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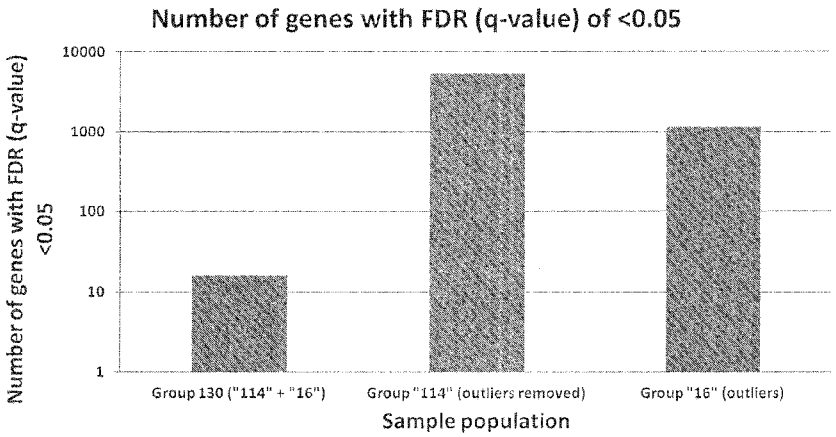


FIGURE 6

(57) Abstract: The present invention provides an *in vitro* method for determining the responsiveness of an individual with Hodgkin's lymphoma to chemotherapeutic drug treatment, the method comprising the steps of providing a protein or mRNA sample from a lymph node of the individual to be tested and then determining the presence and/or amount in the sample of at least two proteins selected from the group identified in Table A, and/or of mRNA encoding the same, wherein the presence and/or amount in the sample of the proteins selected from the group defined in Table A, or of the mRNA encoding the same, is indicative of the responsiveness of the individual with Hodgkin's lymphoma to chemotherapeutic drug treatment. The invention further provides arrays and kits for use in the same.

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NOVEL BIOMARKER SIGNATURE AND USES THEREOF

Field of Invention

The present invention relates to novel biomarkers, and signatures comprising the same, for identifying individuals with Hodgkin's lymphoma who are responsive or resistant to treatment with chemotherapeutic agents.

Background

From a therapeutic perspective the management of patients with Hodgkin's lymphoma (HL) represents a challenging paradigm. As observed in other cancer groups, this is primarily manifested as a variation in the clinical response to chemotherapeutic intervention and presents phenotypically as one of three broad categorical groups: a) response; b) partial response; c) no response [1], [2]. This issue is further compounded by potential side effects elicited by toxicity to non-tumour cells and consequently introduces an additional complication to patient treatment protocols [3], [4], [5]. There is therefore an urgent need for molecular markers that are indicative for appropriate dosing strategies directed specifically towards the individual patient in addition to assays capable of identifying potential resistant/sensitive responses.

At the heart of these clinical issues is the genetic heterogeneity exhibited not only between individual patients with respect to their genomic DNA sequence, but also the somatic mutations that might arise as part of the evolutionary development of the tumour [6], [7], [8]. With respect to the latter, further complexity is exhibited in that mutations have been classified into two broad groups: a) "driver" mutations in which key cellular pathways are abrogated and begin to positively subvert the cellular machinery towards more aggressive phenotypes and b) "passenger" mutations which do not actively promote or abrogate the tumorigenic process but represent "background" noise [9], [10]. The ability to demarcate between mutations that drive aggressive phenotypes from those

that play no significant role in altering the clinical response to chemotherapy would provide potentially useful diagnostic assays with utility for triaging patients into those that may benefit from treatment versus those who are unlikely. With appropriate quantitation, characterisation and validation studies, these markers may also assist in dosing strategies for sensitive patients.

The present invention seeks to provide novel biomarkers for use in predicting the responsiveness of a patient with Hodgkin's lymphoma to chemotherapeutic drug treatment.

Summary of Invention

The invention provides methods of gene expression analysis in which a novel biomarker 'signature' is obtained to predict the responsiveness of a Hodgkin's lymphoma patient to chemotherapy, wherein the signature corresponds to quantitative information about the amount of a plurality of proteins (or mRNA encoding the same) which have been identified as characteristic of the responsiveness of said patient.

Thus, a first aspect of the invention provides an *in vitro* method for determining the responsiveness of an individual with Hodgkin's lymphoma to chemotherapeutic drug treatment, the method comprising the steps of:

(a) providing a protein or mRNA sample from a lymph node of the individual to be tested;

(b) determining the presence and/or amount in the sample of at least two proteins selected from the group identified in Table 1, and/or of mRNA encoding the same

wherein one or more of the at least two proteins selected from the group identified in Table A is not identified in Table B

and wherein the presence and/or amount in the sample of the proteins selected from the group identified in Table A, or of the mRNA encoding the same, is indicative of the responsiveness of the individual with Hodgkin's lymphoma to chemotherapeutic drug treatment.

Table A lists all of the biomarkers identified herein as being differentially expressed (*i.e.* having an adjusted 'p'-value ['q'-value] of less than 0.05 in patients exhibiting a typical gene expression profile; see Example A) in chemotherapy-responsive *versus* chemotherapy-resistant Hodgkin's lymphoma patients (see Example A below).

Table B lists eighty-six biomarkers previously known or suggested in the art as being of potential diagnostic value in differentiating chemotherapy-responsive from chemotherapy-resistant Hodgkin's lymphoma patients (see ref [34], in particular Table S5 of supplementary appendix therein; the disclosures of which are incorporated herein by reference).

In all tables herein, a positive log-fold change ('LogFC') indicates increased expression in chemotherapy-responsive *versus* chemotherapy-resistant Hodgkin's lymphoma patients, whilst a negative log-fold change ('LogFC') indicates increased expression in chemotherapy-resistant *versus* chemotherapy-responsive Hodgkin's lymphoma patients.

The individual being tested is typically a human. However, it will be appreciated that the methods may also be used for the diagnosis of any domestic or farm mammal (such as a horse, pig, cow, sheep, dog or cat).

By "chemotherapeutic drug treatment" we include any of the chemotherapeutic drug regimes commonly used clinically in the treatment of Hodgkin's lymphoma. For example, most people with early stage Hodgkin's lymphoma have 2 to 4 cycles of ABVD chemotherapy, which contains the drugs adriamycin (doxorubicin), bleomycin, vinblastine and dacarbazine. For advanced stage Hodgkin's lymphoma some people have ABVD for up to 8 cycles.

Other possible chemotherapeutic drug combinations include:

ChlvPP - chlorambucil, vinblastine, procarbazine and prednisolone

Stanford V - mustine, doxorubicin, vinblastine, vincristine, bleomycin, etoposide and steroids

BEACOPP - bleomycin, etoposide, doxorubicin, cyclophosphamide, vincristine, procarbazine and prednisolone

If chemotherapy does not work well or the lymphoma comes back some people have "BEAM" chemotherapy with a stem cell transplant:

B = Carmustine (BiCNU)

E = Etoposide

A = Cytarabine (Ara-C, cytosine arabinoside)

M = Melphalan

By "responsiveness" in the context of chemotherapeutic drug treatment of an individual with Hodgkin's lymphoma we include the therapeutic effectiveness of the treatment with respect to Hodgkin's lymphoma. Thus, "responsiveness" includes the ability of chemotherapeutic drug treatment to reduce and most preferably prevent a clinically significant deficit in the activity, function and response of the individual with Hodgkin's lymphoma. For example, the measure of responsiveness may encompass the effect of the chemotherapeutic drug treatment on one or more of the following:

- the reduction of lymphoma cells within the individual;
- the growth and/or proliferation of lymphoma cells within the individual;
- the growth of tumours within the individual;
- the extent and/or rate of metastasis of tumours within the individual; and
- the life expectancy of the individual.

Step (a) of the methods of the invention comprises providing a protein or mRNA sample from the individual to be tested.

Typically, the sample is a lymph node tumour biopsy sample (which may have been excised from the individual previously, for example at the time of diagnosis).

Alternatively, the sample may be a blood or serum sample.

It will be appreciated by persons skilled in the art that the samples may be fresh-frozen or formalin-fixed.

In one embodiment, step (b) comprises measuring the presence and/or amount in the sample of at least three proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least four, five, six, seven, eight, nine, ten,

eleven, twelve, thirteen, fourteen, fifteen or more proteins selected from the group identified in Table A, and/or mRNA encoding the same.

Thus, step (b) may comprise measuring the presence and/or amount in the sample of at least 20 proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least 30, 40, 50, 100, 200, 500, 1000, or more proteins selected from the group identified in Table A, and/or mRNA encoding the same

In one embodiment, the proteins and/or mRNA encoding the same measured in step (b) are selected from one of the following sub-groups defined in Table A:

(a) Biomarker nos. 1 to 10;
(b) Biomarker nos. 1 to 20;
(c) Biomarker nos. 1 to 30;
(d) Biomarker nos. 1 to 40;
(e) Biomarker nos. 1 to 50;
(f) Biomarker nos. 1 to 100;
(g) Biomarker nos. 1 to 200;
(h) Biomarker nos. 1 to 500;
(i) Biomarker nos. 1 to 1000;
(j) Biomarker nos. 1 to 2000;
(k) Biomarker nos. 1 to 3000; or
(l) Biomarker nos. 1 to 4000.

wherein the biomarker number is given in the first column of Table A ("No.").

For example, step (b) may comprise measuring the presence and/or amount in the sample of biomarker nos. 1 to 10 in Table A (i.e. the first ten biomarkers listed in Table A) and/or mRNA encoding the same

In one embodiment, none of the proteins from Table A selected in step (b) are identified in Table B. For example, the proteins selected may be absent from the tables of known differentially-expressed biomarkers disclosed in reference 34 (*e.g.* in supplementary tables 2, 3, 4 and/or 5).

In one preferred embodiment, step (b) comprises measuring the presence and/or amount in the sample of at least one protein, and/or mRNA encoding the same, selected from the group consisting of:

(a) Zinc finger protein 644 (ZNF644) ;
(b) Colipase, pancreatic (CLPS) ;
(c) EST tu05b03.x1;
(d) relaxin 1 (RLN1);
(e) phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D);
(f) EMI domain containing 2 (EMID2);
(g) heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa; HSPA5));
(h) spermatogenesis associated 12 (SPATA12);
(i) kinectin 1 (kinesin receptor; KTN1);
(j) pentraxin 3, long (PTX3);
(k) erythropoietin receptor (EPOR);
(l) DC-STAMP domain containing 2 (DCST2);
(m) golgi to ER traffic protein 4 homolog (*S. cerevisiae*; GET4);
(n) mitogen-activated protein kinase 14 (MAPK14); and
(o) chromosome 1 open reading frame 163 (C1orf163).

For example, (b) may comprise measuring the presence and/or amount in the sample of all of biomarkers 'a' to 'o' above, and/or mRNA encoding the same (see Table C).

Table C lists all of the biomarkers identified herein as being differentially expressed (*i.e.* having an adjusted 'p'-value ['q'-value] of less than 0.05 in patients; see Example A) in all chemotherapy-responsive versus chemotherapy-resistant Hodgkin's lymphoma patients (see Example A below).

Optionally, biomarkers 'a' to 'o' above are measured at the mRNA level using the probe sets ("Probe ID's") identified in Table A (from the Affymetrix GeneChip Human Genome U133 Plus 2.0 array, from Affymetrix Inc, Santa Clara, USA). For example, mRNA levels for heat shock 70kDa protein 5 may be determined using Affymetrix probe set 211936_at.

It will be appreciated by persons skilled in the art that gene expression of the biomarkers of the invention may be determined at either the protein or mRNA level (or both).

In one embodiment, step (b) comprises measuring the presence and/or amount in the sample of mRNA encoding the proteins selected from the group identified in Table A. Thus, measuring the presence and/or amount in the sample of the mRNA may be performed using binding agents capable of binding to the said mRNA, for example using oligonucleotides with a nucleotide sequence complementary to the target mRNA in a hybridisation assay.

In an alternative embodiment, step (b) comprises measuring the presence and/or amount in the sample of the proteins selected from the group identified in Table A, for example using binding agents capable of binding to said proteins. Suitable binding agents may comprise or consist of an antibody or an antigen-binding fragment thereof, such as intact antibodies, Fv fragments (*e.g.* single chain Fv and disulphide-bonded Fv), Fab-like fragments (*e.g.* Fab fragments, Fab' fragments and $F(ab)_2$ fragments), single variable domains (*e.g.* V_H and V_L domains) and domain antibodies (dAbs, including single and dual formats [*i.e.* dAb-linker-dAb]).

Suitable assays for detecting proteins include enzyme linked immunosorbent assays (ELISA), radioimmunoassay (RIA), immunoradiometric assays (IRMA) and immunoenzymatic assays (IEMA), including sandwich assays using monoclonal and/or polyclonal antibodies. Exemplary sandwich assays are described by David *et al* in US Patent Nos. 4,376,110 and 4,486,530, hereby incorporated by reference. Antibody staining of cells on slides may be used in methods well known in cytology laboratory diagnostic tests, as well known to those skilled in the art.

For example, the presence and/or amount of the proteins selected from Table A may be determined by ELISA.

Conveniently, the binding agent comprises or consists of an antibody-like binding agent, for example an affibody or aptamer.

It will be appreciated by persons skilled in the art the proteins and/or mRNA in the sample may be labelled with a detectable moiety prior to performing step (b). A suitable detectable moiety is selected from the group consisting of: a fluorescent moiety; a luminescent moiety; a chemiluminescent moiety; a radioactive moiety; an enzymatic moiety.

In one embodiment, measuring the presence and/or amount of the proteins, or mRNA encoding the same, in the sample is performed using a gene expression profiling array. Suitable arrays include surface-based arrays and bead-based arrays, which may be macroarrays, microarrays or nanoarrays.

Conveniently, the gene expression profiling array is commercially available. For example, such as the GeneChip Human Genome U133 Plus 2.0 array, from Affymetrix Inc, Santa Clara, USA.

Optionally, the method of the first aspect of the invention further comprises step (c) of comparing the presence and/or amount of the proteins, or mRNA encoding the same, with one or more reference values for said proteins or mRNA.

By "reference value" we mean a numerical value corresponding to the amount of a biomarker protein (or its mRNA) associated with a defined group of individuals.

Thus, in one embodiment the reference values correspond to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals selected from a group consisting of healthy individuals, individuals diagnosed with Hodgkin's lymphoma who are responsive to chemotherapeutic drug treatment and individuals diagnosed with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment.

For example, the reference values may correspond to the amount of the biomarker proteins or mRNA associated with individuals from the GEO dataset (Expression series GSE17920) diagnosed with Hodgkin's lymphoma who are responsive to chemotherapeutic drug treatment and individuals from the GEO diagnosed with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment (see Example A below).

It will be appreciated by persons skilled in the art that the amount of the proteins, or mRNA encoding the same, obtained in step (b) and the reference values for said proteins or mRNA may be normalised prior to being compared.

The comparison in step (c) may be performed manually but more typically will be performed using computer-based tools.

In one embodiment, step (c) comprises the use of a predictive model, such as a computer-implemented adaptive learning algorithm.

In one preferred embodiment, the adaptive learning algorithm is an artificial neural network, *e.g.* a multilayer perceptron (see Example A below).

One of the significant advantages of the methods of the present invention is the improved predictive accuracy of the biomarker signatures relative to existing methods for determining the responsiveness of Hodgkin's lymphoma patients to chemotherapy. For example, in reference 34 (Steidl *et al.*, 2010 *NEJM*, **362**:875-885) a biomarker signature for determining the responsiveness of Hodgkin's lymphoma patients to chemotherapy is reported with a predictive accuracy (AUC) of 0.837 based on gene expression profile data from 130 Hodgkin's lymphoma patients (GEO expression series GSE17920), compared to a predictive accuracy of only 0.625 using a clinical model based on the International Prognostic Score.

Using gene expression profile data from the same 130 Hodgkin's lymphoma patients, the methods of the present invention achieved a predictive accuracy (AUC) of 0.926 for all patients (see Example A below). However, following the identification and removal of patients with atypical gene expression profiles (so-called "outliers", of which 16 were identified), then 100% predictive accuracy was achieved with the remaining 114 patients. Moreover, a separate biomarker signature identified for use in the atypical "outlier" patient group also achieved 100% predictive accuracy (in the 16 patients).

From a clinical perspective, such improvements in predictive accuracy are highly significant, enabling clinicians to determine with much greater certainty an effective therapeutic regime for each individual patient.

Thus, in one embodiment, the methods of the invention utilize a predictive model having an accuracy of at least 90% for determining the responsiveness of Hodgkin's lymphoma patients to chemotherapy. For example, the predictive model may have an accuracy of at least 95% for such patient classification, and preferably at least 99%.

It will be appreciated that such predictive accuracy may be determined relative to any given population of Hodgkin's lymphoma patients. In one embodiment, however, the predictive accuracy is determined relative to the 130 patients used in Example A (Expression series GSE17920 from the Gene Expression Omnibus [GEO] data repository).

The studies detailed in Example A below reveal that some proteins exhibit increased expression in individuals with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment whilst some proteins exhibit decreased expression in individuals with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment (compared to the expression of said proteins in individuals with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment).

In one embodiment,

(a) an elevation in the amount of one or more of the following proteins (or mRNA encoding the same) relative to reference values corresponding to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment

HSPA5, PTX3, C1orf163, KTN1, MAPK14 and/or EPOR

and/or

(b) a decrease in the amount of one or more of the following proteins (or mRNA encoding the same) relative to reference values corresponding to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment

ZNF644, EMID2, RLN1, SPATA12, CLPS, EST tu05b03.x1, PDE6D, GET 4 and/or DCST2

is indicative of the individual with Hodgkin's lymphoma being responsive to chemotherapeutic drug treatment.

Likewise, in another embodiment,

(a) an elevation in the amount of one or more of the following proteins (or mRNA encoding the same) relative to reference values corresponding to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals with Hodgkin's lymphoma who are responsive to chemotherapeutic drug treatment

ZNF644, EMID2, RLN1, SPATA12, CLPS, EST tu05b03.x1, PDE6D, GET 4 and/or DCST2

and/or

(b) a decrease in the amount of one or more of the following proteins (or mRNA encoding the same) relative to reference values corresponding to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals with Hodgkin's lymphoma who are responsive to chemotherapeutic drug treatment

HSPA5, PTX3, C1orf163, KTN1, MAPK14 and/or EPOR

is indicative of the individual with Hodgkin's lymphoma being resistant to chemotherapeutic drug treatment.

In a further embodiment of the methods of the invention, step (c) comprises identifying the individual as exhibiting atypical gene expression.

By "atypical gene expression" we mean that the gene expression profile for the dataset (*e.g.* patient group or sub-group) is qualitatively and/or quantitatively different from the gene expression profile most commonly observed in that dataset. In particular, the presence and/or amount of one or more proteins (or their respective mRNAs) may be quantitatively different from the presence and/or amount of said proteins or mRNAs most commonly observed in that dataset.

For example, in the case of patients with Hodgkin's lymphoma, the presence and/or amount of one or more (*e.g.* all) proteins in Table C may be atypical for a given sub-group of those patients (*e.g.* patients responsive or resistant to chemotherapy).

Having identified a given patient as falling within the "outlier" subgroup, a different biomarker signature may be used to determiner whether said patient is responsive or resistant to chemotherapy.

For example, the methods of the invention may further comprise step (d) of determining the presence and/or amount in the sample of at least two proteins selected from the group identified in Table D, and/or of mRNA encoding the same.

Table D lists all of the biomarkers identified herein as being differentially expressed (*i.e.* having an adjusted 'p'-value ['q'-value] of less than 0.05 in patients exhibiting an atypical or "outlier" gene expression profile; see Example A) in chemotherapy-responsive versus chemotherapy-resistant Hodgkin's lymphoma patients (see Example A below).

It will be appreciated by persons skilled in that art that the methods described above in relation to step (b) may be used in step (d).

In one embodiment, step (d) comprises measuring the presence and/or amount in the sample of at least three proteins selected from the group identified in Table D, and/or mRNA encoding the same, for example at least four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen or more proteins selected from the group identified in Table D, and/or mRNA encoding the same.

For example, step (d) may comprise measuring the presence and/or amount in the sample of at least 20 proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least 30, 40, 50, 100, 200, 500, 1000, or more proteins selected from the group identified in Table D, and/or mRNA encoding the same.

In one embodiment, the proteins, and/or mRNA encoding the same, measured in step (d) are selected from one of the following groups defined in Table D:

(a) Biomarker nos. 1 to 10;

(b) Biomarker nos. 1 to 20;
(c) Biomarker nos. 1 to 30;
(d) Biomarker nos. 1 to 40;
(e) Biomarker nos. 1 to 50;
(f) Biomarker nos. 1 to 100;
(g) Biomarker nos. 1 to 200;
(h) Biomarker nos. 1 to 500; or
(i) Biomarker nos. 1 to 1000.

wherein the biomarker number is shown in first column of Table D ("No.").

Thus, step (d) may comprise measuring the presence and/or amount in the sample of at least one protein, and/or mRNA encoding the same, selected from the group consisting of

(a) CD93 molecule (CD93);
(b) Gap junction protein, delta 3, 31.9 kDa (GJD3);
(c) Paired related homeobox 1 (PRRX1);
(d) Neuropilin 1 (NRP1);
(e) Cytoglobin (CYGB);
(f) Gamma-glutamyl transferase 5 (GGT5);
(g) Collagen, type VI, alpha 2 (COL6A2);
(h) Lysosomal protein transmembrane 4 beta (LAPTM4B);
(i) Dimethylarginine dimethylaminohydrolase 1 (DDAH1); and
(j) Zinc finger, DHHC-type containing 9 (ZDHHC9).

For example, Step (d) comprises measuring the presence and/or amount in the sample of all of the following proteins, and/or mRNA encoding the same:

(a) CD93 molecule (CD93);
(b) Gap junction protein, delta 3, 31.9 kDa (GJD3);
(c) Paired related homeobox 1 (PRRX1); and
(d) Neuropilin 1 (NRP1).

In one embodiment, the method further comprises step (e) of comparing the presence and/or amount of the proteins, or mRNA encoding the same, with one or more reference values for said proteins or mRNA.

As in Step (b) above, the reference values may correspond to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals selected from a group consisting of healthy individuals, individuals diagnosed with Hodgkin's lymphoma who are responsive to chemotherapeutic drug treatment and individuals diagnosed with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment.

Likewise, it will be appreciated by persons skilled in the art that the amount of the proteins, or mRNA encoding the same, obtained in step (e) and the reference values for said proteins or mRNA may be normalised prior to being compared.

In a further embodiment of the first aspect of the invention, the method further comprises the step of determining the medical history of the individual.

For example, the medical history of the individual may comprise determining whether the patient has taken any HIV drug therapies prior to providing the sample.

A second aspect of the invention provides a method for treating an individual with Hodgkin's lymphoma comprising:

(a) identifying an individual with Hodgkin's lymphoma who is responsive to chemotherapeutic drug treatment using a method according to the first aspect of the invention; and

(b) administering a chemotherapeutic drug to the individual identified in step (a).

Suitable chemotherapeutic drug regimes effective in the treatment of Hodgkin's lymphoma are known to those skilled in the art.

For example, the individual may be administered 2 to 4 cycles of ABVD chemotherapy, which contains the drugs adriamycin (doxorubicin), bleomycin, vinblastine and dacarbazine. For advanced stage Hodgkin's lymphoma some people have ABVD for up to 8 cycles.

Other possible chemotherapeutic drug combinations include:

ChlvPP - chlorambucil, vinblastine, procarbazine and prednisolone
Stanford V - mustine, doxorubicin, vinblastine, vincristine, bleomycin, etoposide and steroids
BEACOPP - bleomycin, etoposide, doxorubicin, cyclophosphamide, vincristine, procarbazine and prednisolone

A related, third aspect of the invention provides a method for treating an individual with Hodgkin's lymphoma comprising:

(a) identifying an individual with Hodgkin's lymphoma who is resistant to chemotherapeutic drug treatment using a method according to the first aspect of the invention; and
(b) administering a therapeutic agent other than a chemotherapeutic drug to the individual identified in step (a).

Suitable non-chemotherapeutic treatment regimes effective in the treatment of Hodgkin's lymphoma are known to those skilled in the art, for example radiotherapy.

A fourth aspect of the invention provides a method for treating an individual with Hodgkin's lymphoma comprising:

(a) determining the responsiveness of an individual with Hodgkin's lymphoma to chemotherapeutic drug treatment using a method according to the first aspect of the invention;
(b) identifying an effective therapeutic agent for administration to the individual based on the responsiveness of the patient to chemotherapeutic drug treatment; and
(c) administering said effective therapeutic agent identified in step (b) to the individual.

A fifth aspect of the invention provides an array for use in a method according to the first aspect of the invention the array comprising binding agents for two or more of the proteins identified in Table A and/or D, or mRNA encoding the same.

Arrays *per se* are well known in the art. Typically they are formed of a linear or two-dimensional structure having spaced apart (*i.e.* discrete) regions ("spots"), each having a finite area, formed on the surface of a solid support. An array can also be a bead structure where each bead can be identified by a molecular code or colour code or identified in a continuous flow. Analysis can also be performed sequentially where the sample is passed over a series of spots each adsorbing the class of molecules from the solution. The solid support is typically glass or a polymer, the most commonly used polymers being cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene. The solid supports may be in the form of tubes, beads, discs, silicon chips, microplates, polyvinylidene difluoride (PVDF) membrane, nitrocellulose membrane, nylon membrane, other porous membrane, non-porous membrane (e.g. plastic, polymer, perspex, silicon, amongst others), a plurality of polymeric pins, or a plurality of microtitre wells, or any other surface suitable for immobilising proteins, polynucleotides and other suitable molecules and/or conducting an immunoassay. The binding processes are well known in the art and generally consist of cross-linking covalently binding or physically adsorbing a protein molecule, polynucleotide or the like to the solid support. Alternatively, affinity coupling of the probes via affinity-tags or similar constructs may be employed. By using well-known techniques, such as contact or non-contact printing, masking or photolithography, the location of each spot can be defined. For reviews see Jenkins, R.E., Pennington, S.R. (2001, *Proteomics*, **2**,13-29) and Lal *et al* (2002, *Drug Discov Today* **15**;7(18 Suppl):S143-9).

Typically the array is a microarray. By "microarray" we include the meaning of an array of regions having a density of discrete regions of at least about 100/cm^2, and preferably at least about 1000/cm^2. The regions in a microarray have typical dimensions, *e.g.* diameter, in the range of between about 10-250 μm, and are separated from other regions in the array by about the same distance. The array may alternatively be a macroarray or a nanoarray.

In one embodiment, the array comprises binding agents for fewer then 1000 different proteins, or mRNA coding the same, for example fewer than 500, 400, 300, 200, 100, 50, 25, or 20 different proteins, or mRNA coding the same.

In one embodiment, the array comprises binding agents for all of the proteins defined in Table 1, or mRNA encoding the same.

For example, the array may comprise:

(a) binding agents for all of the proteins identified in Table C, or mRNA encoding the same;
(b) binding agents for all of the proteins identified in Table A, or mRNA encoding the same;
(c) binding agents for all of the proteins identified in Table D, or mRNA encoding the same;
(d) binding agents for all of the proteins identified in Tables A and D; and/or
(e) binding agents for mRNA encoding all of the proteins in Tables A and D.

In one embodiment, the binding agents are immobilised.

In one embodiment, the array is a surface-based array or bead-based array.

In one embodiment, the array is suitable for use with high-throughput screening methods of gene profiling.

A sixth aspect of the invention provides a kit for performing a method according to the first aspect of the invention comprising:

(a) an array according to the fifth aspect of the invention; and
(b) instructions for performing a method according to the first aspect of the invention.

In one embodiment, the kit further comprises one or more reagents for use in a method according to the first aspect of the invention.

In one embodiment, the kit further comprises a positive control sample and/or a negative control sample.

A seventh aspect of the invention provides a computer-implemented method for classifying a sample from an individual with Hodgkin's lymphoma, comprising:

(a) providing a dataset associated with the sample, wherein said dataset comprises quantitative data for at least two proteins, and/or mRNA encoding the same, selected from the group defined in Table A;
(b) inputting said dataset into an analytical process on a computer that compares said dataset against one or more reference datasets; and
(c) classifying said sample according to the output of said analytical process

wherein one or more of the at least two proteins selected from the group defined in Table A is not identified in Table B.

and wherein in step (c) the sample is classified as from an individual with Hodgkin's lymphoma who is responsive to chemotherapeutic drug treatment or from an individual with Hodgkin's lymphoma who is resistant to chemotherapeutic drug treatment.

In one embodiment, the dataset in step (a) comprises quantitative data for zinc finger protein 644 (ZNF644) and/or heat shock 70kDa protein 5 (HSPA5), and/or mRNA encoding the same.

In one embodiment, the dataset in step (a) comprises quantitative data for at least three proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen or more proteins selected from the group identified in Table A, and/or mRNA encoding the same.

For example, the dataset in step (a) may comprise quantitative data for at least 20 proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least 30, 40, 50, 100, 200, 500, 1000, or more proteins selected from the group identified in Table A, and/or mRNA encoding the same.

In one embodiment, the proteins, and/or mRNA encoding the same, for which quantitative data are provided in step (a) are selected from one of the following groups defined in Table A:

(a) Biomarker nos. 1 to 10;
(b) Biomarker nos. 1 to 20;
(c) Biomarker nos. 1 to 30;
(d) Biomarker nos. 1 to 40;
(e) Biomarker nos. 1 to 50;
(f) Biomarker nos. 1 to 100;
(g) Biomarker nos. 1 to 200;
(h) Biomarker nos. 1 to 500;
(i) Biomarker nos. 1 to 1000;
(j) Biomarker nos. 1 to 2000;
(k) Biomarker nos. 1 to 3000; or
(l) Biomarker nos. 1 to 4000.

In one embodiment, none of the at least two proteins selected from the group identified in Table A are identified in Table B.

In one embodiment, the dataset in step (a) may comprise quantitative data for at least one protein, and/or mRNA encoding the same, selected from the group consisting of:

(a) Zinc finger protein 644 (ZNF644) ;
(b) Colipase, pancreatic (CLPS) ;
(c) EST tu05b03.x1;
(d) relaxin 1 (RLN1);
(e) phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D);
(f) EMI domain containing 2 (EMID2);
(g) heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa; HSPA5));
(h) spermatogenesis associated 12 (SPATA12);
(i) kinectin 1 (kinesin receptor; KTN1);
(j) pentraxin 3, long (PTX3);
(k) erythropoietin receptor (EPOR);
(l) DC-STAMP domain containing 2 (DCST2);
(m) golgi to ER traffic protein 4 homolog (*S. cerevisiae*; GET4);
(n) mitogen-activated protein kinase 14 (MAPK14); and
(o) chromosome 1 open reading frame 163 (C1orf163).

For example, the dataset in step (a) may comprise quantitative data for all of biomarkers 'a' to 'o' above, and/or mRNA encoding the same.

Optionally, the dataset in step (a) comprises quantitative data for biomarkers 'a' to 'o' above as measured at the mRNA level using the probe sets ("Probe ID's") identified in Table A (from the Affymetrix GeneChip Human Genome U133 Plus 2.0 array, from Affymetrix Inc, Santa Clara, USA). For example, mRNA levels for heat shock 70kDa protein 5 may be determined using Affymetrix probe set 211936_at.

In one embodiment, the dataset in step (a) comprises quantitative data for at least two proteins selected from the group identified in Table D, and/or of mRNA encoding the same.

Thus, the dataset in step (a) comprises quantitative data for at least three proteins selected from the group identified in Table D, and/or mRNA encoding the same, for example at least four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen or more proteins selected from the group identified in Table D, and/or mRNA encoding the same. For example, the dataset in step (a) comprises quantitative data for at least 20 proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least 30, 40, 50, 100, 200, 500, 1000, or more proteins selected from the group identified in Table D, and/or mRNA encoding the same.

In one embodiment, the proteins, and/or mRNA encoding the same, for which quantitative data are provided in step (a) are selected from one of the following groups defined in Table D:

(a) Biomarker nos. 1 to 10;
(b) Biomarker nos. 1 to 20;
(c) Biomarker nos. 1 to 30;
(d) Biomarker nos. 1 to 40;
(e) Biomarker nos. 1 to 50;
(f) Biomarker nos. 1 to 100;
(g) Biomarker nos. 1 to 200;
(h) Biomarker nos. 1 to 500; or
(i) Biomarker nos. 1 to 1000.

In one embodiment, the dataset in step (a) comprises quantitative data for at least one protein, and/or mRNA encoding the same, selected from the group consisting of:

(a) CD93 molecule (CD93);
(b) Gap junction protein, delta 3, 31.9 kDa (GJD3);
(c) Paired related homeobox 1 (PRRX1);
(d) Neuropilin 1 (NRP1);
(e) Cytoglobin (CYGB);
(f) Gamma-glutamyl transferase 5 (GGT5);
(g) Collagen, type VI, alpha 2 (COL6A2);
(h) Lysosomal protein transmembrane 4 beta (LAPTM4B);
(i) Dimethylarginine dimethylaminohydrolase 1 (DDAH1); and
(j) Zinc finger, DHHC-type containing 9 (ZDHHC9).

For example, the dataset in step (a) may comprise quantitative data for all of biomarkers 'a' to 'j' above, and/or mRNA encoding the same.

In one embodiment, the dataset in step (a) comprises quantitative data for all of the following proteins, and/or mRNA encoding the same:

(a) CD93 molecule (CD93);
(b) Gap junction protein, delta 3, 31.9 kDa (GJD3);
(c) Paired related homeobox 1 (PRRX1); and
(d) Neuropilin 1 (NRP1).

Optionally, the dataset in step (a) may comprises quantitative data for biomarkers 'a' to 'j' above as measured at the mRNA level using the probe sets ("Probe ID's") identified in Table A (from the Affymetrix GeneChip Human Genome U133 Plus 2.0 array, from Affymetrix Inc, Santa Clara, USA).

In one embodiment, wherein the dataset in step (a) and the reference datasets are normalised.

In one embodiment, said analytical process in step (b) comprises the use of a predictive model based on the one or more reference datasets.

For example, step (b) may comprise the use of a Linear Discriminant Analysis (LDA) model, a support vector machine classification algorithm, a recursive feature elimination model, a prediction analysis of microarray model, a Logistic Regression model, a CART algorithm, a FlexTree algorithm, a LART algorithm, a random forest algorithm, a MART algorithm, or a Machine Learning algorithm.

In one embodiment, said one or more reference datasets comprise quantitative data obtained from one or more individuals selected from a group consisting of healthy individuals, individuals diagnosed with Hodgkin's lymphoma who are responsive to chemotherapeutic drug treatment and individuals diagnosed with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment.

In one embodiment, the analytical process in step (b) comprises use of an adaptive learning algorithm, such as an artificial neural network.

For example, the artificial neural network may be a multilayer perceptron.

In one embodiment, the predictive model has an accuracy of at least 90% for determining the responsiveness of Hodgkin's lymphoma patients to chemotherapy. For example, the predictive model may have an accuracy of at least 95% for such patient classification, and preferably at least 99%.

It will be appreciated that such predictive accuracy may be determined relative to any given population of Hodgkin's lymphoma patients. In one embodiment, however, the predictive accuracy is determined relative to the 130 patients used in Example A (Expression series GSE17920 from the Gene Expression Omnibus [GEO] data repository).

An eighth aspect of the invention provides a computer system for performing a computer-implemented method according to the seventh aspect of the invention, wherein the system comprises a digital computer and computer readable program means for enabling the computer to perform said computer-implemented method.

It will be appreciated that the computer readable program may be contained within the internal or external memory of the computer system, for example on a RAM chip, hard-drive, CD-ROM, DVD-ROM, USB memory pen and the like.

In one embodiment, the computer system further comprises a computer-readable storage medium comprising reference datasets (*i.e.* from step 'b' of the computer-implemented method of the invention).

Using such a system, the operator simply needs to input the dataset associated with the sample to be tested (*i.e.* step 'a' of the computer-implemented method of the invention) and then run the program.

A ninth aspect of the invention provides a computer-readable storage medium comprising computer readable program means for enabling the computer to perform a computer-implemented method according to the seventh aspect of the invention.

In one embodiment, the computer-readable storage medium further comprises reference datasets (*i.e.* from step 'b' of the computer-implemented method of the invention).

Preferred, non-limiting examples which embody certain aspects of the invention will now be described, with reference to the following figures.

Figure 1: Box plots for resistant (samples 1-38) and sensitive (samples 39-130) patient microarray values (n=54,675) taken from log2 normalised expression values. The black boxes (■) represent the median value and suggests that the data are median centred and therefore appropriate for comparative analyses. Low and high part of the box represents the 25th and 75th percentile respectively. Minimum and maximum values are shown by the vertical thin lines.

Figure 2: A general overview of a multi-layer perceptron back propagation network. Input signals are fed forward in a unidirectional manner (through weighted links) and transformed by an activation function into a predicted classification result. Error in classification is back propagated resulting in incremental changes to the weighted links and a minimisation of classification error.

Figure 3: Receiver Operating Characteristic (ROC) curve for 100 models retained after training for run 5 (sample seed variation). Plots represent the values obtained from all predictions made within training, testing and validation datasets. The true positive class

(sensitivity) represents patients who responded to treatment (i.e. chemo-sensitive). The true negative class (specificity) are indicative of patients who did not respond to treatment (i.e. chemo-resistant).

Figure 4:
(A) Average predictive accuracy (%) for each sample. The mean value represents an average taken from 100 models per run with a total of 10 runs. A random sample seed with fixed network seed values were used to select training, testing and validation datasets and to initialise the network respectively. Chemotherapy failure patients are listed between sample numbers 1-38 and chemotherapy sensitive patients between sample numbers 39-130 respectively. Confidence intervals are shown at $p<0.05$ two-tail t-distribution and 9 degrees of freedom (based upon 10 runs (generating 20,000 models per run)).
(B) Average predictive accuracy (%) for each sample. The mean value represents an average taken from 100 models per run with a total of 10 runs. A fixed sample seed with random network seed values were used to select training, testing and validation datasets and to initialise the network respectively. Chemotherapy failure patients are listed between sample numbers 1-38 and chemotherapy sensitive patients between sample numbers 39-130 respectively. Confidence intervals are shown at $p<0.05$ two-tail t-distribution and 9 degrees of freedom (based upon 10 runs (generating 20,000 models per run)).

Figure 5: Average predictive accuracy for outlier samples. The mean value represents an average taken from 100 models per run with a total of 10 runs. A random sample seed with fixed network seed values were used to select training/testing/validation datasets and to initialise the network respectively. Chemotherapy failure patients (class F) and chemotherapy sensitive patients (class S) from "Sequential" and "Randomised" sample presentation are listed respectively. Confidence intervals are shown at $p<0.05$ two-tail t-distribution and 9 degrees of freedom (based upon 10 runs (generating 20,000 models per run)).

Figure 6: Number of genes with reported back from GEO2R as having adjusted p-values ("q-values") with FDR <0.05. Group 130 includes all 130 samples from the original study. Group 114 includes 114 samples with outlier samples removed. Group 16 includes the original 16 outlier samples only. Group 130, Group 114 and Group 16 contain both chemotherapy sensitive and resistant patient samples.

Figure 7: Receiver Operating Characteristic (ROC) curve for 100 models for Group 130 samples using top 4 predictors identified as having the most significant adjusted p-values for Group 16 outlier samples. Plots represent the values obtained from all predictions made within training, testing and validation datasets. The true positive class (sensitivity) represents patients who responded to treatment (i.e. chemo-sensitive). The true negative class (specificity) are indicative of patients who did not respond to treatment (i.e. chemo-resistant).

