13	5265	SERPINA1	NM_000295	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitryps
202836_s_at	1.09	0.04	0.18	0.15	10907	TXNL4A	NM_006701	thioredoxin-like 4A
202844_s_at	1.19	0.01	0.28	0.26	10928	RALBP1	NM_006788	ralA binding protein 1
202848_s_at	1.12	3.73e-03	0.14	0.19	2870	GRK6	NM_001004106	G protein-coupled receptor kinase 6
202880_s_at	1.07	0.03	0.12	0.17	9267	PSCD1	NM_004762	pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1)
202900_s_at	1.11	0.03	0.21	0.20	4927	NUP88	NM_002532	nucleoporin 88kDa
202901_x_at	1.08	0.03	0.14	0.18	1520	CTSS	NM_004079	cathepsin S
202907_s_at	1.12	8.34e-03	0.16	0.23	4683	NBS1	NM_002485	Nijmegen breakage syndrome 1 (nibrin)
202909_at	1.16	0.01	0.24	0.19	9852	EPM2AIP1	NM_014805	EPM2A (laforin) interacting protein 1
202927_at	1.20	0.02	0.29	0.39	5300	PIN1	NM_006221	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1
202942_at	1.10	0.04	0.20	0.27	2109	ETFB	NM_001985	electron-transfer-flavoprotein, beta polypeptide
203028_s_at	1.09	1.05e-03	0.10	0.11	1535	CYBA	NM_000101	cytochrome b-245, alpha polypeptide
203039_s_at	1.08	0.02	0.14	0.16	4719	NDUFS1	NM_005006	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
203059_s_at	0.85	0.01	0.29	0.24	9060	PAPSS2	NM_004670	3'-phosphoadenosine 5'-phosphosulfate synthase 2
203062_s_at	1.12	0.02	0.19	0.19	9656	MDC1	NM_014641	mediator of DNA damage checkpoint 1
203080_s_at	1.10	0.03	0.18	0.23	29994	BAZ2B	NM_013450	bromodomain adjacent to zinc finger domain, 2B
203082_at	1.09	0.02	0.15	0.21	9790	BMS1L	NM_014753	BMS1-like, ribosome assembly protein (yeast)
203090_at	1.07	6.53e-03	0.08	0.12	6388	SDF2	NM_006923	stromal cell-derived factor 2
203094_at	1.15	2.48e-03	0.18	0.25	9587	MAD2L1BP	NM_014628	MAD2L1 binding protein
203098_at	1.09	0.03	0.16	0.22	9425	CDYL	NM_004824	chromodomain protein, Y-like
203106_s_at	1.22	0.01	0.35	0.26	27072	VPS41	NM_014396	vacuolar protein sorting 41 (yeast)
203109_at	1.11	0.02	0.19	0.16	9040	UBE2M	NM_003969	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)
203158_s_at	0.92	0.03	0.20	0.13	2744	GLS	NM_014905	glutaminase
203171_s_at	1.12	0.03	0.21	0.25	23378	KIAA0409	NM_015324	KIAA0409 protein
203175_at	1.08	0.02	0.14	0.18	391	RHOG	NM_001665	ras homolog gene family, member G (rho G)
203186_s_at	1.09	4.86e-03	0.12	0.13	6275	S100A4	NM_002961	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine pla

203189_s_at	1.15	0.03	0.27	0.30	4728	NDUFS8	NM_002496	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
203206_at	1.15	1.18e-03	0.19	0.14	9679	FAM53B	NM_014661	family with sequence similarity 53, member B
203218_at	1.18	0.02	0.27	0.27	5601	MAPK9	NM_002752	mitogen-activated protein kinase 9
203254_s_at	1.24	0.02	0.42	0.38	7094	TLN1	NM_006289	talin 1
203310_at	1.09	0.04	0.17	0.19	6814	STXBP3	NM_007269	syntaxin binding protein 3
203315_at	1.12	6.21e-03	0.16	0.20	8440	NCK2	NM_003581	NCK adaptor protein 2
203330_s_at	1.09	8.95e-03	0.13	0.13	6811	STX5A	NM_003164	syntaxin 5A
203342_at	1.18	8.95e-04	0.20	0.18	10245	TIMM17B	NM_005834	translocase of inner mitochondrial membrane 17 homolog B (yeast)
203366_at	1.16	9.16e-03	0.25	0.26	5428	POLG	NM_002693	polymerase (DNA directed), gamma
203370_s_at	1.16	0.02	0.29	0.33	9260	PDLIM7	NM_005451	PDZ and LIM domain 7 (enigma)
203371_s_at	1.06	0.04	0.12	0.20	4709	NDUFB3	NM_002491	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
203378_at	1.10	0.02	0.16	0.22	51585	PCF11	NM_015885	pre-mRNA cleavage complex II protein Pcf11
203379_at	1.10	7.58e-03	0.13	0.16	6195	RPS6KA1	NM_002953	ribosomal protein S6 kinase, 90kDa, polypeptide 1
203384_s_at	1.08	0.02	0.11	0.17	2800	GOLGA1	NM_002077	golgi autoantigen, golgin subfamily a, 1
203395_s_at	1.23	0.01	0.36	0.43	3280	HES1	NM_005524	hairy and enhancer of split 1, (Drosophila)
203414_at	1.26	0.01	0.43	0.42	23531	MMD	NM_012329	monocyte to macrophage differentiation-associated
203415_at	1.07	0.01	0.12	0.12	10016	PDCD6	NM_013232	programmed cell death 6
203416_at	1.06	0.03	0.12	0.09	963	CD53	NM_000560	CD53 antigen
203451_at	1.09	0.04	0.17	0.19	8861	LDB1	NM_003893	LIM domain binding 1
203455_s_at	1.10	0.01	0.15	0.15	6303	SAT	NM_002970	spermidine/spermine N1-acetyltransferase
203489_at	1.13	0.01	0.21	0.17	10572	SIVA	NM_006427	CD27-binding (Siva) protein
203502_at	1.10	0.02	0.16	0.18	669	BPGM	NM_001724	2,3-bisphosphoglycerate mutase
203506_s_at	1.10	0.03	0.19	0.20	9968	MED12	NM_005120	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)
203533_s_at	1.18	0.03	0.34	0.26	8065	CUL5	NM_003478	cullin 5
203535_at	1.11	0.02	0.22	0.13	6280	S100A9	NM_002965	S100 calcium binding protein A9 (calgranulin B)
203597_s_at	1.16	0.03	0.25	0.26	11193	WBP4	NM_007187	WW domain binding protein 4 (formin binding protein 21)
203613_s_at	1.10	0.01	0.16	0.19	4712	NDUFB6	NM_002493	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa
203615_x_at	1.19	4.01e-03	0.24	0.38	6817	SULT1A1	NM_001055	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1
203645_s_at	0.88	0.02	0.26	0.20	9332	CD163	NM_004244	CD163 antigen
203669_s_at	1.12	0.02	0.19	0.22	8694	DGAT1	NM_012079	diacylglycerol O-acyltransferase homolog 1 (mouse)
203703_s_at	0.87	3.3e-03	0.17	0.17	9654	TTLL4	NM_014640	tubulin tyrosine ligase-like family, member 4

203728_at	1.09	0.02	0.16	0.20	578	BAK1	NM_001188	BCL2-antagonist/killer 1
203752_s_at	1.09	5.28e-03	0.12	0.12	3727	JUND	NM_005354	jun D proto-oncogene
203765_at	1.11	1.02e-03	0.11	0.15	25801	GCA	NM_012198	grancalcin, EF-hand calcium binding protein
203788_s_at	0.85	4.4e-03	0.21	0.21	10512	SEMA3C	NM_006379	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3
203858_s_at	0.89	7.09e-03	0.17	0.15	1352	COX10	NM_001303	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (ye
203897_at	1.10	0.02	0.16	0.20	57149	LOC57149	NM_020424	hypothetical protein A-211C6.1
203898_at	1.12	0.01	0.18	0.18	27297	RCP9	AU154853	calcitonin gene-related peptide-receptor component protein
203906_at	1.10	0.01	0.15	0.19	9922	IQSEC1	AI652645	IQ motif and Sec7 domain 1
203907_s_at	1.09	8.21e-03	0.12	0.17	9922	IQSEC1	NM_014869	IQ motif and Sec7 domain 1
203983_at	1.16	4.49e-04	0.16	0.18	7257	TSNAX	NM_005999	translin-associated factor X
204000_at	1.13	0.04	0.26	0.25	10681	GNB5	NM_016194	guanine nucleotide binding protein (G protein), beta 5
204012_s_at	1.12	4.3e-03	0.18	0.14	9836	LCMT2	NM_014793	leucine carboxyl methyltransferase 2
204022_at	1.07	0.03	0.12	0.17	11060	WWP2	NM_007014	WW domain containing E3 ubiquitin protein ligase 2
204036_at	1.20	0.04	0.41	0.37	1902	EDG2	NM_001401	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
204070_at	1.19	0.01	0.27	0.31	5920	RARRES3	NM_004585	retinoic acid receptor responder (tazarotene induced) 3
204071_s_at	1.14	0.03	0.25	0.24	10210	TOPORS	NM_005802	topoisomerase I binding, arginine/serine-rich
204081_at	1.30	0.03	0.54	0.43	4900	NRGN	NM_006176	neurogranin (protein kinase C substrate, RC3)
204122_at	1.09	4.68e-03	0.12	0.14	7305	TYROBP	NM_003332	TYRO protein tyrosine kinase binding protein
204162_at	1.20	2.83e-03	0.23	0.37	10403	KNTC2	NM_006101	kinetochore associated 2
204170_s_at	0.87	0.01	0.22	0.22	1164	CKS2	NM_001827	CDC28 protein kinase regulatory subunit 2
204206_at	1.11	0.01	0.18	0.18	4335	MNT	NM_020310	MAX binding protein
204208_at	1.19	0.01	0.30	0.29	8732	RNGTT	NM_003800	RNA guanylyltransferase and 5'-phosphatase
204212_at	1.11	0.02	0.19	0.26	10005	PTE1	NM_005469	peroxisomal acyl-CoA thioesterase
204218_at	1.08	0.04	0.17	0.17	25906	DKFZP564M082	NM_014042	DKFZP564M082 protein
204225_at	1.12	8.58e-03	0.16	0.19	9759	HDAC4	NM_006037	histone deacetylase 4
204232_at	1.10	0.02	0.18	0.21	2207	FCER1G	NM_004106	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
204254_s_at	1.14	0.01	0.21	0.21	7421	VDR	NM_000376	vitamin D (1,25- dihydroxyvitamin D3) receptor
204265_s_at	1.10	4.03e-03	0.14	0.12	63940	GPSM3	NM_022107	G-protein signalling modulator 3 (AGS3-like, C. elegans)
204269_at	1.14	0.04	0.27	0.25	11040	PIM2	NM_006875	pim-2 oncogene

204279_at	1.11	8.76e-03	0.17	0.19	5698	PSMB9	NM_002800	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease
204280_at	1.15	0.02	0.29	0.29	10636	RGS14	NM_006480	regulator of G-protein signalling 14
204307_at	1.13	0.03	0.24	0.34	9895	KIAA0329	AB002295	KIAA0329
204308_s_at	1.12	0.04	0.22	0.25	9895	KIAA0329	NM_014844	KIAA0329
204336_s_at	1.08	0.02	0.14	0.16	10287	RGS19	NM_005873	regulator of G-protein signalling 19
204396_s_at	1.11	0.02	0.18	0.14	2869	GRK5	NM_005308	G protein-coupled receptor kinase 5
204435_at	1.10	0.02	0.19	0.17	9818	NUPL1	AB007870	nucleoporin like 1
204436_at	1.10	0.03	0.19	0.18	80301	pp9099	NM_025201	PH domain-containing protein
204480_s_at	1.09	0.04	0.19	0.12	79095	C9orf16	NM_024112	chromosome 9 open reading frame 16
204510_at	1.08	0.03	0.15	0.17	8317	CDC7	NM_003503	CDC7 cell division cycle 7 (S. cerevisiae)
204513_s_at	0.92	0.04	0.18	0.14	9844	ELMO1	NM_014800	engulfment and cell motility 1 (ced-12 homolog, C. elegans)
204542_at	1.18	0.01	0.26	0.31	10610	ST6GALNAC2	NM_006456	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha
204572_s_at	0.90	0.01	0.20	0.14	5303	PIN4	NM_006223	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
204745_x_at	1.12	9.18e-03	0.16	0.33	4495	MT1G	NM_005950	metallothionein 1G
204762_s_at	0.88	0.02	0.19	0.21	2775	GNAO1	NM_020988	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide
204774_at	1.06	0.04	0.12	0.17	2123	EVI2A	NM_014210	ecotropic viral integration site 2A
204806_x_at	1.08	0.04	0.17	0.14	3134	HLA-F	NM_018950	major histocompatibility complex, class I, F
204809_at	1.10	0.02	0.16	0.21	10845	CLPX	NM_006660	ClpX caseinolytic protease X homolog (E. coli)
204812_at	0.92	0.01	0.12	0.12	9183	ZW10	NM_004724	ZW10 homolog, centromere/kinetochore protein (Drosophila)
204849_at	1.15	0.03	0.27	0.22	10732	TCFL5	NM_006602	transcription factor-like 5 (basic helix-loop-helix)
204882_at	1.09	0.02	0.15	0.19	9938	ARHGAP25	NM_014882	Rho GTPase activating protein 25
204909_at	1.22	7.11e-03	0.29	0.24	1656	DDX6	NM_004397	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
204937_s_at	1.07	0.01	0.12	0.15	10782	ZNF274	NM_016325	zinc finger protein 274
204949_at	1.09	0.01	0.14	0.17	3385	ICAM3	NM_002162	intercellular adhesion molecule 3
204955_at	0.85	0.04	0.27	0.27	8406	SRPX	NM_006307	sushi-repeat-containing protein, X-linked
204959_at	1.08	0.02	0.17	0.13	4332	MNDA	NM_002432	myeloid cell nuclear differentiation antigen
204970_s_at	1.16	0.03	0.29	0.32	4097	MAFG	NM_002359	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)
204982_at	1.12	6.97e-03	0.16	0.23	9815	GIT2	NM_014776	G protein-coupled receptor kinase interactor 2
205037_at	1.17	0.01	0.27	0.24	11020	RABL4	NM_006860	RAB, member of RAS oncogene family-like 4
205077_s_at	1.08	0.01	0.13	0.17	5281	PIGF	NM_002643	phosphatidylinositol glycan, class F
205139_s_at	0.84	2.43e-03	0.24	0.18	10090	UST	NM_005715	uronyl-2-sulfotransferase
205180_s_at	1.09	0.02	0.15	0.18	101	ADAM8	NM_001109	a disintegrin and metalloproteinase domain 8

205197_s_at	1.19	0.02	0.36	0.27	538	ATP7A	NM_000052	ATPase, Cu++ transporting, alpha
polypeptide (Menkes syndrome)								
205198_s_at	1.09	0.02	0.15	0.17	538	ATP7A	NM_000052	ATPase, Cu++ transporting, alpha
polypeptide (Menkes syndrome)								
205202_at	1.10	0.03	0.18	0.19	5110	PCMT1	NM_005389	protein-L-isoaspartate (D-aspartate) O-
methyltransferase								
205230_at	1.25	7.78e-03	0.37	0.30	22895	RPH3A	NM_014954	rabphilin 3A homolog (mouse)
205300_s_at	1.08	0.02	0.13	0.15	11066	U1SNRNPBP	NM_022717	U11/U12 snRNP 35K
205306_x_at	0.88	0.03	0.22	0.25	8564	KMO	NM_003679	kynurenine 3-monooxygenase (kynurenine
3-hydroxylase)								
205323_s_at	1.15	3.61e-03	0.21	0.20	4520	MTF1	NM_005955	metal-regulatory transcription factor 1
205370_x_at	1.09	0.02	0.17	0.13	1629	DBT	NM_001918	dihydrolipoamide branched chain
transacylase E2								
205436_s_at	1.08	0.03	0.15	0.16	3014	H2AFX	NM_002105	H2A histone family, member X
205442_at	1.38	2.74e-03	0.60	0.38	9848	MFAP3L	NM_021647	microfibrillar-associated protein 3-like
205474_at	1.08	1.78e-03	0.08	0.12	51379	CRLF3	NM_015986	cytokine receptor-like factor 3
205510_s_at	1.18	4.16e-03	0.26	0.23	55056	FLJ10038	AK000900	hypothetical protein FLJ10038
205511_at	1.21	0.01	0.32	0.37	55056	FLJ10038	AK000900	hypothetical protein FLJ10038
205545_x_at	1.08	0.02	0.12	0.18	22826	DNAJC8	NM_014280	DnaJ (Hsp40) homolog, subfamily C,
member 8								
205585_at	1.11	0.04	0.22	0.20	2120	ETV6	NM_001987	ets variant gene 6 (TEL oncogene)
205588_s_at	0.87	0.01	0.21	0.20	11116	FGFR1OP	NM_007045	FGFR1 oncogene partner
205607_s_at	1.10	0.01	0.14	0.18	57147	PACE-1	NM_020423	ezrin-binding partner PACE-1
205628_at	1.17	0.03	0.27	0.31	5558	PRIM2A	NM_000947	primase, polypeptide 2A, 58kDa
205690_s_at	1.05	0.02	0.09	0.12	8896	G10	NM_003910	maternal G10 transcript
205740_s_at	1.11	0.03	0.20	0.17	79171	MGC10433	NM_024321	hypothetical protein MGC10433
205773_at	1.13	0.02	0.24	0.37	22849	CPEB3	NM_014912	cytoplasmic polyadenylation element
binding protein 3								
205781_at	1.17	0.02	0.33	0.27	9605	C16orf7	NM_004913	chromosome 16 open reading frame 7
205849_s_at	1.10	0.04	0.20	0.19	7381	UQCRB	NM_006294	ubiquinol-cytochrome c reductase binding
protein								
205887_x_at	1.25	0.01	0.35	0.43	4437	MSH3	NM_002439	mutS homolog 3 (E. coli)
205960_at	0.80	0.01	0.36	0.33	5166	PDK4	NM_002612	pyruvate dehydrogenase kinase, isoenzyme 4
206026_s_at	1.17	0.03	0.33	0.56	7130	TNFAIP6	NM_007115	tumor necrosis factor, alpha-induced
protein 6								
206059_at	0.88	0.02	0.20	0.20	7644	ZNF91	NM_003430	zinc finger protein 91 (HPF7, HTF10)
206074_s_at	1.16	0.04	0.33	0.32	3159	HMGA1	NM_002131	high mobility group AT-hook 1
206082_at	1.11	0.04	0.20	0.22	10866	HCP5	NM_006674	HLA complex P5
206087_x_at	0.86	0.01	0.20	0.28	3077	HFE	NM_000410	hemochromatosis
206129_s_at	0.85	0.02	0.31	0.26	411	ARSB	NM_000046	arylsulfatase B
206138_s_at	1.08	0.02	0.15	0.15	5298	PIK4CB	NM_002651	phosphatidylinositol 4-kinase, catalytic,
beta polypeptide								
206167_s_at	1.34	3.0e-03	0.44	0.33	395	ARHGAP6	NM_001174	Rho GTPase activating protein 6
206194_at	1.14	0.04	0.27	0.25	3221	HOXC4	BC050442	homeo box C4
206284_x_at	1.15	5.1e-03	0.21	0.20	1212	CLTB	NM_001834	clathrin, light polypeptide (Lcb)

206493_at	1.36	0.03	0.61	0.49	3674	ITGA2B	NM_000419	integrin, alpha 2b (platelet glycoprotein IIb
of IIb/IIIa complex, antigen CD41B)								
206565_x_at	0.74	0.01	0.36	0.41	10571	SMA3	NM_006780	SMA3
206574_s_at	1.18	0.01	0.27	0.31	11156	PTP4A3	NM_007079	protein tyrosine phosphatase type IVA,
member 3								
206590_x_at	1.11	0.03	0.23	0.24	1813	DRD2	NM_000795	dopamine receptor D2
206655_s_at	1.43	0.02	0.65	0.59	2812	GP1BB	NM_000407	glycoprotein Ib (platelet), beta polypeptide
206656_s_at	1.10	0.04	0.20	0.25	57136	C20orf3	NM_020531	chromosome 20 open reading frame 3
206687_s_at	1.09	6.23e-03	0.14	0.13	5777	PTPN6	NM_002831	protein tyrosine phosphatase, non-receptor
type 6								
206782_s_at	1.14	0.01	0.23	0.18	3338	DNAJC4	NM_005528	DnaJ (Hsp40) homolog, subfamily C,
member 4								
206789_s_at	1.10	0.01	0.16	0.17	5451	POU2F1	NM_002697	POU domain, class 2, transcription factor 1
206792_x_at	1.09	0.03	0.18	0.11	5143	PDE4C	NM_000923	phosphodiesterase 4C, cAMP-specific
(phosphodiesterase E1 dunce homolog, Drosophila)								
206807_s_at	1.40	5.86e-04	0.35	0.41	119	ADD2	NM_017482	adducin 2 (beta)
206874_s_at	1.09	0.01	0.15	0.15	9748	SLK	AL138761	STE20-like kinase (yeast)
206874_s_at	1.09	0.01	0.15	0.15	1308	COL17A1	AL138761	collagen, type XVII, alpha 1
207071_s_at	0.92	0.03	0.12	0.15	48	ACO1	NM_002197	aconitase 1, soluble
207081_s_at	1.09	0.02	0.15	0.19	5297	PIK4CA	NM_002650	phosphatidylinositol 4-kinase, catalytic,
alpha polypeptide								
207093_s_at	0.87	8.98e-03	0.21	0.19	4974	OMG	NM_002544	oligodendrocyte myelin glycoprotein
207122_x_at	1.17	1.74e-03	0.19	0.31	6799	SULT1A2	NM_001054	sulfotransferase family, cytosolic, 1A,
phenol-preferring, member 2								
207131_x_at	1.11	0.02	0.17	0.22	2678	GGT1	NM_013430	gamma-glutamyltransferase 1
207133_x_at	1.18	0.03	0.32	0.24	80216	ALPK1	NM_025144	alpha-kinase 1
207176_s_at	0.90	0.04	0.23	0.19	941	CD80	NM_005191	CD80 antigen (CD28 antigen ligand 1, B7-1
antigen)								
207198_s_at	1.12	0.04	0.22	0.19	3987	LIMS1	NM_004987	LIM and senescent cell antigen-like
domains 1								
207253_s_at	1.11	0.04	0.21	0.22	29855	UBN1	NM_016936	ubinuclein 1
207332_s_at	1.11	0.01	0.18	0.19	7037	TFRC	NM_003234	transferrin receptor (p90, CD71)
207335_x_at	1.12	0.01	0.18	0.19	521	ATP5I	NM_007100	ATP synthase, H+ transporting,
mitochondrial F0 complex, subunit e								
207428_x_at	1.13	6.14e-03	0.18	0.20	984	CDC2L1	NM_001787	cell division cycle 2-like 1 (PITSLRE
proteins)								
207435_s_at	1.14	0.04	0.28	0.23	23524	SRRM2	NM_016333	serine/arginine repetitive matrix 2
207474_at	1.14	0.02	0.23	0.25	54861	SNRK	NM_017719	SNF-1 related kinase
207490_at	1.09	0.04	0.16	0.21	80086	TUBA4	NM_025019	tubulin, alpha 4
207509_s_at	1.64	0.01	0.68	0.44	3904	LAIR2	NM_002288	leukocyte-associated Ig-like receptor 2
207522_s_at	1.13	0.02	0.22	0.22	489	ATP2A3	NM_005173	ATPase, Ca++ transporting, ubiquitous
207574_s_at	1.10	0.04	0.19	0.23	4616	GADD45B	NM_015675	growth arrest and DNA-damage-
inducible, beta								
207705_s_at	1.19	0.03	0.29	0.30	22981	KIAA0980	NM_025176	KIAA0980 protein
207765_s_at	1.11	0.02	0.18	0.26	80256	KIAA1539	NM_025182	KIAA1539

207805_s_at	1.09	0.01	0.14	0.14	5715	PSMD9	NM_002813	proteasome (prosome, macropain) 26S
subunit, non-ATPase, 9								
207821_s_at	0.91	0.04	0.17	0.18	5747	PTK2	NM_005607	PTK2 protein tyrosine kinase 2
207842_s_at	1.09	0.04	0.17	0.18	22794	CASC3	NM_007359	cancer susceptibility candidate 3
207845_s_at	1.18	0.02	0.26	0.22	10393	ANAPC10	NM_014885	anaphase promoting complex subunit 10
207988_s_at	1.12	1.1e-03	0.15	0.13	10109	ARPC2	NM_005731	actin related protein 2/3 complex, subunit
2, 34kDa								
208002_s_at	1.15	0.02	0.25	0.26	11332	BACH	NM_007274	brain acyl-CoA hydrolase
208021_s_at	1.13	0.01	0.21	0.20	5981	RFC1	NM_002913	replication factor C (activator 1) 1, 145kDa
208030_s_at	1.08	0.04	0.16	0.16	118	ADD1	NM_001119	adducin 1 (alpha)
208052_x_at	1.11	0.01	0.16	0.18	1084	CEACAM3	NM_001815	carcinoembryonic antigen-related cell
adhesion molecule 3								
208091_s_at	1.08	0.01	0.14	0.13	81552	DKFZP564K0822	NM_030796	hypothetical protein
DKFZp564K0822								
208112_x_at	1.08	0.02	0.15	0.15	10938	EHD1	NM_006795	EH-domain containing 1
208284_x_at	1.09	0.04	0.17	0.21	2678	GGT1	NM_013421	gamma-glutamyltransferase 1
208336_s_at	1.12	0.02	0.21	0.19	9524	GPSN2	NM_004868	glycoprotein, synaptic 2
208374_s_at	1.10	2.04e-03	0.12	0.14	829	CAPZA1	NM_006135	capping protein (actin filament) muscle
Z-line, alpha 1								
208549_x_at	1.16	0.03	0.28	0.22	5757	PTMA	NM_002823	prothymosin, alpha (gene sequence 28)
208636_at	1.09	0.01	0.13	0.18	87	ACTN1	AI082078	actinin, alpha 1
208655_at	1.10	8.94e-03	0.15	0.15	10983	CCNI	NM_006835	cyclin I
208659_at	1.08	2.27e-03	0.09	0.12	1192	CLIC1	NM_001288	chloride intracellular channel 1
208673_s_at	1.11	0.02	0.19	0.18	6428	SFRS3	NM_003017	splicing factor, arginine/serine-rich 3
208709_s_at	1.10	0.02	0.17	0.20	4898	NRD1	NM_002525	nardilysin (N-arginine dibasic convertase)
208728_s_at	1.12	7.39e-03	0.17	0.15	998	CDC42	NM_001791	cell division cycle 42 (GTP binding
protein, 25kDa)								
208732_at	1.08	0.02	0.13	0.14	5862	RAB2	AI743756	RAB2, member RAS oncogene family
208736_at	1.09	2.31e-03	0.10	0.13	10094	ARPC3	NM_005719	actin related protein 2/3 complex, subunit
3, 21kDa								
208737_at	1.11	1.35e-03	0.12	0.15	9550	ATP6V1G1	NM_004888	ATPase, H+ transporting, lysosomal
13kDa, V1 subunit G isoform 1								
208739_x_at	1.09	0.01	0.14	0.12	6613	SUMO2	NM_006937	SMT3 suppressor of mif two 3 homolog 2
(yeast)								
208743_s_at	1.07	0.04	0.14	0.13	7529	YWHAB	NM_003404	tyrosine 3-monooxygenase/tryptophan 5-
monooxygenase activation protein, beta polypept								
208749_x_at	1.11	0.02	0.19	0.21	10211	FLOT1	NM_005803	flotillin 1
208788_at	1.10	9.58e-04	0.09	0.15	60481	ELOVL5	NM_021814	ELOVL family member 5, elongation of
long chain fatty acids (FEN1/Elo2, SUR4/Elo3-lik								
208792_s_at	1.35	0.04	0.67	0.48	1191	CLU	NM_001831	clusterin (complement lysis inhibitor, SP-
40,40, sulfated glycoprotein 2, testosteron								
208806_at	1.13	0.03	0.26	0.29	1107	CHD3	AK096555	chromodomain helicase DNA binding protein
3								
208809_s_at	1.11	3.17e-03	0.12	0.17	81688	C6orf62	NM_030939	chromosome 6 open reading frame 62

208810_at	1.09	0.03	0.17	0.15	10049	DNAJB6	NM_005494	DnaJ (Hsp40) homolog, subfamily B, member 6
208827_at	1.11	0.01	0.18	0.16	5694	PSMB6	NM_002798	proteasome (prosome, macropain) subunit, beta type, 6
208830_s_at	1.12	2.15e-03	0.14	0.16	6830	SUPT6H	NM_003170	suppressor of Ty 6 homolog (S. cerevisiae)
208841_s_at	1.10	0.01	0.15	0.18	9908	G3BP2	NM_203505	Ras-GTPase activating protein SH3 domain-binding protein 2
208865_at	1.06	0.03	0.12	0.13	1452	CSNK1A1	AF447582	casein kinase 1, alpha 1
208869_s_at	1.12	0.02	0.20	0.22	23710	GABARAPL1	NM_031412	GABA(A) receptor-associated protein like 1
208924_at	1.11	0.01	0.19	0.17	26994	RNF11	NM_014372	ring finger protein 11
208942_s_at	1.13	5.97e-03	0.18	0.21	7095	TLOC1	NM_003262	translocation protein 1
208965_s_at	1.08	0.04	0.16	0.33	3428	IFI16	NM_005531	interferon, gamma-inducible protein 16
208967_s_at	0.91	0.03	0.17	0.14	204	AK2	NM_001625	adenylate kinase 2
208979_at	1.08	0.01	0.13	0.13	23054	NCOA6	NM_014071	nuclear receptor coactivator 6
208988_at	1.12	4.37e-03	0.15	0.19	22992	FBXL11	NM_012308	F-box and leucine-rich repeat protein 11
208995_s_at	1.14	0.03	0.23	0.26	9360	PPIG	NM_004792	peptidyl-prolyl isomerase G (cyclophilin G)
208998_at	1.11	0.01	0.19	0.17	7351	UCP2	NM_003355	uncoupling protein 2 (mitochondrial, proton carrier)
209004_s_at	1.06	0.01	0.09	0.13	26234	FBXL5	NM_012161	F-box and leucine-rich repeat protein 5
209023_s_at	1.20	4.42e-03	0.31	0.23	10735	STAG2	NM_006603	stromal antigen 2
209039_x_at	1.08	0.01	0.13	0.14	10938	EHD1	NM_006795	EH-domain containing 1
209046_s_at	1.06	0.02	0.09	0.16	11345	GABARAPL2	NM_007285	GABA(A) receptor-associated protein-like 2
209061_at	1.07	0.02	0.13	0.16	8202	NCOA3	NM_181659	nuclear receptor coactivator 3
209081_s_at	1.41	8.37e-04	0.40	0.54	80781	COL18A1	NM_030582	collagen, type XVIII, alpha 1
209082_s_at	1.26	4.49e-03	0.36	0.31	80781	COL18A1	NM_030582	collagen, type XVIII, alpha 1
209089_at	1.07	0.02	0.12	0.16	5868	RAB5A	NM_004162	RAB5A, member RAS oncogene family
209102_s_at	1.07	0.03	0.12	0.15	26959	HBP1	NM_012257	HMG-box transcription factor 1
209112_at	1.11	1.21e-03	0.11	0.15	1027	CDKN1B	NM_004064	cyclin-dependent kinase inhibitor 1B (p27, Kip1)
209117_at	1.12	0.03	0.22	0.26	23558	WBP2	NM_012478	WW domain binding protein 2
209130_at	1.06	0.03	0.10	0.14	8773	SNAP23	NM_003825	synaptosomal-associated protein, 23kDa
209187_at	1.10	0.01	0.17	0.17	1810	DR1	NM_001938	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
209193_at	1.09	0.04	0.17	0.16	5292	PIM1	M24779	pim-1 oncogene
209202_s_at	1.15	0.01	0.24	0.25	2137	EXTL3	NM_001440	exostoses (multiple)-like 3
209217_s_at	1.09	7.89e-03	0.13	0.13	11152	WDR45	NM_007075	WD repeat domain 45
209232_s_at	1.20	4.44e-03	0.24	0.20	84516	MGC3248	NM_032486	dynactin 4
209240_at	1.07	0.03	0.13	0.19	8473	OGT	NM_003605	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptid
209258_s_at	1.18	5.24e-03	0.22	0.31	9126	CSPG6	NM_005445	chondroitin sulfate proteoglycan 6 (bamacan)

209275_s_at	1.12	0.03	0.22	0.27	1201	CLN3	NM_000086	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)
209282_at	1.13	0.01	0.20	0.21	25865	PRKD2	NM_016457	protein kinase D2
209296_at	1.07	0.01	0.10	0.16	5495	PPM1B	NM_177968	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform
209308_s_at	1.12	2.55e-03	0.14	0.17	663	BNIP2	NM_004330	BCL2/adenovirus E1B 19kDa interacting protein 2
209326_at	1.09	6.97e-03	0.14	0.14	7355	SLC35A2	D84454	solute carrier family 35 (UDP-galactose transporter), member A2
209332_s_at	1.10	1.33e-03	0.12	0.12	4149	MAX	NM_002382	MYC associated factor X
209348_s_at	1.17	0.04	0.35	0.31	4094	MAF	AF055376	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
209354_at	1.08	0.01	0.14	0.13	8764	TNFRSF14	NM_003820	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)
209412_at	1.11	0.01	0.18	0.20	7109	TMEM1	NM_003274	transmembrane protein 1
209418_s_at	1.09	0.04	0.17	0.19	8563	C22orf19	NM_001002878	chromosome 22 open reading frame 19
209436_at	0.85	0.02	0.30	0.27	10418	SPON1	NM_006108	spondin 1, extracellular matrix protein
209439_s_at	1.08	0.04	0.15	0.20	5256	PHKA2	NM_000292	phosphorylase kinase, alpha 2 (liver)
209451_at	1.09	0.04	0.17	0.19	10010	TANK	NM_004180	TRAF family member-associated NFKB activator
209463_s_at	1.12	6.78e-03	0.16	0.20	6883	TAF12	NM_005644	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa
209472_at	1.08	0.01	0.12	0.15	56267	KAT3	BC000819	kynurenine aminotransferase III
209477_at	1.21	7.27e-03	0.26	0.26	2010	EMD	NM_000117	emerin (Emery-Dreifuss muscular dystrophy)
209481_at	1.08	0.01	0.12	0.17	54861	SNRK	NM_017719	SNF-1 related kinase
209492_x_at	1.11	0.02	0.19	0.17	521	ATP5I	NM_007100	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e
209515_s_at	1.11	8.37e-03	0.17	0.18	5873	RAB27A	NM_004580	RAB27A, member RAS oncogene family
209563_x_at	1.07	0.04	0.16	0.14	801	CALM1	BC000454	calmodulin 1 (phosphorylase kinase, delta)
209569_x_at	0.78	9.09e-03	0.51	0.40	27065	D4S234E	NM_014392	DNA segment on chromosome 4 (unique) 234 expressed sequence
209586_s_at	1.14	2.84e-03	0.19	0.19	58497	PRUNE	NM_021222	prune homolog (Drosophila)
209606_at	1.08	0.02	0.14	0.12	9595	PSCDBP	NM_004288	pleckstrin homology, Sec7 and coiled-coil domains, binding protein
209607_x_at	1.09	0.04	0.19	0.25	6818	SULT1A3	NM_003166	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3
209636_at	1.18	0.03	0.30	0.31	4791	NFKB2	NM_002502	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
209675_s_at	1.20	0.02	0.33	0.26	11100	HNRPUL1	NM_007040	heterogeneous nuclear ribonucleoprotein U-like 1
209694_at	1.08	0.03	0.17	0.16	5805	PTS	NM_000317	6-pyruvoyltetrahydropterin synthase
209695_at	1.18	5.71e-03	0.25	0.21	11156	PTP4A3	NM_032611	protein tyrosine phosphatase type IVA, member 3

209748_at	1.13	9.39e-03	0.19	0.25	6683	SPG4	NM_014946	spastic paraplegia 4 (autosomal dominant; spastin)
209751_s_at	1.13	0.03	0.24	0.22	6399	TRAPPC2	NM_014563	trafficking protein particle complex 2
209787_s_at	1.10	0.01	0.16	0.15	10473	HMGN4	NM_006353	high mobility group nucleosomal binding domain 4
209795_at	1.26	0.01	0.35	0.27	969	CD69	NM_001781	CD69 antigen (p60, early T-cell activation antigen)
209798_at	1.09	0.03	0.17	0.20	4863	NPAT	NM_002519	nuclear protein, ataxia-telangiectasia locus
209823_x_at	1.23	0.01	0.37	0.49	3119	HLA-DQB1	NM_002123	major histocompatibility complex, class II, DQ beta 1
209860_s_at	1.08	0.03	0.15	0.16	310	ANXA7	NM_001156	annexin A7
209870_s_at	1.13	0.02	0.22	0.35	321	APBA2	NM_005503	amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)
209879_at	1.07	0.01	0.12	0.12	6404	SELPLG	NM_003006	selectin P ligand
209898_x_at	1.10	0.01	0.13	0.19	50618	ITSN2	U61167	intersectin 2
209947_at	1.11	0.01	0.16	0.19	9898	UBAP2L	NM_014847	ubiquitin associated protein 2-like
209967_s_at	1.23	0.02	0.38	0.41	1390	CREM	NM_181571	cAMP responsive element modulator
209969_s_at	1.24	0.04	0.39	0.40	6772	STAT1	NM_139266	signal transducer and activator of transcription 1, 91kDa
209989_at	1.14	5.64e-03	0.18	0.23	10795	ZNF268	NM_003415	zinc finger protein 268
210069_at	1.25	4.77e-03	0.30	0.33	1375	CPT1B	NM_152247	carnitine palmitoyltransferase 1B (muscle)
210075_at	1.22	0.02	0.37	0.31	51257	MARCH2	AF151074	membrane-associated ring finger (C3HC4) 2
210113_s_at	1.12	0.04	0.20	0.24	22861	NALP1	NM_033004	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1
210117_at	1.15	0.04	0.30	0.36	6674	SPAG1	NM_003114	sperm associated antigen 1
210218_s_at	1.14	0.03	0.33	0.61	6672	SP100	NM_003113	nuclear antigen Sp100
210241_s_at	1.19	1.35e-03	0.20	0.22	11257	TP53AP1	NM_007233	TP53 activated protein 1
210243_s_at	1.09	0.02	0.15	0.18	8703	B4GALT3	NM_003779	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3
210247_at	0.84	3.58e-03	0.26	0.21	6854	SYN2	NM_133625	synapsin II
210277_at	1.21	7.56e-03	0.28	0.26	11154	AP4S1	AF155159	adaptor-related protein complex 4, sigma 1 subunit
210346_s_at	1.11	0.01	0.16	0.22	57396	CLK4	NM_020666	CDC-like kinase 4
210361_s_at	1.11	0.04	0.21	0.24	1998	ELF2	NM_201999	E74-like factor 2 (ets domain transcription factor)
210527_x_at	1.14	4.96e-03	0.18	0.19	7278	TUBA2	NM_006001	tubulin, alpha 2
210529_s_at	1.18	0.01	0.24	0.32	9747	KIAA0738	NM_014719	KIAA0738 gene product
210532_s_at	1.10	0.02	0.17	0.17	9556	C14orf2	NM_004894	chromosome 14 open reading frame 2
210580_x_at	1.09	0.04	0.17	0.21	6818	SULT1A3	NM_003166	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3
210635_s_at	0.91	0.01	0.15	0.13	27252	KLHL20	NM_014458	kelch-like 20 (Drosophila)
210685_s_at	1.07	0.04	0.13	0.20	10277	UBE4B	NM_006048	ubiquitination factor E4B (UFD2 homolog, yeast)
210752_s_at	1.13	0.01	0.20	0.23	6945	MLX	NM_198205	MAX-like protein X

210755_at	0.80	0.01	0.25	0.31	3082	HGF	U46010	hepatocyte growth factor (hepapoietin A; scatter factor)
210789_x_at	1.09	0.02	0.16	0.23	1084	CEACAM3	NM_001815	carcinoembryonic antigen-related cell adhesion molecule 3
210818_s_at	0.84	0.02	0.46	0.30	571	BACH1	NM_206866	BTB and CNC homology 1, basic leucine zipper transcription factor 1
210908_s_at	1.08	0.04	0.15	0.13	5204	PFDN5	NM_002624	prefoldin 5
210926_at	1.14	0.04	0.34	0.18	440915	LOC440915	AY014272	similar to FKSG30
210943_s_at	1.17	0.01	0.26	0.24	1130	LYST	NM_000081	lysosomal trafficking regulator
210981_s_at	1.09	0.02	0.17	0.16	2870	GRK6	NM_001004106	G protein-coupled receptor kinase 6
211025_x_at	1.09	0.02	0.16	0.15	1329	COX5B	NM_001862	cytochrome c oxidase subunit Vb
211069_s_at	1.09	3.68e-03	0.11	0.12	7341	SUMO1	NM_003352	SMT3 suppressor of mif two 3 homolog 1 (yeast)
211072_x_at	1.07	0.01	0.11	0.12	10376	K-ALPHA-1	NM_006082	tubulin, alpha, ubiquitous
211074_at	1.25	2.61e-03	0.29	0.30	2348	FOLR1	AF000381	folate receptor 1 (adult)
211105_s_at	1.16	1.29e-03	0.17	0.19	4772	NFATC1	NM_006162	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
211121_s_at	1.08	0.04	0.15	0.19	1796	DOK1	NM_001381	docking protein 1, 62kDa (downstream of tyrosine kinase 1)
211152_s_at	1.09	0.02	0.17	0.19	27429	PRSS25	NM_013247	protease, serine, 25
211160_x_at	1.10	0.04	0.17	0.30	87	ACTN1	NM_001102	actinin, alpha 1
211185_s_at	1.06	0.02	0.10	0.11	23451	SF3B1	NM_012433	splicing factor 3b, subunit 1, 155kDa
211257_x_at	1.10	0.02	0.19	0.17	27332	ZNF638	NM_014497	zinc finger protein 638
211289_x_at	1.17	7.05e-03	0.22	0.23	984	CDC2L1	NM_001787	cell division cycle 2-like 1 (PITSLRE proteins)
211325_x_at	1.11	0.03	0.21	0.28	171220	LOC171220	U72518	destrin-2 pseudogene
211337_s_at	0.90	7.02e-03	0.16	0.13	27229	76P	NM_014444	gamma tubulin ring complex protein (76p gene)
211385_x_at	1.14	7.75e-03	0.18	0.29	6799	SULT1A2	NM_001054	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2
211429_s_at	1.08	0.01	0.13	0.13	5265	SERPINA1	NM_000295	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitryps
211458_s_at	1.13	0.01	0.21	0.22	23710	GABARAPL1	NM_031412	GABA(A) receptor-associated protein like 1
211504_x_at	0.85	5.45e-03	0.27	0.18	9475	ROCK2	NM_004850	Rho-associated, coiled-coil containing protein kinase 2
211543_s_at	1.12	5.65e-03	0.15	0.20	2870	GRK6	NM_001004106	G protein-coupled receptor kinase 6
211546_x_at	1.12	0.02	0.20	0.22	6622	SNCA	NM_000345	synuclein, alpha (non A4 component of amyloid precursor)
211609_x_at	1.08	0.04	0.15	0.17	5710	PSMD4	NM_002810	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
211628_x_at	1.09	0.02	0.18	0.12	2509	FTHP1	J04755	ferritin, heavy polypeptide pseudogene 1
211656_x_at	1.29	0.01	0.46	0.42	3119	HLA-DQB1	NM_002123	major histocompatibility complex, class II, DQ beta 1
211678_s_at	1.05	0.03	0.10	0.13	55905	ZNF313	NM_018683	zinc finger protein 313

211725_s_at	1.08	0.01	0.13	0.16	637	BID	NM_197966	BH3 interacting domain death agonist
211759_x_at	1.07	0.04	0.16	0.14	1155	CKAP1	NM_001281	cytoskeleton associated protein 1
211768_at	1.16	0.01	0.23	0.26	7462	WBSCR5	BC006080	Williams-Beuren syndrome chromosome region 5
211795_s_at	1.07	0.02	0.13	0.14	2533	FYB	NM_199335	FYN binding protein (FYB-120/130)
211795_s_at	1.07	0.02	0.13	0.14	2533	FYB	NM_001465	FYN binding protein (FYB-120/130)
211822_s_at	1.12	0.02	0.21	0.25	22861	NALP1	NM_033004	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1
211824_x_at	1.15	0.02	0.24	0.27	22861	NALP1	NM_033004	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1
211913_s_at	0.85	0.03	0.33	0.28	10461	MERTK	NM_006343	c-mer proto-oncogene tyrosine kinase
211916_s_at	1.10	0.03	0.17	0.20	4640	MYO1A	NM_005379	myosin IA
211924_s_at	1.12	0.02	0.20	0.36	5329	PLAUR	NM_002659	plasminogen activator, urokinase receptor
211950_at	1.10	6.92e-03	0.13	0.17	23352	RBAF600	AB007931	retinoblastoma-associated factor 600
211962_s_at	1.07	0.03	0.14	0.14	677	ZFP36L1	NM_004926	zinc finger protein 36, C3H type-like 1
211965_at	1.32	0.01	0.52	0.58	677	ZFP36L1	NM_004926	zinc finger protein 36, C3H type-like 1
211977_at	1.10	0.01	0.13	0.21	57720	GPR107	AB046844	G protein-coupled receptor 107
211983_x_at	1.10	0.01	0.20	0.09	71	ACTG1	NM_001614	actin, gamma 1
212006_at	1.17	0.02	0.31	0.21	23190	UBXD2	NM_014607	UBX domain containing 2
212025_s_at	1.12	0.01	0.19	0.21	2314	FLII	NM_002018	flightless I homolog (Drosophila)
212027_at	1.15	0.04	0.35	0.22	58517	RBM25	AL832314	RNA binding motif protein 25
212030_at	1.10	0.03	0.19	0.21	58517	RBM25	AL833497	RNA binding motif protein 25
212042_x_at	1.08	0.03	0.16	0.12	6129	RPL7	NM_000971	ribosomal protein L7
212043_at	1.06	0.01	0.09	0.09	10618	TGOLN2	NM_006464	trans-golgi network protein 2
212045_at	1.18	0.01	0.29	0.18	2734	GLG1	AK172806	golgi apparatus protein 1
212048_s_at	1.11	0.04	0.21	0.22	8565	YARS	NM_003680	tyrosyl-tRNA synthetase
212064_x_at	1.14	0.02	0.26	0.21	4150	MAZ	BC041629	MYC-associated zinc finger protein (purine-binding transcription factor)
212082_s_at	1.10	1.57e-03	0.12	0.12	4637	MYL6	NM_021019	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
212108_at	1.08	0.04	0.15	0.16	23197	ETEA	NM_014613	expressed in T-cells and eosinophils in atopic dermatitis
212132_at	1.10	0.04	0.20	0.17	26065	C19orf13	NM_015578	chromosome 19 open reading frame 13
212156_at	1.12	0.03	0.23	0.27	23339	VPS39	NM_015289	vacuolar protein sorting 39 (yeast)
212207_at	1.12	0.03	0.22	0.29	23389	THRAP2	NM_015335	thyroid hormone receptor associated protein 2
212209_at	1.14	8.74e-03	0.19	0.23	23389	THRAP2	NM_015335	thyroid hormone receptor associated protein 2
212242_at	1.17	5.34e-04	0.19	0.19	7277	TUBA1	NM_006000	tubulin, alpha 1 (testis specific)
212255_s_at	1.09	0.01	0.13	0.14	27032	ATP2C1	NM_014382	ATPase, Ca++ transporting, type 2C, member 1
212287_at	1.08	0.01	0.12	0.17	23512	SUZ12	NM_015355	suppressor of zeste 12 homolog (Drosophila)
212293_at	1.16	5.4e-03	0.20	0.28	204851	HIPK1	NM_198268	homeodomain interacting protein kinase 1
212301_at	1.10	7.41e-03	0.13	0.18	23168	KIAA0252	NM_015138	KIAA0252
212331_at	1.10	0.02	0.17	0.17	5934	RBL2	NM_005611	retinoblastoma-like 2 (p130)