TABLE A

Statistical overview of gene biomarkers identified as being differentially expressed between chemotherapy resistant and sensitive Hodgkin's lymphoma patients

No.	*Gene**	*Probe ID***	*Adj. p value*	*P value*	*t*	*B*	*Log FC*
1	HSPA5	211936_at	5.0100E-06	9.16E-11	-7.14	13.91	-7.22E-01
2	ZNF644	229684_s_at	1.5360E-05	5.62E-10	6.78	12.24	3.71E-01
3	FNDC3B	222693_at	6.1720E-05	4.32E-09	-6.36	10.36	-6.90E-01
4	ARSB	232197_x_at	6.1720E-05	4.52E-09	-6.35	10.32	-2.96E-01
5	PTX3	206157_at	1.0542E-04	9.64E-09	-6.19	9.62	-4.99E-01
6	RPL12	214271_x_at	2.5621E-04	3.22E-08	5.93	8.51	3.32E-01
7	PYGL	202990_at	2.5621E-04	3.47E-08	-5.92	8.44	-1.03E+00
8	C1orf163	222883_at	2.5621E-04	3.75E-08	-5.90	8.37	-5.02E-01
9	KTN1	214709_s_at	2.5988E-04	4.28E-08	-5.87	8.25	-4.23E-01
10	EMID2	229080_at	3.9145E-04	8.54E-08	5.72	7.62	2.29E-01
11	RLN1	211753_s_at	3.9145E-04	8.90E-08	5.71	7.58	5.24E-01
12	ASPH	224996_at	3.9145E-04	9.66E-08	-5.70	7.50	-7.67E-01
13	SIAE	224391_s_at	3.9145E-04	9.84E-08	-5.69	7.48	-6.81E-01
14	MAPK14	211087_x_at	3.9145E-04	1.19E-07	-5.65	7.31	-3.39E-01
15	TMED9	208757_at	3.9145E-04	1.24E-07	-5.64	7.27	-4.78E-01
16	MARCKS	201669_s_at	3.9145E-04	1.29E-07	-5.63	7.23	-6.47E-01
17	ATRN	211852_s_at	3.9145E-04	1.30E-07	-5.63	7.23	-5.97E-01
18	RTN4	214629_x_at	3.9145E-04	1.37E-07	-5.62	7.18	-3.91E-01
19	KTN1	200915_x_at	3.9145E-04	1.38E-07	-5.62	7.18	-3.68E-01
20	SPATA12	237807_at	3.9145E-04	1.43E-07	5.61	7.14	2.84E-01
21	CLPS	206131_at	3.9285E-04	1.51E-07	5.60	7.09	2.72E-01
22	ETS2	201328_at	4.3244E-04	1.74E-07	-5.57	6.96	-8.98E-01
23	ITSN1	209298_s_at	4.5032E-04	1.89E-07	-5.55	6.88	-8.31E-01
24	AP2A2	211779_x_at	4.9207E-04	2.16E-07	-5.52	6.76	-8.71E-01
25	GPR135	214503_x_at	4.9708E-04	2.31E-07	5.50	6.70	2.27E-01
26	HLX	214438_at	4.9708E-04	2.47E-07	-5.49	6.64	-5.96E-01
27	APOL1	209546_s_at	4.9708E-04	2.58E-07	-5.48	6.60	-7.40E-01
28	AP2A2	215764_x_at	4.9708E-04	2.68E-07	-5.47	6.57	-5.69E-01
29	KCNK6	223658_at	4.9708E-04	2.85E-07	-5.46	6.51	-4.76E-01
30	HRH1	205579_at	4.9708E-04	2.86E-07	-5.46	6.51	-9.28E-01
31	PRNP	215707_s_at	4.9708E-04	2.92E-07	-5.45	6.49	-6.46E-01
32	DCUN1D3	239648_at	4.9708E-04	3.11E-07	-5.44	6.43	-4.56E-01
33	FZD5	221245_s_at	4.9708E-04	3.12E-07	-5.44	6.43	-8.30E-01
34	RPL22	221775_x_at	4.9708E-04	3.33E-07	5.42	6.37	2.72E-01
35	PPP2CB	201375_s_at	4.9708E-04	3.34E-07	-5.42	6.36	-5.12E-01
36	CD93	202878_s_at	4.9708E-04	3.44E-07	-5.41	6.33	-1.27E+00
37	FLJ10357	220326_s_at	4.9708E-04	3.65E-07	-5.40	6.28	-3.85E-01
38	CTBP2	201218_at	4.9708E-04	3.70E-07	-5.40	6.27	-6.17E-01
39	DUSP3	201536_at	4.9708E-04	3.72E-07	-5.40	6.26	-5.22E-01
40	MCOLN1	219952_s_at	4.9708E-04	3.74E-07	-5.39	6.26	-7.41E-01
41	EDEM3	223243_s_at	4.9708E-04	3.79E-07	-5.39	6.25	-5.42E-01
42	CEBPD	213006_at	4.9708E-04	3.82E-07	-5.39	6.24	-6.13E-01
43	RPL12	200809_x_at	5.0044E-04	3.94E-07	5.38	6.21	3.00E-01
44	CP	204846_at	5.0439E-04	4.14E-07	-5.37	6.17	-1.22E+00
45	ITSN1	209297_at	5.0439E-04	4.15E-07	-5.37	6.16	-6.65E-01
46	TBXAS1	208130_s_at	5.1517E-04	4.33E-07	-5.36	6.12	-6.30E-01
47	SLCO2B1	203473_at	5.1886E-04	4.46E-07	-5.35	6.10	-7.81E-01
48		235892_at	5.2987E-04	4.65E-07	5.35	6.06	2.45E-01
49	ERO1L	222646_s_at	5.6223E-04	5.04E-07	-5.33	5.99	-7.88E-01
50		236280_at	5.7129E-04	5.22E-07	5.32	5.95	7.37E-01
51	LHFP	218656_s_at	6.1657E-04	5.81E-07	-5.29	5.85	-8.81E-01
52	PDE6D	231065_at	6.1657E-04	5.86E-07	5.29	5.85	3.02E-01
53	CD300C	207270_x_at	6.3176E-04	6.17E-07	-5.28	5.80	-3.56E-01
54		229373_at	6.3176E-04	6.33E-07	-5.28	5.78	-8.51E-01
55	UBE3A	214980_at	6.3176E-04	6.36E-07	5.27	5.77	3.51E-01
56	PLOD1	200827_at	6.4343E-04	6.59E-07	-5.27	5.74	-8.30E-01
57	TMBIM1	217730_at	7.2267E-04	7.60E-07	-5.23	5.61	-5.22E-01
58	PRNP	201300_s_at	7.2267E-04	7.67E-07	-5.23	5.60	-5.12E-01
59	ZNF85	206572_x_at	7.5625E-04	8.17E-07	5.22	5.54	5.11E-01
60	C1S	1555229_a_at	7.5625E-04	8.51E-07	-5.21	5.51	-1.65E+00
61	CTNNA1	1558214_s_at	7.5625E-04	8.55E-07	-5.21	5.50	-5.23E-01
62	F13A1	203305_at	7.5625E-04	8.58E-07	-5.21	5.50	-1.52E+00