212356_at	1.11	0.04	0.24	0.19	23351	KIAA0323	NM_015299	KIAA0323
212377_s_at	1.14	2.55e-04	0.12	0.19	4853	NOTCH2	NM_024408	Notch homolog 2 (Drosophila)
212415_at	1.13	0.01	0.21	0.23	23157	SEPT6	NM_145799	septin 6
212430_at	1.13	0.01	0.21	0.13	55544	RNPC1	NM_017495	RNA-binding region (RNP1, RRM)
containing 1								
212450_at	1.12	0.01	0.19	0.21	9728	KIAA0256	NM_014701	KIAA0256 gene product
212493_s_at	1.07	0.03	0.13	0.16	29072	HYPB	NM_014159	huntingtin interacting protein B
212499_s_at	1.16	0.04	0.28	0.25	51077	C14orf111	NM_015962	chromosome 14 open reading frame 111
212521_s_at	0.90	5.49e-03	0.15	0.10	5151	PDE8A	NM_002605	phosphodiesterase 8A
212530_at	1.11	5.3e-03	0.14	0.19	140609	NEK7	AL080111	NIMA (never in mitosis gene a)-related
kinase 7								
212536_at	1.10	0.01	0.15	0.21	23200	ATP11B	AB023173	ATPase, Class VI, type 11B
212544_at	1.10	0.01	0.15	0.15	9326	TRIP3	NM_004773	thyroid hormone receptor interactor 3
212547_at	1.08	0.02	0.15	0.17	266655	FLJ35348	N34842	FLJ35348
212549_at	1.12	0.01	0.17	0.22	6777	STAT5B	NM_012448	signal transducer and activator of
transcription 5B								
212553_at	1.22	0.01	0.32	0.33	23248	KIAA0460	NM_015203	KIAA0460 protein
212576_at	1.14	0.02	0.24	0.25	23295	MGRN1	NM_015246	mahogunin, ring finger 1
212580_at	0.89	9.55e-03	0.17	0.16	831	CAST	NM_173060	calpastatin
212588_at	1.09	8.94e-03	0.16	0.11	5788	PTPRC	NM_002838	protein tyrosine phosphatase, receptor
type, C								
212601_at	1.10	0.03	0.18	0.17	23140	ZZEF1	NM_015113	zinc finger, ZZ type with EF hand domain 1
212625_at	1.08	0.03	0.14	0.20	8677	STX10	NM_003765	syntaxin 10
212628_at	1.09	0.03	0.17	0.24	5586	PKN2	BG292065	protein kinase N2
212639_x_at	1.08	0.02	0.13	0.13	7846	TUBA3	NM_006009	tubulin, alpha 3
212643_at	1.09	0.01	0.15	0.16	93487	C14orf32	NM_144578	chromosome 14 open reading frame 32
212680_x_at	1.11	0.03	0.20	0.19	26472	PPP1R14B	XM_370630	protein phosphatase 1, regulatory
(inhibitor) subunit 14B								
212702_s_at	1.09	0.04	0.18	0.21	23299	BICD2	NM_001003800	bicaudal D homolog 2 (Drosophila)
212714_at	0.87	3.1e-03	0.18	0.17	113251	LOC113251	NM_052879	c-Mpl binding protein
212717_at	1.07	0.03	0.12	0.17	9842	PLEKHM1	NM_014798	pleckstrin homology domain containing,
family M (with RUN domain) member 1								
212744_at	1.14	0.02	0.24	0.20	585	BBS4	NM_033028	Bardet-Biedl syndrome 4
212771_at	0.92	0.03	0.15	0.16	221061	C10orf38	AL050367	chromosome 10 open reading frame 38
212779_at	1.10	0.03	0.17	0.21	84162	KIAA1109	AB029032	KIAA1109
212781_at	1.16	9.92e-03	0.21	0.27	5930	RBBP6	NM_006910	retinoblastoma binding protein 6
212795_at	1.08	0.01	0.10	0.17	23325	KIAA1033	NM_015275	KIAA1033 protein
212813_at	1.24	7.28e-03	0.39	0.34	83700	JAM3	NM_032801	junctional adhesion molecule 3
212814_at	1.10	0.04	0.20	0.19	23382	KIAA0828	NM_015328	KIAA0828 protein
212857_x_at	1.05	0.04	0.11	0.10	10923	PC4	NM_006713	activated RNA polymerase II transcription
cofactor 4								
212876_at	1.19	0.03	0.25	0.28	8702	B4GALT4	NM_212543	UDP-Gal:betaGlcNAc beta 1,4-
galactosyltransferase, polypeptide 4								
212888_at	1.09	0.01	0.15	0.18	23405	DICER1	NM_177438	Dicer1, Dcr-1 homolog (Drosophila)

212919_at	1.09	0.02	0.18	0.19	167227	DCP2	NM_152624	DCP2 decapping enzyme homolog (S. cerevisiae)
212947_at	1.14	8.14e-03	0.19	0.22	23315	SLC9A8	NM_015266	solute carrier family 9 (sodium/hydrogen exchanger), isoform 8
212955_s_at	1.17	5.53e-03	0.22	0.27	5438	POLR2I	NM_006233	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa
212971_at	1.07	0.02	0.11	0.12	833	CARS	NM_139273	cysteinyl-tRNA synthetase
212979_s_at	1.20	0.03	0.36	0.37	9747	KIAA0738	AW293343	KIAA0738 gene product
212988_x_at	1.09	0.02	0.19	0.09	71	ACTG1	NM_001614	actin, gamma 1
212989_at	1.18	7.32e-03	0.23	0.28	259230	TMEM23	NM_147156	transmembrane protein 23
213000_at	1.12	6.92e-03	0.16	0.20	23515	ZCWCC3	NM_015358	zinc finger, CW type with coiled-coil domain 3
213021_at	1.08	0.03	0.15	0.18	9527	GOSR1	BC040072	golgi SNAP receptor complex member 1
213037_x_at	1.04	0.04	0.09	0.10	6780	STAU	AJ132258	staufen, RNA binding protein (Drosophila)
213038_at	1.11	0.02	0.19	0.26	127544	IBRDC3	NM_153341	IBR domain containing 3
213074_at	1.13	0.01	0.18	0.26	55023	PHIP	BG545769	pleckstrin homology domain interacting protein
213080_x_at	1.09	0.03	0.19	0.16	6125	RPL5	NM_000969	ribosomal protein L5
213101_s_at	1.08	8.84e-03	0.14	0.10	10096	ACTR3	NM_005721	ARP3 actin-related protein 3 homolog (yeast)
213102_at	1.08	3.57e-03	0.09	0.12	10096	ACTR3	NM_005721	ARP3 actin-related protein 3 homolog (yeast)
213119_at	1.12	0.04	0.24	0.24	206358	SLC36A1	NM_078483	solute carrier family 36 (proton/amino acid symporter), member 1
213151_s_at	1.06	0.01	0.10	0.12	989	SEPT7	NM_001788	septin 7
213153_at	1.11	0.01	0.18	0.20	23067	KIAA1076	AB028999	KIAA1076 protein
213168_at	1.14	3.7e-03	0.18	0.22	6670	SP3	NM_003111	Sp3 transcription factor
213214_x_at	1.07	0.02	0.15	0.09	71	ACTG1	NM_001614	actin, gamma 1
213227_at	1.13	0.04	0.24	0.26	10424	PGRMC2	AK094949	progesterone receptor membrane component 2
213267_at	1.13	0.03	0.21	0.26	23033	KIAA1117	AL162056	KIAA1117
213279_at	1.09	0.02	0.14	0.20	115817	DHRS1	NM_138452	dehydrogenase/reductase (SDR family) member 1
213311_s_at	1.21	1.99e-03	0.27	0.23	22980	KIAA1049	NM_014972	KIAA1049 protein
213360_s_at	1.09	0.02	0.15	0.15	9883	POM121	NM_172020	POM121 membrane glycoprotein (rat)
213390_at	1.09	0.01	0.13	0.19	23211	C19orf7	AB028987	chromosome 19 open reading frame 7
213475_s_at	1.13	0.04	0.23	0.18	3683	ITGAL	NM_002209	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; al
213490_s_at	1.14	0.03	0.27	0.20	5605	MAP2K2	NM_030662	mitogen-activated protein kinase kinase 2
213513_x_at	1.09	1.16e-03	0.11	0.11	10109	ARPC2	NM_152862	actin related protein 2/3 complex, subunit 2, 34kDa
213514_s_at	1.17	3.55e-03	0.20	0.28	1729	DIAPH1	NM_005219	diaphanous homolog 1 (Drosophila)
213526_s_at	1.12	0.01	0.19	0.19	55957	F25965	NM_019104	protein F25965
213527_s_at	1.11	7.96e-03	0.16	0.16	146542	LOC146542	NM_145271	similar to hypothetical protein MGC13138

213540_at	1.13	0.03	0.23	0.30	7923	HSD17B8	NM_014234	hydroxysteroid (17-beta) dehydrogenase 8
213594_x_at	0.90	4.26e-03	0.14	0.12	10772	FUSIP1	NM_054016	FUS interacting protein (serine-arginine rich) 1
213603_s_at	1.07	0.01	0.12	0.10	5880	RAC2	NM_002872	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac
213669_at	1.08	0.04	0.18	0.17	23149	FCHO1	NM_015122	FCH domain only 1
213682_at	1.11	6.88e-03	0.14	0.18	10762	NUP50	BC039468	nucleoporin 50kDa
213688_at	1.20	3.98e-04	0.18	0.23	801	CALM1	NM_006888	calmodulin 1 (phosphorylase kinase, delta)
213735_s_at	1.08	0.01	0.13	0.14	1329	COX5B	NM_001862	cytochrome c oxidase subunit Vb
213743_at	1.10	0.03	0.19	0.19	905	CCNT2	NM_001241	cyclin T2
213786_at	1.14	0.03	0.26	0.21	8887	TAX1BP1	NM_006024	Tax1 (human T-cell leukemia virus type I) binding protein 1
213795_s_at	1.09	0.04	0.18	0.14	5786	PTPRA	NM_002836	protein tyrosine phosphatase, receptor type, A
213798_s_at	1.09	0.01	0.14	0.12	10487	CAP1	NM_006367	CAP, adenylate cyclase-associated protein 1 (yeast)
213850_s_at	1.08	0.03	0.16	0.14	9169	SFRS2IP	NM_004719	splicing factor, arginine/serine-rich 2, interacting protein
213857_s_at	1.07	0.03	0.12	0.17	961	CD47	NM_001777	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)
213881_x_at	1.10	1.97e-03	0.12	0.11	6613	SUMO2	NM_006937	SMT3 suppressor of mif two 3 homolog 2 (yeast)
213883_s_at	1.18	2.44e-03	0.20	0.21	83941	BBP	NM_032027	beta-amyloid binding protein precursor
213885_at	1.09	3.7e-03	0.11	0.13	10612	TRIM3	NM_006458	tripartite motif-containing 3
213911_s_at	1.06	0.01	0.09	0.13	3015	H2AFZ	NM_002106	H2A histone family, member Z
213916_at	1.12	0.01	0.18	0.21	7568	ZNF20	NM_021143	zinc finger protein 20 (KOX 13)
213923_at	1.07	0.04	0.14	0.14	5912	RAP2B	NM_002886	RAP2B, member of RAS oncogene family
213940_s_at	1.11	0.02	0.18	0.17	23048	FNBP1	NM_015033	formin binding protein 1
213941_x_at	1.07	0.04	0.15	0.13	6201	RPS7	NM_001011	ribosomal protein S7
213971_s_at	1.17	0.02	0.26	0.22	23512	SUZ12	NM_015355	suppressor of zeste 12 homolog (Drosophila)
214047_s_at	1.08	0.01	0.13	0.15	8930	MBD4	NM_003925	methyl-CpG binding domain protein 4
214083_at	1.14	7.24e-03	0.19	0.21	5527	PPP2R5C	AW772123	protein phosphatase 2, regulatory subunit B (B56), gamma isoform
214112_s_at	1.07	0.03	0.14	0.15	91966	CXorf40	NM_178124	chromosome X open reading frame 40
214157_at	0.87	2.75e-03	0.19	0.17	2778	GNAS	AJ224867	GNAS complex locus
214173_x_at	1.19	0.01	0.28	0.29	8725	C19orf2	NM_003796	chromosome 19 open reading frame 2
214198_s_at	1.12	3.0e-03	0.14	0.18	9993	DGCR2	NM_005137	DiGeorge syndrome critical region gene 2
214220_s_at	1.12	0.04	0.22	0.18	7840	ALMS1	NM_015120	Alstrom syndrome 1
214246_x_at	1.14	0.02	0.25	0.26	50488	MINK1	NM_015716	misshapen-like kinase 1 (zebrafish)
214264_s_at	0.86	0.02	0.22	0.26	90141	C14orf143	NM_145231	chromosome 14 open reading frame 143
214273_x_at	1.12	0.02	0.19	0.23	8131	C16orf35	NM_012075	chromosome 16 open reading frame 35
214334_x_at	1.08	8.92e-03	0.12	0.13	9802	DAZAP2	NM_014764	DAZ associated protein 2
214377_s_at	1.12	0.01	0.16	0.21	1506	CTRL	NM_001907	chymotrypsin-like
214441_at	0.87	4.01e-03	0.18	0.18	10228	STX6	NM_005819	syntaxin 6

214512_s_at	1.07	0.03	0.14	0.13	10923	PC4	NM_006713	activated RNA polymerase II transcription cofactor 4
214687_x_at	1.10	2.38e-03	0.12	0.12	226	ALDOA	NM_000034	aldolase A, fructose-bisphosphate
214722_at	1.17	0.04	0.36	0.22	388677	NOTCH2NL	AK022008	Notch homolog 2 (Drosophila) N-terminal like
214723_x_at	1.60	5.85e-04	0.49	0.42	57730	KIAA1641	AB046861	KIAA1641
214772_at	0.81	0.02	0.35	0.32	25758	G2	XM_039515	G2 protein
214844_s_at	0.84	0.02	0.34	0.32	55816	DOK5	NM_018431	docking protein 5
214847_s_at	1.21	0.01	0.32	0.31	63940	GPSM3	NM_022107	G-protein signalling modulator 3 (AGS3-like, C. elegans)
214881_s_at	1.16	6.16e-03	0.23	0.21	7343	UBTF	NM_014233	upstream binding transcription factor, RNA polymerase I
214965_at	1.17	7.51e-03	0.23	0.18	124044	MGC26885	NM_152339	hypothetical protein MGC26885
215001_s_at	1.09	4.25e-03	0.13	0.14	2752	GLUL	NM_002065	glutamate-ammonia ligase (glutamine synthase)
215031_x_at	1.11	0.02	0.19	0.15	55658	RNF126	NM_194460	ring finger protein 126
215043_s_at	0.74	0.02	0.43	0.51	10571	SMA3	NM_006780	SMA3
215049_x_at	0.86	0.01	0.28	0.21	9332	CD163	NM_004244	CD163 antigen
215088_s_at	1.12	0.02	0.20	0.20	6391	SDHC	NM_003001	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa
215135_at	0.84	0.01	0.37	0.21	23549	DNPEP	AK021871	aspartyl aminopeptidase
215235_at	1.14	0.04	0.25	0.23	6709	SPTAN1	AL110273	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
215245_x_at	1.09	0.01	0.14	0.21	2332	FMR1	NM_002024	fragile X mental retardation 1
215299_x_at	1.13	6.24e-03	0.17	0.25	6817	SULT1A1	NM_001055	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1
215378_at	1.20	0.03	0.36	0.36	54882	ANKHD1	AU148255	ankyrin repeat and KH domain containing 1
215424_s_at	1.06	0.03	0.12	0.11	22938	SKIIP	NM_012245	SKI interacting protein
215452_x_at	1.10	0.01	0.18	0.13	387082	SUMO4	NM_001002255	SMT3 suppressor of mif two 3 homolog 4 (yeast)
215467_x_at	1.24	6.46e-03	0.33	0.38	1660	DHX9	AK001442	DEAH (Asp-Glu-Ala-His) box polypeptide 9
215498_s_at	1.11	0.02	0.19	0.18	5606	MAP2K3	NM_002756	mitogen-activated protein kinase kinase 3
215504_x_at	0.89	0.02	0.20	0.19	55608	ANKRD10	AF131777	ankyrin repeat domain 10
215535_s_at	1.14	0.01	0.21	0.22	10554	AGPAT1	NM_006411	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase
215623_x_at	1.17	0.03	0.29	0.32	10051	SMC4L1	AK002200	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)
215628_x_at	1.13	0.03	0.23	0.11	5515	PPP2CA	AL049285	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
215706_x_at	1.14	0.03	0.26	0.30	7791	ZYX	NM_003461	zyxin
215716_s_at	1.12	1.78e-03	0.15	0.16	490	ATP2B1	NM_001001323	ATPase, Ca++ transporting, plasma membrane 1
215732_s_at	1.10	0.04	0.20	0.20	113878	DTX2	NM_020892	deltex homolog 2 (Drosophila)

215737_x_at	1.10	0.03	0.20	0.13	7392	USF2	NM_003367	upstream transcription factor 2, c-fos interacting
215754_at	0.89	0.01	0.19	0.16	950	SCARB2	AK022432	scavenger receptor class B, member 2
215773_x_at	0.89	0.01	0.17	0.16	10038	PARP2	NM_005484	poly (ADP-ribose) polymerase family, member 2
215810_x_at	0.86	0.03	0.35	0.22	7943	D6S1101	AL049215	Dystonia musculorum of mouse, human homolog of
215883_at	0.85	1.17e-03	0.23	0.14	401210	LOC401210	AK022326	hypothetical gene supported by AK022326
215887_at	1.22	9.1e-03	0.31	0.32	11179	ZNF277	AK027128	zinc finger protein (C2H2 type) 277
215952_s_at	1.09	8.44e-04	0.09	0.12	4946	OAZ1	NM_004152	ornithine decarboxylase antizyme 1
215978_x_at	1.13	0.02	0.22	0.19	152719	LOC152719	AK021514	hypothetical protein LOC152719
215985_at	0.91	0.02	0.15	0.15	80869	HCG8	X92110	HLA complex group 8
216088_s_at	1.13	0.02	0.21	0.23	5688	PSMA7	NM_002792	proteasome (prosome, macropain) subunit, alpha type, 7
216092_s_at	1.11	0.04	0.21	0.22	23428	SLC7A8	NM_012244	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8
216121_at	1.14	7.91e-03	0.18	0.24	23369	PUM2	AL080106	pumilio homolog 2 (Drosophila)
216170_at	0.86	3.15e-03	0.21	0.16	54927	CHCHD3	AK025271	coiled-coil-helix-coiled-coil-helix domain containing 3
216174_at	0.85	0.01	0.28	0.21	387535	HCRP1	AK025343	hepatocellular carcinoma-related HCRP1
216203_at	0.90	0.01	0.20	0.14	9517	SPTLC2	U15555	serine palmitoyltransferase, long chain base subunit 2
216213_at	0.80	1.82e-03	0.25	0.25	4750	NEK1	AF155113	NIMA (never in mitosis gene a)-related kinase 1
216267_s_at	1.12	0.04	0.22	0.21	11070	PL6	NM_007024	placental protein 6
216321_s_at	1.09	0.01	0.13	0.18	2908	NR3C1	X03348	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
216323_x_at	1.16	9.19e-04	0.19	0.18	113457	H2-ALPHA	K03460	alpha-tubulin isotype H2-alpha
216341_s_at	0.87	0.04	0.28	0.26	2798	GNRHR	NM_000406	gonadotropin-releasing hormone receptor
216348_at	1.16	0.03	0.30	0.26	7021	TFAP2B	AL049693	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
216348_at	1.16	0.03	0.30	0.26	442216	LOC442216	AL049693	similar to dJ753D5.2 (novel protein similar to RPS17 (40S ribosomal protein S17))
216438_s_at	1.12	0.03	0.25	0.15	7114	TMSB4X	NM_021109	thymosin, beta 4, X-linked
216547_at	1.09	0.03	0.17	0.13	127406	LOC127406	XM_497679	similar to Laminin receptor 1
216661_x_at	0.86	0.03	0.32	0.25	1557	CYP2C19	NM_000769	cytochrome P450, family 2, subfamily C, polypeptide 19
216809_at	0.81	8.37e-03	0.33	0.30	1538	CYLC1	Z22780	cylicin, basic protein of sperm head cytoskeleton 1
216836_s_at	1.14	0.02	0.22	0.26	2064	ERBB2	NM_001005862	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived
216903_s_at	1.08	0.03	0.14	0.22	10367	CBARA1	NM_006077	calcium binding atopy-related autoantigen 1
216933_x_at	1.17	0.04	0.32	0.43	324	APC	NM_000038	adenomatosis polyposis coli

217028_at	1.13	4.51e-04	0.14	0.14	7852	CXCR4	NM_003467	chemokine (C-X-C motif) receptor 4
217042_at	0.89	0.04	0.22	0.21	51109	RDH11	NM_016026	retinol dehydrogenase 11 (all-trans and 9-cis)
217045_x_at	1.10	0.02	0.19	0.16	9436	NCR2	AL136967	natural cytotoxicity triggering receptor 2
217120_s_at	0.84	1.06e-03	0.16	0.20	9282	CRSP2	AK023368	cofactor required for Sp1 transcriptional activation, subunit 2, 150kDa
217211_at	1.15	0.01	0.22	0.26	69	ACTBP9	D50604	actin, beta pseudogene 9
217299_s_at	1.09	0.04	0.17	0.28	4683	NBS1	NM_002485	Nijmegen breakage syndrome 1 (nibrin)
217558_at	0.88	0.02	0.22	0.23	1559	CYP2C9	BC020754	cytochrome P450, family 2, subfamily C, polypeptide 9
217731_s_at	1.11	1.63e-03	0.12	0.13	9445	ITM2B	NM_021999	integral membrane protein 2B
217737_x_at	1.09	6.06e-03	0.11	0.18	51507	C20orf43	NM_016407	chromosome 20 open reading frame 43
217738_at	1.10	0.03	0.18	0.19	10135	PBEF1	NM_005746	pre-B-cell colony enhancing factor 1
217739_s_at	1.09	7.98e-03	0.15	0.13	10135	PBEF1	NM_005746	pre-B-cell colony enhancing factor 1
217745_s_at	1.14	0.02	0.25	0.27	80218	MAK3	NM_025146	Mak3 homolog (S. cerevisiae)
217755_at	1.09	0.02	0.17	0.16	51155	HN1	NM_016185	hematological and neurological expressed 1
217765_at	1.10	0.01	0.15	0.19	29959	NRBP	NM_013392	nuclear receptor binding protein
217783_s_at	1.08	0.02	0.14	0.15	51646	YPEL5	NM_016061	yippee-like 5 (Drosophila)
217801_at	1.13	2.43e-03	0.17	0.15	514	ATP5E	NM_006886	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
217831_s_at	1.12	0.04	0.24	0.29	55968	NSFL1C	NM_016143	NSFL1 (p97) cofactor (p47)
217836_s_at	1.07	0.03	0.13	0.14	55249	YY1AP1	NM_018253	YY1 associated protein 1
217844_at	1.10	0.01	0.17	0.15	58190	CTDSP1	NM_021198	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1
217856_at	1.13	0.01	0.21	0.17	9939	RBM8A	AF182415	RNA binding motif protein 8A
217873_at	1.07	0.01	0.12	0.12	51719	CAB39	NM_016289	calcium binding protein 39
217880_at	1.14	0.02	0.22	0.25	996	CDC27	NM_001256	cell division cycle 27
217887_s_at	1.08	0.04	0.16	0.17	2060	EPS15	NM_001981	epidermal growth factor receptor pathway substrate 15
217917_s_at	1.09	6.74e-03	0.14	0.11	83658	DNCL2A	NM_014183	dynein, cytoplasmic, light polypeptide 2A
217918_at	1.07	0.03	0.14	0.13	83658	DNCL2A	NM_014183	dynein, cytoplasmic, light polypeptide 2A
217923_at	1.12	1.61e-03	0.14	0.17	23578	PEF	NM_012392	PEF protein with a long N-terminal hydrophobic domain (peflin)
217931_at	1.13	0.01	0.23	0.21	10695	TNRC5	NM_183010	trinucleotide repeat containing 5
217931_at	1.13	0.01	0.23	0.21	10695	TNRC5	NM_006586	trinucleotide repeat containing 5
217943_s_at	1.13	3.68e-03	0.16	0.17	55700	FLJ10350	NM_018067	hypothetical protein FLJ10350
217947_at	1.08	0.04	0.18	0.14	54918	CKLFSF6	NM_017801	chemokine-like factor super family 6
217963_s_at	1.28	8.18e-03	0.44	0.45	27018	NGFRAP1	NM_014380	nerve growth factor receptor (TNFRSF16) associated protein 1
217982_s_at	1.08	9.51e-03	0.11	0.13	10933	MORF4L1	NM_006791	mortality factor 4 like 1
217989_at	1.10	0.01	0.13	0.17	51170	DHRS8	NM_016245	dehydrogenase/reductase (SDR family) member 8
217993_s_at	1.10	0.01	0.14	0.17	27430	MAT2B	NM_013283	methionine adenosyltransferase II, beta
218010_x_at	1.25	0.02	0.51	0.21	79144	C20orf149	NM_024299	chromosome 20 open reading frame 149

218011_at	1.09	4.79e-03	0.11	0.14	59286	UBL5	NM_024292	ubiquitin-like 5
218022_at	1.10	1.6e-03	0.12	0.14	51231	VRK3	NM_016440	vaccinia related kinase 3
218037_at	1.14	0.02	0.24	0.21	79137	C2orf17	NM_024293	chromosome 2 open reading frame 17
218061_at	1.13	0.01	0.17	0.24	4201	MEA	NM_014623	male-enhanced antigen
218079_s_at	1.08	0.03	0.15	0.16	79893	ZNF403	NM_024835	zinc finger protein 403
218088_s_at	1.09	0.01	0.14	0.17	64121	RRAGC	NM_022157	Ras-related GTP binding C
218130_at	1.07	0.03	0.12	0.16	79415	MGC4368	NM_024510	hypothetical protein MGC4368
218132_s_at	1.08	0.04	0.15	0.17	79042	LENG5	NM_024075	leukocyte receptor cluster (LRC) member 5
218153_at	1.13	6.67e-03	0.16	0.23	79587	FLJ12118	NM_024537	hypothetical protein FLJ12118
218155_x_at	1.14	0.03	0.24	0.18	55720	FLJ10534	NM_018128	hypothetical protein FLJ10534
218175_at	1.18	0.03	0.31	0.21	80212	FLJ22471	NM_025140	limkain beta 2
218192_at	1.15	2.04e-03	0.16	0.24	51447	IHPK2	NM_016291	inositol hexaphosphate kinase 2
218206_x_at	1.11	0.03	0.21	0.19	51282	SCAND1	NM_016558	SCAN domain containing 1
218230_at	1.13	0.02	0.21	0.25	27236	ARFIP1	AK096509	ADP-ribosylation factor interacting protein 1 (arfaptin 1)
218258_at	1.11	0.04	0.22	0.26	51082	POLR1D	NM_015972	polymerase (RNA) I polypeptide D, 16kDa
218265_at	1.09	0.02	0.15	0.20	79048	SECISBP2	NM_024077	SECIS binding protein 2
218277_s_at	1.08	0.03	0.15	0.19	79665	DHX40	NM_024612	DEAH (Asp-Glu-Ala-His) box polypeptide 40
218282_at	1.08	0.03	0.15	0.17	55741	C20orf31	NM_018217	chromosome 20 open reading frame 31
218292_s_at	1.09	0.01	0.14	0.17	51422	PRKAG2	NM_016203	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
218301_at	1.13	6.77e-03	0.19	0.17	57140	RNPEPL1	NM_018226	arginyl aminopeptidase (aminopeptidase B)-like 1
218306_s_at	1.08	0.04	0.16	0.17	8925	HERC1	NM_003922	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like
218308_at	1.12	0.03	0.20	0.23	10460	TACC3	NM_006342	transforming, acidic coiled-coil containing protein 3
218363_at	0.83	8.68e-04	0.22	0.18	55218	C14orf114	NM_018199	chromosome 14 open reading frame 114
218372_at	1.12	0.03	0.22	0.17	55090	MED9	NM_018019	mediator of RNA polymerase II transcription, subunit 9 homolog (yeast)
218379_at	1.08	0.04	0.16	0.21	10179	RBM7	NM_016090	RNA binding motif protein 7
218391_at	1.08	0.02	0.14	0.13	11267	EAP30	NM_007241	EAP30 subunit of ELL complex
218392_x_at	1.09	0.03	0.17	0.23	94081	SFXN1	NM_022754	sideroflexin 1
218433_at	1.23	0.02	0.33	0.23	79646	PANK3	NM_024594	pantothenate kinase 3
218435_at	1.19	0.03	0.31	0.27	29103	DNAJD1	NM_013238	DnaJ (Hsp40) homolog, subfamily D, member 1
218447_at	1.13	0.01	0.20	0.22	56942	DC13	NM_020188	DC13 protein
218492_s_at	1.10	0.04	0.19	0.20	80764	THAP7	NM_030573	THAP domain containing 7
218518_at	1.11	5.77e-03	0.15	0.17	51306	C5orf5	NM_016603	chromosome 5 open reading frame 5
218531_at	1.11	6.15e-03	0.16	0.15	80194	FLJ21749	NM_025124	hypothetical protein FLJ21749
218570_at	1.12	0.02	0.22	0.22	55709	KBTBD4	NM_018095	kelch repeat and BTB (POZ) domain containing 4
218586_at	1.08	0.04	0.17	0.13	55257	C20orf20	NM_018270	chromosome 20 open reading frame 20

218599_at	1.11	0.02	0.19	0.20	9985	REC8L1	NM_005132	REC8-like 1 (yeast)
218614_at	1.09	0.01	0.14	0.17	55196	FLJ10652	NM_018169	hypothetical protein FLJ10652
218668_s_at	1.17	1.91e-03	0.19	0.24	57826	RAP2C	NM_021183	RAP2C, member of RAS oncogene family
218669_at	1.09	0.04	0.18	0.29	57826	RAP2C	NM_021183	RAP2C, member of RAS oncogene family
218671_s_at	1.09	0.02	0.14	0.19	93974	ATPIF1	NM_016311	ATPase inhibitory factor 1
218679_s_at	1.14	9.29e-03	0.21	0.18	51160	VPS28	NM_016208	vacuolar protein sorting 28 (yeast)
218728_s_at	1.11	0.03	0.21	0.25	29097	HSPC163	NM_014184	HSPC163 protein
218743_at	1.15	1.98e-03	0.19	0.15	79643	FLJ11749	NM_024591	hypothetical protein FLJ11749
218746_at	1.16	0.01	0.24	0.26	55080	TAPBPL	NM_018009	TAP binding protein-like
218747_s_at	1.13	0.04	0.25	0.22	55080	TAPBPL	NM_018009	TAP binding protein-like
218855_at	1.12	0.01	0.20	0.20	131601	GPR175	NM_016372	G protein-coupled receptor 175
218873_at	1.08	0.04	0.15	0.19	54856	FLJ20203	AB046826	hypothetical protein FLJ20203
218915_at	1.15	0.02	0.21	0.22	4771	NF2	NM_016418	neurofibromin 2 (bilateral acoustic neuroma)
218936_s_at	1.12	7.84e-03	0.16	0.19	29080	HSPC128	NM_014167	HSPC128 protein
218961_s_at	1.09	0.04	0.17	0.16	11284	PNKP	NM_007254	polynucleotide kinase 3'-phosphatase
218987_at	1.10	5.06e-03	0.13	0.17	55729	ATF7IP	NM_018179	activating transcription factor 7 interacting protein
218994_s_at	1.13	0.02	0.19	0.24	64940	FLJ13195	AK023257	hypothetical protein FLJ13195 similar to stromal antigen 3
219004_s_at	0.90	0.03	0.21	0.17	54069	C21orf45	NM_018944	chromosome 21 open reading frame 45
219022_at	0.88	0.02	0.23	0.20	64897	FLJ12448	NM_022895	hypothetical protein FLJ12448
219035_s_at	1.05	0.04	0.09	0.10	80196	RNF34	NM_025126	ring finger protein 34
219052_at	1.18	2.17e-03	0.21	0.19	79803	HPS6	NM_024747	Hermansky-Pudlak syndrome 6
219094_at	1.19	4.25e-03	0.23	0.27	25852	ARMC8	NM_014154	armadillo repeat containing 8
219161_s_at	1.07	0.04	0.13	0.19	51192	CKLF	NM_016951	chemokine-like factor
219186_at	1.11	0.03	0.22	0.15	51341	ZBTB7	NM_015898	zinc finger and BTB domain containing 7
219193_at	1.10	0.02	0.17	0.22	55100	FLJ10233	NM_018034	hypothetical protein FLJ10233
219216_at	1.19	0.02	0.31	0.34	54465	ETAA16	NM_019002	ETAA16 protein
219234_x_at	0.84	0.02	0.25	0.32	79634	SCRN3	NM_024583	secernin 3
219238_at	1.12	2.25e-03	0.14	0.17	55650	PIGV	NM_017837	phosphatidylinositol glycan, class V
219242_at	1.08	0.04	0.16	0.21	80254	Cep63	NM_025180	centrosome protein Cep63
219266_at	1.09	0.04	0.18	0.19	59348	ZNF350	NM_021632	zinc finger protein 350
219290_x_at	1.10	0.04	0.21	0.19	27071	DAPP1	NM_014395	dual adaptor of phosphotyrosine and 3-phosphoinositides
219292_at	1.13	0.02	0.20	0.29	55145	THAP1	NM_018105	THAP domain containing, apoptosis associated protein 1
219326_s_at	0.87	0.02	0.23	0.29	10678	B3GNT1	NM_006577	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1
219382_at	1.12	0.03	0.22	0.30	29946	SERTAD3	NM_013368	SERTA domain containing 3
219397_at	1.08	0.02	0.13	0.16	80219	FLJ13448	NM_025147	hypothetical protein FLJ13448
219409_at	1.06	0.03	0.10	0.13	79753	SNIP1	NM_024700	Smad nuclear interacting protein
219433_at	1.12	0.04	0.22	0.23	54880	BCOR	NM_017745	BCL6 co-repressor
219457_s_at	1.08	0.01	0.13	0.12	79890	RIN3	NM_024832	Ras and Rab interactor 3
219472_at	0.88	0.04	0.25	0.22	79172	MGC11266	NM_024322	hypothetical protein MGC11266

219498_s_at	1.11	0.04	0.22	0.24	53335	BCL11A	NM_018014	B-cell CLL/lymphoma 11A (zinc finger protein)
219507_at	1.13	8.8e-03	0.20	0.22	51319	MGC12197	NM_016625	BM-011 protein
219540_at	1.12	0.01	0.19	0.26	10308	ZNF267	NM_003414	zinc finger protein 267
219546_at	1.16	0.04	0.28	0.27	55589	BMP2K	NM_017593	BMP2 inducible kinase
219594_at	1.12	0.03	0.21	0.24	4815	NINJ2	NM_016533	ninjurin 2
219639_x_at	1.08	0.02	0.14	0.12	56965	PARP6	NM_020213	poly (ADP-ribose) polymerase family, member 6
219666_at	0.87	0.01	0.22	0.20	64231	MS4A6A	NM_022349	membrane-spanning 4-domains, subfamily A, member 6A
219696_at	1.17	0.01	0.25	0.29	54530	FLJ20054	NM_019049	hypothetical protein FLJ20054
219802_at	1.17	1.66e-03	0.18	0.27	79912	FLJ22028	NM_024854	hypothetical protein FLJ22028
219807_x_at	1.10	0.01	0.17	0.12	53916	RAB4B	NM_016154	RAB4B, member RAS oncogene family
219880_at	1.16	0.02	0.27	0.24	64942	FLJ23053	NM_022907	hypothetical protein FLJ23053
219939_s_at	1.17	0.03	0.35	0.22	7812	UNR	NM_007158	upstream of NRAS
220038_at	0.86	0.01	0.26	0.22	23678	SGKL	NM_013257	serum/glucocorticoid regulated kinase-like
220052_s_at	1.11	0.04	0.20	0.22	26277	TINF2	NM_012461	TERF1 (TRF1)-interacting nuclear factor 2
220127_s_at	1.08	8.28e-03	0.12	0.11	54850	FBXL12	NM_017703	F-box and leucine-rich repeat protein 12
220167_s_at	0.88	0.01	0.18	0.17	24150	TP53TG3	NM_015369	TP53TG3 protein
220659_s_at	1.16	0.04	0.29	0.29	55262	FLJ10925	NM_018275	hypothetical protein FLJ10925
220703_at	0.88	6.07e-03	0.19	0.16	55853	C10orf110	NM_018470	chromosome 10 open reading frame 110
220753_s_at	1.09	0.02	0.16	0.14	51084	CRYL1	NM_015974	crystallin, lambda 1
220757_s_at	1.15	0.02	0.25	0.21	80700	UBXD1	NM_025241	UBX domain containing 1
220956_s_at	1.10	0.02	0.19	0.21	112398	EGLN2	NM_017555	egl nine homolog 2 (C. elegans)
220964_s_at	1.12	0.02	0.24	0.16	81876	RAB1B	NM_030981	RAB1B, member RAS oncogene family
221080_s_at	1.07	0.02	0.12	0.10	79958	FAM31C	NM_024898	family with sequence similarity 31, member C
221087_s_at	1.13	0.01	0.21	0.25	80833	APOL3	NM_014349	apolipoprotein L, 3
221192_x_at	1.12	0.04	0.23	0.27	79157	ET	NM_024311	hypothetical protein ET
221193_s_at	1.16	5.32e-03	0.21	0.23	54819	ZCCHC10	NM_017665	zinc finger, CCHC domain containing 10
221194_s_at	0.89	0.01	0.19	0.17	51136	LOC51136	NM_016125	PTD016 protein
221423_s_at	0.90	0.01	0.15	0.14	81555	SMAP-5	NM_030799	golgi membrane protein SB140
221428_s_at	1.12	0.04	0.25	0.21	79718	TBL1XR1	NM_024665	transducin (beta)-like 1X-linked receptor 1
221478_at	1.09	0.01	0.14	0.18	665	BNIP3L	NM_004331	BCL2/adenovirus E1B 19kDa interacting protein 3-like
221495_s_at	1.09	0.02	0.16	0.15	22980	KIAA1049	NM_014972	KIAA1049 protein
221507_at	1.09	0.03	0.16	0.14	30000	TNPO2	NM_013433	transportin 2 (importin 3, karyopherin beta 2b)
221515_s_at	1.08	0.03	0.15	0.17	51451	LCMT1	NM_016015	leucine carboxyl methyltransferase 1
221515_s_at	1.08	0.03	0.15	0.17	51451	LCMT1	NM_016309	leucine carboxyl methyltransferase 1
221534_at	1.13	7.97e-03	0.19	0.16	83638	Bles03	NM_031450	basophilic leukemia expressed protein BLES03

221564_at	1.11	0.02	0.19	0.20	3275	HRMT1L1	AL109794	HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae)
221588_x_at	0.91	0.01	0.14	0.14	4329	ALDH6A1	NM_005589	aldehyde dehydrogenase 6 family, member A1
221607_x_at	1.08	0.03	0.19	0.09	71	ACTG1	NM_001614	actin, gamma 1
221613_s_at	1.09	5.19e-03	0.12	0.16	54469	ZA20D3	NM_019006	zinc finger, A20 domain containing 3
221620_s_at	0.90	0.03	0.19	0.19	79135	MGC4825	NM_024122	hypothetical protein MGC4825
221626_at	1.20	0.02	0.31	0.22	91115	ZNF506	AL136548	zinc finger protein 506
221653_x_at	1.25	2.63e-03	0.29	0.29	23780	APOL2	NM_030882	apolipoprotein L, 2
221666_s_at	1.08	0.01	0.13	0.16	29108	PYCARD	NM_013258	PYD and CARD domain containing
221702_s_at	1.06	0.04	0.13	0.13	80213	BLP2	NM_078474	BBP-like protein 2
221732_at	1.22	1.7e-03	0.24	0.22	124583	CANT1	NM_138793	calcium activated nucleotidase 1
221735_at	1.12	0.03	0.22	0.18	57599	WDR48	NM_020839	WD repeat domain 48
221749_at	1.09	0.04	0.18	0.20	253943	YTHDF3	NM_152758	YTH domain family, member 3
221791_s_at	1.11	0.01	0.17	0.15	51372	HSPC016	NM_015933	hypothetical protein HSPC016
221815_at	1.23	0.01	0.39	0.28	11057	ABHD2	BE671816	abhydrolase domain containing 2
221824_s_at	1.09	0.01	0.11	0.22	220972	MARCH8	AL833316	membrane-associated ring finger (C3HC4) 8
221827_at	1.12	0.01	0.18	0.21	10616	C20orf18	BC016301	chromosome 20 open reading frame 18
221832_s_at	1.10	0.04	0.22	0.20	7798	LUZP1	NM_033631	leucine zipper protein 1
221849_s_at	1.18	2.09e-03	0.23	0.22	90379	LOC90379	XM_373433	hypothetical protein BC002926
221856_s_at	1.09	0.03	0.17	0.17	55793	FLJ11280	NM_018379	hypothetical protein FLJ11280
221875_x_at	1.08	0.02	0.16	0.12	3134	HLA-F	NM_018950	major histocompatibility complex, class I, F
221882_s_at	1.12	0.03	0.22	0.20	58986	TMEM8	NM_021259	transmembrane protein 8 (five membrane-spanning domains)
221904_at	1.10	0.01	0.15	0.19	131408	MGC21688	NM_144635	hypothetical protein MGC21688
221905_at	1.10	0.03	0.20	0.16	1540	CYLD	NM_015247	cylindromatosis (turban tumor syndrome)
221952_x_at	1.07	6.23e-03	0.09	0.12	57570	KIAA1393	NM_020810	KIAA1393
221978_at	1.18	8.26e-04	0.19	0.21	3134	HLA-F	NM_018950	major histocompatibility complex, class I, F
221984_s_at	1.11	0.02	0.20	0.21	79137	C2orf17	NM_024293	chromosome 2 open reading frame 17
221998_s_at	1.13	7.9e-03	0.19	0.19	51231	VRK3	NM_016440	vaccinia related kinase 3
222036_s_at	1.13	0.02	0.20	0.19	4173	MCM4	AI859865	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)
222041_at	1.08	0.02	0.13	0.14	124641	OVCA2	NM_080822	candidate tumor suppressor in ovarian cancer 2
222061_at	1.11	0.01	0.18	0.25	965	CD58	AA700015	CD58 antigen, (lymphocyte function-associated antigen 3)
222065_s_at	1.08	0.04	0.17	0.19	2314	FLII	NM_002018	flightless I homolog (Drosophila)
222082_at	1.10	0.03	0.19	0.21	51341	ZBTB7	NM_015898	zinc finger and BTB domain containing 7
222133_s_at	1.11	0.02	0.20	0.18	51105	PHF20L1	NM_016018	PHD finger protein 20-like 1
222151_s_at	1.10	0.01	0.12	0.24	80254	Cep63	NM_025180	centrosome protein Cep63
222206_s_at	1.20	3.19e-03	0.22	0.26	56926	NCLN	NM_020170	nicalin homolog (zebrafish)
222212_s_at	1.07	0.02	0.13	0.17	29956	LASS2	NM_181746	LAG1 longevity assurance homolog 2 (S. cerevisiae)