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
63	RIBC1	235946_at	7.6941E-04	8.87E-07	5.20	5.47	2.50E-01
64	SIPA1L2	233587_s_at	7.8609E-04	9.20E-07	-5.19	5.43	-5.11E-01
65	NCRNA00219	225698_at	8.6294E-04	1.03E-06	5.16	5.33	8.18E-01
66	PDIA4	208658_at	8.6294E-04	1.04E-06	-5.16	5.32	-5.69E-01
67	TMEM37	1554485_s_at	9.1213E-04	1.12E-06	-5.14	5.26	-7.42E-01
68	ELOVL5	215082_at	9.3749E-04	1.17E-06	5.13	5.22	9.46E-01
69	RPL38	202029_x_at	9.3749E-04	1.18E-06	5.13	5.20	2.73E-01
70	MS4A4A	219607_s_at	9.7933E-04	1.25E-06	-5.12	5.15	-1.50E+00
71	ASPH	225008_at	9.9547E-04	1.29E-06	-5.11	5.12	-6.38E-01
72	EPB41L3	212681_at	1.0046E-03	1.33E-06	-5.10	5.10	-8.75E-01
73	SLCO2B1	203472_s_at	1.0046E-03	1.41E-06	-5.09	5.04	-7.72E-01
74	AP2A2	212159_x_at	1.0046E-03	1.42E-06	-5.09	5.04	-8.16E-01
75		235438_at	1.0046E-03	1.43E-06	-5.09	5.03	-6.90E-01
76	PTGS1	215813_s_at	1.0046E-03	1.43E-06	-5.09	5.03	-1.04E+00
77	PRKAR2A	225011_at	1.0046E-03	1.44E-06	-5.09	5.03	-3.87E-01
78	FNDC3B	222692_s_at	1.0046E-03	1.44E-06	-5.09	5.02	-6.58E-01
79	PPAP2B	209355_s_at	1.0046E-03	1.49E-06	-5.08	4.99	-1.15E+00
80	ATN1	211076_x_at	1.0046E-03	1.50E-06	5.08	4.99	2.11E-01
81	ASPH	205808_at	1.0046E-03	1.52E-06	-5.07	4.97	-3.51E-01
82	RPL22	208768_x_at	1.0046E-03	1.53E-06	5.07	4.97	2.64E-01
83	SNHG6	225547_at	1.0046E-03	1.54E-06	5.07	4.97	6.33E-01
84	MBNL1	233015_at	1.0046E-03	1.55E-06	5.07	4.96	4.04E-01
85	RPL12	200088_x_at	1.0046E-03	1.56E-06	5.07	4.95	2.53E-01
86	ACSL1	207275_s_at	1.0871E-03	1.72E-06	-5.05	4.86	-1.03E+00
87	MS4A4A	224357_s_at	1.0871E-03	1.73E-06	-5.04	4.86	-8.75E-01
88	LOC653506///METRNL	225955_at	1.1197E-03	1.80E-06	-5.03	4.82	-1.01E+00
89		237442_at	1.1650E-03	1.90E-06	5.02	4.77	5.91E-01
90	PTAFR	206278_at	1.1650E-03	1.92E-06	-5.02	4.76	-5.28E-01
91	CTNNA1	200764_s_at	1.1684E-03	1.98E-06	-5.01	4.73	-7.05E-01
92	C20orf112	230955_s_at	1.1684E-03	2.00E-06	5.01	4.72	3.30E-01
93	RETSAT	1566472_s_at	1.1684E-03	2.01E-06	-5.01	4.72	-3.82E-01
94	LOC374443	238790_at	1.1684E-03	2.03E-06	5.01	4.71	6.57E-01
95	RTN4	210968_s_at	1.1684E-03	2.04E-06	-5.00	4.71	-5.61E-01
96	RNF19B	213038_at	1.1684E-03	2.05E-06	-5.00	4.70	-7.27E-01
97	HELQ	1554342_s_at	1.1750E-03	2.08E-06	5.00	4.69	5.36E-01
98	APLP2	208702_x_at	1.2063E-03	2.18E-06	-4.99	4.64	-7.07E-01
99	UBC///UBB///RPS27A	208980_s_at	1.2063E-03	2.18E-06	-4.99	4.64	-7.24E-01
100	MANBA	203778_at	1.2236E-03	2.24E-06	-4.98	4.62	-3.47E-01
101	FCGR2C	211395_x_at	1.2281E-03	2.27E-06	-4.98	4.61	-1.13E+00
102	CFI	1555564_a_at	1.2364E-03	2.31E-06	-4.98	4.59	-6.23E-01
103	TRIM27	212116_at	1.2835E-03	2.42E-06	-4.96	4.55	-3.76E-01
104	PRKACB	235780_at	1.2855E-03	2.45E-06	4.96	4.54	7.45E-01
105	ATP2A2	212361_s_at	1.2980E-03	2.49E-06	-4.96	4.52	-7.47E-01
106	C19orf10	221739_at	1.3520E-03	2.67E-06	-4.94	4.46	-3.75E-01
107		228685_at	1.3520E-03	2.68E-06	-4.94	4.46	-3.55E-01
108	MPZL1	210087_s_at	1.3520E-03	2.69E-06	-4.94	4.45	-5.98E-01
109	AGRN	212283_at	1.3520E-03	2.72E-06	4.94	4.44	3.71E-01
110	RBPJ	207785_s_at	1.3520E-03	2.72E-06	-4.94	4.44	-6.61E-01
111		239237_at	1.3547E-03	2.77E-06	4.93	4.43	5.31E-01
112	CD209	207277_at	1.3547E-03	2.78E-06	-4.93	4.42	-1.47E+00
113	TNFSF12-TNFSF13///TNFSF12///TNFSF13	209500_x_at	1.3730E-03	2.84E-06	-4.93	4.40	-6.52E-01
114	RPL34	200026_at	1.3839E-03	2.89E-06	4.92	4.39	3.16E-01
115	STIP1	213330_s_at	1.3842E-03	2.91E-06	-4.92	4.38	-6.62E-01
116	FAM76B	232048_at	1.3849E-03	2.94E-06	4.92	4.37	2.97E-01
117	TGM2	201042_at	1.3972E-03	3.00E-06	-4.91	4.35	-1.25E+00
118	SP4	236265_at	1.3972E-03	3.03E-06	4.91	4.34	4.93E-01
119	LHFP	231411_at	1.3972E-03	3.07E-06	-4.91	4.33	-5.01E-01
120	TRMT11	218877_s_at	1.3972E-03	3.07E-06	4.91	4.33	3.83E-01
121	FAM20A	226804_at	1.4555E-03	3.22E-06	-4.90	4.29	-9.63E-01
122	RPL22	220960_x_at	1.5163E-03	3.38E-06	4.89	4.24	1.80E-01
123	OSMR	205729_at	1.5299E-03	3.44E-06	-4.88	4.23	-4.76E-01
124	CALHM2	57715_at	1.5540E-03	3.54E-06	-4.87	4.20	-4.86E-01
125	TTL	224908_s_at	1.5540E-03	3.55E-06	-4.87	4.20	-4.19E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
126	EARS2	227374_at	1.5810E-03	3.64E-06	-4.87	4.17	-2.82E-01
127	LOC729513/ //LOC64129 8///LOC5951 01///LOC440 354///SMG1	244766_at	1.6005E-03	3.76E-06	4.86	4.15	5.24E-01
128	RPS20	200949_x_at	1.6005E-03	3.77E-06	4.86	4.14	3.85E-01
129	FILIP1L	204135_at	1.6005E-03	3.80E-06	-4.86	4.14	-7.77E-01
130	MEX3D	91816_f_at	1.6005E-03	3.82E-06	-4.86	4.13	-1.93E-01
131	ITPRIPL2	227514_at	1.6005E-03	3.85E-06	-4.85	4.12	-7.43E-01
132	APP	214953_s_at	1.6005E-03	3.88E-06	-4.85	4.12	-7.70E-01
133	VAMP3	211749_s_at	1.6005E-03	3.91E-06	-4.85	4.11	-7.24E-01
134	PEA15	200788_s_at	1.6005E-03	3.94E-06	-4.85	4.10	-5.81E-01
135	LOC284900	244189_at	1.6005E-03	3.95E-06	4.85	4.10	9.69E-01
136		229716_at	1.6547E-03	4.12E-06	4.84	4.06	9.35E-01
137	C16orf72	220743_at	1.6883E-03	4.23E-06	4.83	4.04	3.83E-01
138	FILIP1	1570515_a_at	1.6946E-03	4.28E-06	-4.83	4.03	-3.82E-01
139	CTNS	36566_at	1.7071E-03	4.34E-06	-4.83	4.02	-4.99E-01
140	RXRA	202449_s_at	1.7302E-03	4.43E-06	-4.82	4.00	-5.69E-01
141	FAM169A	235048_at	1.7365E-03	4.50E-06	4.82	3.98	6.29E-01
142	MS4A4A	1555728_a_at	1.7365E-03	4.51E-06	-4.82	3.98	-1.46E+00
143		1556346_at	1.7365E-03	4.54E-06	4.81	3.97	3.85E-01
144		230856_at	1.7400E-03	4.58E-06	4.81	3.97	5.29E-01
145	CALHM2	221565_s_at	1.7581E-03	4.66E-06	-4.81	3.95	-5.41E-01
146	CCDC57	227783_at	1.7745E-03	4.75E-06	4.80	3.93	4.61E-01
147	KPNB1	213803_at	1.7745E-03	4.77E-06	-4.80	3.93	-6.94E-01
148	ATRN	212517_at	1.7826E-03	4.83E-06	-4.80	3.92	-4.26E-01
149	RBMS1	203748_x_at	1.7826E-03	4.86E-06	-4.80	3.91	-7.04E-01
150	GPATCH2	1556126_s_at	1.7832E-03	4.92E-06	4.80	3.90	4.81E-01
151	RBMS1	207266_x_at	1.7832E-03	4.95E-06	-4.79	3.89	-7.11E-01
152	ELOVL6	204256_at	1.7832E-03	4.96E-06	-4.79	3.89	-3.53E-01
153	DOCK7	225384_at	1.7969E-03	5.03E-06	-4.79	3.88	-4.99E-01
154	SLC44A1	228485_s_at	1.8092E-03	5.10E-06	-4.79	3.87	-4.88E-01
155	ACSL1	201963_at	1.8205E-03	5.16E-06	-4.78	3.86	-7.61E-01
156	GET4	224816_at	1.8301E-03	5.22E-06	4.78	3.85	2.12E-01
157	PLTP	202075_s_at	1.8425E-03	5.34E-06	-4.78	3.83	-1.87E+00
158	ALOX5	204445_s_at	1.8425E-03	5.37E-06	-4.77	3.82	-5.95E-01
159	ANTXR2	225524_at	1.8425E-03	5.39E-06	-4.77	3.82	-7.42E-01
160	CD44	204489_s_at	1.8425E-03	5.43E-06	-4.77	3.81	-5.40E-01
161	CD44	212063_at	1.8425E-03	5.52E-06	-4.77	3.80	-5.25E-01
162	FAU	200019_s_at	1.8425E-03	5.53E-06	4.77	3.79	4.13E-01
163	C19orf10	216483_s_at	1.8425E-03	5.53E-06	-4.77	3.79	-7.15E-01
164	NFE2L2	201146_at	1.8425E-03	5.58E-06	-4.77	3.79	-4.78E-01
165	TTC35	203584_at	1.8425E-03	5.59E-06	-4.76	3.78	-6.23E-01
166	HLA-DRB1	208306_x_at	1.8425E-03	5.59E-06	-4.76	3.78	-6.52E-01
167	C1R	212067_s_at	1.8552E-03	5.72E-06	-4.76	3.76	-9.51E-01
168	ATP1B3	208836_at	1.8552E-03	5.73E-06	-4.76	3.76	-4.03E-01
169	FILIP1L	1554966_a_at	1.8552E-03	5.73E-06	-4.76	3.76	-9.70E-01
170	CXorf36	222911_s_at	1.8577E-03	5.80E-06	-4.76	3.75	-3.53E-01
171	SLCO2B1	211557_x_at	1.8577E-03	5.81E-06	-4.76	3.75	-6.15E-01
172	FAM105B	240834_at	1.8592E-03	5.85E-06	4.75	3.74	2.50E-01
173		225567_at	1.8664E-03	5.98E-06	-4.75	3.72	-8.34E-01
174	GTSF1L	232820_s_at	1.8664E-03	6.05E-06	4.75	3.71	4.33E-01
175	FBLIM1	1554795_a_at	1.8664E-03	6.07E-06	-4.74	3.71	-2.70E-01
176		209353_s_at	1.8664E-03	6.10E-06	4.74	3.70	1.75E-01
177	SIPA1L2	225056_at	1.8664E-03	6.13E-06	-4.74	3.70	-6.16E-01
178	SLC36A2/// RPL24	214143_x_at	1.8664E-03	6.20E-06	4.74	3.69	2.94E-01
179	CD44	210916_s_at	1.8664E-03	6.20E-06	-4.74	3.69	-8.03E-01
180	FKBP1A	214119_s_at	1.8664E-03	6.21E-06	-4.74	3.69	-5.98E-01
181	PTGS1	205128_x_at	1.8664E-03	6.25E-06	-4.74	3.68	-8.34E-01
182		237726_at	1.8664E-03	6.28E-06	4.74	3.68	1.79E-01
183	MARCO	205819_at	1.8664E-03	6.30E-06	-4.74	3.67	-1.28E+00
184	RPL37	200092_s_at	1.8664E-03	6.31E-06	4.74	3.67	1.78E-01
185	THBD	203888_at	1.8664E-03	6.32E-06	-4.74	3.67	-6.36E-01
186	RHBG	220510_at	1.8685E-03	6.38E-06	4.73	3.66	3.05E-01
187	STXBP4	1554328_at	1.8685E-03	6.43E-06	4.73	3.66	1.63E-01
188	P4HB	200656_s_at	1.8685E-03	6.46E-06	-4.73	3.65	-9.32E-01
189	PMS2L1	214756_x_at	1.8685E-03	6.46E-06	4.73	3.65	4.41E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
190		222877_at	1.8738E-03	6.51E-06	-4.73	3.65	-8.01E-01
191	TNFSF13	210314_x_at	1.8943E-03	6.63E-06	-4.72	3.63	-6.81E-01
192	SIGLEC10	1552806_a_at	1.8943E-03	6.67E-06	-4.72	3.62	-1.05E+00
193	FLJ42291	238648_at	1.8943E-03	6.69E-06	4.72	3.62	2.15E-01
194	DNAJA1	200881_s_at	1.9089E-03	6.81E-06	-4.72	3.60	-6.60E-01
195	SIL1	218436_at	1.9089E-03	6.82E-06	-4.72	3.60	-4.41E-01
196	OAF	225510_at	1.9089E-03	6.89E-06	-4.71	3.59	-5.26E-01
197	Sep-02	200015_s_at	1.9089E-03	6.91E-06	-4.71	3.59	-3.51E-01
198	RORB	206443_at	1.9089E-03	6.93E-06	4.71	3.59	1.71E-01
199	CLEC2D	235522_at	1.9089E-03	6.95E-06	4.71	3.59	4.36E-01
200	LOC153328	231372_at	1.9089E-03	7.07E-06	-4.71	3.57	-5.29E-01
201		1557409_at	1.9089E-03	7.11E-06	4.71	3.57	2.26E-01
202	LOC441259/ //PMS2L5/// PMS2L2	213893_x_at	1.9089E-03	7.12E-06	4.71	3.56	4.04E-01
203	RNF135	223591_at	1.9089E-03	7.14E-06	-4.71	3.56	-6.11E-01
204	FKBP11	219118_at	1.9089E-03	7.16E-06	-4.70	3.56	-7.54E-01
205	PRUNE2	212806_at	1.9089E-03	7.16E-06	4.70	3.56	1.95E-01
206	MAFB	222670_s_at	1.9179E-03	7.24E-06	-4.70	3.55	-8.49E-01
207	RPL14	213588_x_at	1.9179E-03	7.26E-06	4.70	3.55	2.67E-01
208	STK17A	202694_at	1.9560E-03	7.44E-06	4.70	3.52	4.42E-01
209	CTTNBP2NL	231822_at	1.9859E-03	7.67E-06	-4.69	3.50	-3.54E-01
210	YME1L1	232216_at	1.9859E-03	7.74E-06	4.69	3.49	4.94E-01
211	GRIN1	211125_x_at	1.9859E-03	7.75E-06	4.69	3.49	3.14E-01
212	ATN1	1555754_s_at	1.9859E-03	7.78E-06	4.68	3.48	2.64E-01
213	ARRB1	218832_x_at	1.9859E-03	7.79E-06	-4.68	3.48	-4.04E-01
214	DPYSL2	200762_at	1.9859E-03	7.80E-06	-4.68	3.48	-7.14E-01
215	SYNCRIP	217834_s_at	1.9859E-03	7.82E-06	-4.68	3.48	-5.29E-01
216	APOD	201525_at	1.9859E-03	7.85E-06	-4.68	3.48	-1.39E+00
217	SPRED1	226837_at	2.0023E-03	7.95E-06	-4.68	3.46	-7.07E-01
218	PPM1K	244011_at	2.0039E-03	8.00E-06	4.68	3.46	2.71E-01
219	NCKIPSD	216114_at	2.0039E-03	8.05E-06	4.68	3.45	2.76E-01
220	FCGR2C	210992_x_at	2.0039E-03	8.09E-06	-4.67	3.45	-9.53E-01
221	PAPSS2	203059_s_at	2.0039E-03	8.10E-06	-4.67	3.45	-4.14E-01
222	ADAM9	202381_at	2.0046E-03	8.17E-06	-4.67	3.44	-7.10E-01
223	RAB7A	211961_s_at	2.0046E-03	8.19E-06	-4.67	3.44	-6.44E-01
224	WIPI1	203827_at	2.0046E-03	8.22E-06	-4.67	3.43	-7.74E-01
225	FAM129A	217967_s_at	2.0046E-03	8.25E-06	-4.67	3.43	-7.76E-01
226	CECR2	223729_at	2.0077E-03	8.31E-06	4.67	3.42	2.33E-01
227	ARMCX3	222444_at	2.0077E-03	8.38E-06	-4.67	3.41	-4.29E-01
228	FCGR3B///FCGR3A	204006_s_at	2.0077E-03	8.41E-06	-4.67	3.41	-1.43E+00
229	MLLT3	1569652_at	2.0077E-03	8.41E-06	4.67	3.41	5.00E-01
230	PFKFB2	226733_at	2.0080E-03	8.45E-06	-4.66	3.41	-3.77E-01
231	CREG1	201200_at	2.0106E-03	8.49E-06	-4.66	3.40	-6.80E-01
232	PUS7L	221025_x_at	2.0138E-03	8.57E-06	4.66	3.39	2.96E-01
233	GTPBP8	221046_s_at	2.0138E-03	8.58E-06	4.66	3.39	5.96E-01
234	RASAL1	233144_s_at	2.0574E-03	8.81E-06	4.65	3.37	2.25E-01
235	EPOR	396_f_at	2.0772E-03	8.93E-06	-4.65	3.36	-3.43E-01
236	SRSF3	208672_s_at	2.0920E-03	9.03E-06	4.65	3.35	3.20E-01
237	NUDT16	228341_at	2.0980E-03	9.09E-06	-4.65	3.34	-4.73E-01
238	PEA15	200787_s_at	2.1006E-03	9.16E-06	-4.64	3.33	-9.92E-01
239	PTTG1IP	200677_at	2.1006E-03	9.18E-06	-4.64	3.33	-5.47E-01
240	GAS5	224741_x_at	2.1290E-03	9.40E-06	4.64	3.31	7.20E-01
241	PHF20	235389_at	2.1290E-03	9.41E-06	4.64	3.31	7.45E-01
242	GZF1	225884_s_at	2.1290E-03	9.46E-06	-4.64	3.30	-4.11E-01
243	MMP14	160020_at	2.1290E-03	9.46E-06	-4.64	3.30	-4.35E-01
244	ZFYVE21	219929_s_at	2.1430E-03	9.56E-06	-4.63	3.29	-4.22E-01
245	CNKSR3	227481_at	2.1489E-03	9.63E-06	-4.63	3.29	-4.90E-01
246	CALR	214315_x_at	2.1536E-03	9.74E-06	-4.63	3.28	-7.32E-01
247	ZBTB47	226484_at	2.1536E-03	9.75E-06	-4.63	3.28	-3.83E-01
248	SURF4	222979_s_at	2.1536E-03	9.77E-06	-4.63	3.28	-4.40E-01
249	C16orf62	203173_s_at	2.1813E-03	9.93E-06	-4.62	3.26	-3.49E-01
250	DAPK3	203890_s_at	2.1974E-03	1.00E-05	-4.62	3.25	-3.35E-01
251	NAGA	1555041_a_at	2.2693E-03	1.04E-05	-4.61	3.21	-7.22E-01
252	MMP11	235908_at	2.2693E-03	1.05E-05	4.61	3.21	2.60E-01
253	MYO1B	212365_at	2.2693E-03	1.05E-05	-4.61	3.21	-4.27E-01
254		226542_at	2.2693E-03	1.06E-05	-4.61	3.20	-3.49E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
255	P4HB	1564494_s_at	2.2693E-03	1.07E-05	-4.61	3.20	-1.24E+00
256	PICALM	215236_s_at	2.2693E-03	1.07E-05	-4.61	3.19	-9.40E-01
257	ICMT	201611_s_at	2.2693E-03	1.07E-05	-4.61	3.19	-5.76E-01
258	CD3D	213539_at	2.2693E-03	1.07E-05	4.61	3.19	5.79E-01
259	TMEM176B	220532_s_at	2.2758E-03	1.08E-05	-4.60	3.19	-9.49E-01
260	CREB5	229228_at	2.2792E-03	1.09E-05	-4.60	3.18	-3.16E-01
261	LOC100131262	1558152_at	2.2792E-03	1.09E-05	-4.60	3.18	-3.03E-01
262	TSHZ3	223393_s_at	2.2792E-03	1.09E-05	-4.60	3.17	-6.14E-01
263	RBM9	213901_x_at	2.3212E-03	1.12E-05	-4.60	3.15	-4.91E-01
264	CMKLR1	229121_at	2.3216E-03	1.12E-05	-4.59	3.15	-7.77E-01
265	TMEM176A	218345_at	2.3380E-03	1.13E-05	-4.59	3.14	-7.21E-01
266	FGFR1	210973_s_at	2.3397E-03	1.14E-05	-4.59	3.14	-3.68E-01
267	LTBR	203005_at	2.3491E-03	1.15E-05	-4.59	3.13	-5.38E-01
268	SESN2	223196_s_at	2.3494E-03	1.15E-05	-4.59	3.13	-3.96E-01
269		1569009_s_at	2.3503E-03	1.16E-05	4.59	3.12	2.30E-01
270	HRH1	205580_s_at	2.3651E-03	1.17E-05	-4.58	3.11	-4.56E-01
271	CTNS	204925_at	2.3702E-03	1.17E-05	-4.58	3.11	-5.95E-01
272	CRELD2	218358_at	2.3783E-03	1.18E-05	-4.58	3.10	-4.47E-01
273		228951_at	2.3877E-03	1.19E-05	-4.58	3.09	-4.44E-01
274	C20orf3	206656_s_at	2.4498E-03	1.23E-05	-4.57	3.07	-4.19E-01
275	COL6A5	1553835_a_at	2.4562E-03	1.24E-05	-4.57	3.06	-1.10E+00
276	EPHX1	202017_at	2.4715E-03	1.25E-05	-4.57	3.05	-1.04E+00
277	MCAM	209087_x_at	2.4912E-03	1.26E-05	-4.57	3.04	-6.68E-01
278	PPAP2B	212230_at	2.4912E-03	1.27E-05	-4.56	3.04	-5.93E-01
279	SETD8	225118_at	2.5019E-03	1.28E-05	-4.56	3.03	-2.84E-01
280	APEX2	204408_at	2.5021E-03	1.29E-05	-4.56	3.02	-4.10E-01
281	CALD1	201617_x_at	2.5021E-03	1.29E-05	-4.56	3.02	-9.37E-01
282		232535_at	2.5021E-03	1.30E-05	4.56	3.02	3.11E-01
283		244798_at	2.5021E-03	1.30E-05	4.56	3.02	1.01E+00
284	APP	200602_at	2.5021E-03	1.30E-05	-4.56	3.01	-7.26E-01
285	CSDA	201160_s_at	2.5021E-03	1.30E-05	-4.56	3.01	-4.04E-01
286	CD44	204490_s_at	2.5021E-03	1.31E-05	-4.56	3.01	-6.26E-01
287	SOD2	221477_s_at	2.5037E-03	1.31E-05	-4.56	3.01	-8.09E-01
288	EPHB2	211165_x_at	2.5053E-03	1.32E-05	-4.55	3.00	-3.72E-01
289	ZCCHC10	1559399_s_at	2.5053E-03	1.32E-05	4.55	3.00	8.39E-01
290	PSMD1	201198_s_at	2.5096E-03	1.34E-05	-4.55	2.99	-8.38E-01
291	JMJD6	212723_at	2.5096E-03	1.34E-05	-4.55	2.99	-3.32E-01
292	HDLBP	200643_at	2.5096E-03	1.34E-05	-4.55	2.98	-6.95E-01
293	BTG1	1559975_at	2.5096E-03	1.34E-05	4.55	2.98	3.22E-01
294	RPN2	208689_s_at	2.5129E-03	1.35E-05	-4.55	2.98	-8.82E-01
295	CPVL	208146_s_at	2.5182E-03	1.36E-05	-4.55	2.97	-8.09E-01
296		1567140_at	2.5182E-03	1.37E-05	4.55	2.97	1.81E-01
297	FNTA	230808_at	2.5182E-03	1.37E-05	4.55	2.97	2.32E-01
298	C4B///C4A	208451_s_at	2.5196E-03	1.38E-05	-4.54	2.96	-1.10E+00
299	SLC39A8	219869_s_at	2.5196E-03	1.38E-05	-4.54	2.96	-1.22E+00
300		237887_at	2.5390E-03	1.40E-05	4.54	2.95	2.90E-01
301		234508_at	2.5390E-03	1.40E-05	4.54	2.95	1.72E-01
302	DSE	218854_at	2.5643E-03	1.42E-05	-4.54	2.94	-5.44E-01
303	ANUBL1	223624_at	2.5689E-03	1.42E-05	4.54	2.93	2.50E-01
304	LILRB1	211336_x_at	2.5793E-03	1.45E-05	-4.53	2.92	-8.51E-01
305	PICALM	203134_at	2.5793E-03	1.45E-05	-4.53	2.92	-2.31E-01
306	P4HB	200654_at	2.5793E-03	1.45E-05	-4.53	2.92	-6.53E-01
307	ZRANB3	224124_at	2.5793E-03	1.45E-05	4.53	2.91	2.02E-01
308	OPTN	202073_at	2.5793E-03	1.46E-05	-4.53	2.91	-5.24E-01
309	TNRC6C	1561041_at	2.5793E-03	1.46E-05	4.53	2.91	4.11E-01
310	WDR62	1553125_x_at	2.5848E-03	1.47E-05	4.53	2.90	2.07E-01
311	C1orf38	210785_s_at	2.5848E-03	1.47E-05	-4.53	2.90	-9.40E-01
312	PPAP2B	212226_s_at	2.6602E-03	1.52E-05	-4.52	2.87	-6.87E-01
313	MAPK14	210449_x_at	2.7048E-03	1.55E-05	-4.51	2.86	-5.07E-01
314	CD99	201028_s_at	2.7097E-03	1.56E-05	-4.51	2.85	-8.58E-01
315	AP3D1	210974_s_at	2.7097E-03	1.56E-05	-4.51	2.85	-6.13E-01
316	CTNNA1	210844_x_at	2.7097E-03	1.57E-05	-4.51	2.85	-5.22E-01
317		1562083_at	2.7098E-03	1.57E-05	4.51	2.84	1.35E-01
318	CFI	203854_at	2.7137E-03	1.58E-05	-4.51	2.84	-1.01E+00
319	C3orf17	225281_at	2.7491E-03	1.60E-05	4.51	2.82	3.19E-01
320		1563472_at	2.7541E-03	1.61E-05	4.50	2.82	2.04E-01
321	RELL1	226430_at	2.7671E-03	1.62E-05	-4.50	2.81	-5.62E-01
322	CEBPB	212501_at	2.7703E-03	1.63E-05	-4.50	2.81	-6.67E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
323	RETSAT	218124_at	2.7703E-03	1.64E-05	-4.50	2.81	-3.61E-01
324	ZBTB44	220243_at	2.8605E-03	1.70E-05	4.49	2.77	3.46E-01
325	RFESD	239142_at	2.8729E-03	1.71E-05	4.49	2.77	5.37E-01
326	LDHA	200650_s_at	2.8809E-03	1.72E-05	-4.49	2.76	-4.03E-01
327	CD44	1557905_s_at	2.8836E-03	1.72E-05	-4.49	2.76	-7.56E-01
328	LOC100131735///CCBL2///RBMX	1556336_at	2.8893E-03	1.74E-05	4.49	2.75	5.08E-01
329	CEBPD	203973_s_at	2.8893E-03	1.74E-05	-4.49	2.75	-7.44E-01
330	RAB1A	208724_s_at	2.9201E-03	1.76E-05	-4.48	2.74	-3.42E-01
331	PCDHA3	211870_s_at	2.9248E-03	1.77E-05	4.48	2.73	2.51E-01
332	PTCSC	233111_at	2.9415E-03	1.79E-05	4.48	2.72	2.58E-01
333		240783_at	2.9415E-03	1.80E-05	4.48	2.72	1.72E-01
334	CCNB1IP1	217988_at	2.9415E-03	1.80E-05	4.48	2.72	7.22E-01
335	NCRNA00032	1559293_x_at	2.9415E-03	1.81E-05	4.48	2.72	1.76E-01
336	FAM13A	202972_s_at	2.9415E-03	1.81E-05	-4.47	2.71	-4.20E-01
337	GAB1	226002_at	2.9415E-03	1.82E-05	-4.47	2.71	-3.84E-01
338	RPSAP19///RPSAP9///RPSAP58///RPSA	213801_x_at	2.9415E-03	1.82E-05	4.47	2.71	2.98E-01
339	ALS2CR8	219834_at	2.9529E-03	1.83E-05	4.47	2.70	3.23E-01
340	ADAMTS2	214454_at	2.9529E-03	1.84E-05	-4.47	2.70	-5.88E-01
341	IKZF5	220086_at	2.9681E-03	1.85E-05	4.47	2.69	2.63E-01
342	RBMS1	225265_at	2.9681E-03	1.86E-05	-4.47	2.69	-5.21E-01
343	SERPINA1	202833_s_at	2.9681E-03	1.87E-05	-4.47	2.69	-1.51E+00
344	FLVCR2	219316_s_at	2.9681E-03	1.87E-05	-4.47	2.69	-6.49E-01
345	LOC440288	238511_at	2.9775E-03	1.88E-05	4.47	2.68	4.15E-01
346	COL6A5	1553834_at	2.9787E-03	1.88E-05	-4.47	2.68	-8.93E-01
347	RTN4	211509_s_at	2.9931E-03	1.91E-05	-4.46	2.67	-3.32E-01
348	C9orf98	230976_at	2.9931E-03	1.91E-05	4.46	2.67	5.82E-01
349	GANAB	211934_x_at	2.9971E-03	1.91E-05	-4.46	2.66	-7.40E-01
350	CTSB	227961_at	2.9971E-03	1.92E-05	-4.46	2.66	-1.10E+00
351	LOC729806	217544_at	3.0259E-03	1.94E-05	4.46	2.65	6.55E-01
352	TFG	217839_at	3.0259E-03	1.95E-05	-4.46	2.65	-3.65E-01
353	TGFBI	201506_at	3.0259E-03	1.95E-05	-4.46	2.64	-7.37E-01
354	CALR	212953_x_at	3.0405E-03	1.97E-05	-4.45	2.64	-3.61E-01
355	PGK1	217356_s_at	3.0424E-03	1.98E-05	-4.45	2.63	-1.06E+00
356	PDIA6	216640_s_at	3.0527E-03	1.99E-05	-4.45	2.63	-6.45E-01
357	SIK2	223430_at	3.0527E-03	2.00E-05	-4.45	2.62	-3.63E-01
358	STAB1	204150_at	3.0527E-03	2.00E-05	-4.45	2.62	-9.02E-01
359	MCAM	210869_s_at	3.0527E-03	2.01E-05	-4.45	2.62	-5.54E-01
360	RXRA	202426_s_at	3.0527E-03	2.01E-05	-4.45	2.62	-2.84E-01
361	HMOX1	203665_at	3.0847E-03	2.04E-05	-4.45	2.61	-8.39E-01
362	LOC100130155	236693_at	3.0869E-03	2.04E-05	4.44	2.60	1.99E-01
363	SP100	237426_at	3.0950E-03	2.05E-05	4.44	2.60	5.17E-01
364	KREMEN1	227250_at	3.1121E-03	2.07E-05	-4.44	2.59	-4.03E-01
365	C13orf31	1553142_at	3.1259E-03	2.09E-05	-4.44	2.58	-2.82E-01
366	SHC1	214853_s_at	3.1259E-03	2.09E-05	-4.44	2.58	-5.74E-01
367	KCTD12	212192_at	3.1381E-03	2.11E-05	-4.44	2.58	-4.68E-01
368	MBTPS2	206473_at	3.1502E-03	2.12E-05	-4.44	2.57	-2.25E-01
369	RAB7A	211960_s_at	3.1502E-03	2.13E-05	-4.43	2.57	-6.10E-01
370	HSPA6	117_at	3.1575E-03	2.14E-05	-4.43	2.56	-6.81E-01
371	MRC1L1///MRC1	204438_at	3.1715E-03	2.15E-05	-4.43	2.56	-1.20E+00
372	HK1	200697_at	3.1917E-03	2.18E-05	-4.43	2.55	-5.02E-01
373	CTSB	200838_at	3.1917E-03	2.18E-05	-4.43	2.55	-1.04E+00
374	TMEM181	225127_at	3.2093E-03	2.20E-05	-4.43	2.54	-4.13E-01
375	RAB34	1555630_a_at	3.2195E-03	2.21E-05	-4.43	2.53	-8.15E-01
376	PFKFB4	228499_at	3.2338E-03	2.22E-05	-4.42	2.53	-4.84E-01
377	HS6ST1	225263_at	3.2436E-03	2.24E-05	-4.42	2.52	-4.23E-01
378	TUBB6	209191_at	3.2723E-03	2.26E-05	-4.42	2.51	-4.85E-01
379	IGHMBP2	31861_at	3.2760E-03	2.28E-05	-4.42	2.51	-2.07E-01
380	HERC2P7	232900_at	3.2760E-03	2.28E-05	4.42	2.50	1.90E-01
381	LAIR1	208071_s_at	3.2760E-03	2.28E-05	-4.42	2.50	-5.98E-01
382	RPS20	214003_x_at	3.2817E-03	2.29E-05	4.42	2.50	1.58E-01
383	NDRG1	200632_s_at	3.2829E-03	2.30E-05	-4.41	2.50	-4.53E-01
384	TLR2	204924_at	3.2829E-03	2.31E-05	-4.41	2.49	-8.10E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
385	FZD1	204452_s_at	3.2996E-03	2.32E-05	-4.41	2.49	-1.92E-01
386		242453_at	3.3261E-03	2.35E-05	4.41	2.48	2.47E-01
387		241904_at	3.3552E-03	2.37E-05	4.41	2.47	3.31E-01
388	FCGR3B	204007_at	3.3568E-03	2.39E-05	-4.41	2.46	-1.02E+00
389	P2RY10	214615_at	3.3568E-03	2.39E-05	4.40	2.46	4.68E-01
390	TMEM37	227190_at	3.3568E-03	2.40E-05	-4.40	2.46	-4.79E-01
391	PDIA6	207668_x_at	3.3568E-03	2.40E-05	-4.40	2.46	-4.15E-01
392	CITED2	209357_at	3.3684E-03	2.42E-05	-4.40	2.45	-7.40E-01
393		214083_at	3.3687E-03	2.43E-05	4.40	2.45	5.19E-01
394	ACTC1	205132_at	3.3687E-03	2.43E-05	-4.40	2.45	-4.76E-01
395	SLCO4A1	219911_s_at	3.3687E-03	2.44E-05	-4.40	2.44	-5.76E-01
396	PPP4R1	201594_s_at	3.3687E-03	2.44E-05	-4.40	2.44	-2.88E-01
397	FN1	214701_s_at	3.3774E-03	2.45E-05	-4.40	2.44	-5.03E-01
398	ILK	201234_at	3.3849E-03	2.46E-05	-4.40	2.43	-4.68E-01
399	TNFSF12-TNFSF13/// TNFSF12/// TNFSF13	209499_x_at	3.3948E-03	2.48E-05	-4.40	2.43	-9.07E-01
400	ANPEP	202888_s_at	3.3948E-03	2.49E-05	-4.39	2.42	-9.74E-01
401	KIAA1143	227493_s_at	3.3948E-03	2.49E-05	4.39	2.42	5.16E-01
402		1558028_x_at	3.3948E-03	2.50E-05	-4.39	2.42	-4.43E-01
403	PTGER2	206631_at	3.3948E-03	2.50E-05	-4.39	2.42	-5.85E-01
404	ZNF136	206240_s_at	3.4326E-03	2.54E-05	4.39	2.41	4.19E-01
405	TSPAN4	209263_x_at	3.4414E-03	2.55E-05	-4.39	2.40	-5.31E-01
406	RPL5	213080_x_at	3.4567E-03	2.57E-05	4.39	2.40	2.10E-01
407	ZNF563	1552770_s_at	3.4797E-03	2.59E-05	4.38	2.39	1.96E-01
408	PLIN3	202122_s_at	3.4797E-03	2.60E-05	-4.38	2.39	-4.73E-01
409	SCARNA2	237137_at	3.4800E-03	2.61E-05	4.38	2.38	5.82E-01
410	OLFML2B	213125_at	3.4800E-03	2.61E-05	-4.38	2.38	-1.00E+00
411	TEAD4	41037_at	3.4886E-03	2.63E-05	-4.38	2.37	-2.90E-01
412	TTC32	226838_at	3.4886E-03	2.64E-05	4.38	2.37	4.74E-01
413	FNTB	1773_at	3.4886E-03	2.64E-05	-4.38	2.37	-2.39E-01
414	C1orf38	207571_x_at	3.4886E-03	2.65E-05	-4.38	2.37	-7.64E-01
415	LOC100133811///LOC100133661///ZNF749///RNASE2///HLA-DRB5///HLA-DRB4///HLA-DRB3///HLA-DRB2///HLA-DRB1	209312_x_at	3.4886E-03	2.66E-05	-4.38	2.36	-7.40E-01
416	CRK	202224_at	3.4886E-03	2.67E-05	-4.38	2.36	-4.93E-01
417	GAS5	224841_x_at	3.4886E-03	2.67E-05	4.38	2.36	6.82E-01
418	CD44	212014_x_at	3.4886E-03	2.68E-05	-4.38	2.36	-6.15E-01
419	LOC100133130	223766_at	3.4886E-03	2.68E-05	4.38	2.36	3.14E-01
420	PHTF1	210191_s_at	3.4886E-03	2.68E-05	-4.38	2.36	-3.37E-01
421	TNFAIP1	201207_at	3.4971E-03	2.70E-05	-4.37	2.35	-5.57E-01
422	ERLIN1	202441_at	3.4971E-03	2.70E-05	-4.37	2.35	-3.37E-01
423	RILPL1	226207_at	3.5155E-03	2.72E-05	-4.37	2.34	-3.69E-01
424	IFNAR1	225661_at	3.5212E-03	2.73E-05	-4.37	2.34	-5.71E-01
425	GLUL	242281_at	3.5320E-03	2.75E-05	-4.37	2.34	-7.88E-01
426	LILRB4	210152_at	3.5702E-03	2.78E-05	-4.37	2.32	-1.12E+00
427	SGPL1	208381_s_at	3.5853E-03	2.81E-05	-4.36	2.32	-4.62E-01
428	CD14	201743_at	3.5853E-03	2.82E-05	-4.36	2.31	-1.01E+00
429	LOC1518	1563445_x_at	3.5853E-03	2.82E-05	-4.36	2.31	-4.68E-01
430	FBLIM1	1555480_a_at	3.5853E-03	2.82E-05	-4.36	2.31	-4.29E-01
431	PICALM	212506_at	3.6379E-03	2.87E-05	-4.36	2.30	-4.91E-01
432	NFE2L1	200759_x_at	3.6379E-03	2.87E-05	-4.36	2.29	-4.35E-01
433	GOSR2	213206_at	3.6402E-03	2.89E-05	-4.36	2.29	-2.60E-01
434	GOSR2	213144_at	3.6402E-03	2.89E-05	-4.36	2.29	-2.93E-01
435	SDF2L1	218681_s_at	3.6515E-03	2.91E-05	-4.35	2.28	-5.05E-01
436		238265_x_at	3.6515E-03	2.92E-05	4.35	2.28	2.41E-01
437	FZD2	210220_at	3.6515E-03	2.92E-05	-4.35	2.28	-8.16E-01
438	DAB2	201279_s_at	3.6519E-03	2.93E-05	-4.35	2.28	-8.23E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
439	NCRNA00275	224915_x_at	3.6519E-03	2.93E-05	4.35	2.28	6.56E-01
440		234510_at	3.6519E-03	2.94E-05	4.35	2.27	1.32E-01
441	ALDH9A1	201612_at	3.6534E-03	2.95E-05	-4.35	2.27	-2.65E-01
442	MUC5AC	217187_at	3.6616E-03	2.97E-05	4.35	2.26	3.12E-01
443	SPIRE1	225018_at	3.6616E-03	2.98E-05	-4.35	2.26	-3.63E-01
444	MAFB	218559_s_at	3.6616E-03	2.98E-05	-4.35	2.26	-6.98E-01
445	CARD9	220162_s_at	3.6616E-03	2.98E-05	-4.35	2.26	-4.79E-01
446	RAB31	217763_s_at	3.6940E-03	3.03E-05	-4.34	2.25	-8.50E-01
447	DCP2	244777_at	3.6940E-03	3.03E-05	4.34	2.25	5.71E-01
448	MMP19	204575_s_at	3.6940E-03	3.03E-05	-4.34	2.25	-5.34E-01
449	DAB2	240873_x_at	3.6940E-03	3.03E-05	-4.34	2.24	-2.80E-01
450	SNX33	227151_at	3.7155E-03	3.06E-05	-4.34	2.24	-3.27E-01
451		215180_at	3.7311E-03	3.08E-05	4.34	2.23	2.56E-01
452		244216_at	3.7343E-03	3.09E-05	4.34	2.23	2.61E-01
453	POU5F1P4////POU5F1P3////POU5F1B////POU5F1	208286_x_at	3.7434E-03	3.10E-05	4.34	2.22	2.35E-01
454	TUBA1B	201090_x_at	3.7434E-03	3.11E-05	-4.34	2.22	-4.41E-01
455	FAM129B	223019_at	3.7434E-03	3.12E-05	-4.34	2.22	-5.18E-01
456	CSF1R	203104_at	3.7527E-03	3.13E-05	-4.34	2.22	-1.03E+00
457	SNX19	1554986_a_at	3.8439E-03	3.21E-05	-4.33	2.19	-1.91E-01
458	DTNBP1	223763_at	3.8439E-03	3.23E-05	4.33	2.19	3.83E-01
459	PLOD3	202185_at	3.8439E-03	3.23E-05	-4.33	2.19	-6.12E-01
460	LAMB1	211651_s_at	3.8439E-03	3.24E-05	-4.33	2.19	-8.32E-01
461	S100A11	200660_at	3.8439E-03	3.24E-05	-4.33	2.18	-7.99E-01
462	DGCR8	219811_at	3.8904E-03	3.29E-05	4.32	2.17	2.73E-01
463	ANXA2P2	208816_x_at	3.8904E-03	3.30E-05	-4.32	2.17	-4.35E-01
464	PDIA3	208612_at	3.8904E-03	3.30E-05	-4.32	2.17	-6.47E-01
465		235513_at	3.8978E-03	3.32E-05	4.32	2.16	4.19E-01
466		235772_at	3.9104E-03	3.33E-05	4.32	2.16	2.45E-01
467	RRAD	204802_at	3.9222E-03	3.35E-05	-4.32	2.15	-6.41E-01
468	DCST2	242988_at	3.9274E-03	3.37E-05	4.32	2.15	1.84E-01
469	SNRPN	228370_at	3.9274E-03	3.37E-05	4.32	2.15	6.80E-01
470	MARCKS	225897_at	3.9551E-03	3.40E-05	-4.32	2.14	-5.66E-01
471	BAT5	224756_s_at	3.9732E-03	3.42E-05	-4.31	2.14	-5.35E-01
472	TNFSF12-TNFSF13///TNFSF12///TNFSF13	211495_x_at	3.9756E-03	3.43E-05	-4.31	2.13	-7.87E-01
473	EIF4G2	200004_at	3.9786E-03	3.44E-05	-4.31	2.13	-2.80E-01
474	UBC///UBB////RPS27A	211296_x_at	3.9839E-03	3.45E-05	-4.31	2.13	-3.95E-01
475	NAIP	204860_s_at	3.9887E-03	3.47E-05	-4.31	2.12	-7.67E-01
476	CD44	209835_x_at	4.0059E-03	3.49E-05	-4.31	2.12	-5.73E-01
477	IGSF22	1553857_at	4.0059E-03	3.49E-05	4.31	2.12	2.87E-01
478	SEC63	201914_s_at	4.0274E-03	3.52E-05	-4.31	2.11	-6.92E-01
479	TRIP6	209129_at	4.0572E-03	3.55E-05	-4.30	2.10	-5.52E-01
480	LOC100133811///LOC100133661///ZNF749///RNASE2///HLA-DRB5///HLA-DRB4///HLA-DRB3///HLA-DRB2///HLA-DRB1	215193_x_at	4.0711E-03	3.58E-05	-4.30	2.09	-7.10E-01
481	C17orf48	223401_at	4.0711E-03	3.59E-05	4.30	2.09	6.15E-01
482		227769_at	4.0711E-03	3.59E-05	-4.30	2.09	-5.14E-01
483	RPS16	213890_x_at	4.0711E-03	3.60E-05	4.30	2.09	1.80E-01
484	ABCB7	209620_s_at	4.1287E-03	3.66E-05	4.30	2.07	3.19E-01
485	LMNA	203411_s_at	4.1287E-03	3.67E-05	-4.30	2.07	-5.85E-01
486	SGPL1	212322_at	4.1287E-03	3.67E-05	-4.30	2.07	-7.15E-01
487	PGM3	210041_s_at	4.1338E-03	3.68E-05	-4.29	2.07	-5.15E-01
488	PANK2	235130_at	4.1444E-03	3.70E-05	4.29	2.07	3.70E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
489	CD99L2	233825_s_at	4.1779E-03	3.74E-05	-4.29	2.06	-4.27E-01
490	ZNF681	238962_at	4.1993E-03	3.76E-05	4.29	2.05	2.58E-01
491	STARD8	206868_at	4.2026E-03	3.78E-05	-4.29	2.05	-4.01E-01
492	GNAQ	224862_at	4.2026E-03	3.78E-05	-4.29	2.05	-5.32E-01
493	KCMF1	240430_at	4.2189E-03	3.80E-05	4.29	2.04	2.19E-01
494	RAD23B	201223_s_at	4.2522E-03	3.84E-05	-4.28	2.03	-2.61E-01
495	TYMS	217684_at	4.2522E-03	3.86E-05	4.28	2.03	1.80E-01
496	C1S	208747_s_at	4.2522E-03	3.86E-05	-4.28	2.03	-5.83E-01
497	PAPSS2	203058_s_at	4.2640E-03	3.88E-05	-4.28	2.02	-6.09E-01
498	TCTN2	239928_at	4.2640E-03	3.89E-05	4.28	2.02	2.02E-01
499		233335_at	4.2640E-03	3.89E-05	4.28	2.02	1.18E-01
500	OXNAD1	227686_at	4.2755E-03	3.91E-05	4.28	2.01	6.72E-01
501	CHST15	203066_at	4.2755E-03	3.92E-05	-4.28	2.01	-7.11E-01
502	TTC22	215106_at	4.2804E-03	3.93E-05	4.28	2.01	1.93E-01
503	TRADD	1729_at	4.3082E-03	3.96E-05	-4.28	2.00	-3.63E-01
504	KIF16B	219570_at	4.3297E-03	3.99E-05	-4.27	2.00	-4.25E-01
505	RAC1	1567458_s_at	4.3388E-03	4.01E-05	-4.27	1.99	-8.53E-01
506	EMILIN1	204163_at	4.4127E-03	4.09E-05	-4.27	1.97	-8.63E-01
507	PRKAR1A	200603_at	4.4127E-03	4.09E-05	-4.27	1.97	-3.85E-01
508	SIT1	205484_at	4.4281E-03	4.11E-05	4.27	1.97	3.88E-01
509	LEMD1	229927_at	4.4427E-03	4.14E-05	4.26	1.96	2.05E-01
510	NAGLU	204360_s_at	4.4427E-03	4.14E-05	-4.26	1.96	-4.55E-01
511	VSIG10L	238654_at	4.4774E-03	4.18E-05	-4.26	1.95	-3.16E-01
512	TUBA1C	211750_x_at	4.4774E-03	4.19E-05	-4.26	1.95	-4.36E-01
513	FOLH1	217483_at	4.5304E-03	4.25E-05	4.26	1.94	1.66E-01
514	DNAJB11	223054_at	4.5366E-03	4.26E-05	-4.26	1.94	-6.14E-01
515		231552_at	4.5374E-03	4.27E-05	4.26	1.93	3.12E-01
516	SETD7	224928_at	4.5435E-03	4.29E-05	-4.25	1.93	-4.82E-01
517	NT5C3	223298_s_at	4.5435E-03	4.30E-05	4.25	1.93	5.99E-01
518	RBMS1	209868_s_at	4.5435E-03	4.30E-05	-4.25	1.93	-9.38E-01
519	HIST1H2AH ///HIST1H2A G///HIST1H2 AM///HIST1 H2AL///HIST 1H2AJ///HIS T1H2AK///HI ST1H2AI	208583_x_at	4.5481E-03	4.32E-05	4.25	1.92	5.73E-01
520	VKORC1	217949_s_at	4.5605E-03	4.34E-05	-4.25	1.92	-6.92E-01
521	ZPBP2	231442_at	4.5972E-03	4.38E-05	4.25	1.91	1.41E-01
522	NCRNA002 75	226227_x_at	4.6147E-03	4.41E-05	4.25	1.91	6.14E-01
523	STK38	1553117_a_at	4.6309E-03	4.43E-05	-4.25	1.90	-5.76E-01
524	ARPC2	213513_x_at	4.6340E-03	4.44E-05	-4.25	1.90	-2.87E-01
525	NDNL2	226008_at	4.6443E-03	4.47E-05	4.24	1.89	2.55E-01
526	PTPN11	209895_at	4.6443E-03	4.48E-05	-4.24	1.89	-2.99E-01
527	LOC390595	232663_s_at	4.6443E-03	4.48E-05	4.24	1.89	2.41E-01
528	RAB3GAP1	213530_at	4.6469E-03	4.50E-05	-4.24	1.89	-2.63E-01
529	SEL1L	230265_at	4.6469E-03	4.50E-05	-4.24	1.89	-4.76E-01
530	ATP5I	209492_x_at	4.6469E-03	4.51E-05	4.24	1.88	5.75E-01
531	NEU1	208926_at	4.6469E-03	4.52E-05	-4.24	1.88	-7.06E-01
532	SEC23B	201583_s_at	4.6469E-03	4.52E-05	-4.24	1.88	-7.21E-01
533	LILRB1	207104_x_at	4.6798E-03	4.56E-05	-4.24	1.88	-8.08E-01
534	TPI1	213011_s_at	4.6813E-03	4.59E-05	-4.24	1.87	-5.59E-01
535		243388_at	4.6813E-03	4.59E-05	4.24	1.87	2.55E-01
536	DCD	1553946_at	4.6813E-03	4.60E-05	4.24	1.87	2.18E-01
537	PVRL2	225418_at	4.6813E-03	4.60E-05	-4.24	1.87	-4.14E-01
538	CD63	200663_at	4.6813E-03	4.61E-05	-4.24	1.87	-4.24E-01
539	SLC39A6	202089_s_at	4.7291E-03	4.67E-05	-4.23	1.85	-7.32E-01
540	RPL36	231658_x_at	4.7291E-03	4.68E-05	4.23	1.85	1.57E-01
541	FNDC3B	229865_at	4.7291E-03	4.68E-05	-4.23	1.85	-4.76E-01
542		233920_at	4.7498E-03	4.71E-05	4.23	1.85	2.48E-01
543	ALDH6A1	204290_s_at	4.7679E-03	4.74E-05	-4.23	1.84	-6.35E-01
544	YWHAG	222985_at	4.7683E-03	4.75E-05	-4.23	1.84	-3.99E-01
545	MPDU1	209208_at	4.7683E-03	4.75E-05	-4.23	1.84	-4.90E-01
546	CTSB	200839_s_at	4.7953E-03	4.79E-05	-4.23	1.83	-6.67E-01
547	NRP2	219367_s_at	4.8823E-03	4.88E-05	-4.22	1.81	-3.42E-01
548	EPHA4	238671_at	4.9116E-03	4.92E-05	4.22	1.81	1.87E-01
549	GGCX	205351_at	4.9343E-03	4.95E-05	-4.22	1.80	-3.89E-01
550	ADRA2B	208544_at	4.9573E-03	4.99E-05	4.22	1.79	3.05E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
551		242980_at	4.9573E-03	5.01E-05	4.21	1.79	1.53E-01
552	QKI	212636_at	4.9573E-03	5.02E-05	-4.21	1.79	-5.47E-01
553	PDXK	202671_s_at	4.9573E-03	5.03E-05	-4.21	1.79	-7.13E-01
554		242629_at	4.9573E-03	5.04E-05	4.21	1.79	1.44E-01
555	DUT	209932_s_at	4.9573E-03	5.05E-05	4.21	1.78	3.55E-01
556	PPARA	223437_at	4.9573E-03	5.05E-05	-4.21	1.78	-4.56E-01
557	CFHR1///CFH	215388_s_at	4.9573E-03	5.06E-05	-4.21	1.78	-6.16E-01
558	WDFY3	212602_at	4.9573E-03	5.06E-05	-4.21	1.78	-4.14E-01
559	MIA3	1569057_s_at	4.9604E-03	5.07E-05	-4.21	1.78	-3.46E-01
560	CTBP2	210554_s_at	4.9704E-03	5.09E-05	-4.21	1.78	-4.52E-01
561		234987_at	4.9767E-03	5.12E-05	-4.21	1.77	-6.43E-01
562	PGAM1	200886_s_at	4.9767E-03	5.13E-05	-4.21	1.77	-3.62E-01
563	GAS5	228238_at	4.9767E-03	5.13E-05	4.21	1.77	6.68E-01
564	LOC284648	231427_at	4.9767E-03	5.13E-05	4.21	1.77	2.13E-01
565	PDXK	222492_at	4.9810E-03	5.15E-05	-4.21	1.77	-3.86E-01
566	ZAK	223519_at	5.0014E-03	5.18E-05	-4.21	1.76	-5.46E-01
567	BLVRA	203771_s_at	5.0014E-03	5.20E-05	-4.21	1.76	-8.30E-01
568		217521_at	5.0014E-03	5.20E-05	4.21	1.76	2.46E-01
569	USP40	225085_at	5.0032E-03	5.21E-05	-4.20	1.75	-3.27E-01
570	C13orf31	228937_at	5.0032E-03	5.22E-05	-4.20	1.75	-6.51E-01
571	STAB1	38487_at	5.0120E-03	5.23E-05	-4.20	1.75	-8.55E-01
572	TNFRSF1A	207643_s_at	5.0214E-03	5.25E-05	-4.20	1.75	-5.87E-01
573	HSP90B1	200599_s_at	5.0348E-03	5.28E-05	-4.20	1.74	-4.74E-01
574	FRMD4A	225167_at	5.0365E-03	5.30E-05	-4.20	1.74	-6.87E-01
575	HSPA8	210338_s_at	5.0365E-03	5.30E-05	-4.20	1.74	-1.03E+00
576	OTUD4	238848_at	5.0365E-03	5.31E-05	-4.20	1.74	-4.25E-01
577	NEDD4L	237498_at	5.0401E-03	5.32E-05	4.20	1.74	1.75E-01
578	GBAP1///GBA	209093_s_at	5.0401E-03	5.33E-05	-4.20	1.73	-5.46E-01
579	DAB2	210757_x_at	5.0401E-03	5.34E-05	-4.20	1.73	-7.10E-01
580	TUBA1C	209251_x_at	5.0516E-03	5.36E-05	-4.20	1.73	-4.13E-01
581	TTC37	1554029_a_at	5.0735E-03	5.39E-05	-4.20	1.72	-2.43E-01
582	FCGR2A	203561_at	5.0962E-03	5.42E-05	-4.19	1.72	-1.04E+00
583	LOC100131043	244029_at	5.1050E-03	5.45E-05	4.19	1.71	5.09E-01
584	KIAA0146	228325_at	5.1050E-03	5.47E-05	-4.19	1.71	-6.72E-01
585	AP1S1	205196_s_at	5.1050E-03	5.48E-05	-4.19	1.71	-3.48E-01
586		1561942_x_at	5.1050E-03	5.48E-05	4.19	1.71	2.58E-01
587	NRP1	210510_s_at	5.1050E-03	5.48E-05	-4.19	1.71	-5.01E-01
588	DHDPSL	239093_at	5.1050E-03	5.49E-05	4.19	1.71	1.92E-01
589	GMPPA	218070_s_at	5.1117E-03	5.51E-05	-4.19	1.70	-3.61E-01
590	PTPN7	1554860_at	5.1117E-03	5.52E-05	4.19	1.70	2.76E-01
591	SPRED1	244439_at	5.1231E-03	5.54E-05	-4.19	1.70	-5.03E-01
592	ZNF410	209944_at	5.1231E-03	5.55E-05	4.19	1.70	3.46E-01
593	GLT25D1	218473_s_at	5.1287E-03	5.57E-05	-4.19	1.69	-4.73E-01
594	EPAS1	200878_at	5.1287E-03	5.58E-05	-4.19	1.69	-7.35E-01
595	NF1	212678_at	5.1287E-03	5.58E-05	-4.19	1.69	-2.90E-01
596	ZNF100	238791_at	5.1287E-03	5.59E-05	4.19	1.69	2.42E-01
597		237965_at	5.1615E-03	5.64E-05	4.18	1.68	2.43E-01
598	PADI1	223739_at	5.1695E-03	5.65E-05	4.18	1.68	1.84E-01
599	LMO4	209205_s_at	5.1722E-03	5.67E-05	-4.18	1.68	-3.52E-01
600	SLC39A1	217778_at	5.1722E-03	5.68E-05	-4.18	1.68	-2.51E-01
601		1563188_at	5.1722E-03	5.69E-05	4.18	1.68	1.39E-01
602		239287_at	5.1858E-03	5.72E-05	4.18	1.67	8.99E-01
603	DUSP3	201537_s_at	5.1858E-03	5.73E-05	-4.18	1.67	-5.59E-01
604	LAMB3	209270_at	5.1858E-03	5.73E-05	-4.18	1.67	-3.68E-01
605		236379_at	5.1905E-03	5.74E-05	4.18	1.67	6.85E-01
606	CCDC3	223316_at	5.2128E-03	5.80E-05	-4.18	1.66	-6.55E-01
607	IL13RA1	211612_s_at	5.2128E-03	5.80E-05	-4.18	1.66	-8.14E-01
608	DPP9	231957_s_at	5.2128E-03	5.80E-05	-4.18	1.66	-2.17E-01
609	APLP2	214875_x_at	5.2128E-03	5.81E-05	-4.18	1.66	-6.09E-01
610	ATXN3	216657_at	5.2128E-03	5.82E-05	4.18	1.66	1.73E-01
611	PDXK	218019_s_at	5.2135E-03	5.83E-05	-4.18	1.65	-4.44E-01
612	CTSC	225647_s_at	5.2758E-03	5.91E-05	-4.17	1.64	-7.36E-01
613	RPS4X	213347_x_at	5.2758E-03	5.92E-05	4.17	1.64	1.86E-01
614		236901_at	5.2758E-03	5.92E-05	-4.17	1.64	-7.89E-01
615	MCAM	209086_x_at	5.2795E-03	5.94E-05	-4.17	1.64	-3.21E-01
616	RRAS	212647_at	5.2847E-03	5.96E-05	-4.17	1.63	-5.43E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
617	CD99	201029_s_at	5.2847E-03	5.98E-05	-4.17	1.63	-4.89E-01
618	COMT	208817_at	5.2847E-03	5.98E-05	-4.17	1.63	-7.00E-01
619	KDELR2	200699_at	5.2847E-03	5.98E-05	-4.17	1.63	-5.94E-01
620	FAHD1	227960_s_at	5.3065E-03	6.03E-05	-4.17	1.62	-4.82E-01
621	ZNF101	1552634_a_at	5.3065E-03	6.03E-05	4.17	1.62	7.36E-01
622	TULP3	221964_at	5.3151E-03	6.06E-05	-4.17	1.62	-2.22E-01
623	COBLL1	211032_at	5.3151E-03	6.06E-05	4.17	1.62	1.82E-01
624	PLD1	215723_s_at	5.3344E-03	6.10E-05	-4.16	1.61	-3.98E-01
625	SPPL2B	225248_at	5.3344E-03	6.11E-05	4.16	1.61	2.61E-01
626		1554224_at	5.3344E-03	6.11E-05	4.16	1.61	2.80E-01
627	RC3H1	225893_at	5.3602E-03	6.15E-05	4.16	1.61	3.21E-01
628		243104_at	5.3721E-03	6.17E-05	4.16	1.60	2.17E-01
629	SUCNR1	223939_at	5.3864E-03	6.20E-05	-4.16	1.60	-1.05E+00
630		221648_s_at	5.3949E-03	6.24E-05	4.16	1.59	6.76E-01
631		229830_at	5.3949E-03	6.24E-05	-4.16	1.59	-4.95E-01
632	FEZ2	202305_s_at	5.3949E-03	6.25E-05	-4.16	1.59	-4.81E-01
633	MLEC	200616_s_at	5.3949E-03	6.27E-05	-4.16	1.59	-5.20E-01
634	GAS7	211067_s_at	5.3949E-03	6.27E-05	-4.16	1.59	-4.59E-01
635	C2orf18	225695_at	5.3949E-03	6.28E-05	-4.16	1.59	-4.89E-01
636	UBE3A	213128_s_at	5.3949E-03	6.28E-05	-4.16	1.59	-3.68E-01
637	SLC35C1	222647_at	5.3949E-03	6.29E-05	-4.16	1.58	-2.89E-01
638	AQP1	207542_s_at	5.3949E-03	6.30E-05	-4.15	1.58	-6.11E-01
639	NSD1	235760_at	5.3949E-03	6.31E-05	4.15	1.58	3.07E-01
640	CD59	212463_at	5.3949E-03	6.32E-05	-4.15	1.58	-4.81E-01
641	IRAK1BP1	238599_at	5.3949E-03	6.32E-05	4.15	1.58	5.07E-01
642	KIAA1432	223826_s_at	5.4006E-03	6.35E-05	-4.15	1.58	-1.63E-01
643	TRIM27	210541_s_at	5.4006E-03	6.35E-05	-4.15	1.58	-7.34E-01
644	RAB3GAP1	239527_at	5.4109E-03	6.37E-05	4.15	1.57	1.63E-01
645	TM9SF1	209150_s_at	5.4170E-03	6.39E-05	-4.15	1.57	-5.31E-01
646	SORD	201562_s_at	5.4170E-03	6.40E-05	-4.15	1.57	-5.20E-01
647	CD59	200984_s_at	5.4201E-03	6.41E-05	-4.15	1.57	-6.23E-01
648	CPNE8	241706_at	5.4201E-03	6.43E-05	-4.15	1.56	-3.25E-01
649	LOC389199	1554809_at	5.4201E-03	6.43E-05	4.15	1.56	2.20E-01
650	FAM127A	201828_x_at	5.4361E-03	6.46E-05	-4.15	1.56	-6.15E-01
651	MAOB	204041_at	5.4937E-03	6.54E-05	-4.14	1.55	-5.18E-01
652	ZNF345	207236_at	5.4937E-03	6.57E-05	4.14	1.54	2.83E-01
653		230599_at	5.4937E-03	6.57E-05	4.14	1.54	6.03E-01
654	H2AFY	214500_at	5.4937E-03	6.57E-05	-4.14	1.54	-8.36E-01
655	CYB561	209163_at	5.4985E-03	6.60E-05	-4.14	1.54	-4.57E-01
656	PDAP1	202290_at	5.4985E-03	6.60E-05	-4.14	1.54	-5.92E-01
657	MTERFD2	214364_at	5.4985E-03	6.62E-05	4.14	1.54	4.71E-01
658		238106_at	5.4985E-03	6.63E-05	4.14	1.54	2.74E-01
659	ARRB2	203388_at	5.4985E-03	6.63E-05	-4.14	1.54	-6.30E-01
660	CDC42BPB	217849_s_at	5.5188E-03	6.67E-05	-4.14	1.53	-5.08E-01
661	ZNRF2	229188_s_at	5.5188E-03	6.67E-05	4.14	1.53	1.81E-01
662		1563297_s_at	5.5381E-03	6.71E-05	4.14	1.53	1.34E-01
663	HIST1H1D	214537_at	5.5381E-03	6.72E-05	4.14	1.53	6.34E-01
664	RRAD	204803_s_at	5.5424E-03	6.73E-05	-4.14	1.52	-5.58E-01
665	CSPG5	39966_at	5.5424E-03	6.75E-05	4.14	1.52	2.14E-01
666	ZNF384	220616_at	5.5424E-03	6.76E-05	4.14	1.52	2.58E-01
667	TRIM47	225868_at	5.5424E-03	6.78E-05	-4.14	1.52	-5.18E-01
668	SLC24A6	218749_s_at	5.5424E-03	6.79E-05	-4.13	1.51	-4.74E-01
669	IL15RA	207375_s_at	5.5424E-03	6.80E-05	-4.13	1.51	-5.85E-01
670	FKBP2	203391_at	5.5424E-03	6.80E-05	-4.13	1.51	-4.68E-01
671	CHP	214665_s_at	5.5424E-03	6.81E-05	-4.13	1.51	-5.96E-01
672	RP9	227849_at	5.5424E-03	6.82E-05	4.13	1.51	1.91E-01
673	FLII	212025_s_at	5.5424E-03	6.82E-05	-4.13	1.51	-7.06E-01
674	CD81	200675_at	5.5424E-03	6.83E-05	-4.13	1.51	-6.50E-01
675	HSP90B1	200598_s_at	5.5461E-03	6.85E-05	-4.13	1.51	-6.94E-01
676	HLA-DRB6	217362_x_at	5.5461E-03	6.86E-05	-4.13	1.51	-5.33E-01
677	AP3D1	206592_s_at	5.5531E-03	6.88E-05	-4.13	1.50	-4.43E-01
678	PDE11A	221110_x_at	5.5531E-03	6.89E-05	4.13	1.50	1.64E-01
679	HSP90AA1	210211_s_at	5.5633E-03	6.92E-05	-4.13	1.50	-3.20E-01
680	COPS7A	209029_at	5.5633E-03	6.92E-05	-4.13	1.50	-3.88E-01
681	KDSR	229850_at	5.5674E-03	6.93E-05	-4.13	1.50	-4.71E-01
682	ARX	231020_at	5.6116E-03	7.01E-05	4.13	1.49	2.88E-01
683	CISH	223961_s_at	5.6116E-03	7.01E-05	-4.13	1.49	-6.93E-01
684	ZSCAN16	219676_at	5.6116E-03	7.03E-05	4.13	1.48	4.39E-01
685		235295_at	5.6116E-03	7.05E-05	-4.13	1.48	-2.64E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
686	Sep-02	1554747_a_at	5.6116E-03	7.05E-05	-4.13	1.48	-5.56E-01
687	HSPH1	208744_x_at	5.6116E-03	7.05E-05	-4.12	1.48	-6.35E-01
688	CD163	203645_s_at	5.6116E-03	7.07E-05	-4.12	1.48	-1.35E+00
689	FCRLB	238452_at	5.6116E-03	7.07E-05	-4.12	1.48	-4.01E-01
690		237954_x_at	5.6133E-03	7.08E-05	4.12	1.48	1.53E-01
691	KIAA0368	212428_at	5.6133E-03	7.09E-05	-4.12	1.48	-7.47E-01
692	SP100	202863_at	5.6141E-03	7.11E-05	4.12	1.47	3.09E-01
693	EDEM3	220926_s_at	5.6167E-03	7.12E-05	-4.12	1.47	-3.63E-01
694	AGBL2	220390_at	5.6328E-03	7.16E-05	4.12	1.47	1.93E-01
695		236109_at	5.6328E-03	7.16E-05	4.12	1.47	3.69E-01
696	PDGFRB	202273_at	5.6396E-03	7.18E-05	-4.12	1.46	-5.80E-01
697		1564389_at	5.6396E-03	7.19E-05	4.12	1.46	1.64E-01
698		236301_at	5.6543E-03	7.23E-05	4.12	1.46	4.21E-01
699	CYP2D6	217468_at	5.6543E-03	7.23E-05	4.12	1.46	2.60E-01
700	DYNLRB2	238116_at	5.6590E-03	7.25E-05	4.12	1.46	4.00E-01
701	CTNNA1	200765_x_at	5.6649E-03	7.26E-05	-4.12	1.45	-5.07E-01
702	CTSC	201487_at	5.6696E-03	7.28E-05	-4.12	1.45	-4.83E-01
703	RPS7	213941_x_at	5.6696E-03	7.29E-05	4.12	1.45	2.28E-01
704	RABGAP1L	213982_s_at	5.6796E-03	7.32E-05	4.12	1.45	4.50E-01
705	KPNA1	213741_s_at	5.6796E-03	7.32E-05	-4.11	1.45	-4.23E-01
706	SEL1L	202061_s_at	5.6898E-03	7.35E-05	-4.11	1.44	-3.97E-01
707	TRAM2	202369_s_at	5.6931E-03	7.36E-05	-4.11	1.44	-7.21E-01
708	CD163	215049_x_at	5.7083E-03	7.39E-05	-4.11	1.44	-1.32E+00
709	GYLTL1B	227829_at	5.7170E-03	7.44E-05	4.11	1.43	2.49E-01
710	CARD8	228641_at	5.7170E-03	7.45E-05	4.11	1.43	5.80E-01
711	DOCK5	230263_s_at	5.7170E-03	7.46E-05	-4.11	1.43	-5.03E-01
712	PSMC3	201267_s_at	5.7170E-03	7.46E-05	-4.11	1.43	-8.38E-01
713	SLC35B1	202433_at	5.7170E-03	7.47E-05	-4.11	1.43	-4.21E-01
714	MDH1	235374_at	5.7170E-03	7.47E-05	4.11	1.43	4.98E-01
715	AMPD2	212360_at	5.7179E-03	7.48E-05	-4.11	1.43	-4.68E-01
716	PVRL2	232079_s_at	5.7307E-03	7.50E-05	-4.11	1.42	-4.56E-01
717		228049_x_at	5.7355E-03	7.52E-05	4.11	1.42	7.30E-01
718	BRCC3	221196_x_at	5.7682E-03	7.57E-05	-4.11	1.42	-4.26E-01
719	ITPRIPL2	227792_at	5.7750E-03	7.61E-05	-4.10	1.41	-6.31E-01
720	PIGT	217770_at	5.7750E-03	7.61E-05	-4.10	1.41	-3.44E-01
721	STMN1	217714_x_at	5.7750E-03	7.62E-05	4.10	1.41	2.74E-01
722	KCND3	213832_at	5.8062E-03	7.68E-05	-4.10	1.40	-4.67E-01
723	FOLR1	211074_at	5.8062E-03	7.69E-05	4.10	1.40	6.15E-01
724	CCL18	32128_at	5.8062E-03	7.70E-05	-4.10	1.40	-1.20E+00
725	TPI1	200822_x_at	5.8062E-03	7.70E-05	-4.10	1.40	-5.13E-01
726	MERTK	211913_s_at	5.8173E-03	7.72E-05	-4.10	1.40	-4.55E-01
727	PRMT5	217786_at	5.8431E-03	7.77E-05	-4.10	1.39	-6.47E-01
728		234417_at	5.8721E-03	7.82E-05	4.10	1.39	2.01E-01
729	TSHZ3	223392_s_at	5.8863E-03	7.85E-05	-4.10	1.38	-4.75E-01
730	MTRF1	244763_at	5.9071E-03	7.89E-05	4.10	1.38	2.41E-01
731	PPARGC1A	1569141_a_at	5.9158E-03	7.91E-05	4.09	1.38	1.98E-01
732	NDUFA2	209223_at	5.9158E-03	7.92E-05	4.09	1.38	2.81E-01
733	PPARG	208510_s_at	5.9441E-03	7.97E-05	-4.09	1.37	-5.67E-01
734	S100A11P1/ //S100A11	208540_x_at	5.9491E-03	7.99E-05	-4.09	1.37	-6.26E-01
735	RCN1	201063_at	5.9571E-03	8.02E-05	-4.09	1.36	-4.71E-01
736	CSDA	201161_s_at	5.9571E-03	8.03E-05	-4.09	1.36	-5.62E-01
737	GNS	212335_at	5.9571E-03	8.03E-05	-4.09	1.36	-8.26E-01
738	YIF1B	226437_at	5.9594E-03	8.05E-05	-4.09	1.36	-4.43E-01
739	SEC61A1	222385_x_at	5.9594E-03	8.06E-05	-4.09	1.36	-8.03E-01
740	HCK	208018_s_at	5.9594E-03	8.07E-05	-4.09	1.36	-7.96E-01
741	GNAQ	224861_at	6.0067E-03	8.17E-05	-4.09	1.35	-4.76E-01
742	GFPT1	202721_s_at	6.0067E-03	8.20E-05	-4.08	1.34	-3.69E-01
743	CCL23	210549_s_at	6.0067E-03	8.20E-05	-4.08	1.34	-1.34E+00
744		215796_at	6.0067E-03	8.21E-05	4.08	1.34	5.67E-01
745	CCL23	210548_at	6.0067E-03	8.22E-05	-4.08	1.34	-1.45E+00
746	CTSZ	210042_s_at	6.0067E-03	8.23E-05	-4.08	1.34	-9.00E-01
747	CSF2RA	211287_x_at	6.0067E-03	8.23E-05	-4.08	1.34	-4.73E-01
748	CLCC1	207855_s_at	6.0067E-03	8.25E-05	-4.08	1.34	-2.75E-01
749	NSFL1C	217831_s_at	6.0067E-03	8.25E-05	-4.08	1.34	-4.55E-01
750	CCDC96	238682_at	6.0067E-03	8.25E-05	-4.08	1.34	-1.67E-01
751	SNORD104	228879_at	6.0067E-03	8.25E-05	4.08	1.34	5.58E-01
752	RANBP9	216125_s_at	6.0067E-03	8.26E-05	-4.08	1.34	-4.28E-01
753	TPD52L2	201379_s_at	6.0261E-03	8.30E-05	-4.08	1.33	-5.64E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
754	ZC3H6	227809_at	6.0314E-03	8.32E-05	4.08	1.33	3.74E-01
755	RAB31	217762_s_at	6.0399E-03	8.34E-05	-4.08	1.33	-7.68E-01
756		235072_s_at	6.0679E-03	8.39E-05	-4.08	1.32	-4.79E-01
757	HSPA5	230031_at	6.0727E-03	8.41E-05	-4.08	1.32	-4.39E-01
758	SCARNA17	240830_at	6.0794E-03	8.43E-05	4.08	1.32	5.94E-01
759	LOC253962	1559061_at	6.1036E-03	8.47E-05	4.08	1.32	2.57E-01
760	PLAG1	205372_at	6.1143E-03	8.52E-05	4.07	1.31	3.74E-01
761	TUBA1B	212639_x_at	6.1143E-03	8.52E-05	-4.07	1.31	-4.67E-01
762	TIMP2	231579_s_at	6.1143E-03	8.54E-05	-4.07	1.31	-8.36E-01
763	GADD45B	209305_s_at	6.1143E-03	8.55E-05	-4.07	1.31	-5.60E-01
764		217615_at	6.1143E-03	8.55E-05	4.07	1.31	2.32E-01
765	LOC100128025	1562765_at	6.1143E-03	8.55E-05	4.07	1.31	2.28E-01
766	NAGA	202943_s_at	6.1341E-03	8.59E-05	-4.07	1.30	-6.42E-01
767	CD69	209795_at	6.1816E-03	8.67E-05	4.07	1.29	6.70E-01
768	PGD	201118_at	6.1965E-03	8.71E-05	-4.07	1.29	-1.02E+00
769	CCT6A	201327_s_at	6.1965E-03	8.72E-05	-4.07	1.29	-3.31E-01
770	ACOT7	208002_s_at	6.1965E-03	8.73E-05	-4.07	1.29	-5.90E-01
771	BCL2L2	209311_at	6.2043E-03	8.75E-05	-4.07	1.29	-4.54E-01
772	LRRC59	222231_s_at	6.2111E-03	8.77E-05	-4.07	1.28	-5.71E-01
773	PMS2L1	214526_x_at	6.2329E-03	8.82E-05	4.07	1.28	4.33E-01
774	ZCRB1	225394_s_at	6.2329E-03	8.82E-05	4.07	1.28	4.09E-01
775	NBR1	201384_s_at	6.2355E-03	8.84E-05	-4.06	1.28	-5.26E-01
776	HIST2H4B///HIST4H4///HIST2H4A///HIST1H4L///HIST1H4E///HIST1H4B///HIST1H4H///HIST1H4C///HIST1H4J///HIST1H4K///HIST1H4F///HIST1H4D///HIST1H4A///HIST1H4I	205967_at	6.2355E-03	8.85E-05	4.06	1.28	7.42E-01
777	ASTE1	221135_s_at	6.2355E-03	8.87E-05	4.06	1.27	3.39E-01
778	ATG7	218673_s_at	6.2355E-03	8.87E-05	-4.06	1.27	-5.80E-01
779	RDH11	217776_at	6.2362E-03	8.89E-05	-4.06	1.27	-2.46E-01
780	CCDC61	228475_at	6.2362E-03	8.90E-05	4.06	1.27	2.04E-01
781	AP1B1	205423_at	6.2750E-03	8.98E-05	-4.06	1.26	-3.67E-01
782	MAPK1	212271_at	6.2750E-03	8.98E-05	-4.06	1.26	-6.85E-01
783	HIST1H2AH///HIST1H2AG///HIST1H2AM///HIST1H2AL///HIST1H2AJ///HIST1H2AK///HIST1H2AI	214542_x_at	6.2750E-03	9.01E-05	4.06	1.26	5.23E-01
784	TPP1	200743_s_at	6.2750E-03	9.02E-05	-4.06	1.26	-6.83E-01
785	IGFBP2	202718_at	6.2750E-03	9.02E-05	-4.06	1.26	-8.59E-01
786	CDK2AP1	201938_at	6.2750E-03	9.02E-05	-4.06	1.26	-4.05E-01
787	SKIV2L2	227447_at	6.2879E-03	9.06E-05	4.06	1.25	3.49E-01
788	OLFM4	212768_s_at	6.2879E-03	9.07E-05	4.06	1.25	1.38E-01
789	GORASP2	207812_s_at	6.2879E-03	9.07E-05	-4.06	1.25	-3.61E-01
790	TMEM214	217899_at	6.2879E-03	9.10E-05	-4.06	1.25	-5.14E-01
791	GNPTG	224887_at	6.2879E-03	9.10E-05	-4.06	1.25	-3.78E-01
792	EIF3B	211501_s_at	6.2879E-03	9.13E-05	-4.06	1.25	-6.90E-01
793	Sep-02	200778_s_at	6.2879E-03	9.13E-05	-4.06	1.25	-4.44E-01
794	ZZZ3	229325_at	6.2879E-03	9.14E-05	4.06	1.25	2.70E-01
795		241883_x_at	6.2879E-03	9.14E-05	4.06	1.25	1.41E-01
796	MVP	202180_s_at	6.3078E-03	9.20E-05	-4.05	1.24	-5.64E-01
797	FTL	213187_x_at	6.3078E-03	9.21E-05	-4.05	1.24	-5.84E-01
798	MGAT1	201126_s_at	6.3078E-03	9.21E-05	-4.05	1.24	-5.29E-01
799	GGT5	205582_s_at	6.3188E-03	9.23E-05	-4.05	1.24	-7.16E-01
800	HSPA6	213418_at	6.3327E-03	9.27E-05	-4.05	1.23	-8.55E-01
801	CD151	204306_s_at	6.3362E-03	9.28E-05	-4.05	1.23	-4.36E-01
802	TGOLN2	203834_s_at	6.3384E-03	9.30E-05	-4.05	1.23	-3.74E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
803	ARMC8	219094_at	6.3529E-03	9.34E-05	4.05	1.23	2.67E-01
804	SLC16A3	202855_s_at	6.3529E-03	9.34E-05	-4.05	1.23	-6.08E-01
805	ETHE1	204034_at	6.3546E-03	9.36E-05	-4.05	1.23	-4.43E-01
806	FKBP4	200895_s_at	6.3654E-03	9.38E-05	-4.05	1.22	-3.94E-01
807	CLTC	200614_at	6.4079E-03	9.46E-05	-4.05	1.22	-3.04E-01
808	TRADD	205641_s_at	6.4084E-03	9.47E-05	-4.05	1.21	-3.39E-01
809	C11orf45	1553787_at	6.4097E-03	9.48E-05	-4.05	1.21	-1.59E-01
810		244028_at	6.4146E-03	9.52E-05	4.05	1.21	2.48E-01
811	ADAMTS1	222486_s_at	6.4146E-03	9.52E-05	-4.05	1.21	-1.94E-01
812	HLA-DPA1	211990_at	6.4146E-03	9.53E-05	-4.04	1.21	-5.15E-01
813	ACRV1	206776_x_at	6.4272E-03	9.56E-05	4.04	1.21	1.66E-01
814	BCKDK	202030_at	6.4282E-03	9.57E-05	-4.04	1.21	-5.04E-01
815	HSP90AA1	211969_at	6.4327E-03	9.62E-05	-4.04	1.20	-5.41E-01
816	PTGR1	231897_at	6.4327E-03	9.62E-05	-4.04	1.20	-6.40E-01
817	TRNP1	227862_at	6.4327E-03	9.63E-05	-4.04	1.20	-1.78E-01
818		242867_x_at	6.4327E-03	9.63E-05	4.04	1.20	1.58E-01
819	DKK3	202196_s_at	6.4327E-03	9.64E-05	-4.04	1.20	-3.43E-01
820	SERPINA1	211429_s_at	6.4327E-03	9.65E-05	-4.04	1.20	-1.09E+00
821	RPN2	213399_x_at	6.4431E-03	9.67E-05	-4.04	1.20	-3.58E-01
822	MAPK4	204708_at	6.4562E-03	9.72E-05	4.04	1.19	1.62E-01
823	EPRS	200841_s_at	6.4562E-03	9.72E-05	-4.04	1.19	-6.09E-01
824	GLG1	214730_s_at	6.4724E-03	9.75E-05	-4.04	1.19	-6.72E-01
825	MBNL1	1558111_at	6.4818E-03	9.78E-05	4.04	1.19	7.32E-01
826	SURF4	222978_at	6.5070E-03	9.83E-05	-4.04	1.18	-5.93E-01
827	ACTR1A	200720_s_at	6.5242E-03	9.87E-05	-4.04	1.18	-5.83E-01
828	CTTNBP2NL	226000_at	6.5242E-03	9.88E-05	-4.04	1.18	-3.80E-01
829	HIST1H3F/// HIST1H3B/// HIST1H3H/// HIST1H3J/// HIST1H3G/// HIST1H3I/// HIST1H3E/// HIST1H3C/// HIST1H3D/// HIST1H3A/// HIST1H2AD	208576_s_at	6.5367E-03	9.92E-05	4.03	1.17	7.65E-01
830	WNT16	224022_x_at	6.5367E-03	9.92E-05	4.03	1.17	1.68E-01
831	SLC2A5	204429_s_at	6.5419E-03	9.96E-05	-4.03	1.17	-5.68E-01
832	PDIA6	208639_x_at	6.5419E-03	9.96E-05	-4.03	1.17	-4.35E-01
833	RAB3GAP1	212932_at	6.5419E-03	9.97E-05	-4.03	1.17	-3.88E-01
834	SESN2	223195_s_at	6.5419E-03	9.98E-05	-4.03	1.17	-3.27E-01
835	TIA1	201447_at	6.5624E-03	1.00E-04	4.03	1.16	4.36E-01
836	NRP2	225566_at	6.5624E-03	1.00E-04	-4.03	1.16	-4.19E-01
837	ZNF880	235913_at	6.5650E-03	1.01E-04	4.03	1.16	5.63E-01
838	ZNF141	206931_at	6.5650E-03	1.01E-04	4.03	1.16	3.59E-01
839	PCSK5	205560_at	6.5650E-03	1.01E-04	-4.03	1.16	-5.69E-01
840	PTAFR	211661_x_at	6.5869E-03	1.01E-04	-4.03	1.15	-9.22E-01
841	OCEL1	205441_at	6.5869E-03	1.01E-04	-4.03	1.15	-2.15E-01
842	MPP1	202974_at	6.5869E-03	1.01E-04	-4.03	1.15	-6.78E-01
843	ZNF138	244743_x_at	6.5966E-03	1.02E-04	4.03	1.15	4.24E-01
844	CHN2	213385_at	6.5966E-03	1.02E-04	-4.03	1.15	-6.58E-01
845	TOMM40L	226059_at	6.5966E-03	1.02E-04	-4.03	1.15	-2.68E-01
846	C17orf108	213195_at	6.6189E-03	1.02E-04	4.03	1.14	3.72E-01
847	PALLD	200907_s_at	6.6287E-03	1.03E-04	-4.02	1.14	-5.09E-01
848	TRIM8	223132_s_at	6.6468E-03	1.03E-04	-4.02	1.14	-6.29E-01
849	RNF146	221430_s_at	6.6806E-03	1.04E-04	-4.02	1.13	-4.24E-01
850		230444_at	6.6889E-03	1.04E-04	4.02	1.13	6.01E-01
851	BOLA2	231500_s_at	6.6889E-03	1.04E-04	4.02	1.13	4.78E-01
852	TM9SF2	201078_at	6.7037E-03	1.05E-04	-4.02	1.13	-4.89E-01
853	NCRNA00275	226835_s_at	6.7037E-03	1.05E-04	4.02	1.12	6.99E-01
854	RRBP1	201206_s_at	6.7037E-03	1.05E-04	-4.02	1.12	-5.51E-01
855	MCAM	211340_s_at	6.7488E-03	1.06E-04	-4.02	1.12	-5.54E-01
856		231431_s_at	6.7559E-03	1.06E-04	-4.02	1.11	-3.94E-01
857	GALNT10	207357_s_at	6.7559E-03	1.06E-04	-4.02	1.11	-4.39E-01
858	ANXA2	201590_x_at	6.7692E-03	1.06E-04	-4.02	1.11	-4.51E-01
859		1561226_at	6.7743E-03	1.06E-04	-4.02	1.11	-3.71E-01
860	L3MBTL2	1555815_a_at	6.8023E-03	1.07E-04	-4.01	1.10	-4.35E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
861	KDM1B	227021_at	6.8108E-03	1.07E-04	-4.01	1.10	-5.50E-01
862	GSPT1	240452_at	6.8108E-03	1.07E-04	4.01	1.10	4.43E-01
863	CALU	214845_s_at	6.8308E-03	1.08E-04	-4.01	1.10	-7.71E-01
864		226311_at	6.8465E-03	1.08E-04	-4.01	1.09	-9.45E-01
865	FBLIM1	225258_at	6.8661E-03	1.09E-04	-4.01	1.09	-5.85E-01
866	DLEU1	205677_s_at	6.8670E-03	1.09E-04	4.01	1.09	6.86E-01
867	CRK	202226_s_at	6.8670E-03	1.09E-04	-4.01	1.09	-5.50E-01
868	CALU	200755_s_at	6.8670E-03	1.09E-04	-4.01	1.09	-6.45E-01
869		234590_x_at	6.8670E-03	1.09E-04	4.01	1.09	1.79E-01
870	VTI1B	225928_at	6.8691E-03	1.10E-04	-4.01	1.08	-4.43E-01
871	SYS1-DBNDD2///DBNDD2	218094_s_at	6.8691E-03	1.10E-04	-4.01	1.08	-4.80E-01
872	ATF7IP	207728_at	6.8691E-03	1.10E-04	4.01	1.08	1.48E-01
873	IL13RA1	201888_s_at	6.8691E-03	1.10E-04	-4.01	1.08	-5.76E-01
874	TMEM43	222418_s_at	6.8691E-03	1.10E-04	-4.01	1.08	-5.12E-01
875		233021_at	6.8691E-03	1.10E-04	4.01	1.08	2.73E-01
876	SELENBP1	214433_s_at	6.8827E-03	1.10E-04	-4.01	1.08	-4.36E-01
877	GIT2	204982_at	6.8886E-03	1.10E-04	4.01	1.08	4.41E-01
878	EMILIN2	224374_s_at	6.8892E-03	1.11E-04	-4.00	1.07	-6.95E-01
879	CALD1	212077_at	6.9027E-03	1.11E-04	-4.00	1.07	-6.10E-01
880	ZNF678	1554922_at	6.9217E-03	1.11E-04	4.00	1.07	1.65E-01
881	ZNF254	242602_x_at	6.9271E-03	1.12E-04	4.00	1.07	3.56E-01
882	VIM	201426_s_at	6.9434E-03	1.12E-04	-4.00	1.06	-6.19E-01
883	TNIP1	207196_s_at	6.9434E-03	1.12E-04	-4.00	1.06	-5.18E-01
884	UBE2F	225787_at	6.9434E-03	1.12E-04	-4.00	1.06	-4.89E-01
885	C21orf33	202217_at	6.9441E-03	1.12E-04	-4.00	1.06	-2.27E-01
886	ABCC6P1	236205_at	6.9565E-03	1.13E-04	4.00	1.06	1.56E-01
887	EIF3E	208697_s_at	6.9565E-03	1.13E-04	4.00	1.06	3.81E-01
888	NCRNA00241	223740_at	6.9808E-03	1.13E-04	4.00	1.05	2.14E-01
889	ADCY3	209321_s_at	6.9808E-03	1.14E-04	-4.00	1.05	-5.11E-01
890	ZNF273	215239_x_at	6.9895E-03	1.14E-04	4.00	1.05	3.56E-01
891	HSP90AB1	214359_s_at	7.0020E-03	1.14E-04	-4.00	1.05	-1.07E+00
892	SLC38A7	56821_at	7.0034E-03	1.14E-04	-4.00	1.04	-4.01E-01
893	PSMD7	201705_at	7.0034E-03	1.14E-04	-4.00	1.04	-3.58E-01
894	RPS27L	218007_s_at	7.0058E-03	1.15E-04	4.00	1.04	4.43E-01
895		231237_x_at	7.0360E-03	1.15E-04	3.99	1.04	3.09E-01
896	STAP1	220059_at	7.0360E-03	1.15E-04	3.99	1.04	1.17E+00
897	TUBA1B	211058_x_at	7.0360E-03	1.16E-04	-3.99	1.04	-3.54E-01
898	ADAMTS1	222162_s_at	7.0360E-03	1.16E-04	-3.99	1.03	-7.54E-01
899	BCOR	223915_at	7.0361E-03	1.16E-04	3.99	1.03	5.33E-01
900	TSPAN4	209264_s_at	7.0361E-03	1.16E-04	-3.99	1.03	-8.38E-01
901	C8orf68	1554978_at	7.0361E-03	1.16E-04	3.99	1.03	2.25E-01
902	FGF22	1566814_at	7.0408E-03	1.16E-04	3.99	1.03	2.02E-01
903	PPYR1	210956_at	7.0413E-03	1.16E-04	3.99	1.03	1.93E-01
904	STOM	201060_x_at	7.0413E-03	1.16E-04	-3.99	1.03	-4.77E-01
905	NDUFA11	228690_s_at	7.0413E-03	1.17E-04	3.99	1.03	4.94E-01
906	ANAPC16	224664_at	7.0546E-03	1.17E-04	3.99	1.02	4.91E-01
907	SEL1L	202062_s_at	7.0987E-03	1.18E-04	-3.99	1.02	-4.90E-01
908		1562546_at	7.1090E-03	1.18E-04	3.99	1.02	2.46E-01
909	GPC1	202756_s_at	7.1090E-03	1.18E-04	-3.99	1.01	-2.74E-01
910	VMA21	235237_at	7.1185E-03	1.19E-04	3.99	1.01	3.35E-01
911	RPS21	214097_at	7.1185E-03	1.19E-04	3.99	1.01	1.00E+00
912	SDF4	224472_x_at	7.1314E-03	1.19E-04	-3.99	1.01	-5.15E-01
913	DLG1	202516_s_at	7.1314E-03	1.19E-04	-3.98	1.01	-1.79E-01
914	TROAP	1568596_a_at	7.1373E-03	1.19E-04	3.98	1.01	4.53E-01
915	TIMP2	224560_at	7.1373E-03	1.19E-04	-3.98	1.01	-9.63E-01
916	FAM167B	223657_at	7.1405E-03	1.20E-04	-3.98	1.00	-3.17E-01
917	DLC1	210762_s_at	7.1625E-03	1.20E-04	-3.98	1.00	-6.89E-01
918		237859_at	7.1638E-03	1.20E-04	3.98	1.00	1.31E-01
919	IFI30	201422_at	7.1638E-03	1.20E-04	-3.98	1.00	-7.49E-01
920		239479_x_at	7.1875E-03	1.21E-04	3.98	0.99	2.96E-01
921	GPR107	211979_at	7.1982E-03	1.21E-04	-3.98	0.99	-3.11E-01
922	PYROXD1	219802_at	7.2240E-03	1.22E-04	3.98	0.99	4.68E-01
923	SERINC3	221473_x_at	7.2240E-03	1.22E-04	-3.98	0.99	-4.77E-01
924	SLC22A18AS	206097_at	7.2351E-03	1.22E-04	3.98	0.98	2.35E-01
925	PASK	216945_x_at	7.2650E-03	1.23E-04	3.98	0.98	7.12E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
926	KIAA0922	235674_at	7.3016E-03	1.24E-04	3.97	0.97	4.56E-01
927		231174_s_at	7.3026E-03	1.24E-04	-3.97	0.97	-2.32E-01
928	COL4A1	211981_at	7.3161E-03	1.24E-04	-3.97	0.97	-9.04E-01
929	RPL18P11	222297_x_at	7.3355E-03	1.25E-04	3.97	0.97	2.16E-01
930	UBR2	215558_at	7.3463E-03	1.25E-04	3.97	0.96	1.82E-01
931	SVIP	230005_at	7.3463E-03	1.25E-04	3.97	0.96	3.56E-01
932	NDUFB1	206790_s_at	7.3463E-03	1.25E-04	3.97	0.96	3.75E-01
933	SNX2	202113_s_at	7.3463E-03	1.26E-04	-3.97	0.96	-7.38E-01
934	IQGAP1	213446_s_at	7.3463E-03	1.26E-04	-3.97	0.96	-7.17E-01
935		231169_at	7.3463E-03	1.26E-04	-3.97	0.96	-4.54E-01
936	ZNF277	215887_at	7.3463E-03	1.26E-04	3.97	0.96	3.54E-01
937	LRPAP1	201186_at	7.3463E-03	1.26E-04	-3.97	0.96	-3.90E-01
938	SDC1	201287_s_at	7.3463E-03	1.26E-04	-3.97	0.95	-8.09E-01
939	CFL1	200021_at	7.3463E-03	1.27E-04	-3.97	0.95	-6.08E-01
940	TOX4	232097_at	7.3463E-03	1.27E-04	3.97	0.95	3.49E-01
941	METTL12/// SNORA57	238680_at	7.3463E-03	1.27E-04	3.97	0.95	2.26E-01
942	TNFRSF25	216042_at	7.3463E-03	1.27E-04	3.97	0.95	2.38E-01
943	ZNF541	232604_at	7.3463E-03	1.27E-04	3.97	0.95	3.02E-01
944	C2///CFB	202357_s_at	7.3463E-03	1.27E-04	-3.97	0.95	-8.27E-01
945	NOP56	200874_s_at	7.3637E-03	1.27E-04	-3.97	0.95	-3.01E-01
946	F2R	203989_x_at	7.3785E-03	1.28E-04	-3.97	0.95	-4.61E-01
947	PNMA1	218224_at	7.3880E-03	1.28E-04	-3.97	0.94	-3.35E-01
948	ZNF493///ZNF738///ZNF273	240155_x_at	7.3880E-03	1.28E-04	3.96	0.94	4.48E-01
949		242839_at	7.3880E-03	1.28E-04	3.96	0.94	2.11E-01
950	LILRA2	211100_x_at	7.3880E-03	1.28E-04	-3.96	0.94	-3.81E-01
951	KLF3	225133_at	7.4084E-03	1.29E-04	-3.96	0.94	-5.24E-01
952	DISP1	235466_s_at	7.4112E-03	1.29E-04	3.96	0.94	8.60E-01
953	COMT	208818_s_at	7.4402E-03	1.30E-04	-3.96	0.93	-5.03E-01
954	LPHN1	203488_at	7.4737E-03	1.31E-04	-3.96	0.93	-2.14E-01
955		227184_at	7.4737E-03	1.31E-04	-3.96	0.92	-5.78E-01
956	TUBA1B	213646_x_at	7.4737E-03	1.31E-04	-3.96	0.92	-4.31E-01
957	TRIP4	203732_at	7.4737E-03	1.31E-04	-3.96	0.92	-4.18E-01
958	LOC400960	227969_at	7.4737E-03	1.31E-04	-3.96	0.92	-3.81E-01
959	ZNF93	208119_s_at	7.4737E-03	1.32E-04	3.96	0.92	2.86E-01
960	CDKN1A	202284_s_at	7.4737E-03	1.32E-04	-3.96	0.92	-5.43E-01
961	DNAJB6	209015_s_at	7.4737E-03	1.32E-04	-3.96	0.92	-5.25E-01
962	RPL32	200674_s_at	7.4737E-03	1.32E-04	3.96	0.92	1.75E-01
963	LRPPRC	1557360_at	7.4737E-03	1.32E-04	3.96	0.92	4.28E-01
964	SERPINF1	202283_at	7.4737E-03	1.32E-04	-3.96	0.92	-8.12E-01
965	SCARB2	224983_at	7.4737E-03	1.32E-04	-3.96	0.91	-7.17E-01
966	LOC643763	1558388_a_at	7.4737E-03	1.32E-04	3.96	0.91	1.02E-01