222229_x_at	1.09	0.03	0.16	0.16	6154	RPL26	NM_000987	ribosomal protein L26
222251_s_at	1.16	1.27e-04	0.15	0.17	26205	GMEB2	NM_012384	glucocorticoid modulatory element binding protein 2
222294_s_at	1.09	0.01	0.13	0.17	27161	EIF2C2	AW971415	eukaryotic translation initiation factor 2C, 2
222390_at	1.09	5.36e-03	0.11	0.15	51322	WAC	NM_016628	WW domain containing adaptor with coiled-coil
222394_at	1.08	0.04	0.16	0.16	10015	PDCD6IP	NM_013374	programmed cell death 6 interacting protein
222396_at	1.07	0.03	0.12	0.14	51155	HN1	NM_016185	hematological and neurological expressed 1
222402_at	1.13	0.02	0.20	0.31	51371	C13orf12	NM_015932	chromosome 13 open reading frame 12
222408_s_at	1.08	0.02	0.13	0.16	51646	YPEL5	NM_016061	yippee-like 5 (Drosophila)
222409_at	1.10	0.03	0.19	0.25	23603	CORO1C	NM_014325	coronin, actin binding protein, 1C
222415_at	1.06	0.04	0.10	0.18	58508	MLL3	BX640742	myeloid/lymphoid or mixed-lineage leukemia 3
222421_at	1.10	0.03	0.19	0.20	7328	UBE2H	AL832212	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
222426_at	1.11	0.02	0.19	0.22	79109	MAPKAP1	NM_024117	mitogen-activated protein kinase associated protein 1
222432_s_at	1.11	0.01	0.19	0.16	57003	GK001	NM_020198	GK001 protein
222435_s_at	0.90	0.04	0.22	0.18	51465	UBE2J1	NM_016021	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
222440_s_at	1.16	1.13e-03	0.19	0.19	9967	THRAP3	AL576205	thyroid hormone receptor associated protein 3
222467_s_at	1.08	0.02	0.14	0.14	55291	C11orf23	NM_018312	chromosome 11 open reading frame 23
222487_s_at	1.16	0.01	0.24	0.25	51065	RPS27L	BC003667	ribosomal protein S27-like
222488_s_at	1.09	0.03	0.17	0.22	51164	DCTN4	NM_016221	dynactin 4 (p62)
222526_at	1.12	0.01	0.17	0.17	54815	p66alpha	AK024670	p66 alpha
222528_s_at	0.87	0.04	0.40	0.28	51312	MSCP	NM_016612	mitochondrial solute carrier protein
222528_s_at	0.87	0.04	0.40	0.28	51312	MSCP	NM_018579	mitochondrial solute carrier protein
222543_at	1.11	0.04	0.21	0.21	79139	DERL1	AF131854	Der1-like domain family, member 1
222556_at	0.88	0.04	0.24	0.26	29880	ALG5	AF102850	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltra
222589_at	1.12	0.03	0.20	0.16	51701	NLK	NM_016231	nemo like kinase
222602_at	1.13	0.01	0.21	0.24	55236	FLJ10808	NM_018227	hypothetical protein FLJ10808
222633_at	1.10	0.02	0.17	0.19	79718	TBL1XR1	NM_024665	transducin (beta)-like 1X-linked receptor 1
222634_s_at	1.16	0.01	0.27	0.19	79718	TBL1XR1	NM_024665	transducin (beta)-like 1X-linked receptor 1
222656_at	1.09	0.04	0.18	0.26	55284	FLJ11011	NM_001001481	hypothetical protein FLJ11011
222660_s_at	0.89	0.03	0.27	0.21	152006	RNF38	NM_022781	ring finger protein 38
222717_at	1.31	0.04	0.57	0.48	8436	SDPR	NM_004657	serum deprivation response (phosphatidylserine binding protein)
222727_s_at	0.89	0.01	0.20	0.16	80024	SLC24A6	NM_024959	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6

222729_at	1.07	0.04	0.15	0.13	55294	FBXW7	NM_033632	F-box and WD-40 domain protein 7
(archipelago homolog, Drosophila)								
222759_at	1.07	0.04	0.13	0.19	51111	SUV420H1	NM_016028	suppressor of variegation 4-20 homolog 1
(Drosophila)								
222780_s_at	0.90	0.04	0.22	0.19	79870	BAALC	NM_024812	brain and acute leukemia, cytoplasmic
222792_s_at	1.20	2.65e-03	0.24	0.23	29080	HSPC128	NM_014167	HSPC128 protein
222815_at	1.15	1.91e-03	0.18	0.21	51132	RNF12	NM_016120	ring finger protein 12
222821_s_at	1.08	6.79e-03	0.11	0.15	79760	GEMIN7	NM_024707	gem (nuclear organelle) associated
protein 7								
222874_s_at	0.89	0.04	0.36	0.26	2055	CLN8	NM_018941	ceroid-lipofuscinosis, neuronal 8 (epilepsy,
progressive with mental retardation)								
222976_s_at	1.06	0.04	0.15	0.10	7170	TPM3	NM_152263	tropomyosin 3
222976_s_at	1.06	0.04	0.15	0.10	7170	TPM3	NM_153649	tropomyosin 3
222988_s_at	1.19	3.47e-04	0.16	0.24	252839	TMEM9	NM_016456	transmembrane protein 9
222994_at	1.13	1.71e-04	0.14	0.10	25824	PRDX5	NM_012094	peroxiredoxin 5
223000_s_at	1.11	0.02	0.18	0.19	50848	F11R	NM_016946	F11 receptor
223009_at	1.12	3.06e-03	0.16	0.16	55004	FLJ20625	NM_017907	hypothetical protein FLJ20625
223017_at	1.09	9.97e-03	0.12	0.16	51060	TLP19	NM_015913	endoplasmic reticulum thioredoxin
superfamily member, 18 kDa								
223023_at	1.10	0.04	0.20	0.17	51272	BET1L	NM_016526	blocked early in transport 1 homolog (S.
cerevisiae) like								
223039_at	1.07	0.04	0.15	0.13	83606	C22orf13	NM_031444	chromosome 22 open reading frame 13
223044_at	1.07	0.04	0.12	0.21	30061	SLC40A1	NM_014585	solute carrier family 40 (iron-regulated
transporter), member 1								
223047_at	1.07	0.01	0.10	0.15	54918	CKLFSF6	NM_017801	chemokine-like factor super family 6
223053_x_at	1.12	0.01	0.20	0.23	29101	HSPC182	NM_014188	HSPC182 protein
223080_at	0.90	0.04	0.23	0.15	2744	GLS	AK025021	glutaminase
223081_at	1.09	0.01	0.14	0.16	79142	MGC2941	NM_024297	hypothetical protein MGC2941
223085_at	1.12	8.73e-03	0.17	0.18	25897	RNF19	NM_183419	ring finger protein 19
223115_at	0.90	0.04	0.17	0.17	9440	CRSP6	NM_004268	cofactor required for Sp1 transcriptional
activation, subunit 6, 77kDa								
223136_at	1.15	8.92e-03	0.21	0.20	51390	AIG1	NM_016108	androgen-induced 1
223140_s_at	1.09	0.02	0.16	0.15	170506	DHX36	NM_020865	DEAH (Asp-Glu-Ala-His) box
polypeptide 36								
223144_s_at	1.09	0.02	0.14	0.20	55122	C6orf166	NM_018064	chromosome 6 open reading frame 166
223158_s_at	1.18	6.1e-03	0.22	0.28	10783	NEK6	NM_014397	NIMA (never in mitosis gene a)-related
kinase 6								
223167_s_at	1.11	0.03	0.21	0.29	29761	USP25	NM_013396	ubiquitin specific protease 25
223238_s_at	1.09	0.02	0.15	0.17	55193	PB1	AF130061	polybromo 1
223239_at	1.07	0.04	0.12	0.21	51527	C14orf129	BC004818	chromosome 14 open reading frame 129
223252_at	1.11	0.01	0.17	0.22	84717	HDGF2	NM_001001520	hepatoma-derived growth factor-related
protein 2								
223260_s_at	0.90	0.03	0.22	0.18	51426	POLK	NM_016218	polymerase (DNA directed) kappa
223268_at	1.11	0.03	0.21	0.22	28970	PTD012	NM_014039	PTD012 protein

223281_s_at	1.18	0.02	0.29	0.29	1355	COX15	NM_078470	COX15 homolog, cytochrome c oxidase assembly protein (yeast)
223303_at	1.09	0.04	0.18	0.15	83706	URP2	NM_178443	UNC-112 related protein 2
223322_at	1.05	0.04	0.10	0.13	83593	RASSF5	NM_182665	Ras association (RalGDS/AF-6) domain family 5
223338_s_at	1.18	5.18e-03	0.27	0.18	93974	ATPIF1	NM_178190	ATPase inhibitory factor 1
223342_at	1.11	0.02	0.18	0.22	50484	RRM2B	NM_015713	ribonucleotide reductase M2 B (TP53 inducible)
223346_at	1.10	0.03	0.19	0.17	57617	VPS18	NM_020857	vacuolar protein sorting protein 18
223376_s_at	1.08	0.02	0.13	0.20	25798	BRI3	NM_015379	brain protein I3
223389_s_at	1.14	3.03e-03	0.19	0.18	51545	ZNF581	NM_016535	zinc finger protein 581
223444_at	1.11	0.04	0.23	0.25	57337	SENP7	NM_020654	SUMO1/sentrin specific protease 7
223451_s_at	1.13	2.35e-03	0.15	0.18	51192	CKLF	NM_016951	chemokine-like factor
223469_at	1.14	0.01	0.21	0.21	83542	MGC10812	BC004942	hypothetical protein MGC10812
223479_s_at	1.12	0.03	0.23	0.15	84269	CHCHD5	NM_032309	coiled-coil-helix-coiled-coil-helix domain containing 5
223548_at	0.92	0.04	0.19	0.13	54823	C1orf26	NM_017673	chromosome 1 open reading frame 26
223562_at	1.11	0.01	0.18	0.24	64098	PARVG	NM_022141	parvin, gamma
223583_at	1.06	0.03	0.11	0.13	79626	FLJ23467	NM_024575	hypothetical protein FLJ23467
223617_x_at	1.10	0.04	0.18	0.21	83858	ATAD3B	NM_031921	ATPase family, AAA domain containing 3B
223620_at	0.81	9.48e-03	0.40	0.34	2857	GPR34	NM_005300	G protein-coupled receptor 34
223626_x_at	1.11	0.02	0.20	0.24	83982	FAM14A	NM_032036	family with sequence similarity 14, member A
223682_s_at	1.12	0.03	0.18	0.27	84285	MGC11102	NM_032325	hypothetical protein MGC11102
223751_x_at	0.90	0.03	0.34	0.19	81793	TLR10	NM_030956	toll-like receptor 10
223776_x_at	1.07	8.91e-03	0.11	0.10	26277	TINF2	BC005030	TERF1 (TRF1)-interacting nuclear factor 2
223916_s_at	1.20	7.72e-03	0.27	0.30	54880	BCOR	NM_017745	BCL6 co-repressor
223982_s_at	1.08	0.02	0.13	0.16	50640	IPLA2(GAMMA)	NM_015723	intracellular membrane-associated calcium-independent phospholipase A2 gamma
223983_s_at	1.13	0.03	0.22	0.22	83636	C19orf12	NM_031448	chromosome 19 open reading frame 12
224016_at	0.90	0.03	0.25	0.17	28996	HIPK2	NM_022740	homeodomain interacting protein kinase 2
224088_at	0.83	3.31e-04	0.19	0.18	56923	NMUR2	NM_020167	neuromedin U receptor 2
224130_s_at	1.10	0.04	0.20	0.16	10011	SRA1	AF293026	steroid receptor RNA activator 1
224132_at	1.10	0.01	0.16	0.15	84772	MGC13008	BC005072	hypothetical protein MGC13008
224173_s_at	0.88	0.02	0.35	0.20	51263	MRPL30	NM_145212	mitochondrial ribosomal protein L30
224180_x_at	0.90	0.04	0.16	0.19	51057	LOC51057	NM_015910	hypothetical protein LOC51057
224232_s_at	1.14	0.01	0.21	0.21	27166	PX19	NM_013237	px19-like protein
224285_at	0.87	0.03	0.34	0.24	84636	GPR174	NM_032553	G protein-coupled receptor 174
224302_s_at	1.08	0.03	0.16	0.16	92259	MRPS36	NM_033281	mitochondrial ribosomal protein S36
224318_s_at	1.11	0.01	0.19	0.12	55683	FLJ10081	NM_017991	hypothetical protein FLJ10081
224332_s_at	1.13	7.79e-03	0.18	0.25	84545	MRPL43	NM_032112	mitochondrial ribosomal protein L43
224395_s_at	0.88	4.75e-03	0.13	0.18	9616	RNF7	NM_014245	ring finger protein 7
224482_s_at	1.16	8.61e-04	0.17	0.18	84440	RAB11FIP4	NM_032932	RAB11 family interacting protein 4 (class II)

224558_s_at	1.09	8.46e-03	0.12	0.15	378938	MALAT1	BX538238	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)
224563_at	1.21	0.03	0.39	0.44	10163	WASF2	NM_006990	WAS protein family, member 2
224565_at	1.10	0.01	0.16	0.15	283131	TncRNA	AF001893	trophoblast-derived noncoding RNA
224567_x_at	1.09	0.03	0.21	0.14	378938	MALAT1	BX538238	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)
224583_at	1.12	7.97e-03	0.18	0.16	23406	COTL1	NM_021149	coactosin-like 1 (Dictyostelium)
224585_x_at	1.07	0.04	0.16	0.08	71	ACTG1	NM_001614	actin, gamma 1
224586_x_at	1.06	0.02	0.11	0.10	10923	PC4	NM_006713	activated RNA polymerase II transcription cofactor 4
224587_at	1.13	0.02	0.22	0.22	10923	PC4	NM_006713	activated RNA polymerase II transcription cofactor 4
224591_at	1.11	5.83e-03	0.15	0.14	50809	HP1-BP74	NM_016287	HP1-BP74
224609_at	1.10	0.02	0.17	0.25	57153	CTL2	NM_020428	CTL2 gene
224611_s_at	1.18	2.46e-04	0.17	0.16	80331	DNAJC5	AL118506	DnaJ (Hsp40) homolog, subfamily C, member 5
224617_at	1.08	3.49e-03	0.10	0.14	9991	ROD1	BC039896	ROD1 regulator of differentiation 1 (S. pombe)
224625_x_at	1.08	0.01	0.12	0.11	10169	SERF2	NM_005770	small EDRK-rich factor 2
224635_s_at	1.11	0.01	0.17	0.19	57448	BIRC6	AK023848	baculoviral IAP repeat-containing 6 (apollon)
224637_at	1.13	0.03	0.27	0.19	400948	LOC400948	XM_376043	similar to RIKEN cDNA 2310016E02
224656_s_at	1.08	5.46e-03	0.11	0.12	136319	MTPN	NM_145808	myotrophin
224662_at	1.09	0.01	0.13	0.17	3799	KIF5B	NM_004521	kinesin family member 5B
224667_x_at	1.10	0.01	0.17	0.11	119504	C10orf104	NM_173473	chromosome 10 open reading frame 104
224680_at	1.15	0.01	0.22	0.21	222068	TMED4	NM_182547	transmembrane emp24 protein transport domain containing 4
224700_at	1.11	0.02	0.18	0.17	201595	SIMP	AK075380	source of immunodominant MHC-associated peptides
224723_x_at	1.22	8.59e-03	0.30	0.29	402587	LOC402587	XM_380139	hypothetical gene supported by BX537645
224732_at	0.91	0.01	0.15	0.12	54921	DERPC	NM_017804	decreased expression in renal and prostate
224739_at	1.14	0.03	0.26	0.22	415116	PIM3	NM_001001852	pim-3 oncogene
224761_at	1.06	0.01	0.10	0.11	10672	GNA13	NM_006572	guanine nucleotide binding protein (G protein), alpha 13
224765_at	1.08	0.03	0.14	0.19	339287	LOC339287	AK125654	hypothetical protein LOC339287
224791_at	1.10	0.03	0.19	0.20	50807	DDEF1	NM_018482	development and differentiation enhancing factor 1
224793_s_at	1.14	3.69e-03	0.20	0.17	7046	TGFBR1	BC071181	transforming growth factor, beta receptor I (activin A receptor type II-like kinase,
224797_at	1.15	0.02	0.24	0.22	57561	ARRDC3	NM_020801	arrestin domain containing 3
224809_x_at	1.05	0.02	0.09	0.10	26277	TINF2	AK023166	TERF1 (TRF1)-interacting nuclear factor 2
224810_s_at	1.08	0.02	0.14	0.17	88455	ANKRD13	NM_033121	ankyrin repeat domain 13
224843_at	1.29	0.03	0.47	0.44	57606	KIAA1458	AB040891	KIAA1458 protein
224844_at	1.06	0.01	0.10	0.11	57606	KIAA1458	XM_044434	KIAA1458 protein

224855_at	1.17	0.01	0.25	0.29	29920	PYCR2	NM_013328	pyrroline-5-carboxylate reductase family, member 2
224916_at	0.91	0.04	0.21	0.17	340061	LOC340061	NM_198282	hypothetical protein LOC340061
224964_s_at	1.10	0.03	0.18	0.17	54331	GNG2	NM_053064	guanine nucleotide binding protein (G protein), gamma 2
224972_at	1.15	3.57e-03	0.19	0.19	140823	C20orf52	AK000548	chromosome 20 open reading frame 52
224974_at	1.14	0.02	0.25	0.26	64426	SDS3	NM_022491	likely ortholog of mouse Sds3
224992_s_at	1.13	9.93e-03	0.19	0.23	80790	CMIP	NM_198390	c-Maf-inducing protein
224997_x_at	0.83	0.01	0.35	0.30	283120	H19	AK056774	H19, imprinted maternally expressed untranslated mRNA
225043_at	1.10	0.03	0.20	0.21	121260	SLC15A4	NM_145648	solute carrier family 15, member 4
225051_at	1.08	0.02	0.15	0.15	2035	EPB41	NM_203343	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)
225071_at	0.86	4.37e-03	0.22	0.19	116150	C6orf68	NM_138459	chromosome 6 open reading frame 68
225117_at	1.10	2.87e-03	0.13	0.14	284058	LOC284058	NM_015443	hypothetical protein LOC284058
225133_at	1.07	0.03	0.12	0.15	51274	KLF3	NM_016531	Kruppel-like factor 3 (basic)
225134_at	1.11	0.02	0.20	0.18	84926	FLJ14800	NM_032840	hypothetical protein FLJ14800
225137_at	1.10	0.02	0.17	0.15	4775	NFATC3	NM_173165	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3
225142_at	1.11	0.04	0.21	0.33	80853	KIAA1718	XM_376680	KIAA1718 protein
225145_at	1.12	0.02	0.20	0.22	57727	NCOA5	NM_020967	nuclear receptor coactivator 5
225148_at	1.07	0.03	0.14	0.15	91582	MGC52010	NM_194326	hypothetical protein MGC52010
225171_at	1.16	0.03	0.29	0.26	93663	ARHGAP18	NM_033515	Rho GTPase activating protein 18
225175_s_at	1.19	1.42e-03	0.24	0.19	57153	CTL2	NM_020428	CTL2 gene
225192_at	1.10	9.58e-03	0.16	0.12	143384	C10orf46	AA044726	chromosome 10 open reading frame 46
225209_s_at	1.12	0.03	0.22	0.21	118424	UBE2J2	NM_194315	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)
225210_s_at	1.10	0.04	0.19	0.20	83640	MGC2560	NM_031452	hypothetical LOC83640
225229_at	1.14	6.78e-03	0.20	0.17	27125	AF5Q31	AK126818	ALL1 fused gene from 5q31
225243_s_at	1.07	0.04	0.15	0.17	7871	SLMAP	NM_007159	sarcolemma associated protein
225244_at	1.06	0.04	0.11	0.15	116841	IMAGE3451454	NM_053052	SVAP1 protein
225263_at	1.08	0.04	0.15	0.16	9394	HS6ST1	BC001196	heparan sulfate 6-O-sulfotransferase 1
225279_s_at	0.91	0.03	0.20	0.15	285338	LOC285338	AK092546	hypothetical protein LOC285338
225294_s_at	1.09	0.03	0.18	0.16	58485	TRAPPC1	NM_021210	trafficking protein particle complex 1
225304_s_at	1.11	0.02	0.19	0.16	126328	NDUFA11	NM_175614	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa
225337_at	1.19	3.18e-03	0.22	0.26	11057	ABHD2	AI346910	abhydrolase domain containing 2
225347_at	1.13	0.03	0.24	0.30	127829	ARL10B	NM_138795	ADP-ribosylation factor-like 10B
225351_at	1.10	0.01	0.12	0.23	404636	FAM45A	NM_207009	family with sequence similarity 45, member A
225364_at	1.06	0.01	0.09	0.09	6789	STK4	NM_006282	serine/threonine kinase 4
225413_at	1.07	0.03	0.15	0.14	84833	USMG5	NM_032747	upregulated during skeletal muscle growth 5
225414_at	1.08	5.48e-03	0.11	0.12	284996	RNF149	NM_173647	ring finger protein 149

225417_at (Drosophila)	1.07	0.04	0.13	0.14	80314	EPC1	NM_025209	enhancer of polycomb homolog 1
225446_at	1.15	0.02	0.25	0.32	54014	WDR9	BC064602	WD repeat domain 9
225456_at	1.14	0.04	0.25	0.19	5469	PPARBP	BC060758	PPAR binding protein
225469_at	1.16	0.01	0.24	0.24	144363	LOC144363	NM_001001660	hypothetical protein LOC144363
225480_at	1.10	0.02	0.16	0.14	127687	FLJ45459	NM_198446	FLJ45459 protein
225493_at	1.09	0.03	0.18	0.17	144438	LOC144438	BX537514	hypothetical protein LOC144438
225497_at	1.13	0.04	0.23	0.20	11101	ATE1	NM_001001976	arginyltransferase 1
225525_at	1.32	0.02	0.47	0.48	85379	KIAA1671	AB051458	KIAA1671 protein
225537_at	1.10	0.04	0.20	0.18	122553	TRAPPC6B	NM_177452	trafficking protein particle complex 6B
225552_x_at	1.07	0.02	0.12	0.11	54998	AKIP	NM_017900	aurora-A kinase interacting protein
225563_at ribonuclease subunit PAN3	1.07	0.02	0.11	0.15	255967	PAN3	NM_175854	PABP1-dependent poly A-specific
225572_at	1.13	0.01	0.18	0.21	1385	CREB1	AI652633	cAMP responsive element binding protein 1
225602_at	1.08	0.02	0.12	0.16	152007	C9orf19	NM_022343	chromosome 9 open reading frame 19
225618_at	1.09	0.02	0.17	0.18	201176	ARHGAP27	NM_199282	Rho GTPase activating protein 27
225624_at	1.08	0.03	0.14	0.22	92017	LOC92017	AK024473	similar to RIKEN cDNA 4933437K13
225630_at	1.15	7.47e-03	0.18	0.26	80820	KIAA1706	NM_030636	KIAA1706 protein
225649_s_at	1.07	0.03	0.12	0.19	140901	STK35	NM_080836	serine/threonine kinase 35
225651_at (UBC4/5 homolog, yeast)	0.91	0.04	0.22	0.17	7325	UBE2E2	NM_152653	ubiquitin-conjugating enzyme E2E 2
225672_at	1.10	4.82e-03	0.13	0.15	2801	GOLGA2	NM_004486	golgi autoantigen, golgin subfamily a, 2
225690_at	1.18	0.01	0.21	0.33	51755	CRK7	NM_016507	CDC2-related protein kinase 7
225695_at	1.12	8.71e-03	0.18	0.18	54978	C2orf18	BX647807	chromosome 2 open reading frame 18
225704_at	1.11	0.02	0.21	0.20	57666	KIAA1545	AB046765	KIAA1545 protein
225707_at protein 6	1.08	0.04	0.16	0.18	151188	ARL6IP6	NM_152522	ADP-ribosylation-like factor 6 interacting
225758_s_at protein 6	1.12	0.02	0.20	0.20	85378	TUBGCP6	NM_020461	tubulin, gamma complex associated
225759_x_at	0.87	0.01	0.23	0.18	79789	CLMN	AK023828	calmin (calponin-like, transmembrane)
225813_at	1.12	0.02	0.22	0.19	54542	MNAB	AA524361	membrane associated DNA binding protein
225814_at	1.10	0.02	0.16	0.25	54464	XRN1	NM_019001	5'-3' exoribonuclease 1
225821_s_at	1.07	0.04	0.12	0.17	57219	KIAA1327	AB037748	KIAA1327 protein
225830_at	1.15	0.04	0.31	0.49	118987	PDZK8	NM_173791	PDZ domain containing 8
225835_at (sodium/potassium/chloride transporters), member 2	1.17	0.02	0.27	0.35	6558	SLC12A2	NM_001046	solute carrier family 12
225838_at (Drosophila)	1.11	0.01	0.16	0.20	26122	EPC2	NM_015630	enhancer of polycomb homolog 2
225845_at	1.10	0.04	0.19	0.25	29068	HSPC063	BG253884	HSPC063 protein
225860_at	1.11	1.78e-03	0.12	0.14	400843	LOC400843	XM_378976	hypothetical LOC400843
225870_s_at	1.16	2.54e-03	0.20	0.18	126003	TRAPPC5	BC042161	trafficking protein particle complex 5
225882_at	1.09	0.04	0.17	0.23	84912	SLC35B4	NM_032826	solute carrier family 35, member B4
225899_x_at	1.06	0.04	0.13	0.13	399844	FLJ45445	NM_001004321	FLJ45445 protein
225912_at protein 1	1.11	0.02	0.16	0.23	94241	TP53INP1	NM_033285	tumor protein p53 inducible nuclear