967	RPPH1	1556684_at	7.4737E-03	1.32E-04	3.96	0.91	2.62E-01
968	BACE1	217904_s_at	7.4737E-03	1.33E-04	-3.96	0.91	-3.68E-01
969	EFR3B	215328_at	7.4737E-03	1.33E-04	3.96	0.91	2.31E-01
970	C10orf31	1560255_at	7.4737E-03	1.33E-04	3.96	0.91	2.00E-01
971	ACBD5	1568877_a_at	7.4737E-03	1.33E-04	-3.95	0.91	-2.97E-01
972	SERINC3	211769_x_at	7.4737E-03	1.33E-04	-3.95	0.91	-6.07E-01
973	RNH1	206050_s_at	7.4737E-03	1.33E-04	-3.95	0.91	-6.10E-01
974	LOC439949	232001_at	7.4737E-03	1.33E-04	3.95	0.91	7.02E-01
975	HIST1H4J	214463_x_at	7.5249E-03	1.34E-04	3.95	0.90	7.40E-01
976	VPS24	217837_s_at	7.5380E-03	1.35E-04	-3.95	0.90	-6.27E-01
977	FAM20C	226722_at	7.5380E-03	1.35E-04	-3.95	0.90	-7.65E-01
978		229968_at	7.5380E-03	1.35E-04	-3.95	0.90	-4.76E-01
979	CCNG2	202769_at	7.5482E-03	1.35E-04	3.95	0.89	3.60E-01
980	SFXN3	217226_s_at	7.5482E-03	1.35E-04	-3.95	0.89	-4.58E-01
981	DENND3	212974_at	7.5482E-03	1.36E-04	-3.95	0.89	-3.13E-01
982	TMBIM6	200803_s_at	7.5482E-03	1.36E-04	-3.95	0.89	-5.09E-01
983	TMEM115	216267_s_at	7.5482E-03	1.36E-04	-3.95	0.89	-3.77E-01
984	MAPKAP1	229846_s_at	7.5541E-03	1.36E-04	-3.95	0.89	-4.47E-01
985		237301_at	7.5680E-03	1.36E-04	3.95	0.89	2.19E-01
986		236609_at	7.5680E-03	1.36E-04	3.95	0.89	2.21E-01
987	MAN2B1	209166_s_at	7.5813E-03	1.37E-04	-3.95	0.88	-5.96E-01
988	MID2	208384_s_at	7.5813E-03	1.37E-04	-3.95	0.88	-1.91E-01
989	NFE2L1	214179_s_at	7.5813E-03	1.37E-04	-3.95	0.88	-3.59E-01
990	BLVRA	203773_x_at	7.5813E-03	1.38E-04	-3.95	0.88	-3.90E-01
991	C1orf85	225401_at	7.5813E-03	1.38E-04	-3.95	0.88	-5.96E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
992	SLC27A4	225779_at	7.5813E-03	1.38E-04	-3.95	0.88	-3.01E-01
993	GLUL	200648_s_at	7.5813E-03	1.38E-04	-3.95	0.88	-1.11E+00
994	ZNF626	1552643_at	7.5813E-03	1.38E-04	3.94	0.88	5.47E-01
995	FNTB	225851_at	7.5813E-03	1.38E-04	-3.94	0.88	-3.63E-01
996	FAM120A	200767_s_at	7.6167E-03	1.39E-04	-3.94	0.87	-3.87E-01
997	SPACA1	220982_s_at	7.6188E-03	1.39E-04	3.94	0.87	1.57E-01
998	LAIR1	210644_s_at	7.6188E-03	1.39E-04	-3.94	0.87	-6.70E-01
999	TUBA1B	211072_x_at	7.6188E-03	1.39E-04	-3.94	0.87	-3.44E-01
1000		1569834_at	7.6188E-03	1.39E-04	3.94	0.87	2.67E-01
1001		1565913_at	7.6343E-03	1.40E-04	3.94	0.86	2.40E-01
1002	GJD3	230025_at	7.6351E-03	1.40E-04	-3.94	0.86	-4.88E-01
1003	SOD2	216841_s_at	7.6493E-03	1.40E-04	-3.94	0.86	-6.43E-01
1004	GCOM1///GRINL1A	212243_at	7.6580E-03	1.41E-04	3.94	0.86	3.27E-01
1005		235697_at	7.6842E-03	1.41E-04	3.94	0.85	3.36E-01
1006	PFKL	201102_s_at	7.6951E-03	1.42E-04	-3.94	0.85	-3.36E-01
1007	ARCN1	201176_s_at	7.6961E-03	1.42E-04	-3.94	0.85	-4.64E-01
1008	CD36	206488_s_at	7.6966E-03	1.42E-04	-3.94	0.85	-8.62E-01
1009	RPN2	213491_x_at	7.7145E-03	1.42E-04	-3.94	0.85	-3.57E-01
1010	FGFR1	222164_at	7.7145E-03	1.43E-04	3.94	0.85	5.45E-01
1011	ANXA2	210427_x_at	7.7596E-03	1.43E-04	-3.93	0.84	-4.38E-01
1012	AP2M1	200613_at	7.7769E-03	1.44E-04	-3.93	0.84	-6.70E-01
1013	CAPNS1	200001_at	7.7934E-03	1.44E-04	-3.93	0.83	-8.92E-01
1014	PCSK2	204870_s_at	7.7977E-03	1.45E-04	3.93	0.83	1.96E-01
1015	HIST1H2BD	222067_x_at	7.8007E-03	1.45E-04	3.93	0.83	6.01E-01
1016	MYOF	211864_s_at	7.8129E-03	1.45E-04	-3.93	0.83	-8.96E-01
1017	HIST1H1B	214534_at	7.8887E-03	1.47E-04	3.93	0.82	5.37E-01
1018	SNCG	209877_at	7.8970E-03	1.47E-04	3.93	0.82	2.66E-01
1019		237883_at	7.9145E-03	1.48E-04	3.93	0.81	2.30E-01
1020	GPT	206709_x_at	7.9145E-03	1.48E-04	3.93	0.81	2.21E-01
1021	CEP63	222151_s_at	7.9145E-03	1.48E-04	-3.93	0.81	-4.01E-01
1022	RUSC1	206949_s_at	7.9145E-03	1.48E-04	-3.93	0.81	-4.08E-01
1023	GTF3A	215091_s_at	7.9145E-03	1.48E-04	3.93	0.81	3.66E-01
1024	CNDP2	217752_s_at	7.9289E-03	1.49E-04	-3.92	0.81	-5.11E-01
1025	GPX3	201348_at	7.9289E-03	1.49E-04	-3.92	0.81	-1.22E+00
1026	LOC285972	1560762_at	7.9289E-03	1.49E-04	3.92	0.81	4.82E-01
1027	GOLM1	217771_at	7.9416E-03	1.49E-04	-3.92	0.80	-8.87E-01
1028	MYL9	201058_s_at	7.9420E-03	1.49E-04	-3.92	0.80	-1.06E+00
1029	ZNF292	212368_at	7.9420E-03	1.49E-04	3.92	0.80	2.93E-01
1030	VPS53	227229_at	7.9526E-03	1.50E-04	-3.92	0.80	-3.39E-01
1031	RCAN1	208370_s_at	7.9868E-03	1.51E-04	-3.92	0.80	-5.64E-01
1032	CCDC93	209689_at	7.9868E-03	1.51E-04	-3.92	0.80	-3.28E-01
1033	CD93	202877_s_at	7.9868E-03	1.51E-04	-3.92	0.79	-6.21E-01
1034	FAM13A	217047_s_at	7.9868E-03	1.51E-04	-3.92	0.79	-5.27E-01
1035	LOC100131015	244659_at	7.9868E-03	1.51E-04	3.92	0.79	3.86E-01
1036	RPS16	226131_s_at	8.0769E-03	1.53E-04	3.92	0.78	1.19E-01
1037	KCND3	215014_at	8.1023E-03	1.54E-04	-3.92	0.78	-1.88E-01
1038	ZNF695	208273_at	8.1023E-03	1.54E-04	3.92	0.78	2.01E-01
1039	TC2N	234970_at	8.1212E-03	1.54E-04	3.91	0.77	4.82E-01
1040	RICTOR	228248_at	8.1212E-03	1.54E-04	3.91	0.77	3.45E-01
1041	MSX2	210319_x_at	8.1212E-03	1.55E-04	-3.91	0.77	-3.54E-01
1042	FTL	212788_x_at	8.1250E-03	1.55E-04	-3.91	0.77	-3.26E-01
1043	LOC653566///SPCS2	201239_s_at	8.1427E-03	1.55E-04	-3.91	0.77	-4.42E-01
1044	PHF7	221930_at	8.1466E-03	1.56E-04	3.91	0.77	1.41E-01
1045	SDF4	221972_s_at	8.1588E-03	1.56E-04	-3.91	0.77	-7.86E-01
1046	FLII	222065_s_at	8.1826E-03	1.57E-04	-3.91	0.76	-6.95E-01
1047		1558876_at	8.1826E-03	1.57E-04	3.91	0.76	1.92E-01
1048	XBP1	200670_at	8.1826E-03	1.57E-04	-3.91	0.76	-6.42E-01
1049	ARPC2	208679_s_at	8.1826E-03	1.57E-04	-3.91	0.76	-4.10E-01
1050	RAB1A	207791_s_at	8.1826E-03	1.58E-04	-3.91	0.76	-7.13E-01
1051		237698_at	8.1826E-03	1.58E-04	3.91	0.76	1.73E-01
1052	NES	218678_at	8.1826E-03	1.58E-04	-3.91	0.76	-4.21E-01
1053	CROCCL1	1569293_x_at	8.1826E-03	1.58E-04	3.91	0.75	3.17E-01
1054	MS4A6A	223922_x_at	8.1826E-03	1.58E-04	-3.91	0.75	-6.47E-01
1055		1557276_at	8.1826E-03	1.58E-04	3.91	0.75	2.27E-01
1056	KIF6	1556233_s_at	8.1826E-03	1.58E-04	3.91	0.75	1.65E-01
1057	CLN5	204084_s_at	8.2018E-03	1.59E-04	-3.91	0.75	-3.89E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1058	DNASE1L1	203912_s_at	8.2018E-03	1.59E-04	-3.91	0.75	-3.71E-01
1059	CDC14B	211347_at	8.2103E-03	1.59E-04	3.91	0.75	1.77E-01
1060	ARAP2	214102_at	8.2103E-03	1.59E-04	3.91	0.75	3.30E-01
1061	RAP1A	1555340_x_at	8.2103E-03	1.59E-04	3.91	0.75	1.79E-01
1062	YIF1B	1554553_s_at	8.2213E-03	1.60E-04	-3.90	0.74	-6.14E-01
1063	LOC126536	1555988_a_at	8.2219E-03	1.60E-04	3.90	0.74	1.43E-01
1064	MOSC1	218865_at	8.2219E-03	1.60E-04	-3.90	0.74	-2.92E-01
1065	ZNF527	1570238_at	8.2219E-03	1.60E-04	3.90	0.74	2.01E-01
1066	HLA-C	216526_x_at	8.2219E-03	1.60E-04	-3.90	0.74	-3.13E-01
1067	RNASEH2B	219056_at	8.2565E-03	1.61E-04	3.90	0.74	4.81E-01
1068	SLC25A13	203775_at	8.2568E-03	1.61E-04	-3.90	0.73	-3.03E-01
1069	PNKD	233177_s_at	8.2637E-03	1.62E-04	-3.90	0.73	-7.28E-01
1070	PLEK	203471_s_at	8.2637E-03	1.62E-04	-3.90	0.73	-5.46E-01
1071		1569802_at	8.3248E-03	1.63E-04	3.90	0.72	1.46E-01
1072		227979_at	8.3306E-03	1.63E-04	3.90	0.72	4.69E-01
1073	LRRC7	242050_at	8.3531E-03	1.64E-04	3.90	0.72	1.67E-01
1074	STIP1	212009_s_at	8.3545E-03	1.64E-04	-3.90	0.72	-7.81E-01
1075	COX7C	213846_at	8.3935E-03	1.65E-04	3.90	0.71	5.72E-01
1076	ZFX	229022_at	8.4062E-03	1.66E-04	3.89	0.71	4.07E-01
1077	PON2	210830_s_at	8.4062E-03	1.66E-04	-3.89	0.71	-6.45E-01
1078	HLA-C	211799_x_at	8.4062E-03	1.66E-04	-3.89	0.71	-5.69E-01
1079	LOC285771	237870_at	8.4062E-03	1.66E-04	3.89	0.71	1.84E-01
1080	KPNA5	227934_at	8.4062E-03	1.66E-04	3.89	0.71	4.64E-01
1081	KDM4B	212495_at	8.4062E-03	1.66E-04	-3.89	0.71	-4.17E-01
1082	PYROXD1	231173_at	8.4062E-03	1.66E-04	3.89	0.71	1.96E-01
1083	PGK1	200738_s_at	8.4062E-03	1.67E-04	-3.89	0.71	-3.80E-01
1084	DCLRE1C	235478_at	8.4062E-03	1.67E-04	3.89	0.71	3.64E-01
1085	FRMD4A	225163_at	8.4133E-03	1.67E-04	-3.89	0.70	-5.95E-01
1086	MET	203510_at	8.4133E-03	1.67E-04	-3.89	0.70	-5.24E-01
1087	RPS15P3/// RPLP1P3/// METTL13/// DNM3	234900_at	8.4364E-03	1.68E-04	3.89	0.70	2.12E-01
1088	FAM129A	217966_s_at	8.4637E-03	1.69E-04	-3.89	0.70	-5.83E-01
1089	FRAT2	209864_at	8.4637E-03	1.69E-04	-3.89	0.69	-4.19E-01
1090	CD59	200983_x_at	8.4881E-03	1.69E-04	-3.89	0.69	-5.18E-01
1091	CYB561	209164_s_at	8.5117E-03	1.70E-04	-3.89	0.69	-4.32E-01
1092	SCARNA15	228930_at	8.5117E-03	1.70E-04	3.89	0.69	4.42E-01
1093	FGFR2	208234_x_at	8.5299E-03	1.71E-04	3.89	0.68	2.81E-01
1094	TADA3	215272_at	8.5299E-03	1.71E-04	3.89	0.68	1.97E-01
1095		1556511_a_at	8.5395E-03	1.71E-04	3.89	0.68	1.63E-01
1096	TTC7B	226152_at	8.5395E-03	1.71E-04	-3.89	0.68	-6.29E-01
1097	YWHAH	201020_at	8.5450E-03	1.71E-04	-3.89	0.68	-6.38E-01
1098		226834_at	8.5450E-03	1.72E-04	-3.89	0.68	-6.44E-01
1099	NR2C1	210530_s_at	8.5518E-03	1.72E-04	3.88	0.68	2.74E-01
1100		236825_at	8.5569E-03	1.72E-04	3.88	0.68	3.20E-01
1101	SLC16A3	202856_s_at	8.5606E-03	1.73E-04	-3.88	0.67	-8.39E-01
1102	RASSF4	49306_at	8.5606E-03	1.73E-04	-3.88	0.67	-6.40E-01
1103	WSB2	201760_s_at	8.5606E-03	1.73E-04	-3.88	0.67	-3.34E-01
1104	KLC1	212878_s_at	8.5608E-03	1.73E-04	-3.88	0.67	-6.42E-01
1105	CTSL1	202087_s_at	8.5625E-03	1.73E-04	-3.88	0.67	-6.36E-01
1106	OS9	200714_x_at	8.5949E-03	1.74E-04	-3.88	0.67	-4.55E-01
1107	CYSLTR1	230866_at	8.5949E-03	1.74E-04	3.88	0.67	4.97E-01
1108	PILRA	222218_s_at	8.5949E-03	1.74E-04	-3.88	0.67	-1.03E+00
1109	CCL11	210133_at	8.6002E-03	1.74E-04	-3.88	0.66	-1.58E+00
1110		242609_x_at	8.6066E-03	1.75E-04	3.88	0.66	2.60E-01
1111	HSP90AB1	1557910_at	8.6084E-03	1.75E-04	-3.88	0.66	-1.04E+00
1112	PCOLCE	202465_at	8.6096E-03	1.75E-04	-3.88	0.66	-8.33E-01
1113		240032_at	8.6677E-03	1.77E-04	3.88	0.65	2.16E-01
1114	FIP1L1	1554424_at	8.6677E-03	1.77E-04	-3.88	0.65	-1.74E-01
1115	CTSB	213274_s_at	8.7316E-03	1.78E-04	-3.87	0.65	-1.14E+00
1116		1558740_s_at	8.7316E-03	1.78E-04	3.87	0.64	4.57E-01
1117	GAB2	203853_s_at	8.7371E-03	1.79E-04	-3.87	0.64	-4.18E-01
1118	DNAJB1	200666_s_at	8.7371E-03	1.79E-04	-3.87	0.64	-5.06E-01
1119	VSIG4	204787_at	8.7371E-03	1.79E-04	-3.87	0.64	-1.41E+00
1120		237034_at	8.7538E-03	1.79E-04	3.87	0.64	2.67E-01
1121	HLA-C	208812_x_at	8.7538E-03	1.79E-04	-3.87	0.64	-3.81E-01
1122	LOC100132 815	227234_at	8.7597E-03	1.80E-04	3.87	0.64	2.79E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1123	FOLR2	204829_s_at	8.8384E-03	1.82E-04	-3.87	0.63	-6.15E-01
1124	AKR1A1	201900_s_at	8.8384E-03	1.82E-04	-3.87	0.63	-3.61E-01
1125	SGSH	204293_at	8.8384E-03	1.82E-04	-3.87	0.63	-3.13E-01
1126	PELI1	232304_at	8.8384E-03	1.82E-04	3.87	0.62	5.45E-01
1127	FLJ10357	58780_s_at	8.8384E-03	1.82E-04	-3.87	0.62	-4.99E-01
1128	PPHLN1	1555351_s_at	8.8384E-03	1.82E-04	3.87	0.62	2.26E-01
1129	BACH1	234938_at	8.8426E-03	1.83E-04	3.87	0.62	1.93E-01
1130	MANF	202655_at	8.8639E-03	1.83E-04	-3.87	0.62	-3.66E-01
1131	CCDC58	235244_at	8.8639E-03	1.83E-04	3.87	0.62	6.99E-01
1132	CISH	221223_x_at	8.9032E-03	1.84E-04	-3.87	0.61	-5.55E-01
1133	MERTK	206028_s_at	8.9109E-03	1.85E-04	-3.86	0.61	-5.67E-01
1134	HSPA1B///HSPA1A	200800_s_at	8.9130E-03	1.85E-04	-3.86	0.61	-8.44E-01
1135	ZNF92	235170_at	8.9255E-03	1.85E-04	3.86	0.61	4.39E-01
1136	ICAM1	215485_s_at	8.9255E-03	1.85E-04	-3.86	0.61	-4.60E-01
1137	STEAP4	225987_at	8.9376E-03	1.86E-04	-3.86	0.61	-1.04E+00
1138	AGPHD1	236150_at	8.9447E-03	1.86E-04	3.86	0.61	2.89E-01
1139	ALDH6A1	221588_x_at	8.9564E-03	1.87E-04	-3.86	0.60	-4.95E-01
1140	NANS	218189_s_at	8.9564E-03	1.87E-04	-3.86	0.60	-4.07E-01
1141	ASS1	207076_s_at	8.9769E-03	1.87E-04	-3.86	0.60	-5.93E-01
1142		222284_at	8.9935E-03	1.88E-04	3.86	0.60	3.33E-01
1143	FHL1	210298_x_at	8.9935E-03	1.88E-04	-3.86	0.60	-4.05E-01
1144	CYB5R3	201885_s_at	8.9939E-03	1.88E-04	-3.86	0.60	-5.03E-01
1145		244600_at	9.0034E-03	1.89E-04	3.86	0.59	5.23E-01
1146	CATSPER2	1553323_a_at	9.0034E-03	1.89E-04	3.86	0.59	1.65E-01
1147	FLOT1	210142_x_at	9.0034E-03	1.89E-04	-3.86	0.59	-3.62E-01
1148	LILRB2	210146_x_at	9.0034E-03	1.89E-04	-3.86	0.59	-1.14E+00
1149	PVRL2	232078_at	9.0100E-03	1.89E-04	-3.86	0.59	-3.71E-01
1150	SNORA72	228047_at	9.0241E-03	1.90E-04	3.86	0.59	3.22E-01
1151	FBXO7	201178_at	9.0241E-03	1.90E-04	-3.86	0.59	-4.52E-01
1152	LOC728613///PDCD6	1568763_s_at	9.0255E-03	1.90E-04	3.86	0.59	5.82E-01
1153	VCAN	215646_s_at	9.0255E-03	1.90E-04	-3.86	0.59	-1.38E+00
1154	CHD2	225951_s_at	9.0255E-03	1.90E-04	3.86	0.58	4.16E-01
1155	SASH1	41644_at	9.0455E-03	1.91E-04	-3.86	0.58	-6.48E-01
1156	BACE1	222463_s_at	9.0501E-03	1.91E-04	-3.86	0.58	-3.34E-01
1157	RHOQ	212120_at	9.0650E-03	1.92E-04	-3.85	0.58	-4.76E-01
1158	PMS2L11	210707_x_at	9.0890E-03	1.93E-04	3.85	0.58	3.46E-01
1159	PCYOX1	203803_at	9.1132E-03	1.93E-04	-3.85	0.57	-6.07E-01
1160	DIAPH2	205726_at	9.1244E-03	1.94E-04	-3.85	0.57	-4.40E-01
1161	LMNA	1554600_s_at	9.1944E-03	1.95E-04	-3.85	0.56	-5.67E-01
1162	TAF1D	222728_s_at	9.1944E-03	1.95E-04	3.85	0.56	3.11E-01
1163	TACC1	1554690_a_at	9.2180E-03	1.96E-04	-3.85	0.56	-5.46E-01
1164	C22orf9	212421_at	9.2343E-03	1.97E-04	-3.85	0.56	-3.21E-01
1165	ATP5I	207335_x_at	9.2343E-03	1.97E-04	3.85	0.56	5.75E-01
1166	ANXA1	201012_at	9.2386E-03	1.97E-04	-3.85	0.55	-7.29E-01
1167	COL6A1	212937_s_at	9.2598E-03	1.98E-04	-3.85	0.55	-4.48E-01
1168	NDUFA7	1557532_at	9.2598E-03	1.98E-04	3.85	0.55	2.60E-01
1169	KLF11	218486_at	9.2637E-03	1.98E-04	-3.85	0.55	-4.72E-01
1170	IFITM3	212203_x_at	9.3440E-03	2.00E-04	-3.84	0.54	-6.11E-01
1171	TRAF3IP3	231932_at	9.3852E-03	2.01E-04	3.84	0.53	2.20E-01
1172	AHCYL1	200848_at	9.3852E-03	2.02E-04	-3.84	0.53	-4.69E-01
1173	SKAP2	225639_at	9.3852E-03	2.02E-04	-3.84	0.53	-3.58E-01
1174	FRYL	1563687_a_at	9.3852E-03	2.02E-04	-3.84	0.53	-2.03E-01
1175	PRCP	201494_at	9.3852E-03	2.02E-04	-3.84	0.53	-3.45E-01
1176	SCN1B	205508_at	9.3852E-03	2.02E-04	-3.84	0.53	-3.83E-01
1177	FNDC3B	225032_at	9.3852E-03	2.02E-04	-3.84	0.53	-5.88E-01
1178	SLC39A8	209267_s_at	9.3852E-03	2.02E-04	-3.84	0.53	-8.15E-01
1179	ZNF101	1552633_at	9.3852E-03	2.03E-04	3.84	0.53	4.99E-01
1180	IL2RA	211269_s_at	9.3852E-03	2.03E-04	-3.84	0.53	-6.72E-01
1181	LOC730631	230738_at	9.3853E-03	2.03E-04	3.84	0.53	3.79E-01
1182		235193_at	9.4205E-03	2.04E-04	3.84	0.52	3.60E-01
1183	COL6A1	212938_at	9.4205E-03	2.04E-04	-3.84	0.52	-2.09E-01
1184	ENG	201809_s_at	9.4347E-03	2.04E-04	-3.84	0.52	-6.99E-01
1185		233115_at	9.4405E-03	2.05E-04	3.84	0.52	1.19E-01
1186	PPFIA1	210235_s_at	9.4405E-03	2.05E-04	-3.84	0.52	-3.24E-01
1187	C17orf39	228452_at	9.4405E-03	2.05E-04	-3.84	0.52	-2.90E-01
1188	ITGA9	206009_at	9.4405E-03	2.05E-04	-3.84	0.52	-2.10E-01
1189	ANXA5	200782_at	9.4438E-03	2.05E-04	-3.84	0.52	-4.16E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1190	CD2AP	236257_at	9.4757E-03	2.06E-04	3.83	0.51	1.95E-01
1191	RHOJ	1555233_at	9.4788E-03	2.07E-04	-3.83	0.51	-3.16E-01
1192	RRN3	222204_s_at	9.4788E-03	2.07E-04	-3.83	0.51	-3.88E-01
1193	DHX30	230871_at	9.5534E-03	2.08E-04	3.83	0.50	6.53E-01
1194	TELO2	209528_s_at	9.5769E-03	2.09E-04	3.83	0.50	2.68E-01
1195	SPIRE1	1554807_a_at	9.5855E-03	2.10E-04	-3.83	0.50	-2.72E-01
1196	RFESD	236305_at	9.5855E-03	2.10E-04	3.83	0.50	2.45E-01
1197	HLA-DPA1	211991_s_at	9.5855E-03	2.10E-04	-3.83	0.50	-7.00E-01
1198	SERPINA3	202376_at	9.5855E-03	2.10E-04	-3.83	0.50	-6.78E-01
1199	SKAP2	216899_s_at	9.5886E-03	2.10E-04	-3.83	0.50	-6.73E-01
1200	FAM60A	220147_s_at	9.6237E-03	2.11E-04	3.83	0.49	3.59E-01
1201	BTN2A1	244063_at	9.6293E-03	2.12E-04	3.83	0.49	2.87E-01
1202	PI4K2A	215134_at	9.6293E-03	2.12E-04	-3.83	0.49	-3.03E-01
1203	BUB3	201458_s_at	9.6293E-03	2.12E-04	3.83	0.49	2.58E-01
1204	MAP3K1	225927_at	9.6293E-03	2.12E-04	3.83	0.49	5.06E-01
1205	GGCX	235413_at	9.6778E-03	2.13E-04	-3.82	0.48	-2.68E-01
1206	CAMKK2	212252_at	9.6778E-03	2.14E-04	-3.82	0.48	-3.99E-01
1207	LOC285074	230588_s_at	9.6778E-03	2.14E-04	3.82	0.48	4.38E-01
1208		1558348_at	9.6847E-03	2.14E-04	3.82	0.48	2.34E-01
1209	RC3H2	220202_s_at	9.6847E-03	2.14E-04	-3.82	0.48	-5.41E-01
1210	WISP1	206796_at	9.6930E-03	2.15E-04	-3.82	0.48	-5.48E-01
1211	CD36	228766_at	9.6930E-03	2.15E-04	-3.82	0.48	-8.86E-01
1212	FOSL2	218880_at	9.7076E-03	2.15E-04	-3.82	0.47	-5.79E-01
1213	TSPAN18	1561449_at	9.7076E-03	2.15E-04	3.82	0.47	2.09E-01
1214	NCR1	217095_x_at	9.7076E-03	2.16E-04	3.82	0.47	2.38E-01
1215		240434_at	9.7208E-03	2.16E-04	3.82	0.47	3.46E-01
1216		244343_at	9.7336E-03	2.17E-04	3.82	0.47	1.69E-01
1217	PRPF31	202407_s_at	9.7336E-03	2.17E-04	-3.82	0.47	-5.04E-01
1218		237774_at	9.7425E-03	2.17E-04	3.82	0.47	2.08E-01
1219	LOC388889	232340_at	9.7784E-03	2.18E-04	3.82	0.46	4.40E-01
1220	FSTL1	208782_at	9.7784E-03	2.18E-04	-3.82	0.46	-8.63E-01
1221	CRLF3	205474_at	9.7784E-03	2.18E-04	3.82	0.46	3.14E-01
1222	IGFBP7	201162_at	9.7951E-03	2.19E-04	-3.82	0.46	-4.80E-01
1223	HSP90AA1	211968_s_at	9.8259E-03	2.20E-04	-3.82	0.46	-5.54E-01
1224	GTSF1L	232821_at	9.8259E-03	2.20E-04	3.82	0.46	4.56E-01
1225	BRCA2	214727_at	9.8462E-03	2.21E-04	3.82	0.45	1.37E-01
1226		222319_at	9.8825E-03	2.22E-04	3.81	0.45	1.91E-01
1227	MINA	1554774_at	9.8835E-03	2.22E-04	-3.81	0.45	-2.64E-01
1228	MAP7D1	217943_s_at	9.8835E-03	2.22E-04	-3.81	0.45	-6.03E-01
1229	RIN2	209684_at	9.8849E-03	2.22E-04	-3.81	0.45	-6.93E-01
1230	TNFAIP3	202643_s_at	9.8988E-03	2.23E-04	-3.81	0.44	-5.44E-01
1231	ACVRL1	226950_at	9.9376E-03	2.24E-04	-3.81	0.44	-5.24E-01
1232	PCSK5	205559_s_at	9.9376E-03	2.24E-04	-3.81	0.44	-7.82E-01
1233	ABCA11P	220159_at	9.9376E-03	2.24E-04	3.81	0.44	3.29E-01
1234	ALDOA	238996_x_at	9.9403E-03	2.24E-04	-3.81	0.44	-5.72E-01
1235	BTRC	1563620_at	9.9800E-03	2.25E-04	3.81	0.43	1.20E-01
1236	RBPMS	209488_s_at	9.9842E-03	2.26E-04	-3.81	0.43	-7.80E-01
1237	STAG3	219753_at	9.9931E-03	2.26E-04	3.81	0.43	6.53E-01
1238	NAAA	227135_at	1.0014E-02	2.27E-04	-3.81	0.43	-4.92E-01
1239	PMS2L1	217485_x_at	1.0017E-02	2.27E-04	3.81	0.43	3.63E-01
1240	TIA1	201449_at	1.0017E-02	2.27E-04	3.81	0.43	4.61E-01
1241	MAPK7	207292_s_at	1.0018E-02	2.27E-04	-3.81	0.43	-2.36E-01
1242	ENO1	217294_s_at	1.0018E-02	2.28E-04	-3.81	0.43	-1.18E+00
1243	HIST2H4B/// HIST4H4///H IST2H4A///H IST1H4L///H IST1H4E///H IST1H4B///H IST1H4H///H IST1H4C///H IST1H4J///HI ST1H4K///HI ST1H4F///HI ST1H4D///HI ST1H4A///HI ST1H4I	208580_x_at	1.0021E-02	2.28E-04	3.81	0.42	7.05E-01
1244	AGFG2	206821_x_at	1.0025E-02	2.28E-04	3.81	0.42	2.76E-01
1245	AARS	201000_at	1.0037E-02	2.29E-04	-3.81	0.42	-3.50E-01
1246	ITSN1	35776_at	1.0038E-02	2.29E-04	-3.81	0.42	-4.81E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1247	SNAPC5	213203_at	1.0038E-02	2.29E-04	3.81	0.42	3.63E-01
1248	FLJ44606	230404_at	1.0094E-02	2.31E-04	3.80	0.41	2.74E-01
1249	SAMD10	233001_at	1.0094E-02	2.31E-04	3.80	0.41	2.01E-01
1250	FAM198B	223204_at	1.0094E-02	2.31E-04	-3.80	0.41	-7.34E-01
1251	MS4A6A	223280_x_at	1.0094E-02	2.31E-04	-3.80	0.41	-6.56E-01
1252	ZNF540	229328_at	1.0094E-02	2.31E-04	3.80	0.41	1.77E-01
1253	DNAJB4	203811_s_at	1.0094E-02	2.31E-04	-3.80	0.41	-2.41E-01
1254	RBM47	222496_s_at	1.0103E-02	2.32E-04	-3.80	0.41	-6.50E-01
1255	ANKS1A	212747_at	1.0111E-02	2.32E-04	-3.80	0.41	-4.04E-01
1256	IDS	1559136_s_at	1.0114E-02	2.32E-04	3.80	0.41	2.17E-01
1257	RPL27	200025_s_at	1.0114E-02	2.33E-04	3.80	0.41	1.99E-01
1258	EPS8L1	221655_x_at	1.0114E-02	2.33E-04	3.80	0.41	2.35E-01
1259	PMS2L1	239699_s_at	1.0117E-02	2.33E-04	3.80	0.40	2.73E-01
1260	MAP4	243_g_at	1.0125E-02	2.33E-04	-3.80	0.40	-4.69E-01
1261	CHRDL1	209763_at	1.0127E-02	2.34E-04	-3.80	0.40	-9.92E-01
1262	KRT84	217031_at	1.0127E-02	2.34E-04	3.80	0.40	1.41E-01
1263	SRP68	224607_s_at	1.0143E-02	2.34E-04	-3.80	0.40	-4.08E-01
1264		236587_at	1.0188E-02	2.36E-04	3.80	0.39	1.68E-01
1265	WDR16	239916_at	1.0188E-02	2.36E-04	3.80	0.39	1.65E-01
1266	FERMT2	209209_s_at	1.0188E-02	2.36E-04	-3.80	0.39	-5.69E-01
1267	MGC40069	243602_at	1.0203E-02	2.36E-04	3.80	0.39	6.44E-01
1268	RPS17	212578_x_at	1.0203E-02	2.37E-04	3.80	0.39	2.59E-01
1269	C10orf78	236027_at	1.0214E-02	2.37E-04	3.80	0.39	5.03E-01
1270	LAMP2	226671_at	1.0215E-02	2.37E-04	-3.80	0.39	-5.10E-01
1271	PXK	1552275_s_at	1.0215E-02	2.38E-04	-3.79	0.39	-5.51E-01
1272	CWF19L1	233568_x_at	1.0215E-02	2.38E-04	3.79	0.39	2.34E-01
1273	ALKBH7	227879_at	1.0215E-02	2.38E-04	3.79	0.38	1.77E-01
1274	COL6A1	212091_s_at	1.0215E-02	2.38E-04	-3.79	0.38	-6.53E-01
1275	TMX2	201175_at	1.0215E-02	2.39E-04	-3.79	0.38	-3.45E-01
1276	FAM26F	229915_at	1.0215E-02	2.39E-04	-3.79	0.38	-3.90E-01
1277	RAP2B	227897_at	1.0215E-02	2.39E-04	-3.79	0.38	-6.28E-01
1278	PDLIM5	203242_s_at	1.0215E-02	2.39E-04	-3.79	0.38	-3.97E-01
1279	SRGAP2	213329_at	1.0215E-02	2.39E-04	-3.79	0.38	-2.58E-01
1280	PARVB	37966_at	1.0226E-02	2.39E-04	-3.79	0.38	-4.76E-01
1281	DLX6	221289_at	1.0250E-02	2.40E-04	3.79	0.38	1.69E-01
1282	ACE	227463_at	1.0250E-02	2.40E-04	-3.79	0.38	-8.30E-01
1283	CD163	216233_at	1.0250E-02	2.41E-04	-3.79	0.38	-6.11E-01
1284	ARSD	223696_at	1.0250E-02	2.41E-04	-3.79	0.37	-4.00E-01
1285	NR1H2	218215_s_at	1.0253E-02	2.41E-04	-3.79	0.37	-5.00E-01
1286	FLOT1	208749_x_at	1.0253E-02	2.41E-04	-3.79	0.37	-3.77E-01
1287	COPA	208684_at	1.0253E-02	2.42E-04	-3.79	0.37	-5.67E-01
1288	THBD	203887_s_at	1.0253E-02	2.42E-04	-3.79	0.37	-6.25E-01
1289	DPEP3	220179_at	1.0266E-02	2.42E-04	3.79	0.37	2.59E-01
1290	NDUFV3	226616_s_at	1.0266E-02	2.42E-04	-3.79	0.37	-3.81E-01
1291	PDCD7	230182_at	1.0266E-02	2.42E-04	3.79	0.37	1.90E-01
1292		233501_at	1.0294E-02	2.43E-04	3.79	0.36	2.37E-01
1293	SLC46A1	1552278_a_at	1.0294E-02	2.43E-04	-3.79	0.36	-3.23E-01
1294	MCCC2	233231_at	1.0300E-02	2.44E-04	3.79	0.36	1.42E-01
1295		230598_at	1.0300E-02	2.44E-04	3.79	0.36	8.18E-01
1296	ZKSCAN1	214900_at	1.0326E-02	2.45E-04	3.79	0.36	1.67E-01
1297	FCGR2B	210889_s_at	1.0340E-02	2.45E-04	-3.79	0.36	-9.53E-01
1298	SERPING1	200986_at	1.0343E-02	2.46E-04	-3.79	0.36	-1.01E+00
1299	FCGRT	218831_s_at	1.0343E-02	2.46E-04	-3.79	0.36	-6.62E-01
1300	RFX1	206321_at	1.0343E-02	2.46E-04	3.79	0.36	1.71E-01
1301	YME1L1	216304_x_at	1.0344E-02	2.46E-04	-3.79	0.35	-2.22E-01
1302		244529_at	1.0346E-02	2.46E-04	3.78	0.35	1.53E-01
1303	TRAT1	217147_s_at	1.0346E-02	2.47E-04	3.78	0.35	7.74E-01
1304	RAB34	224710_at	1.0346E-02	2.47E-04	-3.78	0.35	-5.58E-01
1305	SLC43A3	213113_s_at	1.0346E-02	2.47E-04	-3.78	0.35	-5.62E-01
1306	LOC389906	1564639_at	1.0346E-02	2.47E-04	3.78	0.35	2.03E-01
1307	EHD4	233660_at	1.0346E-02	2.48E-04	-3.78	0.35	-3.08E-01
1308	USP14	201671_x_at	1.0346E-02	2.48E-04	-3.78	0.35	-3.52E-01
1309	TMSB15B/// TMSB15A	205347_s_at	1.0346E-02	2.48E-04	3.78	0.35	1.28E+00
1310	PCDHB18	234479_at	1.0346E-02	2.48E-04	3.78	0.35	1.83E-01
1311	SPRED1	235074_at	1.0347E-02	2.48E-04	-3.78	0.35	-3.66E-01
1312	SULF2	233555_s_at	1.0361E-02	2.49E-04	-3.78	0.34	-8.72E-01
1313	CUZD1	220275_at	1.0361E-02	2.49E-04	3.78	0.34	3.68E-01
1314	TMEM51	218815_s_at	1.0361E-02	2.49E-04	-3.78	0.34	-4.16E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1315	CLEC1A	219761_at	1.0370E-02	2.49E-04	-3.78	0.34	-3.90E-01
1316		228812_at	1.0371E-02	2.50E-04	3.78	0.34	5.47E-01
1317	HIST1H2BC ///HIST1H2B I///HIST1H2 BE///HIST1H 2BF///HIST1 H2BG	208490_x_at	1.0406E-02	2.51E-04	3.78	0.34	5.34E-01
1318	NEUROD1	206282_at	1.0425E-02	2.51E-04	3.78	0.34	1.61E-01
1319		1566702_at	1.0432E-02	2.52E-04	3.78	0.33	2.07E-01
1320	USMG5	225413_at	1.0432E-02	2.52E-04	3.78	0.33	4.05E-01
1321	AHCYL1	200850_s_at	1.0437E-02	2.52E-04	-3.78	0.33	-4.54E-01
1322	SYK	209269_s_at	1.0440E-02	2.52E-04	-3.78	0.33	-3.73E-01
1323	GPR84	223767_at	1.0440E-02	2.53E-04	-3.78	0.33	-8.18E-01
1324	ELL2	226099_at	1.0512E-02	2.55E-04	-3.78	0.32	-5.41E-01
1325	TEX10	1558702_at	1.0512E-02	2.55E-04	3.78	0.32	2.10E-01
1326	LRCH3	1553668_at	1.0512E-02	2.55E-04	-3.78	0.32	-1.39E-01
1327	HIPK1	1552516_a_at	1.0512E-02	2.55E-04	-3.77	0.32	-2.68E-01
1328	KIF5B	201991_s_at	1.0512E-02	2.55E-04	-3.77	0.32	-3.49E-01
1329	C1orf85	1558693_s_at	1.0558E-02	2.57E-04	-3.77	0.32	-5.60E-01
1330	BCKDHB	213321_at	1.0558E-02	2.57E-04	3.77	0.32	2.17E-01
1331	STX5	203330_s_at	1.0558E-02	2.57E-04	-3.77	0.32	-3.28E-01
1332	CX3CR1	205898_at	1.0558E-02	2.57E-04	-3.77	0.32	-5.81E-01
1333	RPL31	200962_at	1.0560E-02	2.57E-04	3.77	0.31	8.59E-01
1334	PSTK	230129_at	1.0560E-02	2.58E-04	3.77	0.31	3.43E-01
1335	KLF7	1555420_a_at	1.0560E-02	2.58E-04	-3.77	0.31	-4.15E-01
1336		228478_at	1.0560E-02	2.58E-04	-3.77	0.31	-4.19E-01
1337	IRAK1	201587_s_at	1.0560E-02	2.58E-04	-3.77	0.31	-3.69E-01
1338	LOC100129 250	78383_at	1.0571E-02	2.59E-04	3.77	0.31	4.99E-01
1339	BRCC3	216521_s_at	1.0582E-02	2.59E-04	-3.77	0.31	-5.12E-01
1340	FOXRED2	231846_at	1.0582E-02	2.59E-04	-3.77	0.31	-2.58E-01
1341	ADAMTS17	1552726_at	1.0625E-02	2.61E-04	3.77	0.30	1.60E-01
1342	RAC1	208641_s_at	1.0625E-02	2.61E-04	-3.77	0.30	-3.84E-01
1343	DAP	201095_at	1.0625E-02	2.61E-04	-3.77	0.30	-4.93E-01
1344	QKI	212262_at	1.0625E-02	2.62E-04	-3.77	0.30	-4.84E-01
1345	NCF2	209949_at	1.0625E-02	2.62E-04	-3.77	0.30	-8.80E-01
1346		234235_at	1.0625E-02	2.62E-04	3.77	0.30	1.22E-01
1347	PTGER1	214391_x_at	1.0625E-02	2.62E-04	3.77	0.30	3.71E-01
1348	ZNF253	242919_at	1.0625E-02	2.62E-04	3.77	0.30	3.60E-01
1349	DHRS4L2/// DHRS4	218021_at	1.0629E-02	2.62E-04	-3.77	0.30	-3.76E-01
1350	WDR1	210936_at	1.0633E-02	2.63E-04	-3.77	0.30	-1.64E-01
1351	CD59	200985_s_at	1.0633E-02	2.63E-04	-3.77	0.30	-4.51E-01
1352	RAB40C	213466_at	1.0668E-02	2.64E-04	3.77	0.29	2.00E-01
1353	VCAN	211571_s_at	1.0706E-02	2.65E-04	-3.76	0.29	-1.20E+00
1354		233951_at	1.0706E-02	2.65E-04	3.76	0.29	2.61E-01
1355	TACC1	217437_s_at	1.0706E-02	2.66E-04	-3.76	0.29	-4.26E-01
1356	ARHGDIA	213606_s_at	1.0706E-02	2.66E-04	-3.76	0.29	-1.68E-01
1357		236084_at	1.0706E-02	2.66E-04	3.76	0.29	1.70E-01
1358	EIF3D	200005_at	1.0713E-02	2.66E-04	-3.76	0.28	-3.99E-01
1359	LEO1	235096_at	1.0716E-02	2.66E-04	-3.76	0.28	-4.44E-01
1360	C1QB	202953_at	1.0732E-02	2.67E-04	-3.76	0.28	-1.19E+00
1361	CYP1B1	202434_s_at	1.0751E-02	2.68E-04	-3.76	0.28	-2.80E-01
1362	DHDDS	218547_at	1.0751E-02	2.68E-04	-3.76	0.28	-2.54E-01
1363	MAP3K6	219278_at	1.0752E-02	2.69E-04	-3.76	0.28	-3.50E-01
1364	ADAP2	222876_s_at	1.0752E-02	2.69E-04	-3.76	0.28	-5.73E-01
1365	RBMS1	215127_s_at	1.0752E-02	2.69E-04	-3.76	0.28	-3.25E-01
1366	BSDC1	222200_s_at	1.0752E-02	2.69E-04	-3.76	0.28	-3.18E-01
1367	RNF19B	36564_at	1.0752E-02	2.69E-04	-3.76	0.28	-5.98E-01
1368	RGL1	209568_s_at	1.0777E-02	2.70E-04	-3.76	0.27	-4.45E-01
1369	LIMA1	217892_s_at	1.0800E-02	2.71E-04	-3.76	0.27	-4.21E-01
1370	HSPH1	206976_s_at	1.0800E-02	2.71E-04	-3.76	0.27	-3.52E-01
1371	WDR1	244672_at	1.0800E-02	2.71E-04	3.76	0.27	2.23E-01
1372		1560156_at	1.0800E-02	2.71E-04	3.76	0.27	3.87E-01
1373	APLP2	208703_s_at	1.0800E-02	2.72E-04	-3.76	0.27	-5.77E-01
1374	NRP1	212298_at	1.0800E-02	2.72E-04	-3.76	0.26	-8.17E-01
1375	VSTM2A	1554530_at	1.0800E-02	2.72E-04	3.76	0.26	1.42E-01
1376	FRMD4A	225168_at	1.0800E-02	2.72E-04	-3.76	0.26	-5.55E-01
1377		229498_at	1.0800E-02	2.72E-04	3.76	0.26	4.94E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1378	CARS	240983_s_at	1.0800E-02	2.72E-04	-3.76	0.26	-4.80E-01
1379		237067_at	1.0800E-02	2.72E-04	3.76	0.26	1.62E-01
1380	YIPF3	216338_s_at	1.0800E-02	2.73E-04	-3.76	0.26	-4.97E-01
1381	C8orf59	1555243_x_at	1.0800E-02	2.73E-04	3.76	0.26	4.72E-01
1382	ERLEC1P1	242766_at	1.0815E-02	2.73E-04	3.76	0.26	1.65E-01
1383	ITGAV	202351_at	1.0831E-02	2.74E-04	-3.75	0.26	-5.62E-01
1384		214349_at	1.0831E-02	2.74E-04	3.75	0.26	9.66E-01
1385	DAB2	201280_s_at	1.0852E-02	2.75E-04	-3.75	0.26	-6.76E-01
1386	C17orf51	238167_at	1.0864E-02	2.75E-04	3.75	0.25	3.06E-01
1387	TKTL1	216370_s_at	1.0865E-02	2.76E-04	3.75	0.25	2.11E-01
1388	EPB41L2	201718_s_at	1.0865E-02	2.76E-04	-3.75	0.25	-5.36E-01
1389	LILRB3	210225_x_at	1.0876E-02	2.77E-04	-3.75	0.25	-5.03E-01
1390	C17orf57	1553626_a_at	1.0876E-02	2.77E-04	3.75	0.25	8.15E-01
1391	FOSL2	225262_at	1.0876E-02	2.77E-04	-3.75	0.25	-5.81E-01
1392	C2	203052_at	1.0928E-02	2.78E-04	-3.75	0.24	-8.35E-01
1393		211106_at	1.0954E-02	2.79E-04	3.75	0.24	5.75E-01
1394	KDSR	1558279_a_at	1.0954E-02	2.79E-04	-3.75	0.24	-3.76E-01
1395	HSPA1B///HSPA1A	200799_at	1.0954E-02	2.79E-04	-3.75	0.24	-7.27E-01
1396	SCN1A	1555246_a_at	1.0974E-02	2.80E-04	3.75	0.24	1.27E-01
1397		226621_at	1.1000E-02	2.81E-04	-3.75	0.24	-5.24E-01
1398	NFKB1	209239_at	1.1016E-02	2.82E-04	-3.75	0.23	-5.20E-01
1399		1569597_at	1.1031E-02	2.82E-04	3.75	0.23	2.62E-01
1400	CCDC102A	232051_at	1.1044E-02	2.83E-04	-3.75	0.23	-2.38E-01
1401	AHSA1	201491_at	1.1050E-02	2.83E-04	-3.75	0.23	-4.91E-01
1402	CLASP2	238224_at	1.1055E-02	2.83E-04	3.75	0.23	1.37E-01
1403	PHF11	221816_s_at	1.1071E-02	2.84E-04	3.74	0.23	2.94E-01
1404	CLN6	222539_at	1.1116E-02	2.85E-04	3.74	0.22	1.89E-01
1405	CCND1	208712_at	1.1118E-02	2.86E-04	-3.74	0.22	-5.11E-01
1406		1564381_s_at	1.1127E-02	2.86E-04	3.74	0.22	2.32E-01
1407	SERPINB6	211474_s_at	1.1128E-02	2.86E-04	-3.74	0.22	-3.57E-01
1408		229754_at	1.1139E-02	2.87E-04	3.74	0.22	3.30E-01
1409	DIRC2	226026_at	1.1155E-02	2.87E-04	-3.74	0.22	-5.09E-01
1410	CD300A	217078_s_at	1.1162E-02	2.88E-04	-3.74	0.21	-6.29E-01
1411	EIF2B5	1558050_at	1.1162E-02	2.88E-04	3.74	0.21	1.92E-01
1412	RENBP	206617_s_at	1.1186E-02	2.89E-04	-3.74	0.21	-5.30E-01
1413	SFRS12	244287_at	1.1194E-02	2.89E-04	-3.74	0.21	-3.50E-01
1414	NEK6	223159_s_at	1.1221E-02	2.90E-04	-3.74	0.21	-4.57E-01
1415	ZNF747	228856_at	1.1221E-02	2.90E-04	-3.74	0.21	-2.80E-01
1416		239988_at	1.1222E-02	2.91E-04	3.74	0.21	3.21E-01
1417	C12orf73	226927_at	1.1224E-02	2.91E-04	3.74	0.20	3.99E-01