225917_at	1.11	7.51e-03	0.15	0.23	55729	ATF7IP	AA766897	activating transcription factor 7 interacting protein
225919_s_at	1.11	9.92e-03	0.14	0.24	203228	C9orf72	NM_018325	chromosome 9 open reading frame 72
225923_at	1.09	0.04	0.18	0.21	9217	VAPB	AW291083	VAMP (vesicle-associated membrane protein)-associated protein B and C
226009_at	0.83	4.04e-03	0.32	0.18	25911	DPCD	NM_015448	deleted in a mouse model of primary ciliary dyskinesia
226018_at	1.17	0.01	0.31	0.22	222166	Ells1	NM_152793	hypothetical protein Ells1
226045_at	1.16	2.96e-03	0.17	0.25	10818	FRS2	AW264515	fibroblast growth factor receptor substrate 2
226053_at	1.16	3.8e-03	0.22	0.21	5609	MAP2K7	NM_145185	mitogen-activated protein kinase kinase 7
226062_x_at	1.15	6.28e-04	0.15	0.17	55793	FLJ11280	AB037811	hypothetical protein FLJ11280
226074_at	1.11	0.01	0.20	0.20	132160	FLJ32332	NM_144641	likely ortholog of mouse protein phosphatase 2C eta
226094_at	0.88	4.89e-03	0.16	0.16	5286	PIK3C2A	AI401379	phosphoinositide-3-kinase, class 2, alpha polypeptide
226100_at	1.12	0.02	0.21	0.23	55904	MLL5	NM_182931	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)
226100_at	1.12	0.02	0.21	0.23	55904	MLL5	NM_018682	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)
226109_at	1.13	5.26e-03	0.17	0.20	54149	C21orf91	NM_017447	chromosome 21 open reading frame 91
226110_at	1.08	9.63e-03	0.12	0.15	375743	PTAR1	AL832683	protein prenyltransferase alpha subunit repeat containing 1
226115_at	1.11	0.01	0.16	0.20	25909	ELYS	BC012307	ELYS transcription factor-like protein TMBS62
226119_at	1.07	0.03	0.12	0.15	115294	LOC115294	NM_052937	similar to hypothetical protein FLJ10883
226128_at	1.08	0.02	0.13	0.15	148362	FLJ32421	N73682	hypothetical protein FLJ32421
226148_at	1.09	0.03	0.18	0.25	29068	HSPC063	BC040658	HSPC063 protein
226155_at	1.12	0.01	0.20	0.23	57700	KIAA1600	AB046820	KIAA1600
226165_at	1.14	0.01	0.20	0.19	401466	LOC401466	XM_376783	hypothetical gene supported by BC055092
226176_s_at	1.22	7.35e-04	0.25	0.24	84132	USP42	XM_374396	ubiquitin specific protease 42
226241_s_at	1.13	0.03	0.26	0.19	122704	MRPL52	NM_178336	mitochondrial ribosomal protein L52
226275_at	1.09	0.04	0.16	0.16	4084	MXD1	BC051693	MAX dimerization protein 1
226317_at	1.14	4.46e-03	0.18	0.26	151987	PPP4R2	AL833216	protein phosphatase 4, regulatory subunit 2
226321_at	1.10	0.02	0.18	0.19	116068	LOC116068	XM_371760	hypothetical protein LOC116068
226326_at	1.13	0.01	0.18	0.20	84333	PCGF5	AK055625	polycomb group ring finger 5
226333_at	1.10	0.01	0.15	0.18	3570	IL6R	NM_000565	interleukin 6 receptor
226353_at	1.06	0.01	0.10	0.13	84888	SPPL2A	NM_032802	putative intramembrane cleaving protease
226358_at	1.13	0.01	0.20	0.20	145842	LOC145842	AK057677	hypothetical protein LOC145842
226372_at	1.16	2.91e-03	0.17	0.21	50515	CHST11	AI123348	carbohydrate (chondroitin 4) sulfotransferase 11
226387_at	1.08	0.04	0.15	0.18	222194	RSBN1L	NM_198467	round spermatid basic protein 1-like
226434_at	1.10	4.41e-03	0.13	0.14	221908	MGC22793	NM_145030	hypothetical protein MGC22793
226437_at	1.09	0.01	0.14	0.16	90522	LOC90522	NM_033557	similar to putative transmembrane protein; homolog of yeast Golgi membrane protein Yi

226438_at	1.14	0.04	0.24	0.26	6641	SNTB1	AK025100	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)
226441_at	1.15	0.01	0.22	0.23	10746	MAP3K2	AA045204	mitogen-activated protein kinase kinase kinase 2
226461_at	0.92	0.03	0.18	0.14	3219	HOXB9	NM_024017	homeo box B9
226465_s_at	1.18	2.13e-03	0.20	0.22	6651	SON	NM_138925	SON DNA binding protein
226482_s_at	1.10	0.02	0.16	0.17	50848	F11R	BC001699	F11 receptor
226505_x_at	1.07	0.04	0.12	0.19	84669	USP32	NM_032582	ubiquitin specific protease 32
226513_at	1.08	0.03	0.15	0.18	145758	LOC145758	AK057921	hypothetical protein LOC145758
226531_at	1.15	2.92e-03	0.19	0.18	84876	FLJ14466	NM_032790	hypothetical protein FLJ14466
226596_x_at	1.16	0.01	0.27	0.22	401307	LOC401307	AK027125	hypothetical gene supported by AK027125
226633_at	1.07	0.01	0.09	0.14	51762	RAB8B	AI807023	RAB8B, member RAS oncogene family
226641_at	1.12	3.86e-03	0.15	0.20	91526	LOC91526	AU157224	hypothetical protein DKFZp434D2328
226660_at	1.08	0.03	0.15	0.15	6198	RPS6KB1	AK091503	ribosomal protein S6 kinase, 70kDa, polypeptide 1
226672_s_at	1.23	0.03	0.42	0.26	83933	HDAC10	NM_032019	histone deacetylase 10
226675_s_at	1.23	2.31e-04	0.19	0.22	378938	MALAT1	BX538238	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)
226691_at	1.09	0.04	0.18	0.16	84629	KIAA1856	XM_376567	KIAA1856 protein
226694_at	1.21	0.01	0.30	0.38	445815	PALM2-AKAP2	NM_007203	PALM2-AKAP2 protein
226739_at	1.07	0.04	0.14	0.18	254225	KIAA1991	XM_495886	hypothetical protein KIAA1991
226780_s_at	1.12	0.02	0.20	0.23	154791	HSPC268	NM_197964	hypothetical protein HSPC268
226786_at	1.08	0.03	0.15	0.17	5989	RFX1	NM_002918	regulatory factor X, 1 (influences HLA class II expression)
226811_at	1.19	0.02	0.32	0.29	54855	FAM46C	NM_017709	family with sequence similarity 46, member C
226842_at	1.08	0.04	0.17	0.13	90110	LOC90110	BC042012	hypothetical protein LOC90110
226845_s_at	1.10	0.01	0.17	0.16	150678	LOC150678	AF487338	helicase/primase complex protein
226879_at	1.14	0.02	0.23	0.22	84329	MGC15619	NM_032369	hypothetical protein MGC15619
226909_at	1.09	0.04	0.18	0.17	85460	KIAA1729	AW270138	KIAA1729 protein
226962_at	1.16	0.04	0.32	0.35	360023	FRBZ1	BC043426	FRBZ1 protein
226967_at	1.15	0.02	0.25	0.21	84922	FLJ14768	NM_032836	hypothetical protein FLJ14768
226968_at	1.18	0.01	0.32	0.24	23095	KIF1B	NM_183416	kinesin family member 1B
226986_at	1.12	0.02	0.22	0.19	26100	WIPI-2	BX537624	WIPI49-like protein 2
226993_at	1.12	7.23e-03	0.17	0.19	9320	TRIP12	AA973551	thyroid hormone receptor interactor 12
227003_at	1.10	0.04	0.18	0.21	9364	RAB28	BC035054	RAB28, member RAS oncogene family
227037_at	1.07	0.03	0.13	0.15	201164	LOC201164	NM_178836	similar to CG12314 gene product
227065_at	1.10	0.02	0.17	0.13	54476	TRIAD3	NM_207111	TRIAD3 protein
227085_at	1.08	0.03	0.15	0.11	94239	H2AFV	AK025785	H2A histone family, member V
227100_at	0.91	0.04	0.15	0.17	145173	B3GTL	NM_194318	beta 3-glycosyltransferase-like
227119_at	1.10	0.02	0.17	0.16	246175	CNOT6L	BF103856	CCR4-NOT transcription complex, subunit 6-like
227143_s_at	1.10	0.02	0.18	0.15	637	BID	NM_197966	BH3 interacting domain death agonist
227152_at	1.11	0.04	0.22	0.21	55019	FLJ20696	AB046771	hypothetical protein FLJ20696

227203_at	1.21	2.27e-03	0.27	0.25	64839	FBXL17	BC018548	F-box and leucine-rich repeat protein 17
227219_x_at	1.21	0.01	0.26	0.30	84557	MAP1LC3A	NM_032514	microtubule-associated protein 1 light chain 3 alpha
227264_at	1.08	0.04	0.16	0.20	7189	TRAF6	AA702531	TNF receptor-associated factor 6
227291_s_at	1.14	0.04	0.25	0.28	388962	LOC388962	NM_212552	similar to RIKEN 1810056O20
227305_s_at	1.10	0.01	0.16	0.16	6470	SHMT1	N25727	serine hydroxymethyltransferase 1 (soluble)
227309_at	1.15	9.56e-03	0.23	0.26	55432	DKFZp451J1719	AL833081	hypothetical DKFZp451J1719
227346_at	1.09	5.98e-03	0.13	0.13	10320	ZNFN1A1	AI741188	zinc finger protein, subfamily 1A, 1 (Ikaros)
227379_at	1.09	0.04	0.17	0.25	154141	OACT1	XM_371801	O-acyltransferase (membrane bound) domain containing 1
227433_at	1.11	0.01	0.16	0.21	205717	KIAA2018	AI651814	similar to K06A9.1b.p
227466_at	1.11	0.01	0.15	0.23	285550	LOC285550	XM_209656	hypothetical protein LOC285550
227467_at	0.91	0.01	0.15	0.14	157506	RDH10	NM_172037	retinol dehydrogenase 10 (all-trans)
227478_at	1.12	0.04	0.23	0.29	284262	LOC284262	AL832945	hypothetical protein LOC284262
227527_at	1.09	0.01	0.14	0.19	8085	MLL2	BC039197	myeloid/lymphoid or mixed-lineage leukemia 2
227540_at	1.14	3.42e-03	0.17	0.14	60678	SELB	NM_021937	elongation factor for selenoprotein translation
227554_at	0.83	0.01	0.28	0.24	402560	LOC402560	AU145805	hypothetical LOC402560
227568_at	0.85	0.03	0.36	0.24	143279	HECTD2	NM_182765	HECT domain containing 2
227569_at	1.13	0.02	0.22	0.27	222484	LNX2	NM_153371	ligand of numb-protein X 2
227598_at	1.21	1.01e-03	0.20	0.31	113763	C7orf29	NM_138434	chromosome 7 open reading frame 29
227618_at	1.11	0.03	0.21	0.24	392490	FLJ44635	AI250910	FLJ44635 protein
227630_at	1.11	0.02	0.20	0.17	5529	PPP2R5E	AW274445	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
227650_at	0.89	7.16e-03	0.14	0.16	51182	HSPA14	BC026226	heat shock 70kDa protein 14
227651_at	1.10	0.02	0.17	0.14	112939	BTBD14B	NM_052876	BTB (POZ) domain containing 14B
227726_at	1.10	0.03	0.18	0.22	115992	RNF166	NM_178841	ring finger protein 166
227728_at	1.12	7.7e-03	0.16	0.19	5494	PPM1A	AA886888	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform
227737_at	0.92	0.03	0.15	0.15	58477	SRPRB	AI160339	signal recognition particle receptor, B subunit
227817_at	1.13	3.95e-03	0.19	0.17	5579	PRKCB1	R51324	protein kinase C, beta 1
227855_at	1.16	0.02	0.27	0.27	55701	FLJ10357	NM_018071	hypothetical protein FLJ10357
227864_s_at	1.13	0.02	0.21	0.22	93343	LOC93343	NM_138401	hypothetical protein BC011840
227869_at	1.13	0.02	0.21	0.27	440474	LOC440474	XM_496260	similar to LOC90736 protein
227878_s_at	1.12	0.03	0.26	0.23	84266	SPATA11	NM_032306	spermatogenesis associated 11
227951_s_at	1.08	0.03	0.15	0.15	147965	LOC147965	NM_174905	hypothetical protein LOC147965
228071_at	1.12	0.04	0.21	0.18	168537	GIMAP7	NM_153236	GTPase, IMAP family member 7
228087_at	1.11	0.01	0.16	0.28	90693	LOC90693	NM_138771	alpha-1,3(6)-mannosylglycoprotein beta-1,6-N-acetyl-glucosaminyltransferase-like
228188_at	1.13	0.03	0.24	0.26	2355	FOSL2	BX647822	FOS-like antigen 2
228261_at	1.13	0.04	0.26	0.22	142678	ZZANK1	NM_080875	zinc finger, ZZ type with ankyrin repeat domain 1
228283_at	1.30	0.03	0.51	0.42	152100	MGC61571	NM_182523	hypothetical protein MGC61571

228287_at	1.13	0.03	0.22	0.24	84289	ING5	NM_032329	inhibitor of growth family, member 5
228392_at	1.13	0.01	0.20	0.23	55900	ZNF302	BF508739	zinc finger protein 302
228471_at	1.15	6.51e-04	0.15	0.18	91526	LOC91526	AA744636	hypothetical protein DKFZp434D2328
228500_at	1.13	2.21e-03	0.16	0.14	199745	THAP8	NM_152658	THAP domain containing 8
228568_at	1.28	0.01	0.40	0.31	145781	Gup1	AK055535	GRINL1A complex upstream protein
228569_at	1.09	0.03	0.16	0.20	10914	PAPOLA	NM_032632	poly(A) polymerase alpha
228606_at	1.13	0.02	0.21	0.25	255758	MGC33212	NM_152773	hypothetical protein MGC33212
228622_s_at	1.13	0.01	0.21	0.18	3338	DNAJC4	BC010145	DnaJ (Hsp40) homolog, subfamily C,
member 4								
228652_at	1.08	0.04	0.17	0.21	284309	FLJ38288	NM_173632	hypothetical protein FLJ38288
228700_at	1.11	0.01	0.17	0.23	159013	CXorf38	AA063608	chromosome X open reading frame 38
228702_at	1.07	0.02	0.11	0.16	378805	FLJ43663	AK125651	hypothetical protein FLJ43663
228708_at	1.24	3.46e-03	0.25	0.30	5874	RAB27B	BF438386	RAB27B, member RAS oncogene family
228721_at	1.16	0.02	0.26	0.29	339903	LOC339903	BC041820	hypothetical protein LOC339903
228730_s_at	1.11	0.04	0.21	0.34	90507	SCRN2	NM_138355	secernin 2
228736_at	1.10	0.03	0.18	0.24	113510	HEL308	NM_133636	DNA helicase HEL308
228745_at	1.12	0.02	0.20	0.23	80006	FLJ13611	AI376997	hypothetical protein FLJ13611
228751_at	1.15	0.01	0.22	0.28	57396	CLK4	NM_020666	CDC-like kinase 4
228805_at	1.10	0.03	0.18	0.19	375484	FLJ44216	NM_198567	FLJ44216 protein
228822_s_at	1.10	0.04	0.20	0.21	10600	USP16	NM_006447	ubiquitin specific protease 16
228867_at	1.15	9.48e-03	0.20	0.24	128387	LOC128387	XM_375838	hypothetical protein LOC128387
229018_at	1.14	0.01	0.23	0.24	84190	FLJ22789	NM_032230	hypothetical protein FLJ22789
229021_at	1.21	8.2e-04	0.21	0.28	55784	MCTP2	AK026984	multiple C2-domains with two
transmembrane regions 2								
229106_at	1.09	0.01	0.14	0.14	140735	Dlc2	AF112997	dynein light chain 2
229113_s_at	1.17	9.99e-04	0.18	0.20	199990	FLJ31031	NM_182533	hypothetical protein FLJ31031
229211_at	1.09	0.04	0.17	0.19	285193	LOC285193	XM_209509	similar to RIKEN cDNA 0710001B24
229217_at	0.89	0.03	0.35	0.20	6670	SP3	NM_003111	Sp3 transcription factor
229232_at	1.10	0.04	0.20	0.20	255252	FLJ36812	NM_153260	hypothetical protein FLJ36812
229264_at	1.15	7.66e-03	0.20	0.25	440667	LOC440667	XM_498810	LOC440667
229325_at	0.92	0.02	0.16	0.13	26009	ZZZ3	BX640658	zinc finger, ZZ domain containing 3
229551_x_at	1.22	9.34e-03	0.30	0.39	195828	ZNF367	AK091289	zinc finger protein 367
229584_at	1.16	2.53e-03	0.16	0.28	120892	LRRK2	AK026776	leucine-rich repeat kinase 2
229630_s_at	1.11	2.3e-03	0.12	0.16	9589	WTAP	NM_004906	Wilms tumor 1 associated protein
229700_at	0.88	0.01	0.20	0.20	148203	LOC148203	BC034499	hypothetical protein LOC148203
229776_at	1.09	0.03	0.17	0.16	28232	SLCO3A1	NM_013272	solute carrier organic anion transporter
family, member 3A1								
229860_x_at	1.09	0.03	0.17	0.17	401115	LOC401115	BC038466	hypothetical gene supported by
BC038466; BC062790								
229862_x_at	1.09	0.04	0.17	0.22	84878	ZNF499	NM_032792	zinc finger protein 499
229872_s_at	1.08	0.04	0.16	0.19	440667	LOC440667	XM_498810	LOC440667
229908_s_at	1.12	0.02	0.19	0.26	65259	C16orf28	BF338332	chromosome 16 open reading frame 28
229939_at	0.93	0.02	0.11	0.12	284131	FLJ35220	AA926664	hypothetical protein FLJ35220
229967_at	1.08	0.03	0.15	0.16	146225	CKLFSF2	NM_144673	chemokine-like factor super family 2
230012_at	1.10	0.02	0.17	0.21	284029	FLJ34790	NM_173621	hypothetical protein FLJ34790

230133_at	0.90	0.04	0.20	0.19	54542	MNAB	BF972355	membrane associated DNA binding protein
230174_at	1.14	0.03	0.25	0.35	127018	LYPLAL1	AI953360	lysophospholipase-like 1
230259_at	1.09	0.04	0.19	0.17	282969	C10orf125	NM_198472	chromosome 10 open reading frame 125
230298_at	1.15	0.02	0.24	0.27	153364	LOC153364	NM_203406	similar to metallo-beta-lactamase superfamily protein
230322_at	1.12	0.04	0.24	0.30	150372	NFAM1	NM_145912	NFAT activating protein with ITAM motif 1
230400_s_at	1.18	0.02	0.28	0.37	401954	LOC401954	XM_377594	similar to sporulation-induced transcript 4-associated protein
230408_at	1.19	4.16e-03	0.24	0.31	10336	PCGF3	BG231712	polycomb group ring finger 3
230520_at	1.15	0.03	0.29	0.19	51390	AIG1	BX640703	androgen-induced 1
230623_x_at	1.23	4.35e-03	0.28	0.24	57646	USP28	NM_020886	ubiquitin specific protease 28
230748_at	1.10	0.03	0.19	0.22	9120	SLC16A6	NM_004694	solute carrier family 16 (monocarboxylic acid transporters), member 6
230753_at	1.19	0.04	0.38	0.42	197135	LOC197135	XM_113825	similar to RIKEN cDNA 4930424G05
230789_at	0.86	4.25e-03	0.25	0.18	140883	SUHW2	NM_080764	suppressor of hairy wing homolog 2 (Drosophila)
230875_s_at	1.09	0.03	0.17	0.22	23250	ATP11A	AW068936	ATPase, Class VI, type 11A
230942_at	1.21	0.02	0.43	0.21	116173	CKLFSF5	NM_138460	chemokine-like factor super family 5
231043_at	0.90	0.03	0.20	0.18	200373	LOC200373	XM_114222	similar to hypothetical protein
231059_x_at	1.12	0.02	0.21	0.16	51282	SCAND1	NM_016558	SCAN domain containing 1
231109_at	1.41	0.04	0.79	0.37	10659	CUGBP2	R44974	CUG triplet repeat, RNA binding protein 2
231577_s_at	1.20	0.01	0.41	0.76	2633	GBP1	NM_002053	guanylate binding protein 1, interferon-inducible, 67kDa
231718_at	1.12	5.17e-03	0.17	0.19	10569	SLU7	NM_006425	step II splicing factor SLU7
231736_x_at	0.88	0.04	0.23	0.24	4257	MGST1	NM_020300	microsomal glutathione S-transferase 1
231806_s_at	0.92	0.02	0.19	0.12	27148	STK36	NM_015690	serine/threonine kinase 36 (fused homolog, Drosophila)
231815_at	1.10	0.02	0.15	0.22	57649	PHF12	AB040956	PHD finger protein 12
231836_at	1.13	0.04	0.23	0.26	284459	HKR1	NM_181786	GLI-Kruppel family member HKR1
231944_at	1.29	4.29e-04	0.28	0.31	56605	ERO1LB	AL045717	ERO1-like beta (S. cerevisiae)
231953_at	0.88	0.01	0.16	0.18	2186	FALZ	AK027184	fetal Alzheimer antigen
231974_at	1.14	0.04	0.27	0.26	8085	MLL2	BC039197	myeloid/lymphoid or mixed-lineage leukemia 2
231975_s_at	1.15	0.02	0.26	0.25	166968	FLJ35954	NM_152622	hypothetical protein FLJ35954
232030_at	1.14	0.02	0.24	0.27	57724	KIAA1632	NM_020964	KIAA1632
232052_at	1.14	2.38e-03	0.16	0.18	440944	LOC440944	BC052961	hypothetical gene supported by AK128398
232169_x_at	1.14	8.72e-03	0.21	0.16	4728	NDUFS8	AK002110	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
232234_at	1.09	0.04	0.19	0.16	84174	SLA2	NM_032214	Src-like-adaptor 2
232253_at	1.24	9.77e-03	0.34	0.42	441108	LOC441108	AL564637	hypothetical gene supported by AK128882
232353_s_at	1.11	0.01	0.17	0.20	51657	DUSP24	NM_016086	dual specificity phosphatase 24 (putative)
232362_at	0.87	9.4e-03	0.21	0.21	343099	NY-SAR-41	AL139421	sarcoma antigen NY-SAR-41

232366_at	1.10	0.01	0.17	0.19	9778	KIAA0232	AF143884	KIAA0232 gene product
232471_at	0.86	9.68e-03	0.30	0.20	4643	MYO1E	BE143535	myosin IE
232520_s_at	1.13	0.01	0.20	0.26	55968	NSFL1C	NM_016143	NSFL1 (p97) cofactor (p47)
232579_at	1.16	2.47e-03	0.19	0.23	80853	KIAA1718	AK026372	KIAA1718 protein
232597_x_at	1.13	6.29e-03	0.18	0.18	9169	SFRS2IP	AK025132	splicing factor, arginine/serine-rich 2, interacting protein
232637_at	1.15	0.01	0.25	0.14	4735	SEPT2	AK025163	septin 2
232652_x_at	1.17	9.36e-03	0.25	0.20	51282	SCAND1	NM_016558	SCAN domain containing 1
232710_at	1.16	0.01	0.24	0.27	441258	LOC441258	AK021477	similar to Williams Beuren syndrome chromosome region 19
232725_s_at	0.79	8.06e-04	0.37	0.26	64231	MS4A6A	NM_152852	membrane-spanning 4-domains, subfamily A, member 6A
232814_x_at	1.12	7.09e-03	0.19	0.11	84334	C14orf153	AK024310	chromosome 14 open reading frame 153
232916_at	0.85	0.04	0.38	0.29	7325	UBE2E2	AK022159	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)
232949_at	1.07	0.02	0.12	0.12	832	CAPZB	AU146181	capping protein (actin filament) muscle Z-line, beta
233049_x_at	1.06	0.02	0.11	0.13	10273	STUB1	NM_005861	STIP1 homology and U-box containing protein 1
233072_at	1.18	0.04	0.35	0.38	84628	NTNG2	NM_032536	netrin G2
233085_s_at	1.08	0.04	0.17	0.18	64859	FLJ22833	NM_022837	hypothetical protein FLJ22833
233089_at	1.20	0.02	0.29	0.29	55278	QRSL1	AK022251	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1
233132_at	1.19	0.02	0.30	0.32	96610	LOC96610	AK026408	hypothetical protein similar to KIAA0187 gene product
233152_x_at	1.16	0.02	0.28	0.22	8658	TNKS	AL049979	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
233173_x_at	1.13	0.03	0.22	0.21	9328	GTF3C5	NM_012087	general transcription factor IIIC, polypeptide 5, 63kDa
233185_at	0.92	0.03	0.19	0.13	9358	ITGBL1	AF339819	integrin, beta-like 1 (with EGF-like repeat domains)
233186_s_at	1.08	0.03	0.14	0.18	54971	BANP	NM_017869	BTG3 associated nuclear protein
233195_at	0.86	7.01e-03	0.29	0.20	27019	DNAI1	AL117535	dynein, axonemal, intermediate polypeptide 1
233239_at	0.85	0.01	0.31	0.22	55628	ZNF407	AK024882	zinc finger protein 407
233270_x_at	1.16	0.01	0.25	0.21	5108	PCM1	AU146939	pericentriolar material 1
233405_at	1.23	1.98e-03	0.25	0.29	81608	FIP1L1	AU155384	FIP1 like 1 (S. cerevisiae)
233480_at	1.08	0.02	0.14	0.16	79188	TMEM43	AK026869	transmembrane protein 43
233655_s_at	0.89	6.05e-03	0.16	0.15	54801	FAM29A	NM_017645	family with sequence similarity 29, member A
233706_at	0.79	0.02	0.33	0.44	4773	NFATC2	AK024800	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2
233775_x_at	1.09	0.04	0.17	0.13	388509	LOC388509	AK023304	similar to hypothetical protein FLJ38281
233813_at	1.16	0.03	0.27	0.31	26051	PPP1R16B	AK026900	protein phosphatase 1, regulatory (inhibitor) subunit 16B

233842_x_at	1.09	3.77e-03	0.10	0.15	51507	C20orf43	NM_016407	chromosome 20 open reading frame 43
234762_x_at	1.10	0.04	0.21	0.17	57486	NLN	AK026655	neurolysin (metallopeptidase M3 family)
234807_x_at	1.15	6.02e-03	0.19	0.18	128668	RPL7AL2	AL121916	ribosomal protein L7a like 2
234875_at	1.20	4.9e-03	0.28	0.30	161406	RPL7AP3	AJ224082	ribosomal protein L7a pseudogene 3
234977_at	0.90	0.04	0.22	0.19	284273	ZADH2	NM_175907	zinc binding alcohol dehydrogenase,
domain containing 2								
235119_at	1.19	0.04	0.33	0.37	83860	TAF3	XM_291729	TAF3 RNA polymerase II, TATA box
binding protein (TBP)-associated factor, 140kDa								
235195_at	1.23	0.01	0.26	0.31	26190	FBXW2	BG109988	F-box and WD-40 domain protein 2
235197_s_at	1.09	0.03	0.16	0.17	28962	OSTM1	AV713913	osteopetrosis associated transmembrane
protein 1								
235348_at	1.12	0.02	0.20	0.23	84945	C13orf6	NM_032859	chromosome 13 open reading frame 6
235349_at	1.13	0.02	0.20	0.38	151393	FLJ32954	AF435956	hypothetical protein FLJ32954
235535_x_at	1.36	0.02	0.52	0.49	2483	FRG1	NM_004477	FSHD region gene 1
235552_at	1.10	0.03	0.18	0.21	57721	KIAA1627	NM_020961	KIAA1627 protein
235698_at	1.15	0.04	0.29	0.32	146198	ZFP90	AB075834	zinc finger protein 90 homolog (mouse)
235766_x_at	1.08	0.02	0.13	0.16	27161	EIF2C2	AA743462	eukaryotic translation initiation factor 2C, 2
235775_at	0.84	0.02	0.37	0.29	160335	DKFZp762A217	NM_152588	hypothetical protein DKFZp762A217
235791_x_at	1.09	0.02	0.16	0.17	1105	CHD1	AU155298	chromodomain helicase DNA binding
protein 1								
235816_s_at	1.12	0.04	0.23	0.38	266747	Rgr	NM_153615	Ral-GDS related protein Rgr
235870_at	1.14	9.23e-03	0.21	0.18	339524	LOC339524	NM_207357	hypothetical protein LOC339524
236265_at	1.14	0.01	0.23	0.25	6671	SP4	BC015512	Sp4 transcription factor
236924_at	1.19	0.01	0.27	0.25	11146	GLMN	AA814383	glomulin, FKBP associated protein
236974_at	1.11	0.02	0.19	0.20	10983	CCNI	AA808018	cyclin I
237563_s_at	1.14	7.29e-03	0.18	0.23	440731	LOC440731	XM_498838	LOC440731
238004_at	1.12	0.01	0.20	0.18	267002	PGBD2	NM_170725	piggyBac transposable element derived 2
238053_at	1.15	0.03	0.28	0.39	207063	DHRSX	NM_145177	dehydrogenase/reductase (SDR family) X-
linked								
238346_s_at	1.10	0.04	0.21	0.25	96764	NCOA6IP	NM_024831	nuclear receptor coactivator 6 interacting
protein								
238490_at	0.90	2.55e-03	0.13	0.12	158358	KIAA2026	AK091373	KIAA2026
238505_at	0.91	0.03	0.15	0.15	141	ADPRH	NM_001125	ADP-ribosylarginine hydrolase
238519_at	0.90	0.04	0.28	0.17	6248	RSC1A1	AF147408	regulatory solute carrier protein, family 1,
member 1								
238538_at	1.13	0.01	0.20	0.23	29123	ANKRD11	NM_013275	ankyrin repeat domain 11
238547_at	1.18	0.02	0.30	0.23	124790	FLJ32384	NM_144608	hypothetical protein MGC39389
238574_at	0.91	0.03	0.16	0.17	92014	MCART1	BF724944	mitochondrial carrier triple repeat 1
238581_at	1.29	0.04	0.66	0.59	115362	GBP5	BG271923	guanylate binding protein 5
238650_x_at	1.07	0.02	0.13	0.13	112840	C14orf150	NM_080666	chromosome 14 open reading frame 150
238846_at	0.82	9.81e-03	0.30	0.29	8792	TNFRSF11A	AW026379	tumor necrosis factor receptor
superfamily, member 11a, activator of NFKB								
238851_at	1.17	0.03	0.28	0.28	88455	ANKRD13	NM_033121	ankyrin repeat domain 13
238996_x_at	1.13	8.24e-03	0.19	0.22	226	ALDOA	NM_000034	aldolase A, fructose-bisphosphate
239007_at	1.15	0.04	0.27	0.39	90317	ZNF616	BC032805	zinc finger protein 616

239031_at	0.89	0.01	0.22	0.16	6752	SSTR2	AK093950	somatostatin receptor 2
239143_x_at	1.20	9.35e-03	0.31	0.35	51444	RNF138	NM_016271	ring finger protein 138
239824_s_at	1.13	0.01	0.19	0.27	84314	MGC10744	NM_032354	hypothetical protein MGC10744
240204_at	1.29	0.03	0.48	0.34	6638	SNRPN	AF400501	small nuclear ribonucleoprotein polypeptide
N								
240592_at	1.17	0.01	0.26	0.30	254251	MLR1	AK055258	transcription factor MLR1
240890_at	1.13	0.03	0.24	0.21	440066	LOC440066	XM_495897	similar to Caspase-4 precursor (CASP-4)
(ICH-2 protease) (TX protease) (ICE(rel)-II)								
241384_x_at	1.14	0.03	0.26	0.32	256356	MGC40579	BX648681	hypothetical protein MGC40579
241672_at	0.78	3.28e-03	0.35	0.30	400120	LOC400120	NM_203451	hypothetical LOC400120
241866_at	1.21	0.03	0.34	0.35	9194	SLC16A7	NM_004731	solute carrier family 16 (monocarboxylic
acid transporters), member 7								
242091_at	0.87	0.02	0.30	0.24	124411	LOC124411	AL832197	hypothetical protein LOC124411
242290_at	1.07	0.03	0.10	0.20	6867	TACC1	AY139007	transforming, acidic coiled-coil containing
protein 1								
242847_at	1.14	0.02	0.23	0.26	56946	C11orf30	BX647398	chromosome 11 open reading frame 30
243_g_at	1.14	0.01	0.20	0.24	4134	MAP4	NM_002375	microtubule-associated protein 4
243196_s_at	1.15	0.01	0.20	0.34	10906	FLN29	NM_006700	FLN29 gene product
243529_at	0.87	7.85e-04	0.19	0.12	92935	MARS2	NM_138395	methionine-tRNA synthetase 2
(mitochondrial)								
243760_at	1.14	0.03	0.25	0.29	387904	LOC387904	XM_370711	hypothetical LOC387904
243916_x_at	1.18	0.01	0.29	0.33	134510	MGC10067	NM_145049	hypothetical protein MGC10067
244103_at	1.12	5.64e-03	0.15	0.22	163859	FLJ35382	NM_152608	hypothetical protein FLJ35382
244227_at	0.86	0.02	0.25	0.27	148281	SYT6	NM_205848	synaptotagmin VI
244310_at	0.89	0.03	0.23	0.20	440283	LOC440283	AW973410	LOC440283
244563_at	0.87	0.03	0.32	0.24	79832	FLJ21924	AK055185	hypothetical protein FLJ21924
31799_at	1.14	0.02	0.22	0.26	56945	MRPS22	AF070618	mitochondrial ribosomal protein S22
31845_at	1.09	0.01	0.14	0.16	2000	ELF4	NM_001421	E74-like factor 4 (ets domain transcription
factor)								
32029_at	1.11	3.27e-03	0.16	0.12	5170	PDPK1	NM_031268	3-phosphoinositide dependent protein
kinase-1								
32029_at	1.11	3.27e-03	0.16	0.12	5170	PDPK1	NM_002613	3-phosphoinositide dependent protein
kinase-1								
32088_at	1.11	0.04	0.20	0.28	8548	BLZF1	U79751	basic leucine zipper nuclear factor 1 (JEM-1)
33778_at	1.08	0.03	0.16	0.16	25771	TBC1D22A	NM_014346	TBC1 domain family, member 22A
34206_at	1.10	8.09e-03	0.15	0.16	116985	CENTD2	NM_139181	centaurin, delta 2
34408_at	1.17	5.56e-03	0.22	0.23	6253	RTN2	NM_005619	reticulon 2
35156_at	1.10	0.02	0.19	0.19	203069	LOC203069	AL050297	hypothetical protein LOC203069
35160_at	1.10	0.04	0.21	0.25	8861	LDB1	NM_003893	LIM domain binding 1
35201_at	1.22	2.83e-03	0.27	0.21	3191	HNRPL	NM_001533	heterogeneous nuclear ribonucleoprotein L
35671_at	1.17	0.01	0.26	0.21	2975	GTF3C1	NM_001520	general transcription factor IIIC, polypeptide
1, alpha 220kDa								
36612_at	1.20	8.03e-03	0.26	0.23	23201	KIAA0280	D87470	KIAA0280 protein
36888_at	0.93	0.04	0.13	0.13	23354	KIAA0841	AB020648	KIAA0841
37549_g_at	1.18	0.02	0.25	0.33	27241	B1	NM_014451	parathyroid hormone-responsive B1 gene

37793_r_at	0.86	8.91e-03	0.22	0.20	5892	RAD51L3	NM_002878	RAD51-like 3 (S. cerevisiae)
37986_at	1.13	0.01	0.19	0.26	2057	EPOR	NM_000121	erythropoietin receptor
38241_at	1.14	0.04	0.24	0.21	10384	BTN3A3	NM_006994	butyrophilin, subfamily 3, member A3
38269_at	1.13	5.79e-03	0.19	0.17	25865	PRKD2	NM_016457	protein kinase D2
38290_at	1.11	0.02	0.16	0.20	10636	RGS14	NM_006480	regulator of G-protein signalling 14
38964_r_at	1.07	0.03	0.14	0.15	7454	WAS	NM_000377	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
39891_at	1.10	0.03	0.18	0.22	374655	DKFZp547K1113	AK160373	hypothetical protein DKFZp547K1113
40225_at	1.07	0.03	0.13	0.13	2580	GAK	NM_005255	cyclin G associated kinase
40255_at	1.09	0.02	0.16	0.16	55794	DDX28	NM_018380	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28
40420_at	1.07	0.02	0.12	0.15	6793	STK10	NM_005990	serine/threonine kinase 10
40829_at	1.10	0.02	0.18	0.20	23038	WDTC1	NM_015023	WD and tetratricopeptide repeats 1
41113_at	1.09	0.03	0.16	0.16	26048	ZNF500	AB011129	zinc finger protein 500
41220_at	1.09	0.01	0.16	0.12	10801	SEPT9	NM_006640	septin 9
41329_at	1.10	0.02	0.17	0.19	57147	PACE-1	NM_020423	ezrin-binding partner PACE-1
41577_at	1.17	6.85e-03	0.20	0.22	26051	PPP1R16B	NM_015568	protein phosphatase 1, regulatory (inhibitor) subunit 16B
43544_at	1.15	3.94e-03	0.21	0.19	10025	THRAP5	NM_005481	thyroid hormone receptor associated protein 5
44146_at	1.07	0.02	0.11	0.15	26205	GMEB2	NM_012384	glucocorticoid modulatory element binding protein 2
44617_at	1.07	0.04	0.14	0.13	79676	FLJ13491	NM_024623	hypothetical protein FLJ13491
44783_s_at	1.15	0.03	0.28	0.41	23462	HEY1	NM_012258	hairy/enhancer-of-split related with YRPW motif 1
45572_s_at	1.08	6.45e-03	0.12	0.11	26088	GGA1	NM_013365	golgi associated, gamma adaptin ear containing, ARF binding protein 1
45653_at	1.07	0.02	0.11	0.14	253980	KCTD13	NM_178863	potassium channel tetramerisation domain containing 13
46323_at	1.10	0.01	0.17	0.15	124583	CANT1	NM_138793	calcium activated nucleotidase 1
47105_at	1.17	5.42e-04	0.17	0.21	54920	FLJ20399	NM_017803	hypothetical protein FLJ20399
47571_at	1.21	4.97e-03	0.31	0.20	7776	ZNF236	NM_007345	zinc finger protein 236
48825_at	1.16	6.26e-04	0.17	0.17	51147	ING4	NM_016162	inhibitor of growth family, member 4
50376_at	1.09	0.03	0.17	0.14	55311	ZNF444	NM_018337	zinc finger protein 444
52731_at	1.15	0.01	0.25	0.22	55626	FLJ20294	NM_017749	hypothetical protein FLJ20294
53202_at	1.16	7.03e-03	0.22	0.22	79020	C7orf25	NM_024054	chromosome 7 open reading frame 25
54051_at	1.09	0.03	0.17	0.18	5316	PKNOX1	NM_004571	PBX/knotted 1 homeobox 1
57532_at	1.09	0.01	0.15	0.15	1856	DVL2	NM_004422	dishevelled, dsh homolog 2 (Drosophila)
59644_at	1.10	0.04	0.20	0.21	55589	BMP2K	NM_017593	BMP2 inducible kinase
63825_at	1.13	0.01	0.20	0.24	11057	ABHD2	AI557319	abhydrolase domain containing 2
64899_at	1.16	0.01	0.22	0.28	64748	LPPR2	NM_022737	lipid phosphate phosphatase-related protein type 2
71933_at	0.88	0.02	0.27	0.21	7475	WNT6	NM_006522	wingless-type MMTV integration site family, member 6
78383_at	1.10	0.02	0.17	0.17	10210	TOPORS	AI150117	topoisomerase I binding, arginine/serine-rich

90610_at	1.07	0.01	0.10	0.14	4034	LRCH4	NM_002319	leucine-rich repeats and calponin homology (CH) domain containing 4
91952_at	1.12	0.03	0.21	0.20	90379	LOC90379	XM_373433	hypothetical protein BC002926
AFFX-HUMISGF3A/M97931.11			0.02	0.21	0.38	6772	STAT1	NM_007315	signal transducer and activator of transcription 1, 91kDa

AMENDED CLAIMS
received by the International Bureau on 08 May 2007 (08.05.2007)

1. A method of testing for one or more colorectal pathologies in a test subject, the method comprising:

(a) providing data representing a level of one or more products of each of at least two biomarkers in a sample isolated and/or derived from said test subject, wherein said biomarkers are genes selected from the group consisting of BCNP1, CD163, CDA, MS4A1, BANK1, and MGC20553; and

(b) applying to said data a formula based on (i) a dataset representing levels of one or more products of each of said biomarkers in each subject of a reference population having said one or more pathologies, and (ii) a dataset representing levels of one or more products of each of said biomarkers in each subject of a reference population not having said one or more pathologies, thus providing an indication of a probability that said test subject has said one or more colorectal pathologies.

2. A computer-based method for testing for one or more colorectal pathologies in a test subject, the method comprising:

inputting, to a computer, data representing a level of products of each of at least two biomarkers in a sample isolated and/or derived from a test subject, wherein said biomarkers are genes selected from the group consisting of BCNP1, CD163, CDA, MS4A1, BANK1 and MGC20553; and

causing said computer to apply to said data, a formula based on (i) a dataset representing levels of one or more products of each of said biomarkers in each subject of a reference population having said one or more pathologies, and (ii) a dataset representing levels of one or more products of each of said biomarkers in each subject of a reference population not having said one or more pathologies, thus providing an indication of a probability that said test subject has said one or more colorectal pathologies.

3. The method of claims 1 or 2, wherein said formula has a form:

$V = C + \Sigma\beta_i X_i$,

wherein V is a value indicating a probability that said test subject has said one or more colorectal pathologies, Xi is a level of products of an ith biomarker of said biomarkers, βi is a coefficient, and C is a constant.

4. The method of claims 1 or 2, wherein said formula has a form:

$V = C + \Sigma\beta_{ij}(X_i / X_j)$,

wherein V is a value indicating a probability that said test subject has said one or more colorectal pathologies, X_i is a level of products of an *i*th biomarker of said biomarkers, X_j is a level of products of a *j*th biomarker of said biomarkers where the *i*th biomarker is not the *j*th biomarker, β_{ij} is a coefficient and C is a constant.

5. The method of claims 1 or 2, wherein said formula is derived by logistic regression.

6. The method of claims 1 or 2, wherein said sample is selected from the group consisting of blood, lymph and lymphoid tissue.

7. The method of claims 1 or 2 wherein said products in said sample are RNA.

8. The method of claims 1 or 2, wherein said sample is selected from the group consisting of a sample of serum-reduced blood, a sample of erythrocyte-reduced blood, a sample of serum-reduced and erythrocyte-reduced blood, a sample of unfractionated cells of lysed blood, and a sample of fractionated blood.

9. The method of claims 1 or 2, wherein said products in said sample are RNA, and whereas said data represents a level of cDNA, EST and/or PCR product derived from said RNA.

10. A kit comprising packaging and containing at least two primer sets, wherein each set of which is able to generate an amplification product by selective amplification of at least a portion of a polynucleotide complementary to one or more RNA products of a biomarker, wherein said biomarker is a gene selected from the group consisting of: BCNP1, CD163, CDA, MS4A1, BANK1, and MGC20553; and wherein each set of said primer sets is selective for a different biomarker of said group.

11. The kit of claim 10, wherein said polynucleotide is selected from the group consisting of total RNA, mRNA, DNA, cDNA and EST.

12. The kit of claim 10, further comprising two or more oligonucleotide probes, wherein each of said probes is capable of selectively hybridizing to either a sense or an antisense strand of said amplification product.

13. The kit of claims 10, 11 or 12, further comprising two or more components selected from the group consisting of: a thermostable polymerase, a reverse transcriptase, deoxynucleotide triphosphates, nucleotide triphosphates and enzyme buffer.

14. The kit of claims 10, 11, 12 or 13, further comprising a computer-readable medium encoded with instructions for applying a formula to data representing levels of said amplification product in a sample isolated and/or derived from a test subject, wherein said formula is said based on (i) a dataset representing levels of one or more products of each of said biomarkers in each subject of a reference population having one or more colorectal pathologies, and (ii) a dataset representing levels of one or more products of each of said biomarkers in each subject of a reference population not having said one or more pathologies, thus providing an indication of a probability that said test subject has said one or more colorectal pathologies.

15. The kit of claim 14, wherein said formula has a form:

$V = C + \Sigma\beta_i X_i$,

wherein V is a value indicating a probability that said test subject has said one or more colorectal pathologies, X*i* is a level of products of an *i*th biomarker of said biomarkers, β_i is a coefficient, and C is a constant.

16. The kit of claim 14, wherein said formula has a form:

$V = C + \Sigma\beta_{ij}(X_i / X_j)$,

wherein V is a value indicating a probability that said test subject has said one or more colorectal pathologies, X_i is a level of products of an *i*th biomarker of said biomarkers, X_j is a level of products of a *j*th biomarker of said biomarkers where the *i*th biomarker is not the *j*th biomarker, β_{ij} is a coefficient, and C is a constant.

17. The kit of claims 14, 15 or 16, wherein said sample is selected from the group consisting of blood, lymph and lymphoid tissue.

18. The kit of claims 14, 15 or 16, wherein said sample is selected from the group consisting of a sample of serum-reduced blood, a sample of erythrocyte-reduced blood, a sample of serum-reduced and erythrocyte-reduced blood, a sample of unfractionated cells of lysed blood and a sample of fractionated blood.