1418	DCUN1D2	219116_s_at	1.1226E-02	2.91E-04	3.74	0.20	2.76E-01
1419	FADS1	208962_s_at	1.1247E-02	2.92E-04	-3.74	0.20	-5.27E-01
1420	GTPBP8	242685_at	1.1248E-02	2.92E-04	3.74	0.20	1.87E-01
1421	TP53I3	210609_s_at	1.1248E-02	2.93E-04	-3.74	0.20	-5.34E-01
1422	SSB	201138_s_at	1.1248E-02	2.93E-04	-3.74	0.20	-4.11E-01
1423	C20orf200	1553205_at	1.1248E-02	2.93E-04	3.74	0.20	2.57E-01
1424	LOXL1	203570_at	1.1248E-02	2.93E-04	-3.74	0.20	-8.32E-01
1425	ANXA2	213503_x_at	1.1248E-02	2.93E-04	-3.74	0.20	-4.18E-01
1426	ZDHHC3	218078_s_at	1.1248E-02	2.93E-04	-3.74	0.20	-4.40E-01
1427	SAA2///SAA1	208607_s_at	1.1248E-02	2.94E-04	-3.74	0.20	-4.29E-01
1428	RPS17	201665_x_at	1.1248E-02	2.94E-04	3.74	0.20	2.76E-01
1429	CKAP4	200999_s_at	1.1248E-02	2.94E-04	-3.73	0.19	-8.34E-01
1430	MRAS	225185_at	1.1248E-02	2.94E-04	-3.73	0.19	-4.49E-01
1431		213691_at	1.1248E-02	2.94E-04	3.73	0.19	2.67E-01
1432	CCDC34	1553666_at	1.1264E-02	2.95E-04	3.73	0.19	1.44E-01
1433		1557238_s_at	1.1274E-02	2.96E-04	3.73	0.19	3.04E-01
1434	APLP2	211404_s_at	1.1274E-02	2.96E-04	-3.73	0.19	-5.01E-01
1435	ZNF702P	206557_at	1.1274E-02	2.96E-04	3.73	0.19	2.53E-01
1436	SVIP	230285_at	1.1274E-02	2.96E-04	3.73	0.19	5.27E-01
1437	RAC1	208640_at	1.1274E-02	2.96E-04	-3.73	0.19	-3.40E-01
1438		237048_at	1.1274E-02	2.97E-04	3.73	0.19	3.40E-01
1439	HLA-DMA	217478_s_at	1.1274E-02	2.97E-04	-3.73	0.19	-6.14E-01
1440	FAM83A	239586_at	1.1282E-02	2.97E-04	3.73	0.19	1.87E-01
1441	AHCYL1	200849_s_at	1.1287E-02	2.97E-04	-3.73	0.18	-4.03E-01
1442	PRKAR2A	225000_at	1.1293E-02	2.98E-04	-3.73	0.18	-3.17E-01
1443	UQCRC1	201903_at	1.1311E-02	2.99E-04	-3.73	0.18	-5.28E-01
1444	DLEU2L///D	215629_s_at	1.1311E-02	2.99E-04	3.73	0.18	3.79E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
	LEU2						
1445		241460_at	1.1311E-02	2.99E-04	3.73	0.18	3.32E-01
1446	LOC338579	1570474_s_at	1.1346E-02	3.00E-04	3.73	0.18	1.61E-01
1447	ENO1	201231_s_at	1.1353E-02	3.00E-04	-3.73	0.18	-5.42E-01
1448	EFEMP2	209356_x_at	1.1380E-02	3.02E-04	-3.73	0.17	-7.76E-01
1449	NIT1	202891_at	1.1380E-02	3.02E-04	-3.73	0.17	-3.13E-01
1450	CSF2RB	205159_at	1.1380E-02	3.02E-04	-3.73	0.17	-4.45E-01
1451	ATP6V1C1	202872_at	1.1420E-02	3.03E-04	-3.73	0.17	-4.67E-01
1452	LYVE1	220037_s_at	1.1420E-02	3.03E-04	-3.73	0.17	-6.22E-01
1453	TMOD3	223077_at	1.1420E-02	3.03E-04	-3.73	0.17	-4.69E-01
1454		1570076_at	1.1435E-02	3.04E-04	3.73	0.17	1.21E-01
1455	POGK	218229_s_at	1.1435E-02	3.05E-04	-3.73	0.16	-5.85E-01
1456	MRFAP1	226091_s_at	1.1435E-02	3.05E-04	-3.72	0.16	-3.82E-01
1457	WBP4	203598_s_at	1.1435E-02	3.05E-04	-3.72	0.16	-3.07E-01
1458	INPP1	202794_at	1.1435E-02	3.05E-04	-3.72	0.16	-3.84E-01
1459		236595_at	1.1435E-02	3.05E-04	3.72	0.16	7.48E-01
1460	PRDXDD1P	237291_at	1.1435E-02	3.05E-04	3.72	0.16	2.27E-01
1461		1560867_a_at	1.1435E-02	3.06E-04	3.72	0.16	1.29E-01
1462	LOC151484	1562689_at	1.1464E-02	3.07E-04	3.72	0.16	2.15E-01
1463	SGSH	35626_at	1.1464E-02	3.07E-04	-3.72	0.16	-3.38E-01
1464	LITAF	1555454_at	1.1483E-02	3.07E-04	-3.72	0.16	-1.29E-01
1465		236568_at	1.1496E-02	3.08E-04	3.72	0.15	1.78E-01
1466	KRAS	1559203_s_at	1.1496E-02	3.08E-04	3.72	0.15	1.33E-01
1467		225284_at	1.1496E-02	3.08E-04	-3.72	0.15	-6.85E-01
1468	CDX1	206430_at	1.1498E-02	3.09E-04	3.72	0.15	2.35E-01
1469	ZEB2	235593_at	1.1499E-02	3.09E-04	-3.72	0.15	-6.07E-01
1470	FBXL14	1553682_at	1.1521E-02	3.10E-04	3.72	0.15	1.73E-01
1471	CLECL1	244413_at	1.1521E-02	3.10E-04	3.72	0.15	9.18E-01
1472	ZBTB47	234338_s_at	1.1521E-02	3.10E-04	3.72	0.15	2.71E-01
1473	FAR1	1558014_s_at	1.1521E-02	3.11E-04	-3.72	0.15	-3.33E-01
1474	FLJ10038	205511_at	1.1521E-02	3.11E-04	3.72	0.15	2.89E-01
1475	C1QTNF1	220975_s_at	1.1521E-02	3.11E-04	-3.72	0.14	-3.82E-01
1476	NT5DC2	1556895_a_at	1.1521E-02	3.11E-04	3.72	0.14	1.58E-01
1477	MSRB3	225790_at	1.1521E-02	3.11E-04	-3.72	0.14	-3.11E-01
1478	SLIT3	203813_s_at	1.1531E-02	3.12E-04	-3.72	0.14	-5.59E-01
1479	TMEM161B	236227_at	1.1531E-02	3.12E-04	3.72	0.14	2.91E-01
1480	ATF7IP2	228381_at	1.1531E-02	3.12E-04	3.72	0.14	7.13E-01
1481	EIF4G1	208625_s_at	1.1564E-02	3.13E-04	-3.72	0.14	-5.86E-01
1482	SCARF1	206995_x_at	1.1575E-02	3.14E-04	-3.72	0.14	-2.86E-01
1483	HELB	1552787_at	1.1575E-02	3.14E-04	3.72	0.14	5.00E-01
1484		239049_at	1.1575E-02	3.14E-04	3.72	0.14	4.46E-01
1485	CHRNB2	206635_at	1.1594E-02	3.15E-04	3.72	0.13	2.02E-01
1486	GPR107	211977_at	1.1594E-02	3.15E-04	-3.72	0.13	-3.46E-01
1487	RAB6A	201047_x_at	1.1630E-02	3.16E-04	-3.71	0.13	-3.56E-01
1488	UBAC1	202151_s_at	1.1634E-02	3.17E-04	-3.71	0.13	-4.64E-01
1489	RTEL1///TNFRSF6B	206467_x_at	1.1634E-02	3.17E-04	-3.71	0.13	-4.42E-01
1490	LOC100131941	1557817_a_at	1.1634E-02	3.17E-04	3.71	0.13	2.80E-01
1491	KIAA1430	226254_s_at	1.1634E-02	3.18E-04	3.71	0.13	2.95E-01
1492	CXCL16	223454_at	1.1634E-02	3.19E-04	-3.71	0.12	-8.66E-01
1493	WARS	200628_s_at	1.1634E-02	3.19E-04	-3.71	0.12	-9.36E-01
1494	SERINC1	208671_at	1.1634E-02	3.19E-04	-3.71	0.12	-5.28E-01
1495	USO1	201831_s_at	1.1634E-02	3.19E-04	-3.71	0.12	-4.36E-01
1496	ZNF709	242028_at	1.1634E-02	3.19E-04	3.71	0.12	4.22E-01
1497	PCDHGA8	210368_at	1.1634E-02	3.19E-04	3.71	0.12	1.82E-01
1498	NRP2	229225_at	1.1634E-02	3.19E-04	-3.71	0.12	-4.18E-01
1499	PALLD	200897_s_at	1.1634E-02	3.20E-04	-3.71	0.12	-4.62E-01
1500		233068_at	1.1634E-02	3.20E-04	3.71	0.12	3.56E-01
1501	OSBPL1A	208158_s_at	1.1634E-02	3.20E-04	-3.71	0.12	-3.91E-01
1502	LILRB2	207697_x_at	1.1634E-02	3.20E-04	-3.71	0.12	-8.53E-01
1503	DLEU2	216870_x_at	1.1634E-02	3.20E-04	3.71	0.12	3.16E-01
1504	TMEM155	230137_at	1.1634E-02	3.20E-04	3.71	0.12	7.76E-01
1505	ARHGDIA	211716_x_at	1.1634E-02	3.21E-04	-3.71	0.12	-5.61E-01
1506	TNPO1	209226_s_at	1.1634E-02	3.21E-04	-3.71	0.12	-4.00E-01
1507	NT5DC4	1560204_at	1.1634E-02	3.21E-04	3.71	0.12	3.65E-01
1508	MGST1	1565162_s_at	1.1645E-02	3.21E-04	-3.71	0.12	-7.87E-01
1509	CAPRIN1	225340_s_at	1.1660E-02	3.22E-04	-3.71	0.11	-2.63E-01
1510	PTRF	208790_s_at	1.1660E-02	3.22E-04	-3.71	0.11	-4.35E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1511	ITGB1	1553530_a_at	1.1660E-02	3.22E-04	-3.71	0.11	-5.68E-01
1512	LOC100287081	228231_at	1.1663E-02	3.23E-04	-3.71	0.11	-3.77E-01
1513	MS4A6A	224356_x_at	1.1664E-02	3.23E-04	-3.71	0.11	-6.73E-01
1514	SAE1	1555618_s_at	1.1702E-02	3.24E-04	-3.71	0.11	-6.37E-01
1515	SLC24A4	1568922_at	1.1712E-02	3.25E-04	3.71	0.11	1.59E-01
1516	CLEC11A	211709_s_at	1.1766E-02	3.26E-04	-3.71	0.10	-6.22E-01
1517	COL4A1	211980_at	1.1801E-02	3.28E-04	-3.70	0.10	-7.60E-01
1518	MCOLN2	1555465_at	1.1801E-02	3.28E-04	-3.70	0.10	-7.31E-01
1519	C1QA	218232_at	1.1801E-02	3.28E-04	-3.70	0.10	-1.20E+00
1520	ZNF808///ZNF701	236589_at	1.1801E-02	3.29E-04	-3.70	0.10	-1.48E-01
1521	CEACAM5	217291_at	1.1801E-02	3.29E-04	3.70	0.10	1.82E-01
1522	WDR72	227174_at	1.1801E-02	3.29E-04	3.70	0.09	1.22E-01
1523	VTI1A	242356_at	1.1801E-02	3.29E-04	3.70	0.09	2.62E-01
1524		1557733_a_at	1.1801E-02	3.30E-04	3.70	0.09	7.07E-01
1525	IDH1	201193_at	1.1801E-02	3.30E-04	-3.70	0.09	-5.09E-01
1526	PFDN4	205361_s_at	1.1801E-02	3.30E-04	3.70	0.09	6.75E-01
1527	DEGS1	207431_s_at	1.1801E-02	3.30E-04	-3.70	0.09	-6.63E-01
1528	EIF4EBP1	221539_at	1.1801E-02	3.30E-04	-3.70	0.09	-4.29E-01
1529	SLC8A1	241752_at	1.1801E-02	3.30E-04	-3.70	0.09	-3.64E-01
1530	ACTA2	200974_at	1.1844E-02	3.32E-04	-3.70	0.09	-9.29E-01
1531		240533_at	1.1844E-02	3.32E-04	3.70	0.09	1.34E-01
1532	LRRC41	201932_at	1.1883E-02	3.33E-04	-3.70	0.08	-4.04E-01
1533	ID1	208937_s_at	1.1897E-02	3.34E-04	-3.70	0.08	-6.50E-01
1534	STK17B	217503_at	1.1910E-02	3.34E-04	3.70	0.08	5.54E-01
1535	TPP1	200742_s_at	1.1918E-02	3.35E-04	-3.70	0.08	-9.86E-01
1536		231272_at	1.1918E-02	3.35E-04	3.70	0.08	1.96E-01
1537	DRAM1	218627_at	1.1918E-02	3.35E-04	-3.70	0.08	-6.00E-01
1538	LOC100131117	231497_at	1.1918E-02	3.35E-04	3.70	0.08	1.97E-01
1539	CCNY	224652_at	1.1918E-02	3.36E-04	-3.70	0.08	-2.90E-01
1540	EIF3J	217364_x_at	1.1918E-02	3.36E-04	-3.70	0.08	-2.05E-01
1541	ARMCX3	217858_s_at	1.1918E-02	3.36E-04	-3.70	0.08	-3.83E-01
1542	GPX3	214091_s_at	1.1940E-02	3.37E-04	-3.70	0.07	-9.67E-01
1543	GOLGA3	202106_at	1.1953E-02	3.37E-04	-3.70	0.07	-3.58E-01
1544	C3orf16	1561928_s_at	1.1976E-02	3.38E-04	3.70	0.07	1.63E-01
1545	CKAP4	200998_s_at	1.1976E-02	3.38E-04	-3.70	0.07	-8.33E-01
1546	EIF2S3	205321_at	1.1983E-02	3.39E-04	3.69	0.07	7.57E-01
1547	TFCP2	207627_s_at	1.1983E-02	3.39E-04	-3.69	0.07	-3.52E-01
1548	PPP5C	201979_s_at	1.1983E-02	3.39E-04	-3.69	0.07	-3.17E-01
1549	ANXA4	201301_s_at	1.1985E-02	3.40E-04	-3.69	0.07	-4.69E-01
1550	SHC1	201469_s_at	1.2021E-02	3.41E-04	-3.69	0.06	-3.45E-01
1551	GGPS1	202322_s_at	1.2021E-02	3.41E-04	3.69	0.06	3.14E-01
1552	TFE3	206649_s_at	1.2021E-02	3.41E-04	-3.69	0.06	-3.60E-01
1553	SEC61A1	217716_s_at	1.2021E-02	3.41E-04	-3.69	0.06	-4.12E-01
1554		216146_at	1.2021E-02	3.42E-04	3.69	0.06	1.41E-01
1555	WBSCR16	221247_s_at	1.2021E-02	3.42E-04	-3.69	0.06	-3.59E-01
1556	DCN	211896_s_at	1.2027E-02	3.42E-04	-3.69	0.06	-1.49E+00
1557	PCYOX1	225274_at	1.2030E-02	3.43E-04	-3.69	0.06	-5.24E-01
1558	TBC1D9B	215994_x_at	1.2032E-02	3.43E-04	-3.69	0.06	-3.80E-01
1559	VAMP3	201336_at	1.2033E-02	3.43E-04	-3.69	0.06	-3.12E-01
1560	NUDT16	235054_at	1.2033E-02	3.44E-04	-3.69	0.06	-3.72E-01
1561	NPM1	200063_s_at	1.2033E-02	3.44E-04	3.69	0.05	1.55E-01
1562		1557712_x_at	1.2033E-02	3.44E-04	3.69	0.05	2.41E-01
1563		233976_at	1.2033E-02	3.44E-04	3.69	0.05	1.93E-01
1564	SLC11A1	210423_s_at	1.2033E-02	3.44E-04	-3.69	0.05	-3.84E-01
1565	CHRNA3	211772_x_at	1.2033E-02	3.45E-04	3.69	0.05	1.25E-01
1566	ASPH	209135_at	1.2033E-02	3.45E-04	-3.69	0.05	-4.28E-01
1567		231013_at	1.2033E-02	3.45E-04	3.69	0.05	6.39E-01
1568	KARS	200079_s_at	1.2033E-02	3.45E-04	-3.69	0.05	-4.36E-01
1569	SPATS2L	222154_s_at	1.2033E-02	3.45E-04	-3.69	0.05	-4.12E-01
1570	ABCA4	210082_at	1.2042E-02	3.46E-04	3.69	0.05	2.13E-01
1571	LOC643955///ZNF727///ZNF479	1554996_at	1.2042E-02	3.47E-04	3.69	0.05	1.20E-01
1572	PI4K2A	209346_s_at	1.2042E-02	3.47E-04	-3.69	0.05	-2.70E-01
1573	GALNS	206335_at	1.2042E-02	3.47E-04	-3.69	0.05	-3.83E-01
1574	EIF3M	202231_at	1.2042E-02	3.47E-04	3.69	0.05	2.54E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1575	FH	203032_s_at	1.2042E-02	3.47E-04	-3.69	0.05	-2.43E-01
1576	COQ7	209746_s_at	1.2042E-02	3.47E-04	3.69	0.05	2.63E-01
1577	COL4A2	211966_at	1.2042E-02	3.47E-04	-3.69	0.05	-8.52E-01
1578	ALOX5	214366_s_at	1.2047E-02	3.48E-04	-3.69	0.05	-6.47E-01
1579	SQSTM1	201471_s_at	1.2054E-02	3.48E-04	-3.69	0.04	-4.96E-01
1580	SNHG10	244786_at	1.2088E-02	3.49E-04	3.69	0.04	4.22E-01
1581	SELS	223209_s_at	1.2100E-02	3.50E-04	-3.69	0.04	-3.99E-01
1582	NDUFC1	203478_at	1.2119E-02	3.51E-04	3.69	0.04	3.20E-01
1583	COPZ1	222386_s_at	1.2119E-02	3.51E-04	-3.68	0.04	-4.94E-01
1584		237275_at	1.2123E-02	3.51E-04	3.68	0.04	1.42E-01
1585	HLA-G	211528_x_at	1.2123E-02	3.51E-04	-3.68	0.04	-4.70E-01
1586	NRP2	214632_at	1.2143E-02	3.52E-04	-3.68	0.03	-2.75E-01
1587	KLF3	222913_at	1.2143E-02	3.52E-04	-3.68	0.03	-1.95E-01
1588	AGGF1	208042_at	1.2170E-02	3.53E-04	-3.68	0.03	-3.90E-01
1589	PSMA3	232648_at	1.2177E-02	3.54E-04	3.68	0.03	3.17E-01
1590	PFDN6	242048_at	1.2179E-02	3.54E-04	3.68	0.03	1.98E-01
1591	ACO2	200793_s_at	1.2179E-02	3.54E-04	-3.68	0.03	-4.99E-01
1592	LOC391020	216565_x_at	1.2231E-02	3.56E-04	-3.68	0.02	-3.79E-01
1593	SSBP1	1562442_a_at	1.2231E-02	3.56E-04	3.68	0.02	2.78E-01
1594		243221_at	1.2254E-02	3.57E-04	-3.68	0.02	-3.91E-01
1595	TK2	204227_s_at	1.2275E-02	3.58E-04	-3.68	0.02	-2.72E-01
1596	COMMD4	209133_s_at	1.2288E-02	3.59E-04	3.68	0.02	1.98E-01
1597	RPS21	200834_s_at	1.2294E-02	3.59E-04	3.68	0.02	3.13E-01
1598		1564129_a_at	1.2294E-02	3.59E-04	3.68	0.02	2.24E-01
1599	RPL7AP12// /RPS4XP2	234807_x_at	1.2311E-02	3.60E-04	3.68	0.01	3.63E-01
1600	TCERG1	238838_at	1.2311E-02	3.60E-04	3.68	0.01	1.32E-01
1601	MYO7A	33197_at	1.2318E-02	3.61E-04	-3.68	0.01	-4.97E-01
1602	CLLU1	1558185_at	1.2318E-02	3.61E-04	3.68	0.01	9.36E-01
1603	PDE3B	222317_at	1.2318E-02	3.61E-04	3.68	0.01	5.15E-01
1604	PEPD	202108_at	1.2318E-02	3.61E-04	-3.68	0.01	-3.32E-01
1605	HIST1H2AB/ //HIST1H2A E	214469_at	1.2339E-02	3.62E-04	3.68	0.01	6.56E-01
1606	EEA1	225885_at	1.2339E-02	3.62E-04	-3.68	0.01	-4.05E-01
1607	SLCO3A1	227367_at	1.2355E-02	3.63E-04	-3.67	0.01	-5.08E-01
1608	NT5C2	236703_at	1.2355E-02	3.63E-04	3.67	0.01	3.21E-01
1609		43511_s_at	1.2412E-02	3.65E-04	-3.67	0.00	-2.98E-01
1610	CCL18	209924_at	1.2454E-02	3.67E-04	-3.67	0.00	-1.06E+00
1611	GTPBP1	205274_at	1.2467E-02	3.67E-04	3.67	0.00	1.89E-01
1612	UBFD1	205687_at	1.2516E-02	3.69E-04	-3.67	-0.01	-3.60E-01
1613		1561546_at	1.2536E-02	3.70E-04	3.67	-0.01	2.17E-01
1614	AK1	202588_at	1.2556E-02	3.71E-04	3.67	-0.01	2.28E-01
1615	HLA-B	208729_x_at	1.2556E-02	3.71E-04	-3.67	-0.01	-6.06E-01
1616		240508_at	1.2556E-02	3.71E-04	3.67	-0.01	1.82E-01
1617	N4BP1	32069_at	1.2587E-02	3.72E-04	-3.67	-0.02	-3.51E-01
1618		229074_at	1.2587E-02	3.72E-04	-3.67	-0.02	-5.58E-01
1619	ATP5B	201322_at	1.2587E-02	3.73E-04	-3.67	-0.02	-4.28E-01
1620	NCR3	211583_x_at	1.2605E-02	3.73E-04	3.67	-0.02	2.53E-01
1621	ODZ3	227050_at	1.2606E-02	3.74E-04	3.67	-0.02	1.86E-01
1622	GNS	203676_at	1.2606E-02	3.74E-04	-3.67	-0.02	-6.53E-01
1623	NNMT	202238_s_at	1.2606E-02	3.74E-04	-3.67	-0.02	-8.82E-01
1624	TNS3	217853_at	1.2606E-02	3.74E-04	-3.67	-0.02	-5.66E-01
1625	ARHGEF19	226857_at	1.2614E-02	3.75E-04	-3.67	-0.02	-2.42E-01
1626		1561065_at	1.2614E-02	3.75E-04	3.67	-0.02	2.64E-01
1627	NBL1	201621_at	1.2614E-02	3.75E-04	-3.67	-0.02	-6.51E-01
1628	TSPO	202096_s_at	1.2621E-02	3.76E-04	-3.66	-0.03	-5.02E-01
1629	TMED9	205812_s_at	1.2621E-02	3.76E-04	-3.66	-0.03	-4.56E-01
1630	SLCO4A1	229239_x_at	1.2621E-02	3.77E-04	3.66	-0.03	1.98E-01
1631	SRCAP	1552630_a_at	1.2621E-02	3.77E-04	3.66	-0.03	1.64E-01
1632	MLN	207473_at	1.2621E-02	3.77E-04	3.66	-0.03	1.79E-01
1633	FAIM	220643_s_at	1.2621E-02	3.77E-04	-3.66	-0.03	-5.01E-01
1634		1564887_at	1.2646E-02	3.78E-04	3.66	-0.03	1.43E-01
1635	PAX3	207680_x_at	1.2650E-02	3.78E-04	3.66	-0.03	2.17E-01
1636		234827_at	1.2657E-02	3.79E-04	3.66	-0.03	1.42E-01
1637	AGGF1	218534_s_at	1.2657E-02	3.79E-04	-3.66	-0.03	-4.25E-01
1638	FCF1	240928_at	1.2753E-02	3.82E-04	3.66	-0.04	2.42E-01
1639	ITFG1	221449_s_at	1.2753E-02	3.82E-04	-3.66	-0.04	-5.03E-01
1640		228498_at	1.2761E-02	3.83E-04	-3.66	-0.04	-5.34E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1641	DCTN4	218013_x_at	1.2774E-02	3.83E-04	-3.66	-0.04	-4.07E-01
1642	EIF3M	215190_at	1.2795E-02	3.84E-04	3.66	-0.04	4.39E-01
1643	PLP2	201136_at	1.2802E-02	3.85E-04	-3.66	-0.05	-5.36E-01
1644	HLA-B	211911_x_at	1.2804E-02	3.85E-04	-3.66	-0.05	-6.25E-01
1645		233661_at	1.2814E-02	3.86E-04	3.66	-0.05	1.50E-01
1646	SH2B3	203320_at	1.2835E-02	3.87E-04	-3.66	-0.05	-5.13E-01
1647	CBX5	242069_at	1.2835E-02	3.87E-04	3.66	-0.05	4.45E-01
1648	METTL8	1554667_s_at	1.2835E-02	3.87E-04	3.66	-0.05	5.89E-01
1649		1555616_at	1.2841E-02	3.87E-04	3.66	-0.05	2.38E-01
1650	COL5A2	221730_at	1.2862E-02	3.88E-04	-3.66	-0.05	-1.23E+00
1651	MYO1C	225080_at	1.2862E-02	3.88E-04	-3.66	-0.05	-5.26E-01
1652	BLVRA	211729_x_at	1.2878E-02	3.89E-04	-3.66	-0.06	-3.87E-01
1653		244498_x_at	1.2899E-02	3.90E-04	3.65	-0.06	2.09E-01
1654		240742_at	1.2899E-02	3.90E-04	3.65	-0.06	1.81E-01
1655	PMS2L1	216843_x_at	1.2899E-02	3.90E-04	3.65	-0.06	3.99E-01
1656	LILRA2	211101_x_at	1.2907E-02	3.91E-04	-3.65	-0.06	-2.82E-01
1657	HUS1B	1553660_at	1.2931E-02	3.92E-04	3.65	-0.06	1.48E-01
1658	CNTD1	231463_at	1.2931E-02	3.92E-04	3.65	-0.06	1.79E-01
1659	LOC440944	232052_at	1.2937E-02	3.93E-04	3.65	-0.06	4.50E-01
1660	PI4K2A	209345_s_at	1.2952E-02	3.93E-04	-3.65	-0.06	-5.98E-01
1661	LOC100133811///LOC100133661///ZNF749///RNASE2///HLA-DRB5///HLA-DRB4///HLA-DRB3///HLA-DRB2///HLA-DRB1	204670_x_at	1.2966E-02	3.94E-04	-3.65	-0.07	-5.41E-01
1662	RBM15	219286_s_at	1.2967E-02	3.94E-04	3.65	-0.07	2.98E-01
1663	C6orf105	215100_at	1.2968E-02	3.95E-04	3.65	-0.07	3.29E-01
1664	P2RY13	220005_at	1.2968E-02	3.95E-04	-3.65	-0.07	-8.44E-01
1665	P2RX4	204088_at	1.2968E-02	3.95E-04	-3.65	-0.07	-6.67E-01
1666	RSBN1L	226387_at	1.3017E-02	3.97E-04	3.65	-0.07	4.12E-01
1667		244749_at	1.3017E-02	3.97E-04	3.65	-0.07	1.76E-01
1668	NCRNA00188	244807_at	1.3079E-02	3.99E-04	3.65	-0.08	1.38E-01
1669	IDH3B	210418_s_at	1.3095E-02	4.00E-04	-3.65	-0.08	-4.79E-01
1670	CXorf65	231377_at	1.3095E-02	4.00E-04	3.65	-0.08	4.46E-01
1671		217152_at	1.3100E-02	4.00E-04	3.65	-0.08	2.55E-01
1672		230761_at	1.3100E-02	4.01E-04	3.65	-0.08	3.62E-01
1673	LOC728485	242070_at	1.3109E-02	4.01E-04	3.65	-0.08	2.21E-01
1674	MS4A1	231418_at	1.3109E-02	4.01E-04	3.65	-0.08	1.05E+00
1675	FAM20A	241981_at	1.3115E-02	4.02E-04	-3.65	-0.08	-5.78E-01
1676	IPO7	200992_at	1.3116E-02	4.02E-04	-3.65	-0.08	-3.84E-01
1677		240655_at	1.3116E-02	4.02E-04	3.65	-0.09	2.15E-01
1678	TIMP3	201150_s_at	1.3119E-02	4.03E-04	-3.65	-0.09	-8.76E-01
1679		235856_at	1.3119E-02	4.03E-04	-3.65	-0.09	-2.82E-01
1680	SLC15A3	219593_at	1.3119E-02	4.03E-04	-3.65	-0.09	-7.26E-01
1681	PATL1	235234_at	1.3119E-02	4.03E-04	-3.64	-0.09	-2.30E-01
1682	BRPF3	225217_s_at	1.3119E-02	4.04E-04	-3.64	-0.09	-2.72E-01
1683		232111_at	1.3124E-02	4.04E-04	3.64	-0.09	1.53E-01
1684	RERG	244745_at	1.3133E-02	4.05E-04	-3.64	-0.09	-2.78E-01
1685	TUBA1A	209118_s_at	1.3151E-02	4.05E-04	-3.64	-0.09	-2.81E-01
1686	DGCR2	227028_s_at	1.3176E-02	4.06E-04	3.64	-0.09	2.08E-01
1687	DDAH2	215537_x_at	1.3187E-02	4.07E-04	-3.64	-0.10	-4.27E-01
1688	SLC25A43	1557411_s_at	1.3187E-02	4.07E-04	-3.64	-0.10	-5.10E-01
1689	RAB2A	208730_x_at	1.3187E-02	4.07E-04	3.64	-0.10	2.48E-01
1690	MFI2	220043_s_at	1.3191E-02	4.08E-04	3.64	-0.10	2.01E-01
1691	RPS17	211487_x_at	1.3200E-02	4.08E-04	3.64	-0.10	2.50E-01
1692	DNPEP	201937_s_at	1.3200E-02	4.09E-04	-3.64	-0.10	-5.19E-01
1693	SCAMP3	201771_at	1.3200E-02	4.09E-04	-3.64	-0.10	-3.41E-01
1694	LOC541471///NCRNA00152	225799_at	1.3200E-02	4.09E-04	3.64	-0.10	5.63E-01
1695	ALB	214837_at	1.3200E-02	4.09E-04	3.64	-0.10	1.11E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1696	SLC43A2	226629_at	1.3230E-02	4.10E-04	-3.64	-0.10	-3.31E-01
1697	RHOQ	214449_s_at	1.3266E-02	4.12E-04	-3.64	-0.11	-4.80E-01
1698	C12orf65	223477_s_at	1.3274E-02	4.13E-04	3.64	-0.11	2.97E-01
1699	SLAMF8	219385_at	1.3274E-02	4.13E-04	-3.64	-0.11	-7.36E-01
1700	IL6ST	234967_at	1.3274E-02	4.13E-04	3.64	-0.11	1.70E-01
1701	HM13	224615_x_at	1.3274E-02	4.13E-04	-3.64	-0.11	-3.31E-01
1702	BAX	211833_s_at	1.3288E-02	4.14E-04	-3.64	-0.11	-4.63E-01
1703	SPATA19	1559138_a_at	1.3288E-02	4.14E-04	3.64	-0.11	2.03E-01
1704	PICALM	215832_x_at	1.3316E-02	4.15E-04	-3.64	-0.11	-3.78E-01
1705	IPO4	218305_at	1.3316E-02	4.15E-04	-3.64	-0.11	-2.97E-01
1706	PDGFC	218718_at	1.3316E-02	4.15E-04	-3.64	-0.11	-8.41E-01
1707	SQSTM1	239004_at	1.3318E-02	4.16E-04	3.64	-0.11	3.49E-01
1708	CD3G	206804_at	1.3329E-02	4.16E-04	3.64	-0.12	4.94E-01
1709	TNFRSF12A	218368_s_at	1.3358E-02	4.18E-04	-3.64	-0.12	-5.07E-01
1710	SMC1A	217555_at	1.3358E-02	4.18E-04	3.63	-0.12	1.91E-01
1711	PTPN18	213521_at	1.3373E-02	4.18E-04	-3.63	-0.12	-3.79E-01
1712	PML	239582_at	1.3373E-02	4.19E-04	-3.63	-0.12	-2.26E-01
1713	NAAA	214765_s_at	1.3391E-02	4.20E-04	-3.63	-0.12	-5.55E-01
1714	RCOR3	218344_s_at	1.3391E-02	4.20E-04	3.63	-0.12	3.46E-01
1715	LPP	202821_s_at	1.3400E-02	4.20E-04	-3.63	-0.12	-3.51E-01
1716	UBE2V1P2///TMEM189-UBE2V1///TMEM189///UBE2V1///RNPEP	201003_x_at	1.3400E-02	4.21E-04	-3.63	-0.12	-4.10E-01
1717	LAPTM4B	208767_s_at	1.3432E-02	4.22E-04	-3.63	-0.13	-6.27E-01
1718	DUSP6	208891_at	1.3435E-02	4.22E-04	-3.63	-0.13	-2.87E-01
1719	YKT6	217784_at	1.3435E-02	4.23E-04	-3.63	-0.13	-4.48E-01
1720	VEGFA	211527_x_at	1.3435E-02	4.23E-04	-3.63	-0.13	-2.30E-01
1721	ITPRIPL2	227954_at	1.3483E-02	4.24E-04	-3.63	-0.13	-4.42E-01
1722	TRAJ17///TRAV20///TRD@///TRA@	234849_at	1.3483E-02	4.25E-04	3.63	-0.13	5.53E-01
1723	MSL3	207551_s_at	1.3529E-02	4.26E-04	3.63	-0.14	3.76E-01
1724	GAPDH	AFFX-HUMGAPDH/M33197_5_at	1.3549E-02	4.27E-04	-3.63	-0.14	-9.04E-01
1725	LOC641518	243363_at	1.3551E-02	4.28E-04	3.63	-0.14	2.90E-01
1726	MAP3K3	203514_at	1.3551E-02	4.28E-04	-3.63	-0.14	-4.29E-01
1727	FKBP8	40850_at	1.3551E-02	4.28E-04	-3.63	-0.14	-2.17E-01
1728	STAT3	208992_s_at	1.3551E-02	4.29E-04	-3.63	-0.14	-5.86E-01
1729		227585_at	1.3551E-02	4.29E-04	3.63	-0.14	2.14E-01
1730	C8orf59	1555241_at	1.3551E-02	4.29E-04	3.63	-0.14	5.72E-01
1731	BECN1	1561652_at	1.3551E-02	4.29E-04	3.63	-0.14	1.21E-01
1732		231316_at	1.3551E-02	4.29E-04	3.63	-0.14	3.62E-01
1733	CALCR	207887_s_at	1.3551E-02	4.30E-04	3.63	-0.14	1.35E-01
1734	QTRTD1	219178_at	1.3559E-02	4.30E-04	-3.63	-0.14	-3.30E-01
1735		232130_at	1.3564E-02	4.30E-04	-3.63	-0.15	-2.77E-01
1736	OBFC1	228781_at	1.3565E-02	4.31E-04	-3.63	-0.15	-1.57E-01
1737	PITPNA	201191_at	1.3565E-02	4.31E-04	-3.63	-0.15	-4.85E-01
1738	NAP1L5	228062_at	1.3576E-02	4.32E-04	-3.63	-0.15	-3.38E-01
1739	MPHOSPH9	215731_s_at	1.3576E-02	4.32E-04	3.63	-0.15	4.11E-01
1740	AP2B1	200615_s_at	1.3576E-02	4.32E-04	-3.62	-0.15	-5.03E-01
1741	MBD4	214047_s_at	1.3576E-02	4.33E-04	3.62	-0.15	3.36E-01
1742		1557021_s_at	1.3576E-02	4.33E-04	3.62	-0.15	2.30E-01
1743	NUDC	210574_s_at	1.3576E-02	4.33E-04	-3.62	-0.15	-4.77E-01
1744	LOC729915///LOC728093///POM121L3P///POM121L10P///LOC440821///POM121L4P///POM121L8P///POM121L9P///POM121L1P	1553818_x_at	1.3576E-02	4.33E-04	3.62	-0.15	1.94E-01
1745	MAP1B	214577_at	1.3576E-02	4.34E-04	-3.62	-0.15	-1.80E-01
1746	NHSL1	226490_at	1.3576E-02	4.34E-04	-3.62	-0.15	-4.44E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1747	RBPJ	211974_x_at	1.3576E-02	4.34E-04	-3.62	-0.15	-4.44E-01
1748	ADAP2	219358_s_at	1.3576E-02	4.34E-04	-3.62	-0.15	-5.20E-01
1749		244827_at	1.3596E-02	4.35E-04	-3.62	-0.16	-1.53E-01
1750		1562314_at	1.3596E-02	4.35E-04	3.62	-0.16	2.24E-01
1751	HSPD1	200806_s_at	1.3596E-02	4.35E-04	-3.62	-0.16	-5.85E-01
1752	BRAF	243829_at	1.3613E-02	4.36E-04	3.62	-0.16	3.76E-01
1753	HSP90AB1	200064_at	1.3616E-02	4.37E-04	-3.62	-0.16	-6.17E-01
1754	LLGL2	1554006_a_at	1.3618E-02	4.37E-04	3.62	-0.16	1.58E-01
1755	LRRC28	1553940_a_at	1.3618E-02	4.38E-04	-3.62	-0.16	-2.09E-01
1756	PHLDA2	209803_s_at	1.3618E-02	4.38E-04	-3.62	-0.16	-5.00E-01
1757		240489_at	1.3618E-02	4.38E-04	3.62	-0.16	1.32E-01
1758	C10orf110	220703_at	1.3618E-02	4.38E-04	3.62	-0.16	1.42E-01
1759		1560779_a_at	1.3627E-02	4.38E-04	3.62	-0.16	1.37E-01
1760	DLG5	201681_s_at	1.3701E-02	4.41E-04	-3.62	-0.17	-5.14E-01
1761	ZNF280D	1568951_at	1.3701E-02	4.41E-04	3.62	-0.17	2.50E-01
1762	PEX19	201706_s_at	1.3721E-02	4.42E-04	-3.62	-0.17	-3.66E-01
1763	FCN1	205237_at	1.3721E-02	4.42E-04	-3.62	-0.17	-8.38E-01
1764	GART	217445_s_at	1.3721E-02	4.43E-04	-3.62	-0.17	-2.14E-01
1765	PRLR	211917_s_at	1.3766E-02	4.44E-04	3.62	-0.17	9.36E-02
1766	GORASP1	215749_s_at	1.3766E-02	4.45E-04	-3.62	-0.17	-4.64E-01
1767	TBC1D9B	212054_x_at	1.3766E-02	4.45E-04	-3.62	-0.18	-3.45E-01
1768	LOC283028	1560744_at	1.3773E-02	4.45E-04	3.62	-0.18	1.77E-01
1769	LOC440944	1555858_at	1.3782E-02	4.46E-04	3.62	-0.18	3.62E-01
1770	HSPB1	201841_s_at	1.3818E-02	4.47E-04	-3.62	-0.18	-5.81E-01
1771	LYPD3	204952_at	1.3829E-02	4.48E-04	-3.61	-0.18	-3.15E-01
1772		228918_at	1.3837E-02	4.49E-04	-3.61	-0.18	-4.72E-01
1773	TMED10	212352_s_at	1.3837E-02	4.49E-04	-3.61	-0.18	-3.33E-01
1774	PCDHGA1/// PCDHGA2/// PCDHGA3/// PCDHGA4/// PCDHGA5/// PCDHGA6/// PCDHGA7/// PCDHGA9/// PCDHGA10/ //PCDHGA1 1///PCDHGB 1///PCDHGB 2///PCDHGB 3///PCDHGB 5///PCDHGB 6///PCDHGB 7///PCDHGC 4///PCDHGC 5///PCDHGA 12///PCDHG A8///PCDHG B4///PCDHG C3	215836_s_at	1.3837E-02	4.49E-04	-3.61	-0.18	-3.96E-01
1775	ARF1	208750_s_at	1.3838E-02	4.49E-04	-3.61	-0.18	-7.02E-01
1776	GATA6	229282_at	1.3873E-02	4.51E-04	3.61	-0.19	2.47E-01
1777	LRCH3	1559490_at	1.3913E-02	4.52E-04	3.61	-0.19	4.13E-01
1778	SAP18	208741_at	1.3913E-02	4.53E-04	-3.61	-0.19	-3.28E-01
1779	MTRF1	219822_at	1.3913E-02	4.53E-04	3.61	-0.19	4.73E-01
1780	C14orf178	1564816_at	1.3913E-02	4.53E-04	3.61	-0.19	1.65E-01
1781	CYB5R3	1554574_a_at	1.3916E-02	4.53E-04	-3.61	-0.19	-4.38E-01
1782	C10orf84	222617_s_at	1.3948E-02	4.55E-04	3.61	-0.19	4.16E-01
1783		215738_at	1.3948E-02	4.55E-04	3.61	-0.20	1.66E-01
1784		215304_at	1.3968E-02	4.56E-04	3.61	-0.20	1.59E-01
1785	HDLBP	221767_x_at	1.3968E-02	4.56E-04	-3.61	-0.20	-4.97E-01
1786	MIB2	241541_at	1.3999E-02	4.57E-04	3.61	-0.20	2.09E-01
1787		229629_at	1.4001E-02	4.58E-04	3.61	-0.20	4.75E-01
1788	ALDH1A3	203180_at	1.4001E-02	4.58E-04	-3.61	-0.20	-1.04E+00
1789	ZSCAN12	206507_at	1.4006E-02	4.58E-04	3.61	-0.20	2.86E-01
1790	RGS5	1555725_a_at	1.4012E-02	4.59E-04	-3.61	-0.20	-5.47E-01
1791	TAGLN2	210978_s_at	1.4012E-02	4.59E-04	-3.61	-0.20	-7.37E-01
1792	NCRNA00168	1561127_at	1.4015E-02	4.59E-04	3.61	-0.20	1.68E-01
1793	PIK3R6	1558770_a_at	1.4015E-02	4.60E-04	-3.61	-0.20	-3.64E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1794	TBXA2R	211590_x_at	1.4029E-02	4.60E-04	-3.61	-0.21	-1.89E-01
1795	OFD1	241751_at	1.4035E-02	4.61E-04	3.61	-0.21	3.06E-01
1796	DDR2	227561_at	1.4049E-02	4.61E-04	-3.61	-0.21	-5.47E-01
1797	GPI	208308_s_at	1.4074E-02	4.63E-04	-3.61	-0.21	-6.29E-01
1798		233629_at	1.4074E-02	4.63E-04	3.61	-0.21	1.47E-01
1799	PDHA1	200979_at	1.4074E-02	4.63E-04	-3.61	-0.21	-3.03E-01
1800		1560579_s_at	1.4074E-02	4.63E-04	3.61	-0.21	2.24E-01
1801		243493_at	1.4089E-02	4.64E-04	3.60	-0.21	1.92E-01
1802	ACO1	207071_s_at	1.4090E-02	4.64E-04	-3.60	-0.21	-4.53E-01
1803	ERLIN1	202444_s_at	1.4122E-02	4.66E-04	-3.60	-0.22	-3.50E-01
1804	ICAM1	202637_s_at	1.4122E-02	4.66E-04	-3.60	-0.22	-6.08E-01
1805	TBC1D7	1563839_at	1.4139E-02	4.67E-04	3.60	-0.22	1.10E-01
1806		241271_at	1.4167E-02	4.68E-04	3.60	-0.22	9.90E-02
1807	FAM169A	213954_at	1.4172E-02	4.68E-04	3.60	-0.22	2.46E-01
1808	ZNF639	222624_s_at	1.4199E-02	4.70E-04	3.60	-0.22	3.81E-01
1809	EFEMP1	201842_s_at	1.4221E-02	4.71E-04	-3.60	-0.23	-9.02E-01
1810	ZEB2	203603_s_at	1.4221E-02	4.71E-04	-3.60	-0.23	-5.54E-01
1811	SDF4	217855_x_at	1.4277E-02	4.73E-04	-3.60	-0.23	-4.01E-01
1812	FTH1	200748_s_at	1.4303E-02	4.74E-04	-3.60	-0.23	-6.12E-01
1813	ADAM9	1555326_a_at	1.4327E-02	4.75E-04	-3.60	-0.23	-4.83E-01
1814		236520_at	1.4327E-02	4.75E-04	3.60	-0.23	2.00E-01
1815	NBR1	201383_s_at	1.4347E-02	4.76E-04	-3.60	-0.24	-4.82E-01
1816	IQGAP1	200791_s_at	1.4347E-02	4.77E-04	-3.60	-0.24	-3.04E-01
1817	MAN2C1	238089_at	1.4347E-02	4.77E-04	3.60	-0.24	2.69E-01
1818	NRF1	211279_at	1.4347E-02	4.77E-04	3.60	-0.24	1.99E-01
1819	UBE2Q1	222480_at	1.4347E-02	4.78E-04	-3.60	-0.24	-2.91E-01
1820	PPARD	242218_at	1.4347E-02	4.78E-04	3.60	-0.24	1.86E-01
1821	CSDE1	222975_s_at	1.4347E-02	4.78E-04	-3.60	-0.24	-4.85E-01
1822	GPKOW	203776_at	1.4347E-02	4.79E-04	-3.60	-0.24	-3.68E-01
1823	PPM1N	229559_at	1.4347E-02	4.79E-04	-3.60	-0.24	-3.44E-01
1824	GART	212378_at	1.4347E-02	4.79E-04	-3.60	-0.24	-4.36E-01
1825	GINS4	240778_at	1.4347E-02	4.79E-04	3.60	-0.24	1.47E-01
1826	SNAPC2	204104_at	1.4347E-02	4.79E-04	-3.60	-0.24	-2.59E-01
1827	CD99L2	223041_at	1.4347E-02	4.79E-04	-3.60	-0.24	-3.55E-01
1828		229006_at	1.4351E-02	4.80E-04	3.59	-0.24	1.72E-01
1829	KLF6	208960_s_at	1.4371E-02	4.81E-04	-3.59	-0.24	-6.95E-01
1830	KCNJ2	231513_at	1.4407E-02	4.83E-04	-3.59	-0.25	-9.12E-01
1831	GAPDH	AFFX-HUMGAPDH/M33197_M_at	1.4407E-02	4.83E-04	-3.59	-0.25	-6.29E-01
1832	LYVE1	219059_s_at	1.4407E-02	4.83E-04	-3.59	-0.25	-8.79E-01
1833		237763_at	1.4407E-02	4.83E-04	3.59	-0.25	1.88E-01
1834	TFB1M	228075_x_at	1.4429E-02	4.84E-04	3.59	-0.25	4.27E-01
1835		222296_at	1.4448E-02	4.85E-04	-3.59	-0.25	-2.06E-01
1836	TMPRSS6	214955_at	1.4448E-02	4.86E-04	3.59	-0.25	1.67E-01
1837	VIPAR	233140_s_at	1.4448E-02	4.86E-04	-3.59	-0.25	-2.20E-01
1838	ZNF358	226260_x_at	1.4448E-02	4.86E-04	3.59	-0.25	2.26E-01
1839	CD97	202910_s_at	1.4450E-02	4.86E-04	-3.59	-0.25	-4.32E-01
1840	RPL36	219762_s_at	1.4467E-02	4.87E-04	3.59	-0.26	4.22E-01
1841	ZEB2	228333_at	1.4502E-02	4.88E-04	-3.59	-0.26	-3.93E-01
1842	SRPX	204955_at	1.4511E-02	4.89E-04	-3.59	-0.26	-1.14E+00
1843	CTTN	227473_at	1.4511E-02	4.89E-04	-3.59	-0.26	-4.34E-01
1844		238796_at	1.4522E-02	4.90E-04	3.59	-0.26	3.36E-01
1845	AIM1	212543_at	1.4543E-02	4.91E-04	-3.59	-0.26	-4.36E-01
1846	CAPRIN1	200723_s_at	1.4553E-02	4.91E-04	-3.59	-0.26	-4.64E-01
1847	ERI1	226416_at	1.4564E-02	4.92E-04	-3.59	-0.27	-5.04E-01
1848	BCAS4	228787_s_at	1.4564E-02	4.93E-04	3.59	-0.27	3.51E-01
1849	NECAP2	220731_s_at	1.4564E-02	4.93E-04	-3.59	-0.27	-3.05E-01
1850	FAM109B	226504_at	1.4564E-02	4.93E-04	-3.59	-0.27	-3.15E-01
1851	PRPF40A	213729_at	1.4586E-02	4.94E-04	-3.59	-0.27	-5.47E-01
1852	WHAMML2//WHAMML1	1560662_s_at	1.4586E-02	4.94E-04	3.59	-0.27	1.28E-01
1853	HAPLN2	220142_at	1.4588E-02	4.94E-04	3.59	-0.27	1.54E-01
1854	GEMIN4	217099_s_at	1.4594E-02	4.95E-04	-3.59	-0.27	-3.26E-01
1855	MTHFD1	202309_at	1.4598E-02	4.95E-04	-3.59	-0.27	-3.99E-01
1856		238243_at	1.4602E-02	4.96E-04	3.59	-0.27	1.90E-01
1857	CCND2	200951_s_at	1.4609E-02	4.96E-04	-3.59	-0.27	-6.07E-01
1858	SECTM1	213716_s_at	1.4621E-02	4.97E-04	-3.58	-0.27	-6.76E-01
1859	TDH	1553493_a_at	1.4624E-02	4.97E-04	3.58	-0.27	2.94E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1860	SLC27A1	226728_at	1.4624E-02	4.98E-04	-3.58	-0.28	-3.57E-01
1861	CREBL2	201988_s_at	1.4628E-02	4.98E-04	-3.58	-0.28	-5.63E-01
1862	DRG2	203267_s_at	1.4630E-02	4.98E-04	-3.58	-0.28	-4.53E-01
1863		207748_at	1.4656E-02	4.99E-04	3.58	-0.28	2.26E-01
1864	HNRNPUL2	66053_at	1.4665E-02	5.00E-04	-3.58	-0.28	-4.24E-01
1865		1563320_at	1.4684E-02	5.01E-04	3.58	-0.28	1.49E-01
1866	NUP210	213945_s_at	1.4715E-02	5.02E-04	3.58	-0.28	2.61E-01
1867	UBE2J1	217826_s_at	1.4718E-02	5.03E-04	-3.58	-0.28	-4.40E-01
1868	MAN1B1	65884_at	1.4722E-02	5.03E-04	-3.58	-0.28	-3.06E-01
1869	SERP2	239890_s_at	1.4746E-02	5.04E-04	3.58	-0.29	1.44E-01
1870		224006_at	1.4759E-02	5.05E-04	3.58	-0.29	2.05E-01
1871	ANKRD32	1558076_at	1.4781E-02	5.06E-04	3.58	-0.29	1.41E-01
1872	KLC4	225596_at	1.4827E-02	5.08E-04	3.58	-0.29	1.89E-01
1873	WIPI1	213836_s_at	1.4827E-02	5.08E-04	-3.58	-0.29	-4.41E-01
1874	CFD	205382_s_at	1.4859E-02	5.09E-04	-3.58	-0.30	-7.88E-01
1875	LRRFIP1	201862_s_at	1.4890E-02	5.11E-04	-3.58	-0.30	-5.63E-01
1876	FANCD2	242560_at	1.4890E-02	5.11E-04	3.58	-0.30	4.11E-01
1877	EIF4G1	208624_s_at	1.4894E-02	5.11E-04	-3.58	-0.30	-5.76E-01
1878	PRKCD	202545_at	1.4901E-02	5.12E-04	-3.58	-0.30	-6.76E-01
1879	COPB2	201098_at	1.4901E-02	5.12E-04	-3.58	-0.30	-2.85E-01
1880	GPHN	220773_s_at	1.4901E-02	5.12E-04	-3.58	-0.30	-3.69E-01
1881	ACSL4	202422_s_at	1.4926E-02	5.14E-04	-3.58	-0.30	-3.35E-01
1882	MAPK14	211561_x_at	1.4985E-02	5.16E-04	-3.57	-0.31	-3.71E-01
1883	DAGLB	225833_at	1.4999E-02	5.17E-04	-3.57	-0.31	-2.69E-01
1884	KIAA1279	212453_at	1.5071E-02	5.20E-04	-3.57	-0.31	-4.19E-01
1885	CD302	203799_at	1.5071E-02	5.20E-04	-3.57	-0.31	-5.69E-01
1886	NDUFV3	226209_at	1.5071E-02	5.20E-04	-3.57	-0.31	-2.69E-01
1887	PCGF5	226326_at	1.5091E-02	5.21E-04	3.57	-0.32	3.98E-01
1888	LOC283737	237687_at	1.5151E-02	5.23E-04	3.57	-0.32	1.67E-01
1889	RNASET2	217983_s_at	1.5181E-02	5.24E-04	-3.57	-0.32	-5.75E-01
1890	RNF217	235492_at	1.5186E-02	5.25E-04	-3.57	-0.32	-2.00E-01
1891	SFMBT1	213370_s_at	1.5189E-02	5.25E-04	3.57	-0.32	2.76E-01
1892		229031_at	1.5189E-02	5.26E-04	3.57	-0.32	3.78E-01
1893	STOM	201061_s_at	1.5190E-02	5.26E-04	-3.57	-0.32	-3.66E-01
1894	LOC728323/ //NCRNA00 266///PCMT D2	232953_at	1.5198E-02	5.26E-04	3.57	-0.33	1.88E-01
1895	EPB41L3	211776_s_at	1.5207E-02	5.27E-04	-3.57	-0.33	-7.26E-01
1896	IMMP1L	229025_s_at	1.5208E-02	5.27E-04	3.57	-0.33	7.71E-01
1897	LRRC33	235359_at	1.5211E-02	5.28E-04	-3.57	-0.33	-6.55E-01
1898	ZCCHC7	226496_at	1.5211E-02	5.28E-04	3.57	-0.33	4.93E-01
1899	DHX29	212648_at	1.5214E-02	5.28E-04	-3.57	-0.33	-2.99E-01
1900	RPS25	200091_s_at	1.5305E-02	5.32E-04	3.56	-0.33	2.35E-01
1901	CARD6	224414_s_at	1.5305E-02	5.32E-04	-3.56	-0.34	-3.18E-01
1902	MANEA	222805_at	1.5305E-02	5.33E-04	-3.56	-0.34	-4.09E-01
1903	MS4A7	223344_s_at	1.5305E-02	5.33E-04	-3.56	-0.34	-1.03E+00
1904	NF1	243476_at	1.5305E-02	5.33E-04	3.56	-0.34	1.44E-01
1905	TRAK1	201283_s_at	1.5350E-02	5.35E-04	-3.56	-0.34	-1.69E-01
1906	TMEM106B	233666_at	1.5362E-02	5.36E-04	3.56	-0.34	1.46E-01
1907	C6orf145	212923_s_at	1.5377E-02	5.36E-04	-3.56	-0.34	-4.05E-01
1908	C8orf76	1554063_at	1.5382E-02	5.37E-04	3.56	-0.34	2.90E-01
1909	LYPD4	231266_at	1.5382E-02	5.37E-04	3.56	-0.34	1.61E-01
1910		242359_at	1.5382E-02	5.37E-04	3.56	-0.34	2.64E-01
1911	TNS1	221748_s_at	1.5392E-02	5.38E-04	-3.56	-0.34	-8.66E-01
1912	KIF20B	205235_s_at	1.5436E-02	5.40E-04	3.56	-0.35	2.62E-01
1913	SNORD116 @	232976_at	1.5436E-02	5.40E-04	3.56	-0.35	2.39E-01
1914	ZNF382	1557260_a_at	1.5442E-02	5.41E-04	3.56	-0.35	1.97E-01
1915	ARID1B	1566990_x_at	1.5444E-02	5.41E-04	3.56	-0.35	3.53E-01
1916	PSIP1P2///T MSB4Y	216376_x_at	1.5445E-02	5.41E-04	3.56	-0.35	1.59E-01
1917	TM4SF1	209386_at	1.5445E-02	5.42E-04	-3.56	-0.35	-5.26E-01
1918		244336_at	1.5446E-02	5.42E-04	3.56	-0.35	1.15E-01
1919	ZNF697	227080_at	1.5451E-02	5.42E-04	-3.56	-0.35	-4.66E-01
1920	MT1P2	211456_x_at	1.5488E-02	5.44E-04	-3.56	-0.35	-7.55E-01
1921	KLF4	221841_s_at	1.5512E-02	5.45E-04	-3.56	-0.36	-6.84E-01
1922	C6orf89	224988_at	1.5517E-02	5.46E-04	-3.56	-0.36	-3.11E-01
1923	C9orf47	1564274_at	1.5517E-02	5.46E-04	3.56	-0.36	1.73E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1924	TAAR5	221459_at	1.5543E-02	5.47E-04	3.56	-0.36	1.76E-01
1925	GK	215977_x_at	1.5543E-02	5.47E-04	-3.56	-0.36	-5.61E-01
1926	DNAJC3	208499_s_at	1.5556E-02	5.48E-04	-3.56	-0.36	-3.39E-01
1927	ARSF	214490_at	1.5556E-02	5.49E-04	3.56	-0.36	2.12E-01
1928	LOC100128836///LOC730246///LOC729366///LOC729102///LOC728732///LOC728643///LOC728170///HNRPA1P5///HNRPA1L-2///LOC645001///LOC644037///LOC642817///LOC440125///LOC402112///LOC391670///HNRNPA1L2///LOC120364///HNRNPA1	217353_at	1.5556E-02	5.49E-04	-3.56	-0.36	-1.72E-01
1929	LGALS3BP	200923_at	1.5556E-02	5.49E-04	-3.56	-0.36	-9.13E-01
1930	FAM101A	227320_at	1.5556E-02	5.49E-04	-3.56	-0.36	-3.68E-01
1931	CST3	201360_at	1.5563E-02	5.50E-04	-3.56	-0.36	-7.82E-01
1932	TIMP3	201149_s_at	1.5577E-02	5.50E-04	-3.55	-0.37	-8.54E-01
1933	ARSA	204443_at	1.5579E-02	5.51E-04	-3.55	-0.37	-4.58E-01
1934	LRP1	200785_s_at	1.5583E-02	5.51E-04	-3.55	-0.37	-3.06E-01
1935	LAMB1	201505_at	1.5583E-02	5.51E-04	-3.55	-0.37	-8.93E-01
1936	ADCK2	221893_s_at	1.5603E-02	5.52E-04	-3.55	-0.37	-5.39E-01
1937	LOC100129852	244175_at	1.5606E-02	5.53E-04	3.55	-0.37	2.07E-01
1938	psiTPTE22	243952_at	1.5654E-02	5.55E-04	3.55	-0.37	1.45E-01
1939	CDH10	220115_s_at	1.5654E-02	5.55E-04	3.55	-0.37	1.19E-01
1940	SCAMP5	234568_at	1.5654E-02	5.55E-04	3.55	-0.37	2.51E-01
1941	MATN1	206904_at	1.5655E-02	5.56E-04	3.55	-0.37	1.57E-01
1942	DNAJB1	200664_s_at	1.5655E-02	5.56E-04	-3.55	-0.37	-4.42E-01
1943		232903_at	1.5660E-02	5.57E-04	-3.55	-0.38	-1.62E-01
1944	SST	213921_at	1.5665E-02	5.57E-04	3.55	-0.38	1.40E-01
1945	MSN	200600_at	1.5671E-02	5.57E-04	-3.55	-0.38	-6.24E-01
1946	GALNT2	217788_s_at	1.5693E-02	5.59E-04	-3.55	-0.38	-5.42E-01
1947	CDC42EP1	204693_at	1.5693E-02	5.59E-04	-3.55	-0.38	-3.17E-01
1948	PAPOLG	224427_s_at	1.5739E-02	5.61E-04	3.55	-0.38	2.78E-01
1949	TNS1	221246_x_at	1.5739E-02	5.61E-04	-3.55	-0.38	-3.84E-01
1950	FAM104B	227869_at	1.5747E-02	5.62E-04	3.55	-0.38	3.90E-01
1951		1561272_at	1.5760E-02	5.62E-04	3.55	-0.38	1.24E-01
1952		232956_at	1.5760E-02	5.63E-04	3.55	-0.38	1.37E-01
1953	SUSD4	223821_s_at	1.5760E-02	5.63E-04	3.55	-0.39	1.26E-01
1954	ACE	209749_s_at	1.5760E-02	5.63E-04	-3.55	-0.39	-1.64E-01
1955		49111_at	1.5760E-02	5.64E-04	-3.55	-0.39	-2.46E-01
1956	CYP1B1	202435_s_at	1.5771E-02	5.64E-04	-3.55	-0.39	-7.54E-01
1957	ZDHHC7	218606_at	1.5771E-02	5.65E-04	-3.55	-0.39	-4.41E-01
1958		237153_at	1.5788E-02	5.65E-04	3.55	-0.39	1.64E-01
1959	HCLS1	202957_at	1.5790E-02	5.66E-04	-3.55	-0.39	-6.43E-01
1960	NAA35	220925_at	1.5806E-02	5.67E-04	-3.55	-0.39	-4.40E-01
1961	RICTOR	226312_at	1.5806E-02	5.67E-04	3.55	-0.39	3.43E-01
1962	RUFY1	233380_s_at	1.5806E-02	5.67E-04	-3.55	-0.39	-4.36E-01
1963		239489_at	1.5812E-02	5.68E-04	3.55	-0.39	2.81E-01
1964	SYK	207540_s_at	1.5812E-02	5.68E-04	-3.55	-0.39	-3.25E-01
1965	SERBP1	217725_x_at	1.5812E-02	5.68E-04	-3.55	-0.39	-4.01E-01
1966	RBM12///CPNE1	212170_at	1.5812E-02	5.69E-04	3.55	-0.39	3.49E-01
1967	ASGR2	206130_s_at	1.5818E-02	5.69E-04	-3.55	-0.39	-4.10E-01
1968	AKD1	1564002_a_at	1.5824E-02	5.70E-04	3.54	-0.40	4.76E-01
1969	TMEM70	219448_at	1.5864E-02	5.71E-04	3.54	-0.40	3.27E-01
1970	NUDT10	241596_at	1.5882E-02	5.72E-04	3.54	-0.40	1.59E-01
1971	MSI2	225237_s_at	1.5914E-02	5.74E-04	3.54	-0.40	2.93E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1972	SPIN3	1555883_s_at	1.5914E-02	5.74E-04	3.54	-0.40	2.35E-01
1973		239131_at	1.5914E-02	5.75E-04	3.54	-0.40	2.96E-01
1974	TRPM7	223323_x_at	1.5914E-02	5.75E-04	3.54	-0.40	2.52E-01
1975	RPS16P1/// RPS16	226130_at	1.5914E-02	5.75E-04	3.54	-0.40	3.07E-01
1976	FKBP4	200894_s_at	1.5914E-02	5.75E-04	-3.54	-0.40	-3.54E-01
1977	GGA2	214190_x_at	1.5914E-02	5.76E-04	-3.54	-0.41	-2.93E-01
1978	LOC150166	229295_at	1.5914E-02	5.76E-04	-3.54	-0.41	-4.38E-01
1979	AMDHD1	229596_at	1.5914E-02	5.76E-04	3.54	-0.41	2.07E-01
1980	LOC374443	240572_s_at	1.5914E-02	5.76E-04	3.54	-0.41	6.40E-01
1981	ARHGAP15	218870_at	1.5914E-02	5.77E-04	3.54	-0.41	4.43E-01
1982	KLF6	208961_s_at	1.5930E-02	5.77E-04	-3.54	-0.41	-5.19E-01
1983	GNB1	200745_s_at	1.5965E-02	5.79E-04	-3.54	-0.41	-5.96E-01
1984	SNRPD2	200826_at	1.5978E-02	5.80E-04	3.54	-0.41	4.81E-01
1985	ITGB2	1555349_a_at	1.5978E-02	5.81E-04	-3.54	-0.41	-9.10E-01
1986	TMEM93	221255_s_at	1.5978E-02	5.81E-04	3.54	-0.41	3.20E-01
1987		1562046_at	1.5978E-02	5.81E-04	3.54	-0.41	1.41E-01
1988	QRSL1	241933_at	1.5978E-02	5.81E-04	3.54	-0.41	3.53E-01
1989	C2orf34	1554875_at	1.5981E-02	5.81E-04	3.54	-0.41	1.53E-01
1990	RET	205879_x_at	1.6011E-02	5.83E-04	3.54	-0.42	2.14E-01
1991	SEZ6L2	233337_s_at	1.6011E-02	5.83E-04	-3.54	-0.42	-2.47E-01
1992	PPP1R3B	222662_at	1.6011E-02	5.84E-04	-3.54	-0.42	-3.97E-01
1993	COPA	214336_s_at	1.6011E-02	5.84E-04	-3.54	-0.42	-3.28E-01
1994	MFSD4	229254_at	1.6011E-02	5.84E-04	3.54	-0.42	2.28E-01
1995		242680_at	1.6031E-02	5.85E-04	-3.54	-0.42	-4.30E-01
1996	GANAB	214626_s_at	1.6092E-02	5.88E-04	-3.54	-0.42	-3.27E-01
1997	PDE4DIP	212392_s_at	1.6092E-02	5.88E-04	-3.54	-0.42	-1.79E-01
1998		237566_at	1.6092E-02	5.88E-04	3.54	-0.42	1.01E-01
1999	CD96	1555120_at	1.6095E-02	5.88E-04	3.54	-0.42	6.43E-01
2000	CD40	35150_at	1.6125E-02	5.90E-04	-3.53	-0.43	-4.58E-01
2001		1558764_at	1.6125E-02	5.90E-04	3.53	-0.43	1.00E-01
2002	CENPM	218741_at	1.6125E-02	5.90E-04	3.53	-0.43	4.15E-01
2003	CD74	1567628_at	1.6133E-02	5.91E-04	-3.53	-0.43	-1.08E+00
2004		1556982_at	1.6138E-02	5.92E-04	3.53	-0.43	2.09E-01
2005	LOC100129720	235475_at	1.6152E-02	5.92E-04	3.53	-0.43	4.88E-01
2006	PDIA3	227033_at	1.6156E-02	5.93E-04	-3.53	-0.43	-4.08E-01
2007	EIF3A	200596_s_at	1.6260E-02	5.97E-04	-3.53	-0.44	-3.41E-01
2008	PIK3C2A	241905_at	1.6264E-02	5.97E-04	3.53	-0.44	3.18E-01
2009	FST	204948_s_at	1.6270E-02	5.98E-04	-3.53	-0.44	-5.39E-01
2010	EFCAB6	234853_s_at	1.6270E-02	5.98E-04	3.53	-0.44	1.04E-01
2011	ADAM10	202604_x_at	1.6303E-02	6.00E-04	-3.53	-0.44	-3.39E-01
2012	LOC339505	1557373_at	1.6314E-02	6.01E-04	3.53	-0.44	1.44E-01
2013	CLASP2	1555469_a_at	1.6314E-02	6.01E-04	3.53	-0.44	1.64E-01
2014		208421_at	1.6314E-02	6.01E-04	3.53	-0.44	1.42E-01
2015		237065_s_at	1.6314E-02	6.02E-04	3.53	-0.44	2.87E-01
2016	POR	208928_at	1.6314E-02	6.02E-04	-3.53	-0.44	-4.36E-01
2017	DPYD	204646_at	1.6314E-02	6.02E-04	-3.53	-0.45	-4.23E-01
2018	C15orf40	1552310_at	1.6314E-02	6.02E-04	3.53	-0.45	5.42E-01
2019	LRRC27	1558484_s_at	1.6437E-02	6.07E-04	-3.53	-0.45	-2.35E-01
2020	ZNF319	228460_at	1.6437E-02	6.08E-04	-3.53	-0.45	-2.33E-01
2021	THY1	208851_s_at	1.6437E-02	6.08E-04	-3.53	-0.45	-4.89E-01
2022	TTL	224896_s_at	1.6437E-02	6.08E-04	-3.53	-0.45	-3.34E-01
2023		226885_at	1.6439E-02	6.08E-04	-3.53	-0.45	-3.63E-01
2024	TAPT1	238798_at	1.6439E-02	6.09E-04	3.53	-0.45	1.69E-01
2025	FTHL5	211628_x_at	1.6448E-02	6.09E-04	-3.53	-0.46	-3.44E-01
2026	CXorf26	224177_s_at	1.6450E-02	6.10E-04	-3.52	-0.46	-4.53E-01
2027	HYDIN	1554907_a_at	1.6450E-02	6.10E-04	3.52	-0.46	1.65E-01
2028	RPL30	200062_s_at	1.6459E-02	6.10E-04	3.52	-0.46	1.48E-01
2029	NRBP1	217765_at	1.6502E-02	6.12E-04	-3.52	-0.46	-3.80E-01
2030		228611_s_at	1.6513E-02	6.13E-04	3.52	-0.46	3.18E-01
2031	PSMD3	201388_at	1.6513E-02	6.13E-04	-3.52	-0.46	-4.31E-01
2032		240790_at	1.6532E-02	6.14E-04	3.52	-0.46	1.71E-01
2033		239122_at	1.6550E-02	6.15E-04	3.52	-0.46	4.28E-01
2034	ERAP1	210385_s_at	1.6558E-02	6.16E-04	-3.52	-0.47	-4.03E-01
2035	GIGYF1	228755_at	1.6558E-02	6.16E-04	3.52	-0.47	2.83E-01
2036	NOL10	218591_s_at	1.6558E-02	6.17E-04	3.52	-0.47	1.31E-01
2037	ARID1B	1566989_at	1.6572E-02	6.17E-04	3.52	-0.47	3.38E-01
2038	HLA-G	211529_x_at	1.6572E-02	6.18E-04	-3.52	-0.47	-4.38E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2039	PPM1K	235061_at	1.6572E-02	6.18E-04	3.52	-0.47	4.52E-01
2040	MAP2K5	216765_at	1.6581E-02	6.19E-04	3.52	-0.47	1.86E-01
2041	MAPK13	210058_at	1.6589E-02	6.19E-04	-3.52	-0.47	-3.46E-01
2042		235102_x_at	1.6607E-02	6.20E-04	3.52	-0.47	1.21E+00
2043	TAGLN	1555724_s_at	1.6610E-02	6.21E-04	-3.52	-0.47	-8.08E-01
2044	AKIRIN2	223143_s_at	1.6610E-02	6.22E-04	-3.52	-0.47	-1.70E-01
2045	SPATA24	238027_at	1.6610E-02	6.22E-04	3.52	-0.47	2.17E-01
2046	TMEM223	220934_s_at	1.6610E-02	6.22E-04	3.52	-0.47	3.76E-01
2047	KLC1	212877_at	1.6610E-02	6.22E-04	-3.52	-0.47	-2.28E-01
2048	PALMD	218736_s_at	1.6610E-02	6.23E-04	-3.52	-0.48	-5.12E-01
2049		1570014_at	1.6610E-02	6.23E-04	3.52	-0.48	1.44E-01
2050	GNB2	200852_x_at	1.6610E-02	6.23E-04	-3.52	-0.48	-7.16E-01
2051	KIAA0101	202503_s_at	1.6610E-02	6.23E-04	3.52	-0.48	6.78E-01
2052	ARPC1B	201954_at	1.6619E-02	6.24E-04	-3.52	-0.48	-3.66E-01
2053	EBLN2	219906_at	1.6619E-02	6.24E-04	3.52	-0.48	3.05E-01
2054	SCARB1	1552256_a_at	1.6619E-02	6.24E-04	-3.52	-0.48	-5.42E-01
2055	TIMP1	201666_at	1.6619E-02	6.25E-04	-3.52	-0.48	-8.76E-01
2056	TMBIM6	200804_at	1.6619E-02	6.25E-04	-3.52	-0.48	-4.35E-01
2057	BCAP31	200837_at	1.6619E-02	6.25E-04	-3.52	-0.48	-4.30E-01
2058	SNX20	229045_at	1.6619E-02	6.26E-04	-3.52	-0.48	-2.58E-01
2059	GAA	202812_at	1.6619E-02	6.26E-04	-3.52	-0.48	-4.96E-01
2060	NINJ1	203045_at	1.6628E-02	6.26E-04	-3.52	-0.48	-6.35E-01
2061	TBC1D8	241017_at	1.6633E-02	6.27E-04	3.52	-0.48	6.56E-01
2062	PLXNB2	208890_s_at	1.6637E-02	6.28E-04	-3.52	-0.48	-5.64E-01
2063		238113_at	1.6637E-02	6.28E-04	3.52	-0.48	1.25E-01
2064		233867_at	1.6638E-02	6.28E-04	3.52	-0.48	5.98E-01
2065	CALU	200756_x_at	1.6643E-02	6.29E-04	-3.52	-0.48	-5.10E-01
2066	SCAMP2	218143_s_at	1.6645E-02	6.29E-04	-3.52	-0.48	-4.44E-01
2067	RBM33	231834_at	1.6645E-02	6.29E-04	3.52	-0.48	1.60E-01
2068	TMEM68	227936_at	1.6645E-02	6.30E-04	3.52	-0.49	6.57E-01
2069	IFITM2	201315_x_at	1.6645E-02	6.30E-04	-3.52	-0.49	-5.08E-01
2070	PRKAB1	201835_s_at	1.6661E-02	6.31E-04	-3.51	-0.49	-4.43E-01
2071	GLIPR2	225602_at	1.6661E-02	6.31E-04	-3.51	-0.49	-3.25E-01
2072	FBXW2	218941_at	1.6672E-02	6.32E-04	-3.51	-0.49	-3.49E-01
2073	ELL3	219517_at	1.6698E-02	6.33E-04	3.51	-0.49	7.54E-01
2074	ZNF708	239482_x_at	1.6698E-02	6.33E-04	3.51	-0.49	4.36E-01
2075		244371_at	1.6747E-02	6.36E-04	3.51	-0.49	1.92E-01
2076	COL7A1	217312_s_at	1.6792E-02	6.38E-04	-3.51	-0.50	-1.90E-01
2077	LYRM7	240344_x_at	1.6793E-02	6.38E-04	3.51	-0.50	3.41E-01
2078	REPS1	215201_at	1.6795E-02	6.38E-04	3.51	-0.50	2.21E-01
2079	RAB31	217764_s_at	1.6795E-02	6.39E-04	-3.51	-0.50	-5.26E-01
2080	POSTN	1555777_at	1.6795E-02	6.39E-04	-3.51	-0.50	-2.95E-01
2081	C10orf10	209183_s_at	1.6832E-02	6.41E-04	-3.51	-0.50	-5.87E-01
2082	ALDOA	200966_x_at	1.6841E-02	6.41E-04	-3.51	-0.50	-4.97E-01
2083	TMEM106C	201764_at	1.6843E-02	6.42E-04	3.51	-0.50	4.93E-01
2084	FCER1G	1554899_s_at	1.6843E-02	6.42E-04	-3.51	-0.50	-1.04E+00
2085	MIB1	224722_at	1.6845E-02	6.42E-04	3.51	-0.50	3.27E-01
2086	ZNF146	1554433_a_at	1.6859E-02	6.43E-04	-3.51	-0.50	-4.44E-01
2087		244187_at	1.6859E-02	6.44E-04	-3.51	-0.50	-1.97E-01
2088	SDK2	234073_at	1.6882E-02	6.45E-04	3.51	-0.51	1.62E-01
2089	ZFAND3	222493_s_at	1.6882E-02	6.45E-04	-3.51	-0.51	-3.22E-01
2090	AG2	227099_s_at	1.6882E-02	6.45E-04	-3.51	-0.51	-8.74E-01
2091	AK7	241326_at	1.6929E-02	6.48E-04	3.51	-0.51	2.04E-01
2092	LOC100129250	221979_at	1.6929E-02	6.48E-04	3.51	-0.51	4.37E-01
2093	APOA1	204450_x_at	1.6929E-02	6.48E-04	3.51	-0.51	1.49E-01
2094	TARBP1	202813_at	1.6940E-02	6.49E-04	3.51	-0.51	3.20E-01
2095	SHMT1	209980_s_at	1.6955E-02	6.50E-04	-3.51	-0.51	-2.88E-01
2096	MYO1E	203072_at	1.6955E-02	6.50E-04	-3.51	-0.51	-3.42E-01
2097	ECM1	209365_s_at	1.6955E-02	6.50E-04	-3.51	-0.51	-6.51E-01
2098	HIST3H2A	221582_at	1.6969E-02	6.51E-04	3.51	-0.52	6.33E-01
2099	VPS24	222436_s_at	1.6969E-02	6.51E-04	-3.51	-0.52	-4.33E-01
2100	SPARCL1	200795_at	1.6999E-02	6.53E-04	-3.50	-0.52	-4.79E-01
2101	BAX	208478_s_at	1.6999E-02	6.53E-04	-3.50	-0.52	-4.62E-01
2102	FGFR1OP2	223262_s_at	1.7010E-02	6.54E-04	3.50	-0.52	2.75E-01
2103	UBE2NL	217393_x_at	1.7012E-02	6.54E-04	3.50	-0.52	1.57E-01
2104		1558275_at	1.7049E-02	6.56E-04	3.50	-0.52	2.45E-01
2105	OR2F2///OR2F1	208525_s_at	1.7049E-02	6.57E-04	3.50	-0.52	1.26E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2106		216431_at	1.7049E-02	6.57E-04	3.50	-0.52	1.67E-01
2107	PSMC2	201068_s_at	1.7049E-02	6.57E-04	-3.50	-0.52	-2.71E-01
2108	RPS26P57// /ODZ1	234885_at	1.7068E-02	6.58E-04	3.50	-0.52	2.03E-01
2109	NLGN3	234751_s_at	1.7103E-02	6.60E-04	3.50	-0.53	1.69E-01
2110	MGC21881	1555874_x_at	1.7103E-02	6.60E-04	3.50	-0.53	3.10E-01
2111		221725_at	1.7136E-02	6.62E-04	-3.50	-0.53	-4.89E-01
2112	SASH1	226022_at	1.7136E-02	6.62E-04	-3.50	-0.53	-6.82E-01
2113	CAST	207467_x_at	1.7139E-02	6.63E-04	-3.50	-0.53	-3.75E-01
2114	PSAP	200866_s_at	1.7139E-02	6.63E-04	-3.50	-0.53	-7.82E-01
2115	EFTUD1	218973_at	1.7141E-02	6.63E-04	-3.50	-0.53	-3.27E-01
2116	LILRB1	229937_x_at	1.7141E-02	6.63E-04	-3.50	-0.53	-5.80E-01
2117	TRIM59	235476_at	1.7147E-02	6.64E-04	3.50	-0.53	3.77E-01
2118	CR1	208488_s_at	1.7147E-02	6.65E-04	-3.50	-0.53	-2.89E-01
2119	DNTTIP1	234942_s_at	1.7147E-02	6.65E-04	-3.50	-0.53	-5.99E-01
2120	S100A10	200872_at	1.7147E-02	6.65E-04	-3.50	-0.53	-4.66E-01
2121	FKBP10	219249_s_at	1.7147E-02	6.65E-04	-3.50	-0.53	-2.99E-01
2122		241003_at	1.7153E-02	6.66E-04	3.50	-0.53	1.86E-01
2123	RAPGEF6	230078_at	1.7158E-02	6.66E-04	3.50	-0.54	4.30E-01
2124	RPL15	221475_s_at	1.7162E-02	6.67E-04	3.50	-0.54	2.86E-01
2125	HTATSF1	202602_s_at	1.7195E-02	6.68E-04	-3.50	-0.54	-4.30E-01
2126	UBR5	1555888_at	1.7213E-02	6.69E-04	3.50	-0.54	4.38E-01
2127	MYO7A	208189_s_at	1.7213E-02	6.70E-04	-3.50	-0.54	-5.08E-01
2128		241568_at	1.7225E-02	6.71E-04	3.50	-0.54	1.79E-01
2129	MEMO1	219065_s_at	1.7225E-02	6.71E-04	3.50	-0.54	2.92E-01
2130	EXOSC8	215136_s_at	1.7231E-02	6.71E-04	3.50	-0.54	4.06E-01
2131	FXR1	201635_s_at	1.7240E-02	6.72E-04	-3.50	-0.54	-5.05E-01
2132	KRCC1	222585_x_at	1.7240E-02	6.72E-04	3.50	-0.54	4.91E-01
2133	HSPA8	221891_x_at	1.7244E-02	6.73E-04	-3.50	-0.54	-2.65E-01
2134	HLA-C	214459_x_at	1.7272E-02	6.74E-04	-3.50	-0.55	-3.82E-01
2135	PEX13	1558164_s_at	1.7272E-02	6.74E-04	3.50	-0.55	2.57E-01
2136	LCP1	208885_at	1.7272E-02	6.75E-04	-3.50	-0.55	-6.66E-01
2137	RNF24	210706_s_at	1.7277E-02	6.75E-04	-3.49	-0.55	-3.45E-01
2138	SEPN1	224659_at	1.7277E-02	6.76E-04	-3.49	-0.55	-5.61E-01
2139	SGMS2	227038_at	1.7313E-02	6.77E-04	-3.49	-0.55	-5.04E-01
2140	GK	207387_s_at	1.7316E-02	6.78E-04	-3.49	-0.55	-7.03E-01
2141	PDPN	204879_at	1.7323E-02	6.78E-04	-3.49	-0.55	-6.07E-01
2142	LOC100287 037	1554194_at	1.7347E-02	6.80E-04	3.49	-0.55	1.74E-01
2143	CMAS	218111_s_at	1.7347E-02	6.80E-04	-3.49	-0.55	-2.63E-01
2144	DPAGT1	209509_s_at	1.7348E-02	6.80E-04	-3.49	-0.55	-3.40E-01
2145		237345_at	1.7356E-02	6.81E-04	3.49	-0.56	2.42E-01
2146	HYOU1	200825_s_at	1.7356E-02	6.81E-04	-3.49	-0.56	-5.25E-01
2147	C1orf46	216718_at	1.7365E-02	6.82E-04	3.49	-0.56	1.39E-01
2148	PSMD1	201199_s_at	1.7373E-02	6.83E-04	-3.49	-0.56	-3.01E-01
2149	TGFB1	203085_s_at	1.7385E-02	6.83E-04	-3.49	-0.56	-8.77E-01
2150		236531_at	1.7385E-02	6.84E-04	3.49	-0.56	1.85E-01
2151	Sep-08	208999_at	1.7387E-02	6.84E-04	-3.49	-0.56	-5.29E-01
2152	PSEN1	203460_s_at	1.7389E-02	6.85E-04	-3.49	-0.56	-2.91E-01
2153	SFRS12IP1	1553581_s_at	1.7389E-02	6.85E-04	3.49	-0.56	4.12E-01
2154	C5orf42	219381_at	1.7445E-02	6.87E-04	3.49	-0.56	1.58E-01
2155	CMIP	224991_at	1.7511E-02	6.90E-04	-3.49	-0.57	-5.18E-01
2156	ROCK1	230239_at	1.7511E-02	6.91E-04	3.49	-0.57	2.20E-01
2157	GINS2	221521_s_at	1.7513E-02	6.91E-04	3.49	-0.57	6.39E-01
2158		239497_at	1.7571E-02	6.94E-04	3.49	-0.57	1.86E-01
2159	BRWD1	1553227_s_at	1.7571E-02	6.94E-04	3.49	-0.57	2.12E-01
2160	C14orf148	231566_at	1.7590E-02	6.95E-04	3.49	-0.57	1.45E-01
2161	ZNF33B	215022_x_at	1.7590E-02	6.96E-04	3.49	-0.57	3.40E-01
2162		227796_at	1.7590E-02	6.96E-04	3.49	-0.57	3.36E-01
2163	TAF8	229412_at	1.7590E-02	6.96E-04	3.49	-0.57	2.74E-01
2164		240656_at	1.7590E-02	6.96E-04	3.49	-0.57	1.82E-01
2165	HSPA4	211015_s_at	1.7601E-02	6.97E-04	-3.49	-0.58	-6.46E-01
2166		1563577_at	1.7637E-02	6.99E-04	3.48	-0.58	2.44E-01
2167	ACTL9	243208_x_at	1.7647E-02	7.00E-04	3.48	-0.58	1.45E-01
2168	EIF4H	206621_s_at	1.7647E-02	7.00E-04	-3.48	-0.58	-6.33E-01
2169	JAK1	1562103_at	1.7647E-02	7.00E-04	3.48	-0.58	1.64E-01
2170	SERPINE1	202627_s_at	1.7647E-02	7.01E-04	-3.48	-0.58	-7.03E-01
2171	ACLY	210337_s_at	1.7647E-02	7.01E-04	-3.48	-0.58	-4.65E-01
2172		1558885_at	1.7647E-02	7.02E-04	3.48	-0.58	1.12E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2173	UCKL1	232727_at	1.7647E-02	7.02E-04	3.48	-0.58	2.11E-01
2174	ATP6V0C	200954_at	1.7647E-02	7.02E-04	-3.48	-0.58	-6.12E-01
2175	ITPR2	202662_s_at	1.7647E-02	7.02E-04	-3.48	-0.58	-4.24E-01
2176		242696_at	1.7647E-02	7.03E-04	3.48	-0.58	2.85E-01
2177	RHOJ	235489_at	1.7647E-02	7.03E-04	-3.48	-0.58	-4.68E-01
2178		1556728_at	1.7677E-02	7.04E-04	3.48	-0.58	2.55E-01
2179		1566110_at	1.7679E-02	7.05E-04	3.48	-0.59	2.17E-01
2180	SPATA1	221057_at	1.7687E-02	7.05E-04	3.48	-0.59	1.20E-01
2181	LGMN	201212_at	1.7711E-02	7.07E-04	-3.48	-0.59	-6.34E-01
2182	PECAM1	208983_s_at	1.7732E-02	7.08E-04	-3.48	-0.59	-7.00E-01
2183	NAA25	227245_at	1.7734E-02	7.08E-04	-3.48	-0.59	-2.75E-01
2184	ITPRIPL2	1568619_s_at	1.7738E-02	7.09E-04	-3.48	-0.59	-6.89E-01
2185	AP1S3	1555734_x_at	1.7738E-02	7.09E-04	3.48	-0.59	1.59E-01
2186	CSTA	204971_at	1.7767E-02	7.10E-04	3.48	-0.59	7.24E-01
2187	C21orf129	1553918_at	1.7770E-02	7.11E-04	3.48	-0.59	1.58E-01
2188	C6orf162	213312_at	1.7770E-02	7.11E-04	3.48	-0.59	5.32E-01
2189	LOC348761	240590_at	1.7770E-02	7.11E-04	3.48	-0.59	1.59E-01
2190	WDR45	209216_at	1.7783E-02	7.12E-04	-3.48	-0.59	-3.25E-01
2191	MTDH	212251_at	1.7823E-02	7.14E-04	-3.48	-0.60	-3.34E-01
2192	PRKG2	207505_at	1.7848E-02	7.16E-04	3.48	-0.60	1.72E-01
2193	NFIC	213298_at	1.7849E-02	7.16E-04	-3.48	-0.60	-4.44E-01
2194	SLC16A1	202234_s_at	1.7849E-02	7.17E-04	-3.48	-0.60	-2.94E-01
2195	AKAP10	236007_at	1.7849E-02	7.17E-04	3.48	-0.60	5.63E-01
2196	SFRS18	226412_at	1.7855E-02	7.17E-04	3.48	-0.60	5.16E-01
2197	MS4A6A	219666_at	1.7876E-02	7.18E-04	-3.48	-0.60	-5.93E-01
2198	AK3L2///AK4	204348_s_at	1.7882E-02	7.19E-04	-3.48	-0.60	-5.66E-01
2199	LOC100131801	226006_at	1.7882E-02	7.19E-04	3.48	-0.60	4.57E-01
2200		1565788_at	1.7882E-02	7.20E-04	3.48	-0.60	1.03E-01
2201	C14orf2	202279_at	1.7882E-02	7.20E-04	3.48	-0.60	4.96E-01
2202	MIF4GD	231727_s_at	1.7882E-02	7.20E-04	-3.48	-0.60	-5.12E-01
2203	TIGD1	1553099_at	1.7947E-02	7.23E-04	3.47	-0.61	4.57E-01
2204	PGLS	230699_at	1.7963E-02	7.24E-04	3.47	-0.61	1.99E-01
2205	MPZL3	227747_at	1.7963E-02	7.25E-04	3.47	-0.61	2.99E-01
2206		227727_at	1.7963E-02	7.25E-04	-3.47	-0.61	-4.63E-01
2207	PELI3	244214_at	1.7991E-02	7.26E-04	3.47	-0.61	1.64E-01
2208	FLJ36031	229521_at	1.8008E-02	7.27E-04	-3.47	-0.61	-4.03E-01
2209	HMGCL	202772_at	1.8013E-02	7.28E-04	-3.47	-0.61	-2.24E-01
2210	GLUD2	215794_x_at	1.8020E-02	7.28E-04	-3.47	-0.61	-4.64E-01
2211	IFNAR1	225669_at	1.8024E-02	7.29E-04	-3.47	-0.62	-4.03E-01
2212	SFRP2	223121_s_at	1.8024E-02	7.29E-04	-3.47	-0.62	-1.76E+00
2213	EHD1	209038_s_at	1.8024E-02	7.30E-04	-3.47	-0.62	-4.08E-01
2214	FBXO42	221812_at	1.8024E-02	7.30E-04	3.47	-0.62	1.95E-01
2215	C2orf81	228265_at	1.8024E-02	7.30E-04	3.47	-0.62	1.12E-01
2216	FAH	202862_at	1.8031E-02	7.31E-04	-3.47	-0.62	-3.51E-01
2217	CNRIP1	226751_at	1.8032E-02	7.31E-04	-3.47	-0.62	-5.98E-01
2218	GNA11	213944_x_at	1.8032E-02	7.32E-04	-3.47	-0.62	-2.05E-01
2219	RIC8A	221647_s_at	1.8043E-02	7.32E-04	-3.47	-0.62	-3.06E-01
2220	EEF2K	225545_at	1.8063E-02	7.33E-04	-3.47	-0.62	-3.53E-01
2221	POSTN	1555778_a_at	1.8068E-02	7.34E-04	-3.47	-0.62	-1.67E+00
2222	LOC440288	239792_at	1.8068E-02	7.34E-04	3.47	-0.62	3.63E-01
2223		1556332_at	1.8082E-02	7.35E-04	-3.47	-0.62	-2.87E-01
2224		220902_at	1.8114E-02	7.37E-04	3.47	-0.63	1.32E-01
2225	SNRPD1	202691_at	1.8174E-02	7.40E-04	3.47	-0.63	4.06E-01
2226	CYP1B1	202437_s_at	1.8186E-02	7.41E-04	-3.47	-0.63	-8.24E-01
2227	NSFL1C	220248_x_at	1.8186E-02	7.41E-04	-3.47	-0.63	-3.87E-01
2228	NSFL1C	232520_s_at	1.8186E-02	7.42E-04	-3.47	-0.63	-3.48E-01
2229	RAB6C///RAB6A	210406_s_at	1.8186E-02	7.42E-04	-3.47	-0.63	-3.11E-01
2230	CEPT1	1561884_at	1.8186E-02	7.42E-04	3.47	-0.63	2.79E-01
2231		1562933_at	1.8186E-02	7.42E-04	3.47	-0.63	1.44E-01
2232		244068_at	1.8199E-02	7.43E-04	3.47	-0.63	1.86E-01
2233	FAM168B	229946_at	1.8199E-02	7.43E-04	-3.47	-0.63	-1.73E-01
2234	SLC1A6	1554593_s_at	1.8236E-02	7.45E-04	3.47	-0.63	1.07E-01
2235	TRIO	209011_at	1.8247E-02	7.46E-04	-3.47	-0.64	-2.72E-01
2236	RASGRP1	205590_at	1.8247E-02	7.46E-04	3.47	-0.64	4.11E-01
2237	HERC4	233509_at	1.8252E-02	7.47E-04	3.46	-0.64	1.54E-01
2238	TAPBP	1555565_s_at	1.8252E-02	7.47E-04	-3.46	-0.64	-3.09E-01
2239	PFDN5	210908_s_at	1.8252E-02	7.47E-04	3.46	-0.64	4.42E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2240	PANX1	204715_at	1.8267E-02	7.49E-04	-3.46	-0.64	-3.61E-01
2241		215993_at	1.8267E-02	7.49E-04	3.46	-0.64	1.05E-01
2242	CDC5L	222179_at	1.8267E-02	7.49E-04	3.46	-0.64	1.15E-01
2243		239086_at	1.8267E-02	7.50E-04	3.46	-0.64	3.64E-01
2244	RPS4XP17///RPS4XP7///RPS4XP13///RPS4X	216342_x_at	1.8267E-02	7.50E-04	3.46	-0.64	2.58E-01
2245	SLC5A9	232378_at	1.8270E-02	7.50E-04	3.46	-0.64	1.54E-01
2246	C10orf78	238794_at	1.8271E-02	7.51E-04	3.46	-0.64	6.04E-01
2247	SYNGR1	204287_at	1.8277E-02	7.52E-04	3.46	-0.64	1.92E-01
2248		1562557_at	1.8277E-02	7.52E-04	3.46	-0.64	2.35E-01
2249	ING3	231863_at	1.8277E-02	7.52E-04	3.46	-0.64	5.27E-01
2250	VIPR1	205019_s_at	1.8277E-02	7.53E-04	3.46	-0.64	3.09E-01
2251	NR2F6	209262_s_at	1.8277E-02	7.53E-04	-3.46	-0.64	-3.67E-01
2252	C8orf59	226165_at	1.8277E-02	7.53E-04	3.46	-0.64	5.51E-01
2253	KLF9	203543_s_at	1.8277E-02	7.53E-04	-3.46	-0.64	-4.79E-01
2254	MT2A	212185_x_at	1.8282E-02	7.54E-04	-3.46	-0.65	-7.87E-01
2255	PIK3AP1	1554508_at	1.8282E-02	7.54E-04	-3.46	-0.65	-5.69E-01
2256	EIF2B4	215482_s_at	1.8283E-02	7.54E-04	-3.46	-0.65	-2.23E-01
2257	CD59	228748_at	1.8301E-02	7.56E-04	-3.46	-0.65	-2.09E-01
2258	TMCO3	220240_s_at	1.8301E-02	7.56E-04	-3.46	-0.65	-3.44E-01
2259	NUS1	225070_at	1.8303E-02	7.56E-04	-3.46	-0.65	-5.02E-01
2260	ZNF436	226114_at	1.8321E-02	7.57E-04	-3.46	-0.65	-2.32E-01
2261	DKFZP547L112	234912_at	1.8321E-02	7.58E-04	3.46	-0.65	1.75E-01
2262	C10orf72	235471_at	1.8328E-02	7.58E-04	-3.46	-0.65	-1.87E-01
2263	TMCO3	230317_x_at	1.8361E-02	7.60E-04	3.46	-0.65	1.48E-01
2264	SLC38A7	218727_at	1.8379E-02	7.61E-04	-3.46	-0.65	-4.17E-01
2265		1559316_at	1.8379E-02	7.61E-04	3.46	-0.65	1.51E-01
2266	PARVB	204629_at	1.8379E-02	7.62E-04	-3.46	-0.65	-4.97E-01
2267	CAPZB	37012_at	1.8379E-02	7.62E-04	-3.46	-0.65	-4.32E-01
2268	LMF1	1569048_s_at	1.8394E-02	7.64E-04	3.46	-0.66	1.87E-01
2269	MICAL3	229474_at	1.8394E-02	7.64E-04	3.46	-0.66	2.06E-01
2270	HSD17B12	1554122_a_at	1.8394E-02	7.64E-04	3.46	-0.66	2.95E-01
2271	SURF4	222977_at	1.8394E-02	7.64E-04	-3.46	-0.66	-4.66E-01
2272		1565701_at	1.8394E-02	7.64E-04	3.46	-0.66	2.09E-01
2273	KBTBD2	223585_x_at	1.8394E-02	7.65E-04	-3.46	-0.66	-4.13E-01
2274	EPHA7	238533_at	1.8426E-02	7.66E-04	3.46	-0.66	1.22E-01
2275	HLA-G	210514_x_at	1.8429E-02	7.67E-04	-3.46	-0.66	-5.20E-01
2276	ADAM3A	216276_s_at	1.8436E-02	7.67E-04	3.46	-0.66	1.30E-01
2277	PWRN1	1562873_at	1.8440E-02	7.68E-04	3.46	-0.66	1.60E-01
2278	AK3L2///AK4	225342_at	1.8440E-02	7.68E-04	-3.46	-0.66	-6.92E-01
2279	TMEM189-UBE2V1///UBE2V1	201001_s_at	1.8443E-02	7.69E-04	3.46	-0.66	2.66E-01
2280	DEK	200934_at	1.8460E-02	7.70E-04	-3.46	-0.66	-2.68E-01
2281		237800_at	1.8461E-02	7.70E-04	3.46	-0.66	1.32E-01
2282	PLEKHB2	201410_at	1.8462E-02	7.71E-04	-3.46	-0.66	-3.32E-01
2283	CCDC48	233259_at	1.8468E-02	7.71E-04	3.46	-0.67	1.22E-01
2284	CSDE1	202646_s_at	1.8468E-02	7.72E-04	-3.45	-0.67	-2.81E-01
2285	SRSF11	213742_at	1.8468E-02	7.73E-04	3.45	-0.67	4.29E-01
2286	ACTR1A	200721_s_at	1.8468E-02	7.73E-04	-3.45	-0.67	-4.56E-01
2287		230415_at	1.8468E-02	7.73E-04	3.45	-0.67	3.67E-01
2288	COL15A1	203477_at	1.8468E-02	7.73E-04	-3.45	-0.67	-1.10E+00
2289	EMP3	203729_at	1.8468E-02	7.73E-04	-3.45	-0.67	-5.35E-01
2290	BPY2	208331_at	1.8468E-02	7.74E-04	3.45	-0.67	1.27E-01
2291	MAGED1	209014_at	1.8468E-02	7.74E-04	-3.45	-0.67	-5.63E-01
2292	MALT1	210017_at	1.8468E-02	7.74E-04	3.45	-0.67	4.14E-01
2293		233376_at	1.8482E-02	7.75E-04	3.45	-0.67	1.56E-01
2294	NKX6-2	235832_at	1.8482E-02	7.75E-04	3.45	-0.67	1.68E-01
2295	TUBB3	213476_x_at	1.8508E-02	7.77E-04	-3.45	-0.67	-4.97E-01
2296	ASCC3	212815_at	1.8513E-02	7.78E-04	-3.45	-0.67	-3.20E-01
2297	TBC1D10B	220947_s_at	1.8513E-02	7.78E-04	-3.45	-0.67	-3.09E-01
2298	NKX2-2	206915_at	1.8528E-02	7.79E-04	3.45	-0.67	1.20E-01
2299	MICA///HLA-B	209140_x_at	1.8540E-02	7.80E-04	-3.45	-0.68	-3.92E-01
2300	XPNPEP1	208453_s_at	1.8551E-02	7.81E-04	-3.45	-0.68	-5.62E-01
2301	FLVCR2	222866_s_at	1.8551E-02	7.81E-04	-3.45	-0.68	-5.12E-01