19. A computer-readable medium having instructions stored thereon that are operable when executed by a computer to apply a formula to data representing a level of one or more products of each of at least two biomarkers in a sample isolated and/or derived from a test subject, wherein said biomarkers are genes selected from the group consisting of BCNP1, CD163, CDA, MS4A1, BANK1, and MGC20553, wherein said formula is based on (i) a dataset representing levels of one or more products of each of said biomarkers in each subject of a reference population having one or more colorectal pathologies, and (ii) a dataset representing levels of one or more products of each of said biomarkers in each subject of a reference population not having said one or more pathologies, thus providing an indication of a probability that said test subject has said one or more colorectal pathologies.

20. The computer-readable medium of claim 19, wherein said formula has a form:

$V = C + \Sigma\beta_i X_i$,

wherein V is a value indicating a probability that said test subject has said one or more colorectal pathologies, X_i is a level of products of an ith biomarker of said biomarkers, β_i is a coefficient, and C is a constant.

21. The computer-readable medium of claim 19, wherein said formula has a form:

$V = C + \Sigma\beta_{ij}(X_i / X_j)$,

wherein V is a value indicating a probability that said test subject has said one or more colorectal pathologies, X_i is a level of products of an *i*th biomarker of said biomarkers, and Xj is a level of products of a *j*th biomarker of said biomarkers, where the *i*th biomarker is not the *j*th biomarker, β_{ij} is a coefficient and C is a constant.

22. The computer-readable medium of claim 19 wherein said formula is derived by logistic regression.

23. The computer-readable medium of claim 19 wherein said sample is selected from the group consisting of blood, lymph and lymphoid tissue.

24. The computer-readable medium of claims 19 wherein said products in said sample are RNA.

25. The computer-readable medium of claim 19, wherein said sample is selected from the group consisting of a sample of serum-reduced blood, a sample of erythrocyte-reduced blood, a sample of serum-reduced and erythrocyte-reduced blood, a sample of unfractionated cells of lysed blood, and a sample of fractionated blood.

26. The computer-readable medium of claim 19 wherein said products in said sample are RNA, and whereas said data represents a level of cDNA, EST and/or PCR product derived from said RNA.

27. A computer system for providing an indication of a probability that a test subject has one or more colorectal pathologies, the computer system comprising

a processor; and

a memory configured with instructions that, when executed, cause said processor to provide a user with said indication, wherein said instructions comprise applying a formula to data representing a level of one or more products of each of at least two biomarkers in a sample isolated and/or derived from said test subject, wherein said biomarkers are genes selected from the group consisting of BCNP1, CD163, CDA, MS4A1, BANK1, and MGC20553; and wherein said formula is based on (i) a dataset representing levels of one or more products of each of said biomarkers in each subject of a reference population having said one or more pathologies, and (ii) a dataset representing levels of one or more products of each of said biomarkers in each subject of a reference population not having said one or more pathologies, thus providing said indication of said probability that said test subject has said one or more colorectal pathologies.

28. The system of claim 27, wherein said formula has a form:

$V = C + \Sigma\beta_i X_i$,

wherein V is a value indicating a probability that said test subject has said one or more colorectal pathologies, X_i is a level of products of an *i*th biomarker of said biomarkers, β_i is a coefficient, and C is a constant.

29. The system of claim 27, wherein said formula has a form:

$V = C + \Sigma\beta_{ij}(X_i / X_j)$,

wherein V is a value indicating a probability that said test subject has said one or more colorectal pathologies, X_i is a level of products of an *i*th biomarker of said biomarkers, and X_j is a level of products of a *j*th biomarker of said biomarkers, where the *i*th biomarker is not the *j*th biomarker, β_{ij} is a coefficient, and C is a constant.

30. The system of claim 27, wherein said formula is derived by logistic regression.

31. The system of claim 27, wherein said sample is selected from the group consisting of blood, lymph and lymphoid tissue.

32. The system of claim 27, wherein said products in said sample are RNA.

33. The system of claim 27 wherein said sample is selected from the group consisting of a sample of serum-reduced blood, a sample of erythrocyte-reduced blood, a sample of serum-reduced and erythrocyte-reduced blood, a sample of unfractionated cells of lysed blood, and a sample of fractionated blood.

34. The system of claim 27 wherein said products in said sample are RNA, and whereas said data represents a level of cDNA, EST and/or PCR product derived from said RNA.

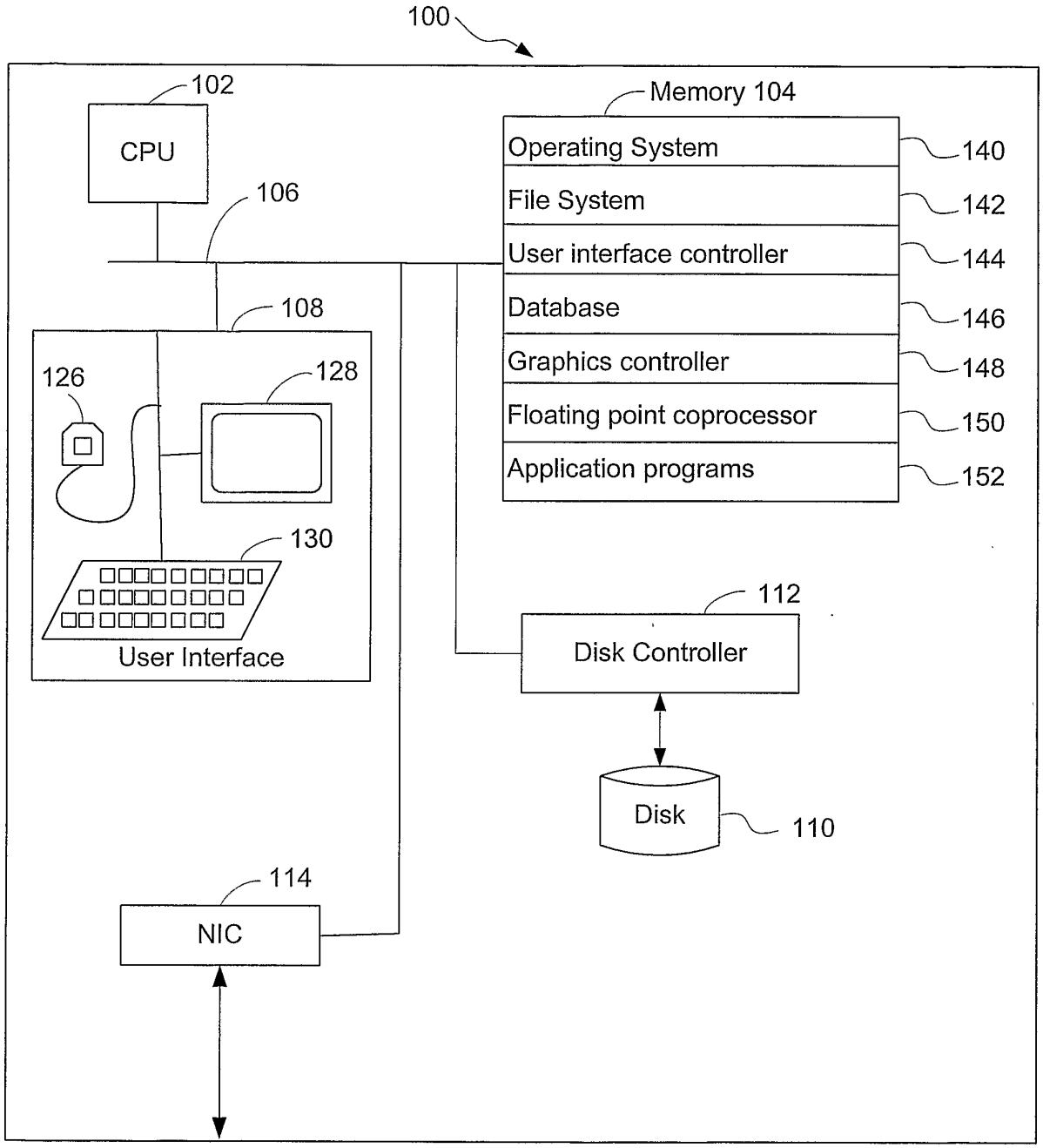

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Memory 104
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File System
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User interface controller
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Database
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Graphics controller
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Floating point coprocessor
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User Interface
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Disk Controller
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FIG. 1

FIGURE 2

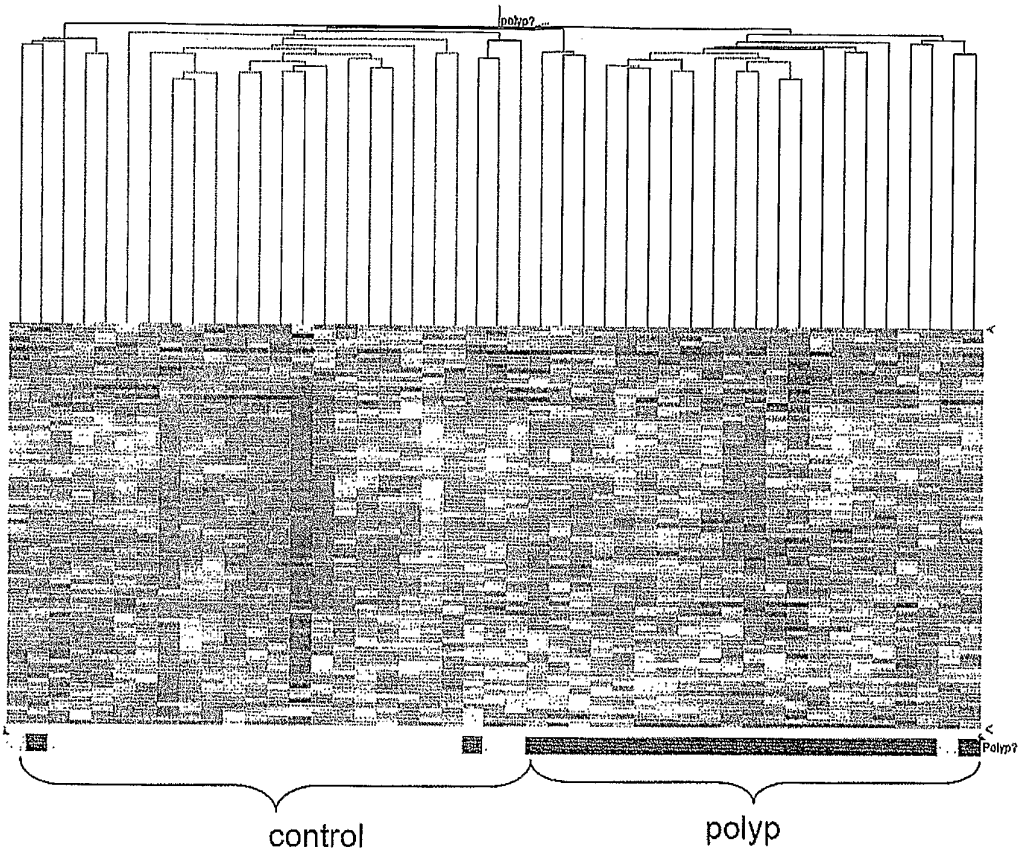


FIGURE 3

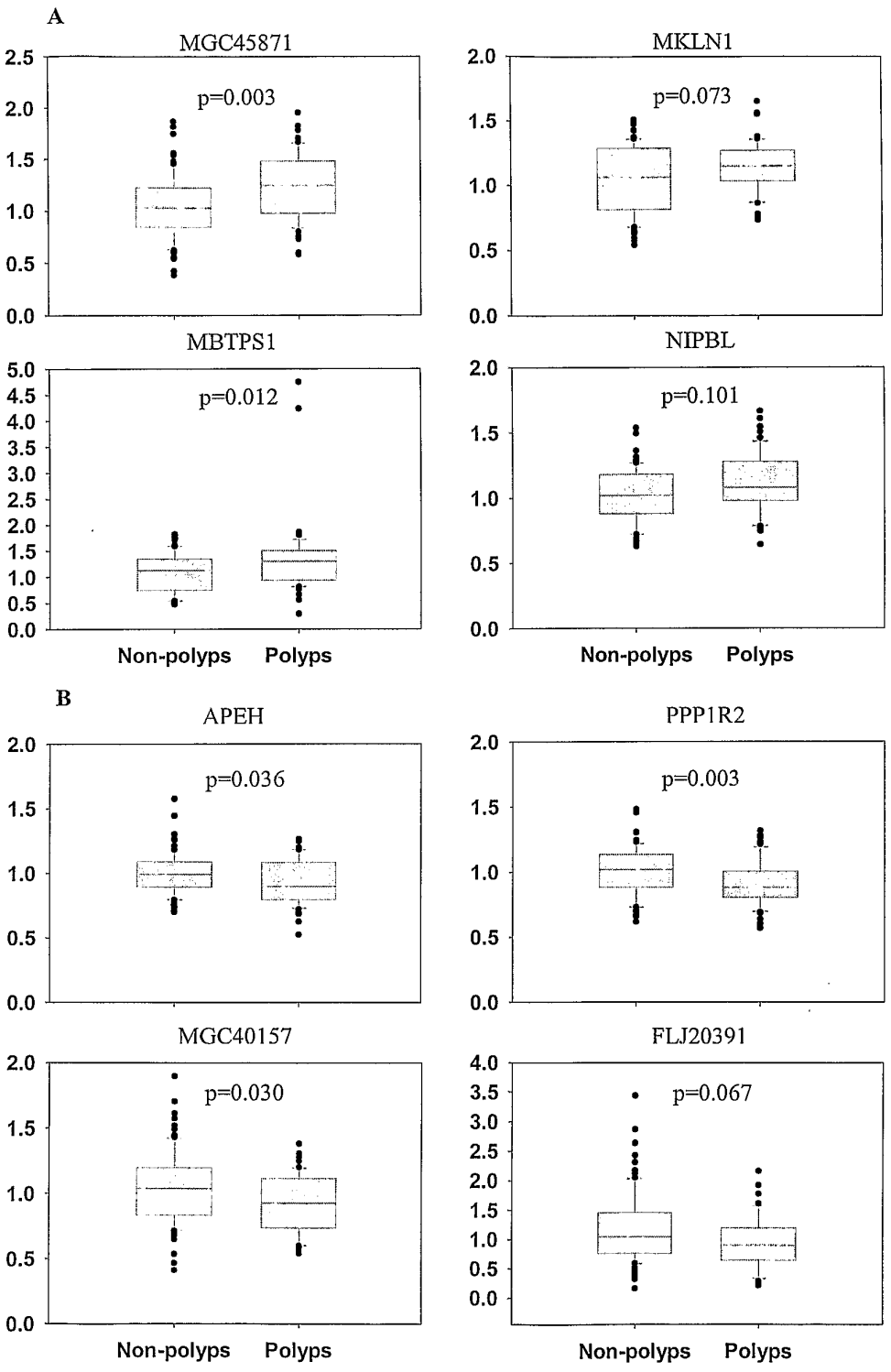

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FIGURE 4

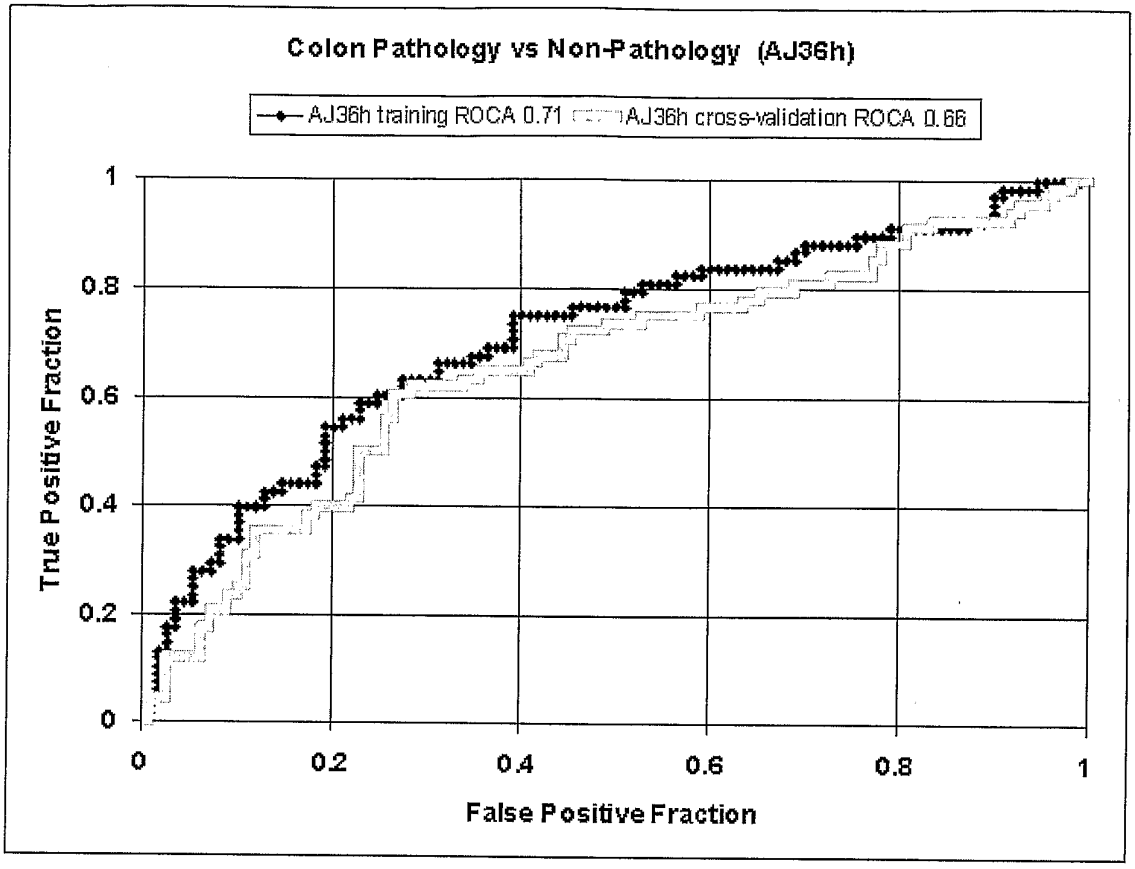

Colon Pathology vs Non-Pathology (AJ36h)
AJ36h training ROCA 0.71
AJ36h cross-validation ROCA 0.66
True Positive Fraction
False Positive Fraction
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0.4
0.6
0.8
1

Figure 5

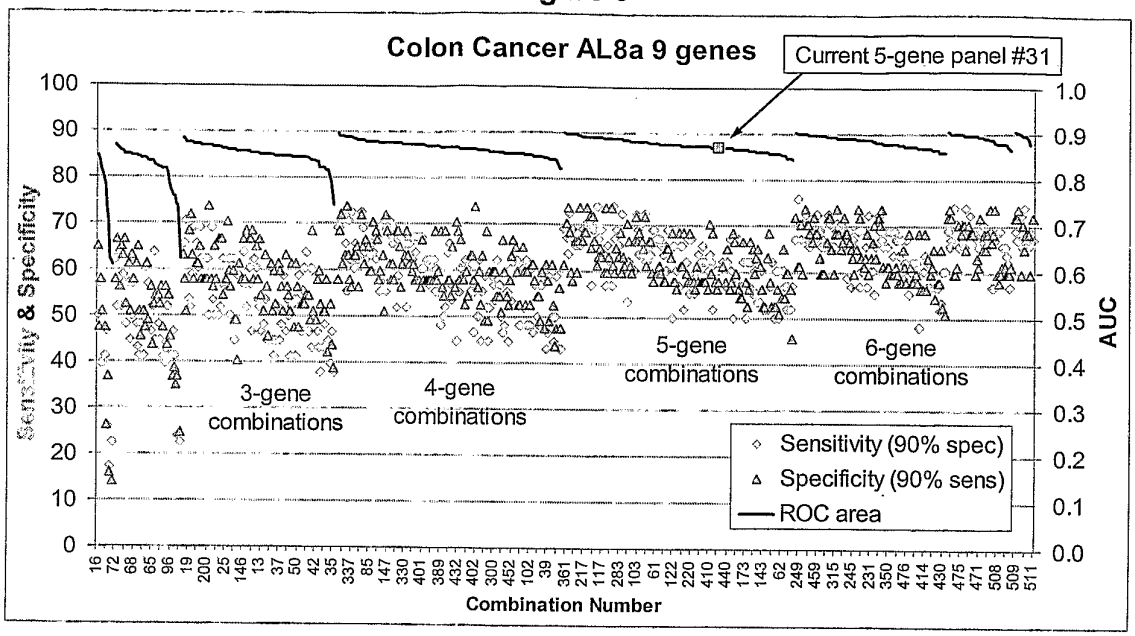
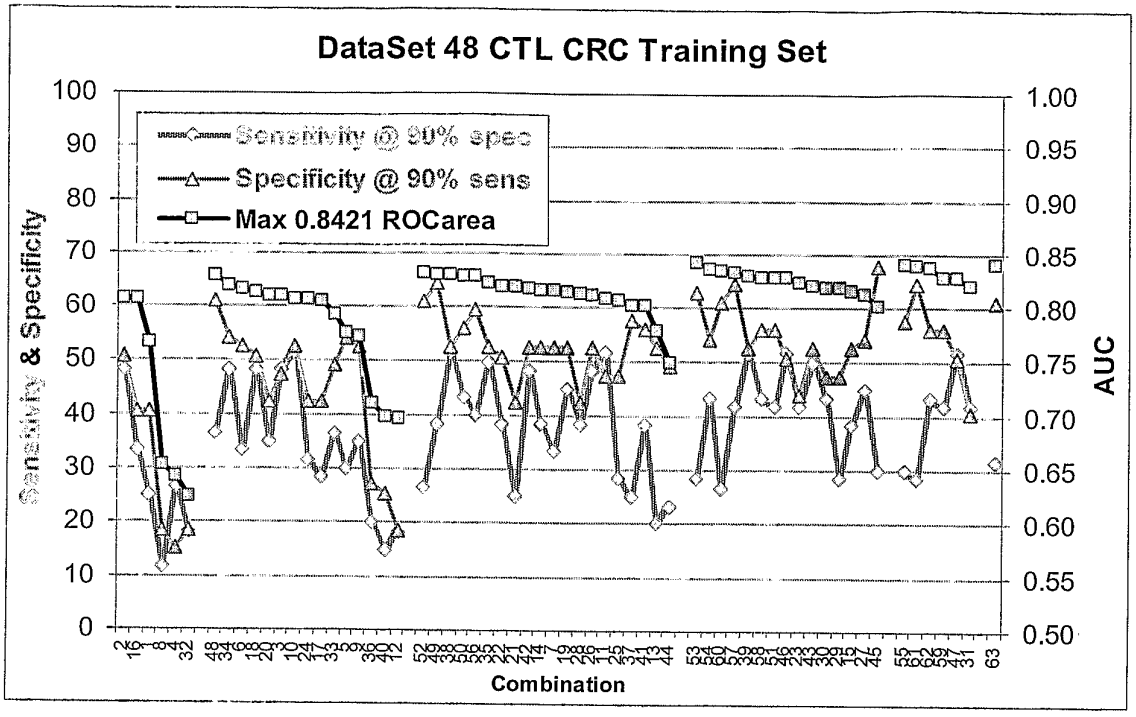

Colon Cancer AL8a 9 genes
Current 5-gene panel #31
Sensitivity & Specificity
AUC
3-gene combinations
4-gene combinations
5-gene combinations
6-gene combinations
Sensitivity (90% spec)
Specificity (90% sens)
ROC area
Combination Number

Figure 6


DataSet 48 CTL CRC Training Set
Sensitivity @ 90% spec
Specificity @ 90% sens
Max 0.8421 ROCarea
Sensitivity & Specificity
AUC
Combination
100
90
80
70
60
50
40
30
20
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