2302		243491_at	1.8551E-02	7.81E-04	3.45	-0.68	1.93E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2303	VWCE	242957_at	1.8595E-02	7.83E-04	3.45	-0.68	2.56E-01
2304	ZNF74	205881_at	1.8600E-02	7.84E-04	-3.45	-0.68	-1.72E-01
2305	C4orf39	1553711_a_at	1.8600E-02	7.84E-04	3.45	-0.68	1.40E-01
2306	CCT8L2	220508_at	1.8610E-02	7.85E-04	3.45	-0.68	1.85E-01
2307	CISH	223377_x_at	1.8610E-02	7.85E-04	-3.45	-0.68	-5.21E-01
2308	BCL2L10	221320_at	1.8610E-02	7.86E-04	3.45	-0.68	1.87E-01
2309	GADD45B	209304_x_at	1.8610E-02	7.86E-04	-3.45	-0.68	-3.96E-01
2310	MAPK13	210059_s_at	1.8614E-02	7.87E-04	-3.45	-0.68	-2.45E-01
2311		1563706_at	1.8614E-02	7.87E-04	3.45	-0.68	1.55E-01
2312		238531_x_at	1.8614E-02	7.88E-04	-3.45	-0.68	-4.93E-01
2313	SRPX2	205499_at	1.8614E-02	7.88E-04	-3.45	-0.69	-5.64E-01
2314	CASD1	231244_at	1.8614E-02	7.88E-04	3.45	-0.69	1.59E-01
2315	MPND	233651_s_at	1.8614E-02	7.88E-04	-3.45	-0.69	-5.46E-01
2316	TUBGCP4	211337_s_at	1.8614E-02	7.88E-04	-3.45	-0.69	-3.02E-01
2317	PRKAG2	222582_at	1.8659E-02	7.91E-04	3.45	-0.69	4.18E-01
2318	CYP1B1	202436_s_at	1.8669E-02	7.91E-04	-3.45	-0.69	-7.60E-01
2319		239081_at	1.8670E-02	7.92E-04	3.45	-0.69	4.55E-01
2320	NCAPH2	209718_at	1.8670E-02	7.92E-04	3.45	-0.69	2.37E-01
2321	SLC41A2	235299_at	1.8670E-02	7.93E-04	-3.45	-0.69	-5.49E-01
2322	YIF1A	202418_at	1.8670E-02	7.93E-04	-3.45	-0.69	-4.44E-01
2323	SNX9	223027_at	1.8670E-02	7.94E-04	-3.45	-0.69	-4.90E-01
2324	GUSBP3///SMA5///SMA4	215043_s_at	1.8670E-02	7.94E-04	-3.45	-0.69	-4.93E-01
2325	GLUL	217202_s_at	1.8670E-02	7.94E-04	-3.45	-0.69	-8.18E-01
2326	C21orf67	1552528_at	1.8695E-02	7.95E-04	3.45	-0.69	1.45E-01
2327	ITGB3BP	205176_s_at	1.8709E-02	7.97E-04	3.45	-0.69	7.26E-01
2328	UBE2D4	65521_at	1.8709E-02	7.97E-04	3.45	-0.69	2.14E-01
2329	RPL9	200032_s_at	1.8709E-02	7.97E-04	3.45	-0.69	2.24E-01
2330	ZNF430	206829_x_at	1.8720E-02	7.98E-04	3.45	-0.70	3.78E-01
2331	HK3	205936_s_at	1.8783E-02	8.01E-04	-3.44	-0.70	-6.39E-01
2332	RPS10	200095_x_at	1.8810E-02	8.02E-04	3.44	-0.70	1.70E-01
2333		1557118_a_at	1.8831E-02	8.04E-04	3.44	-0.70	2.85E-01
2334	DPH5	222360_at	1.8866E-02	8.05E-04	3.44	-0.70	3.42E-01
2335	RAB2A	208734_x_at	1.8866E-02	8.06E-04	-3.44	-0.70	-3.61E-01
2336	RAB7B	1553982_a_at	1.8870E-02	8.06E-04	-3.44	-0.71	-2.18E-01
2337	AKAP8L	240554_at	1.8889E-02	8.08E-04	3.44	-0.71	2.50E-01
2338	MAZ	229807_s_at	1.8889E-02	8.08E-04	3.44	-0.71	2.46E-01
2339	CD74	209619_at	1.8909E-02	8.09E-04	-3.44	-0.71	-5.86E-01
2340	TMEM131	212507_at	1.8945E-02	8.11E-04	-3.44	-0.71	-4.93E-01
2341	SS18L2	218283_at	1.8945E-02	8.11E-04	3.44	-0.71	5.36E-01
2342	CCDC23	226723_at	1.8994E-02	8.14E-04	3.44	-0.71	5.83E-01
2343		215667_x_at	1.9035E-02	8.16E-04	3.44	-0.72	2.97E-01
2344	IQGAP1	210840_s_at	1.9037E-02	8.16E-04	-3.44	-0.72	-3.01E-01
2345		1562826_at	1.9042E-02	8.17E-04	3.44	-0.72	1.76E-01
2346	CUL4A	201423_s_at	1.9071E-02	8.18E-04	-3.44	-0.72	-2.70E-01
2347	NFE2L2	1567013_at	1.9098E-02	8.20E-04	-3.44	-0.72	-3.06E-01
2348	IVD	216958_s_at	1.9126E-02	8.21E-04	-3.44	-0.72	-3.31E-01
2349	LMLN	244881_at	1.9129E-02	8.22E-04	-3.44	-0.72	-3.69E-01
2350	BAG3	217911_s_at	1.9141E-02	8.23E-04	-3.44	-0.72	-4.74E-01
2351		240892_at	1.9141E-02	8.23E-04	3.44	-0.72	1.99E-01
2352	FAM110B	221959_at	1.9166E-02	8.25E-04	-3.44	-0.73	-2.01E-01
2353	PELI1	218319_at	1.9166E-02	8.25E-04	3.44	-0.73	2.90E-01
2354	ZNF77	229000_at	1.9220E-02	8.28E-04	3.43	-0.73	3.45E-01
2355	ARF3	200734_s_at	1.9220E-02	8.28E-04	-3.43	-0.73	-5.44E-01
2356		1568802_at	1.9220E-02	8.29E-04	3.43	-0.73	1.22E-01
2357	ACP2	202767_at	1.9220E-02	8.29E-04	-3.43	-0.73	-5.20E-01
2358	OLFML3	218162_at	1.9220E-02	8.29E-04	-3.43	-0.73	-1.02E+00
2359	TOMM20	212773_s_at	1.9227E-02	8.30E-04	3.43	-0.73	5.79E-01
2360	KRTAP1-3	234880_x_at	1.9268E-02	8.32E-04	3.43	-0.73	3.04E-01
2361	DAK	218688_at	1.9303E-02	8.34E-04	-3.43	-0.73	-2.75E-01
2362	DLGAP4	202572_s_at	1.9308E-02	8.34E-04	-3.43	-0.74	-2.67E-01
2363	TIPRL	1553677_a_at	1.9308E-02	8.34E-04	3.43	-0.74	3.41E-01
2364	G0S2	213524_s_at	1.9337E-02	8.36E-04	-3.43	-0.74	-6.12E-01
2365	LILRB3	211135_x_at	1.9351E-02	8.37E-04	-3.43	-0.74	-4.90E-01
2366	AQP1	209047_at	1.9354E-02	8.38E-04	-3.43	-0.74	-8.73E-01
2367	ZNF673	206583_at	1.9361E-02	8.38E-04	3.43	-0.74	3.14E-01
2368	TIPRL	214773_x_at	1.9361E-02	8.39E-04	3.43	-0.74	3.30E-01
2369	GPR174	224285_at	1.9361E-02	8.39E-04	3.43	-0.74	2.91E-01
2370		236143_at	1.9382E-02	8.40E-04	3.43	-0.74	1.87E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2371		237201_at	1.9382E-02	8.41E-04	3.43	-0.74	4.08E-01
2372		235423_at	1.9393E-02	8.41E-04	3.43	-0.74	3.20E-01
2373	WT1	206067_s_at	1.9402E-02	8.42E-04	-3.43	-0.74	-5.29E-01
2374	WDR13	222138_s_at	1.9406E-02	8.43E-04	-3.43	-0.74	-3.44E-01
2375	CMTM6	217947_at	1.9413E-02	8.43E-04	-3.43	-0.74	-3.10E-01
2376	ELMO2	221528_s_at	1.9435E-02	8.45E-04	-3.43	-0.75	-4.48E-01
2377		235821_at	1.9448E-02	8.46E-04	-3.43	-0.75	-5.68E-01
2378	ALDOA	214687_x_at	1.9448E-02	8.46E-04	-3.43	-0.75	-4.70E-01
2379	COL4A2	211964_at	1.9448E-02	8.47E-04	-3.43	-0.75	-9.34E-01
2380	TKT	208699_x_at	1.9448E-02	8.47E-04	-3.43	-0.75	-7.00E-01
2381	SLC35E1	229410_at	1.9470E-02	8.48E-04	-3.43	-0.75	-2.85E-01
2382	HDGF	216484_x_at	1.9479E-02	8.49E-04	-3.43	-0.75	-2.85E-01
2383		242731_x_at	1.9480E-02	8.49E-04	3.43	-0.75	1.42E-01
2384		240969_at	1.9495E-02	8.50E-04	3.43	-0.75	1.39E-01
2385		234239_at	1.9495E-02	8.51E-04	3.43	-0.75	1.51E-01
2386	GRN	216041_x_at	1.9495E-02	8.51E-04	-3.43	-0.75	-7.33E-01
2387	ALKBH5	228034_x_at	1.9495E-02	8.51E-04	3.43	-0.75	1.79E-01
2388	HEG1	212822_at	1.9567E-02	8.55E-04	-3.42	-0.76	-4.36E-01
2389	BACE2	217867_x_at	1.9567E-02	8.55E-04	-3.42	-0.76	-5.72E-01
2390	GTF3A	201338_x_at	1.9587E-02	8.56E-04	3.42	-0.76	3.31E-01
2391	SIGLEC7	207224_s_at	1.9618E-02	8.58E-04	-3.42	-0.76	-5.12E-01
2392	GPR172A	222155_s_at	1.9671E-02	8.61E-04	-3.42	-0.76	-4.76E-01
2393	SRPR	200918_s_at	1.9671E-02	8.61E-04	-3.42	-0.76	-5.61E-01
2394	ATP13A3	212297_at	1.9671E-02	8.61E-04	-3.42	-0.76	-2.79E-01
2395	MARCKS	213002_at	1.9690E-02	8.62E-04	-3.42	-0.76	-3.96E-01
2396	LYZL4	231306_at	1.9701E-02	8.63E-04	3.42	-0.77	1.82E-01
2397	HLA-DPB2	239975_at	1.9701E-02	8.64E-04	3.42	-0.77	3.75E-01
2398		238129_s_at	1.9708E-02	8.64E-04	-3.42	-0.77	-3.07E-01
2399	TM9SF1	209149_s_at	1.9712E-02	8.65E-04	-3.42	-0.77	-4.20E-01
2400	COL1A2	202403_s_at	1.9749E-02	8.67E-04	-3.42	-0.77	-1.06E+00
2401	C21orf49	1557782_s_at	1.9758E-02	8.68E-04	3.42	-0.77	1.41E-01
2402	TMC5	240304_s_at	1.9758E-02	8.68E-04	3.42	-0.77	1.43E-01
2403	LOC645513	1561759_at	1.9787E-02	8.70E-04	3.42	-0.77	1.49E-01
2404	WARS2	218766_s_at	1.9798E-02	8.71E-04	3.42	-0.77	4.14E-01
2405	PGBD4	243815_at	1.9798E-02	8.71E-04	3.42	-0.77	3.64E-01
2406		233680_at	1.9821E-02	8.72E-04	3.42	-0.77	1.35E-01
2407	CLTA	204050_s_at	1.9850E-02	8.74E-04	-3.42	-0.78	-2.86E-01
2408	UBE2J1	217823_s_at	1.9864E-02	8.75E-04	-3.42	-0.78	-3.59E-01
2409	ASPH	210896_s_at	1.9864E-02	8.75E-04	-3.42	-0.78	-4.94E-01
2410	FLJ10038	236164_at	1.9933E-02	8.79E-04	3.42	-0.78	2.18E-01
2411	CHIC1	1557786_s_at	1.9964E-02	8.80E-04	3.42	-0.78	1.62E-01
2412	LAP3	217933_s_at	2.0002E-02	8.82E-04	-3.42	-0.79	-4.08E-01
2413	FBXO9	238472_at	2.0016E-02	8.83E-04	3.41	-0.79	2.52E-01
2414	ITGAM	205786_s_at	2.0018E-02	8.84E-04	-3.41	-0.79	-6.24E-01
2415	TAX1BP3	209154_at	2.0020E-02	8.84E-04	-3.41	-0.79	-5.04E-01
2416	EIF3J	208985_s_at	2.0043E-02	8.86E-04	-3.41	-0.79	-2.35E-01
2417	LEPREL2	204854_at	2.0043E-02	8.86E-04	-3.41	-0.79	-2.32E-01
2418	RGS10	204316_at	2.0044E-02	8.87E-04	3.41	-0.79	4.06E-01
2419	SASH1	213236_at	2.0044E-02	8.87E-04	-3.41	-0.79	-6.76E-01
2420	C5AR1	220088_at	2.0044E-02	8.88E-04	-3.41	-0.79	-5.69E-01
2421	EHBP1L1	91703_at	2.0044E-02	8.88E-04	-3.41	-0.79	-5.29E-01
2422	EEF1A1	213614_x_at	2.0044E-02	8.88E-04	-3.41	-0.79	-1.12E-01
2423	ATP5L	207573_x_at	2.0052E-02	8.89E-04	3.41	-0.79	3.92E-01
2424	FLJ36848	231698_at	2.0052E-02	8.90E-04	-3.41	-0.79	-4.21E-01
2425	FZD1	204451_at	2.0052E-02	8.90E-04	-3.41	-0.79	-6.09E-01
2426	PPM1L	239855_at	2.0052E-02	8.90E-04	3.41	-0.79	1.74E-01
2427	RRP7B///RRP7A	202938_x_at	2.0130E-02	8.94E-04	-3.41	-0.80	-2.07E-01
2428	PDE4DIP	214130_s_at	2.0136E-02	8.94E-04	-3.41	-0.80	-2.72E-01
2429	RNASE1	201785_at	2.0136E-02	8.95E-04	-3.41	-0.80	-1.01E+00
2430	C12orf45	226349_at	2.0159E-02	8.96E-04	3.41	-0.80	5.66E-01
2431	WDR1	210935_s_at	2.0161E-02	8.97E-04	-3.41	-0.80	-7.63E-01
2432	HCP5	206082_at	2.0161E-02	8.97E-04	3.41	-0.80	3.57E-01
2433	IL13RA1	210904_s_at	2.0188E-02	8.99E-04	-3.41	-0.80	-7.95E-01
2434	LOC728216///LOC644165	1553592_x_at	2.0188E-02	9.00E-04	-3.41	-0.80	-1.08E-01
2435	HIST1H2AM	214481_at	2.0188E-02	9.00E-04	3.41	-0.80	2.75E-01
2436	MGST1	231736_x_at	2.0188E-02	9.00E-04	-3.41	-0.80	-9.27E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2437	PHF6	224442_at	2.0188E-02	9.01E-04	3.41	-0.80	1.70E-01
2438		241219_at	2.0188E-02	9.01E-04	3.41	-0.80	1.60E-01
2439	ZNF259P1/// ZNF259	217185_s_at	2.0188E-02	9.02E-04	-3.41	-0.80	-4.15E-01
2440	CUX1	214743_at	2.0188E-02	9.02E-04	-3.41	-0.80	-4.91E-01
2441	SPPL2A	226353_at	2.0188E-02	9.02E-04	-3.41	-0.80	-3.56E-01
2442	ANO6	224906_at	2.0188E-02	9.02E-04	-3.41	-0.80	-2.89E-01
2443	MRPL47	223480_s_at	2.0188E-02	9.02E-04	3.41	-0.81	4.02E-01
2444	PHF20L1	227523_s_at	2.0188E-02	9.02E-04	-3.41	-0.81	-3.80E-01
2445	SPATA3	240340_at	2.0192E-02	9.03E-04	-3.41	-0.81	-1.49E-01
2446	PLAU	211668_s_at	2.0192E-02	9.03E-04	-3.41	-0.81	-6.02E-01
2447	SOD2	215223_s_at	2.0196E-02	9.04E-04	-3.41	-0.81	-7.47E-01
2448	C16orf57	1554016_a_at	2.0196E-02	9.04E-04	-3.41	-0.81	-4.24E-01
2449	SIRT2	220605_s_at	2.0217E-02	9.06E-04	-3.41	-0.81	-2.11E-01
2450		226832_at	2.0226E-02	9.06E-04	-3.41	-0.81	-4.89E-01
2451		215376_at	2.0234E-02	9.07E-04	3.41	-0.81	2.37E-01
2452	ZNF284	239462_at	2.0234E-02	9.08E-04	3.41	-0.81	2.19E-01
2453	LOC728769	238039_at	2.0234E-02	9.08E-04	3.41	-0.81	4.95E-01
2454	LEPROT	202378_s_at	2.0260E-02	9.09E-04	-3.41	-0.81	-5.20E-01
2455	ABCC9	1557374_at	2.0271E-02	9.10E-04	3.41	-0.81	1.59E-01
2456		1556613_s_at	2.0271E-02	9.11E-04	3.41	-0.81	3.37E-01
2457	VRK1	203856_at	2.0271E-02	9.11E-04	3.41	-0.81	4.09E-01
2458	TFB2M	1566930_at	2.0277E-02	9.12E-04	3.41	-0.81	8.57E-02
2459	LRRC20	218550_s_at	2.0347E-02	9.16E-04	-3.40	-0.82	-2.12E-01
2460	NKD1	1553115_at	2.0347E-02	9.17E-04	3.40	-0.82	1.96E-01
2461	C9orf163	1553642_at	2.0347E-02	9.17E-04	3.40	-0.82	1.99E-01
2462	EFNB1	202711_at	2.0347E-02	9.17E-04	-3.40	-0.82	-1.95E-01
2463	UQCRB	209065_at	2.0347E-02	9.17E-04	3.40	-0.82	5.61E-01
2464	HSPA8	208687_x_at	2.0353E-02	9.17E-04	-3.40	-0.82	-5.19E-01
2465	ETF1	201574_at	2.0368E-02	9.18E-04	-3.40	-0.82	-3.32E-01
2466	GAS2	205848_at	2.0379E-02	9.19E-04	3.40	-0.82	2.65E-01
2467	CTSB	213275_x_at	2.0386E-02	9.20E-04	-3.40	-0.82	-5.93E-01
2468		1554963_at	2.0386E-02	9.20E-04	3.40	-0.82	1.25E-01
2469	CLTA	200960_x_at	2.0386E-02	9.21E-04	-3.40	-0.82	-2.08E-01
2470	HADHA	208631_s_at	2.0412E-02	9.22E-04	-3.40	-0.82	-5.08E-01
2471		230446_at	2.0445E-02	9.24E-04	3.40	-0.83	5.00E-01
2472	NSA2	201922_at	2.0445E-02	9.24E-04	3.40	-0.83	3.81E-01
2473	IGFBP4	201508_at	2.0459E-02	9.25E-04	-3.40	-0.83	-8.24E-01
2474	TRIM26	242812_at	2.0502E-02	9.28E-04	3.40	-0.83	2.51E-01
2475		1569487_at	2.0518E-02	9.29E-04	3.40	-0.83	2.07E-01
2476	PAM	214620_x_at	2.0518E-02	9.29E-04	-3.40	-0.83	-2.62E-01
2477		1562965_at	2.0518E-02	9.30E-04	3.40	-0.83	1.52E-01
2478	GNB1	200744_s_at	2.0528E-02	9.30E-04	-3.40	-0.83	-5.31E-01
2479	ZNF492	215532_x_at	2.0544E-02	9.31E-04	3.40	-0.83	1.67E-01
2480		223930_at	2.0545E-02	9.32E-04	3.40	-0.83	2.13E-01
2481	FAM84B	228870_at	2.0558E-02	9.33E-04	3.40	-0.84	2.58E-01
2482	ARHGAP1	202117_at	2.0558E-02	9.34E-04	-3.40	-0.84	-5.21E-01
2483	MSI2	225240_s_at	2.0558E-02	9.34E-04	3.40	-0.84	5.18E-01
2484		226377_at	2.0558E-02	9.34E-04	-3.40	-0.84	-6.05E-01
2485	DCTN2	200932_s_at	2.0558E-02	9.34E-04	-3.40	-0.84	-2.24E-01
2486	B4GALT4	210540_s_at	2.0561E-02	9.35E-04	-3.40	-0.84	-2.90E-01
2487	IVD	203682_s_at	2.0623E-02	9.38E-04	-3.40	-0.84	-2.29E-01
2488	OS9	215399_s_at	2.0623E-02	9.38E-04	-3.40	-0.84	-5.49E-01
2489		236829_at	2.0632E-02	9.39E-04	3.40	-0.84	2.44E-01
2490		240226_at	2.0632E-02	9.40E-04	3.40	-0.84	1.31E-01
2491	C21orf58	1559439_s_at	2.0651E-02	9.41E-04	3.40	-0.84	1.34E-01
2492	ZNF780B	243294_at	2.0661E-02	9.42E-04	3.40	-0.84	1.74E-01
2493	CFLAR	211317_s_at	2.0671E-02	9.43E-04	-3.40	-0.84	-6.59E-01
2494		241823_at	2.0706E-02	9.45E-04	3.39	-0.85	2.31E-01
2495	PPFIA1	202065_s_at	2.0736E-02	9.46E-04	-3.39	-0.85	-3.23E-01
2496	TPM4	212481_s_at	2.0757E-02	9.48E-04	-3.39	-0.85	-3.73E-01
2497	NELL2	203413_at	2.0811E-02	9.50E-04	3.39	-0.85	7.15E-01
2498	TRADD	213443_at	2.0814E-02	9.51E-04	3.39	-0.85	1.22E-01
2499	SEL1L	202064_s_at	2.0846E-02	9.53E-04	-3.39	-0.85	-3.65E-01
2500	COMMD6	225312_at	2.0846E-02	9.53E-04	3.39	-0.85	4.78E-01
2501	MARVELD1	223095_at	2.0878E-02	9.55E-04	-3.39	-0.86	-4.60E-01
2502	PPP6R2	1570210_x_at	2.0892E-02	9.56E-04	3.39	-0.86	3.66E-01
2503	CDC14A	210440_s_at	2.0892E-02	9.56E-04	3.39	-0.86	1.68E-01
2504	LMNA	212086_x_at	2.0899E-02	9.57E-04	-3.39	-0.86	-3.52E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2505	RGS5	209070_s_at	2.0901E-02	9.58E-04	-3.39	-0.86	-8.02E-01
2506	AZI1	214742_at	2.0931E-02	9.59E-04	3.39	-0.86	2.90E-01
2507	SLC22A14	207408_at	2.0937E-02	9.60E-04	3.39	-0.86	1.96E-01
2508	BIRC5	210334_x_at	2.0952E-02	9.61E-04	3.39	-0.86	3.55E-01
2509	TSPAN3	200972_at	2.0969E-02	9.62E-04	-3.39	-0.86	-3.82E-01
2510		238156_at	2.0978E-02	9.63E-04	3.39	-0.86	5.34E-01
2511	TMEM205	225003_at	2.1039E-02	9.66E-04	-3.39	-0.87	-4.65E-01
2512	CYGB	226632_at	2.1039E-02	9.67E-04	-3.39	-0.87	-4.60E-01
2513	FLJ40606	1560162_at	2.1039E-02	9.67E-04	3.39	-0.87	1.93E-01
2514		1559867_at	2.1051E-02	9.68E-04	3.39	-0.87	2.03E-01
2515	QKI	236154_at	2.1051E-02	9.68E-04	-3.39	-0.87	-2.26E-01
2516	SLC16A6	207038_at	2.1070E-02	9.70E-04	3.39	-0.87	2.03E-01
2517	GLUL	215001_s_at	2.1082E-02	9.71E-04	-3.39	-0.87	-4.30E-01
2518		235378_at	2.1082E-02	9.71E-04	-3.39	-0.87	-1.47E-01
2519	FKBP15	212663_at	2.1086E-02	9.72E-04	-3.39	-0.87	-3.51E-01
2520	TXNDC5	221253_s_at	2.1086E-02	9.72E-04	-3.39	-0.87	-6.36E-01
2521	LRRC34	236918_s_at	2.1091E-02	9.72E-04	3.39	-0.87	1.98E-01
2522		1560144_at	2.1100E-02	9.74E-04	3.39	-0.87	2.57E-01
2523		239175_at	2.1100E-02	9.74E-04	3.39	-0.87	4.75E-01
2524	SH3PXD2B	231823_s_at	2.1110E-02	9.75E-04	-3.39	-0.87	-6.58E-01
2525	B4GALT5	221484_at	2.1175E-02	9.78E-04	-3.38	-0.88	-5.48E-01
2526	RBM11	232549_at	2.1203E-02	9.80E-04	3.38	-0.88	2.25E-01
2527	ZNF230	1557322_at	2.1203E-02	9.80E-04	3.38	-0.88	2.15E-01
2528	RPRD1A	228566_at	2.1203E-02	9.80E-04	3.38	-0.88	3.21E-01
2529	NLGN4X	1554689_a_at	2.1205E-02	9.81E-04	-3.38	-0.88	-1.51E-01
2530	TNFRSF10B	209294_x_at	2.1247E-02	9.83E-04	-3.38	-0.88	-2.39E-01
2531	FCER1G	204232_at	2.1287E-02	9.85E-04	-3.38	-0.88	-8.71E-01
2532	DDX3Y	205001_s_at	2.1288E-02	9.86E-04	-3.38	-0.88	-8.96E-01
2533	TCTN3	212121_at	2.1292E-02	9.87E-04	-3.38	-0.88	-4.70E-01
2534	LINS1	220121_at	2.1292E-02	9.87E-04	3.38	-0.88	3.49E-01
2535	ZNF547///TRAPPC2P1///TRAPPC2	219351_at	2.1306E-02	9.88E-04	3.38	-0.89	4.43E-01
2536	HDDC2	203259_s_at	2.1307E-02	9.89E-04	3.38	-0.89	3.84E-01
2537	AKAP7	205771_s_at	2.1307E-02	9.89E-04	3.38	-0.89	5.95E-01
2538	ARHGDIA	201168_x_at	2.1307E-02	9.89E-04	-3.38	-0.89	-4.55E-01
2539	PTPN1	202716_at	2.1307E-02	9.89E-04	-3.38	-0.89	-4.55E-01
2540		235740_at	2.1333E-02	9.92E-04	-3.38	-0.89	-6.09E-01
2541	ARF1	200065_s_at	2.1333E-02	9.92E-04	-3.38	-0.89	-4.25E-01
2542	ASRGL1	222764_at	2.1333E-02	9.92E-04	-3.38	-0.89	-2.35E-01
2543	MYBPC3	208040_s_at	2.1377E-02	9.94E-04	3.38	-0.89	1.93E-01
2544	PLEKHO2	204436_at	2.1387E-02	9.95E-04	-3.38	-0.89	-3.84E-01
2545		229108_at	2.1390E-02	9.96E-04	3.38	-0.89	1.51E-01
2546	KIAA1704	229078_s_at	2.1390E-02	9.96E-04	3.38	-0.89	2.31E-01
2547	HSPB8	221667_s_at	2.1390E-02	9.97E-04	-3.38	-0.89	-4.27E-01
2548	PDIA3	229453_at	2.1390E-02	9.97E-04	-3.38	-0.89	-2.40E-01
2549	TMED5	242263_at	2.1390E-02	9.98E-04	-3.38	-0.89	-3.75E-01
2550	OR12D3	221431_s_at	2.1390E-02	9.98E-04	-3.38	-0.89	-1.17E-01
2551	PITPNA	201190_s_at	2.1424E-02	1.00E-03	-3.38	-0.90	-3.57E-01
2552	HSD11B1L	1569905_at	2.1470E-02	1.00E-03	3.38	-0.90	1.84E-01
2553	NUPL1	223984_s_at	2.1474E-02	1.00E-03	-3.38	-0.90	-3.07E-01
2554	ODF3	233795_at	2.1479E-02	1.00E-03	3.38	-0.90	2.10E-01
2555	KCNN3	205903_s_at	2.1495E-02	1.00E-03	-3.38	-0.90	-2.79E-01
2556		1570134_at	2.1495E-02	1.00E-03	3.38	-0.90	1.05E-01
2557	VAC14	218169_at	2.1519E-02	1.01E-03	-3.38	-0.90	-5.05E-01
2558		1560002_at	2.1536E-02	1.01E-03	3.38	-0.90	1.37E-01
2559	HSPA8	224187_x_at	2.1536E-02	1.01E-03	-3.38	-0.90	-4.57E-01
2560	LANCL2	222560_at	2.1549E-02	1.01E-03	3.37	-0.90	1.70E-01
2561	ZNF532	220617_s_at	2.1549E-02	1.01E-03	3.37	-0.90	2.40E-01
2562	FILIP1	1556325_at	2.1549E-02	1.01E-03	-3.37	-0.90	-2.09E-01
2563	RPL23AP82///FAM41C///RPL23AP7	232899_at	2.1556E-02	1.01E-03	3.37	-0.91	2.52E-01
2564	SMOC2	223235_s_at	2.1573E-02	1.01E-03	-3.37	-0.91	-9.22E-01
2565	KIF21A	231875_at	2.1599E-02	1.01E-03	-3.37	-0.91	-2.41E-01
2566	ATF6	203952_at	2.1638E-02	1.02E-03	-3.37	-0.91	-3.14E-01
2567	RBM6	230742_at	2.1638E-02	1.02E-03	3.37	-0.91	4.79E-01
2568	PDE7A	1552343_s_at	2.1638E-02	1.02E-03	3.37	-0.91	3.59E-01
2569	ALDH7A1	208950_s_at	2.1638E-02	1.02E-03	-3.37	-0.91	-2.91E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2570	RASSF4	221578_at	2.1649E-02	1.02E-03	-3.37	-0.91	-4.77E-01
2571	APOL2	221653_x_at	2.1673E-02	1.02E-03	-3.37	-0.91	-4.06E-01
2572		241227_at	2.1673E-02	1.02E-03	3.37	-0.91	2.28E-01
2573	DOLK	204488_at	2.1673E-02	1.02E-03	-3.37	-0.91	-3.06E-01
2574	E2F2	207042_at	2.1675E-02	1.02E-03	3.37	-0.91	1.70E-01
2575	LOC283481	230351_at	2.1675E-02	1.02E-03	3.37	-0.91	1.84E-01
2576	CDR2L	213230_at	2.1675E-02	1.02E-03	-3.37	-0.91	-2.05E-01
2577	FAM20A	242945_at	2.1729E-02	1.02E-03	-3.37	-0.92	-4.58E-01
2578	PRKACB	202741_at	2.1738E-02	1.03E-03	3.37	-0.92	3.03E-01
2579	SLC39A6	1556551_s_at	2.1738E-02	1.03E-03	-3.37	-0.92	-4.35E-01
2580		236662_at	2.1746E-02	1.03E-03	-3.37	-0.92	-1.32E-01
2581		232319_at	2.1746E-02	1.03E-03	3.37	-0.92	2.07E-01
2582	CDADC1	233647_s_at	2.1746E-02	1.03E-03	3.37	-0.92	2.92E-01
2583	JAM2	229127_at	2.1746E-02	1.03E-03	-3.37	-0.92	-4.82E-01
2584	C9orf135	243610_at	2.1748E-02	1.03E-03	3.37	-0.92	1.37E-01
2585		228773_at	2.1758E-02	1.03E-03	3.37	-0.92	6.87E-01
2586	H19	224997_x_at	2.1758E-02	1.03E-03	-3.37	-0.92	-3.84E-01
2587	SLC25A28	221432_s_at	2.1763E-02	1.03E-03	-3.37	-0.92	-4.75E-01
2588	ZCRB1	227416_s_at	2.1848E-02	1.03E-03	3.37	-0.93	3.12E-01
2589	GART	244822_at	2.1848E-02	1.03E-03	3.37	-0.93	2.53E-01
2590	LOC284933	240754_at	2.1856E-02	1.04E-03	3.37	-0.93	1.96E-01
2591		227069_at	2.1879E-02	1.04E-03	-3.37	-0.93	-2.65E-01
2592	RPL23	214744_s_at	2.1879E-02	1.04E-03	3.37	-0.93	6.31E-01
2593	HSPA2	211538_s_at	2.1881E-02	1.04E-03	-3.37	-0.93	-4.04E-01
2594	TYMP	204858_s_at	2.1924E-02	1.04E-03	-3.37	-0.93	-5.68E-01
2595	MLF1IP	218883_s_at	2.1924E-02	1.04E-03	3.37	-0.93	6.08E-01
2596		236202_at	2.1924E-02	1.04E-03	3.37	-0.93	2.38E-01
2597	SLC39A6	202088_at	2.1938E-02	1.04E-03	-3.36	-0.93	-3.00E-01
2598	EIF3B	203462_x_at	2.1941E-02	1.04E-03	-3.36	-0.93	-5.10E-01
2599	GHRHR	211545_at	2.1943E-02	1.04E-03	3.36	-0.93	1.48E-01
2600	GTDC1	220853_at	2.1945E-02	1.04E-03	3.36	-0.93	1.74E-01
2601	TWIST2	229404_at	2.1945E-02	1.04E-03	-3.36	-0.93	-2.89E-01
2602	NPHP4	213471_at	2.1951E-02	1.05E-03	-3.36	-0.94	-2.53E-01
2603	LOC100132999	229872_s_at	2.1951E-02	1.05E-03	3.36	-0.94	3.45E-01
2604		244075_at	2.1951E-02	1.05E-03	3.36	-0.94	3.90E-01
2605	MTHFD2L	239562_at	2.1951E-02	1.05E-03	3.36	-0.94	2.11E-01
2606	LITAF	200704_at	2.1951E-02	1.05E-03	-3.36	-0.94	-3.53E-01
2607	CAP1	200625_s_at	2.2031E-02	1.05E-03	-3.36	-0.94	-2.88E-01
2608	RHOB	212099_at	2.2073E-02	1.05E-03	-3.36	-0.94	-7.56E-01
2609	FLJ35776	238432_at	2.2073E-02	1.05E-03	3.36	-0.94	3.24E-01
2610	SELP	206049_at	2.2089E-02	1.05E-03	-3.36	-0.94	-5.22E-01
2611	SLC39A9	216011_at	2.2089E-02	1.05E-03	3.36	-0.94	1.67E-01
2612	CXCL12	203666_at	2.2090E-02	1.06E-03	-3.36	-0.94	-8.27E-01
2613	TMEM182	238867_at	2.2090E-02	1.06E-03	3.36	-0.94	1.91E-01
2614	GAPDH	217398_x_at	2.2107E-02	1.06E-03	-3.36	-0.95	-4.63E-01
2615	CLIC4	201560_at	2.2107E-02	1.06E-03	-3.36	-0.95	-4.48E-01
2616	RPL14P1/// RPL14	200074_s_at	2.2132E-02	1.06E-03	3.36	-0.95	2.36E-01
2617	CRISPLD2	221541_at	2.2132E-02	1.06E-03	-3.36	-0.95	-1.03E+00
2618	VCL	200931_s_at	2.2132E-02	1.06E-03	-3.36	-0.95	-4.95E-01
2619	C11orf51	204218_at	2.2133E-02	1.06E-03	3.36	-0.95	2.84E-01
2620	GAS7	207704_s_at	2.2163E-02	1.06E-03	-3.36	-0.95	-2.58E-01
2621	RHEB	213409_s_at	2.2163E-02	1.06E-03	3.36	-0.95	2.61E-01
2622	VN1R95P	235322_at	2.2163E-02	1.06E-03	3.36	-0.95	3.28E-01
2623	EPS15	217886_at	2.2163E-02	1.06E-03	-3.36	-0.95	-2.42E-01
2624	LOC401431	229094_at	2.2163E-02	1.06E-03	3.36	-0.95	1.56E-01
2625	CXXC4	220277_at	2.2163E-02	1.06E-03	3.36	-0.95	2.23E-01
2626	ZNF485	1552427_at	2.2163E-02	1.06E-03	3.36	-0.95	1.70E-01
2627	MYO10	201976_s_at	2.2163E-02	1.06E-03	-3.36	-0.95	-5.19E-01
2628	TMF1	215855_s_at	2.2191E-02	1.07E-03	3.36	-0.95	2.78E-01
2629	FTSJ2	218356_at	2.2191E-02	1.07E-03	-3.36	-0.95	-2.58E-01
2630	TARDBP	1558208_at	2.2194E-02	1.07E-03	3.36	-0.95	1.94E-01
2631	IL1RL1	207526_s_at	2.2206E-02	1.07E-03	-3.36	-0.96	-2.09E-01
2632	EXOSC6	1558044_s_at	2.2214E-02	1.07E-03	3.36	-0.96	2.40E-01
2633	C21orf91	220941_s_at	2.2256E-02	1.07E-03	3.36	-0.96	5.31E-01
2634	RXFP2	1553326_at	2.2260E-02	1.07E-03	3.36	-0.96	1.03E-01
2635	CD52	34210_at	2.2268E-02	1.07E-03	3.36	-0.96	5.45E-01
2636	C8orf40	225534_at	2.2268E-02	1.07E-03	3.36	-0.96	5.54E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2637	ERC1	226049_at	2.2268E-02	1.07E-03	-3.36	-0.96	-3.08E-01
2638	COL6A1	213428_s_at	2.2273E-02	1.07E-03	-3.36	-0.96	-9.53E-01
2639	ANGEL2	221826_at	2.2273E-02	1.08E-03	3.36	-0.96	3.54E-01
2640	NBL1	37005_at	2.2299E-02	1.08E-03	-3.35	-0.96	-7.06E-01
2641	C2orf74	1568658_at	2.2299E-02	1.08E-03	-3.35	-0.96	-4.12E-01
2642	CFL1	1555730_a_at	2.2299E-02	1.08E-03	-3.35	-0.96	-9.91E-01
2643	ZC3H10	227430_at	2.2299E-02	1.08E-03	-3.35	-0.96	-2.47E-01
2644	NSDHL	209279_s_at	2.2299E-02	1.08E-03	-3.35	-0.96	-2.90E-01
2645		237829_at	2.2299E-02	1.08E-03	3.35	-0.96	1.41E-01
2646	TRIM11	228267_at	2.2306E-02	1.08E-03	3.35	-0.96	1.41E-01
2647	VPS37C	219053_s_at	2.2314E-02	1.08E-03	-3.35	-0.96	-3.43E-01
2648	PCCB	212694_s_at	2.2332E-02	1.08E-03	-3.35	-0.97	-3.47E-01
2649	CD274	227458_at	2.2332E-02	1.08E-03	-3.35	-0.97	-6.99E-01
2650		216625_at	2.2332E-02	1.08E-03	3.35	-0.97	8.87E-02
2651		231602_at	2.2332E-02	1.08E-03	3.35	-0.97	2.02E-01
2652	MYLK	1563466_at	2.2332E-02	1.08E-03	3.35	-0.97	1.04E-01
2653	C6orf57	238504_at	2.2332E-02	1.08E-03	3.35	-0.97	5.45E-01
2654	LOC100129510	1560163_at	2.2356E-02	1.09E-03	3.35	-0.97	1.45E-01
2655	ZAK	225662_at	2.2373E-02	1.09E-03	-3.35	-0.97	-4.17E-01
2656	C11orf24	218299_at	2.2373E-02	1.09E-03	-3.35	-0.97	-3.11E-01
2657	MS4A6A	232725_s_at	2.2373E-02	1.09E-03	-3.35	-0.97	-2.17E-01
2658		1562730_a_at	2.2373E-02	1.09E-03	3.35	-0.97	1.30E-01
2659	MGAT4B	220189_s_at	2.2373E-02	1.09E-03	-3.35	-0.97	-4.87E-01
2660	SERPINH1	207714_s_at	2.2375E-02	1.09E-03	-3.35	-0.97	-8.06E-01
2661	C14orf102	227575_s_at	2.2375E-02	1.09E-03	-3.35	-0.97	-1.79E-01
2662	C2orf24	207511_s_at	2.2375E-02	1.09E-03	-3.35	-0.97	-2.26E-01
2663	SVOPL	1554300_a_at	2.2386E-02	1.09E-03	3.35	-0.97	1.29E-01
2664	ITGA9	227297_at	2.2386E-02	1.09E-03	-3.35	-0.97	-5.89E-01
2665	LYRM5	231640_at	2.2386E-02	1.09E-03	3.35	-0.97	2.19E-01
2666	APOE	203381_s_at	2.2386E-02	1.09E-03	-3.35	-0.97	-7.96E-01
2667	RHOC	200885_at	2.2386E-02	1.09E-03	-3.35	-0.97	-5.24E-01
2668	SYNCRIP	209024_s_at	2.2391E-02	1.09E-03	-3.35	-0.97	-5.05E-01
2669	PCDHGA1/// PCDHGA2/// PCDHGA3/// PCDHGA4/// PCDHGA5/// PCDHGA6/// PCDHGA7/// PCDHGA9/// PCDHGA10/ //PCDHGA1 1///PCDHGB 1///PCDHGB 2///PCDHGB 3///PCDHGB 5///PCDHGB 6///PCDHGB 7///PCDHGC 4///PCDHGC 5///PCDHGA 12///PCDHG A8///PCDHG B4///PCDHG C3	209079_x_at	2.2406E-02	1.09E-03	-3.35	-0.98	-3.34E-01
2670	NRXN3	205795_at	2.2435E-02	1.10E-03	-3.35	-0.98	-1.65E-01
2671	DCN	211813_x_at	2.2452E-02	1.10E-03	-3.35	-0.98	-1.18E+00
2672	CCDC88C	231288_at	2.2461E-02	1.10E-03	3.35	-0.98	2.44E-01
2673	LOC100288009	1570362_at	2.2475E-02	1.10E-03	3.35	-0.98	1.80E-01
2674	IDH1	1555037_a_at	2.2502E-02	1.10E-03	-3.35	-0.98	-5.71E-01
2675	SLC16A2	204462_s_at	2.2507E-02	1.10E-03	-3.35	-0.98	-2.79E-01
2676	CYP3A7	243609_at	2.2524E-02	1.10E-03	3.35	-0.98	1.36E-01
2677	RHOQ	212119_at	2.2545E-02	1.10E-03	-3.35	-0.98	-4.27E-01
2678	TIMM23B///LOC10431	218119_at	2.2545E-02	1.10E-03	-3.35	-0.98	-5.02E-01
2679	MTUS1	212095_s_at	2.2574E-02	1.11E-03	-3.35	-0.99	-4.39E-01
2680	PDLIM4	211564_s_at	2.2574E-02	1.11E-03	-3.35	-0.99	-4.78E-01
2681	GRN	211284_s_at	2.2601E-02	1.11E-03	-3.35	-0.99	-6.60E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2682	TM2D1	212963_at	2.2601E-02	1.11E-03	3.35	-0.99	3.01E-01
2683	EPB41L3	206710_s_at	2.2601E-02	1.11E-03	-3.35	-0.99	-8.55E-01
2684	ZNF519	1557283_a_at	2.2601E-02	1.11E-03	3.35	-0.99	1.41E-01
2685	HDGF	200896_x_at	2.2601E-02	1.11E-03	-3.35	-0.99	-4.11E-01
2686	B3GNT4	221240_s_at	2.2601E-02	1.11E-03	3.35	-0.99	1.91E-01
2687	SS18	202816_s_at	2.2601E-02	1.11E-03	-3.35	-0.99	-3.48E-01
2688	C17orf90	221797_at	2.2601E-02	1.11E-03	3.35	-0.99	2.35E-01
2689	CRYAB	209283_at	2.2611E-02	1.11E-03	-3.35	-0.99	-5.08E-01
2690	GADD45A	203725_at	2.2611E-02	1.11E-03	-3.35	-0.99	-4.62E-01
2691	MT1F	213629_x_at	2.2620E-02	1.11E-03	-3.34	-0.99	-7.47E-01
2692		239170_at	2.2629E-02	1.11E-03	3.34	-0.99	2.00E-01
2693	HSF5	230718_at	2.2630E-02	1.11E-03	3.34	-0.99	3.52E-01
2694	GAS6	202177_at	2.2630E-02	1.12E-03	-3.34	-0.99	-5.59E-01
2695	PAK2	208878_s_at	2.2630E-02	1.12E-03	-3.34	-0.99	-3.07E-01
2696	CTTN	201059_at	2.2630E-02	1.12E-03	-3.34	-0.99	-5.34E-01
2697	RGS10	214000_s_at	2.2639E-02	1.12E-03	3.34	-0.99	4.42E-01
2698	C10orf46	227257_s_at	2.2639E-02	1.12E-03	-3.34	-0.99	-5.80E-01
2699	GGTA1	228376_at	2.2669E-02	1.12E-03	-3.34	-1.00	-5.11E-01
2700	ZBTB25	214482_at	2.2669E-02	1.12E-03	3.34	-1.00	3.92E-01
2701		233698_at	2.2672E-02	1.12E-03	3.34	-1.00	1.71E-01
2702	GSN	214040_s_at	2.2700E-02	1.12E-03	-3.34	-1.00	-3.49E-01
2703	ADCK2	44120_at	2.2700E-02	1.12E-03	-3.34	-1.00	-2.73E-01
2704	PHKB	202739_s_at	2.2713E-02	1.12E-03	-3.34	-1.00	-3.40E-01
2705	DNAJB5	207453_s_at	2.2713E-02	1.12E-03	-3.34	-1.00	-1.84E-01
2706	CP	227253_at	2.2716E-02	1.12E-03	-3.34	-1.00	-6.88E-01
2707	TRIM49	221154_at	2.2723E-02	1.13E-03	3.34	-1.00	1.18E-01
2708		242366_at	2.2723E-02	1.13E-03	-3.34	-1.00	-3.69E-01
2709	RPS15	200819_s_at	2.2736E-02	1.13E-03	3.34	-1.00	1.69E-01
2710	ATP6V0D1	212041_at	2.2739E-02	1.13E-03	-3.34	-1.00	-5.41E-01
2711	LACTB	1552486_s_at	2.2742E-02	1.13E-03	-3.34	-1.00	-6.88E-01
2712	NCRNA00115	220399_at	2.2742E-02	1.13E-03	3.34	-1.00	2.47E-01
2713	FEM1B	212367_at	2.2748E-02	1.13E-03	-3.34	-1.00	-2.83E-01
2714	RPS19	202649_x_at	2.2759E-02	1.13E-03	3.34	-1.00	1.56E-01
2715	TAX1BP3	215464_s_at	2.2771E-02	1.13E-03	-3.34	-1.01	-6.30E-01
2716	TMEM164	223201_s_at	2.2777E-02	1.13E-03	-3.34	-1.01	-2.24E-01
2717	SERBP1	217724_at	2.2810E-02	1.13E-03	-3.34	-1.01	-2.94E-01
2718	SPTLC2	203128_at	2.2810E-02	1.13E-03	-3.34	-1.01	-2.23E-01
2719	LOC728153	1560199_x_at	2.2901E-02	1.14E-03	3.34	-1.01	3.01E-01
2720	FAM55D	220645_at	2.2901E-02	1.14E-03	3.34	-1.01	1.54E-01
2721	NKAIN4	230771_at	2.2922E-02	1.14E-03	3.34	-1.01	1.42E-01
2722	FAM65A	45749_at	2.2922E-02	1.14E-03	-3.34	-1.01	-2.91E-01
2723	ENPEP	204844_at	2.2922E-02	1.14E-03	-3.34	-1.01	-3.21E-01
2724	AZI2	227905_s_at	2.2924E-02	1.14E-03	-3.34	-1.01	-2.63E-01
2725	ADAM7	239079_at	2.2924E-02	1.14E-03	3.34	-1.01	1.42E-01
2726	LIME1	219541_at	2.2942E-02	1.14E-03	3.34	-1.02	3.03E-01
2727	BTN3A3	204821_at	2.2942E-02	1.14E-03	-3.34	-1.02	-4.50E-01
2728		237791_at	2.2946E-02	1.14E-03	3.34	-1.02	1.29E-01
2729	RWDD3	205087_at	2.2966E-02	1.15E-03	3.34	-1.02	4.76E-01
2730	ZRANB2	223016_x_at	2.3042E-02	1.15E-03	3.33	-1.02	2.38E-01
2731	PPAP2A	209147_s_at	2.3042E-02	1.15E-03	-3.33	-1.02	-4.88E-01
2732	PDCD1LG2	220049_s_at	2.3076E-02	1.15E-03	-3.33	-1.02	-4.06E-01
2733		239808_at	2.3150E-02	1.16E-03	3.33	-1.03	3.16E-01
2734	LIMK2	210582_s_at	2.3175E-02	1.16E-03	-3.33	-1.03	-4.43E-01
2735	UBIAD1	229348_at	2.3188E-02	1.16E-03	3.33	-1.03	2.28E-01
2736	PRELID1	223032_x_at	2.3188E-02	1.16E-03	-3.33	-1.03	-3.42E-01
2737	ZNF292	212366_at	2.3188E-02	1.16E-03	3.33	-1.03	2.99E-01
2738	MME	203434_s_at	2.3191E-02	1.16E-03	-3.33	-1.03	-9.53E-01
2739	TMEM126B	1554537_at	2.3194E-02	1.16E-03	3.33	-1.03	1.74E-01
2740	SNRPE	215450_at	2.3195E-02	1.16E-03	3.33	-1.03	5.52E-01
2741		237459_at	2.3214E-02	1.16E-03	3.33	-1.03	2.02E-01
2742	PQLC1	218208_at	2.3214E-02	1.16E-03	-3.33	-1.03	-2.72E-01
2743	SRP72	208800_at	2.3227E-02	1.17E-03	-3.33	-1.03	-4.82E-01
2744	LAMP1	213728_at	2.3227E-02	1.17E-03	-3.33	-1.03	-2.30E-01
2745	HIST1H3D/// HIST1H2AD	214522_x_at	2.3229E-02	1.17E-03	3.33	-1.03	4.51E-01
2746	SENP5	222110_at	2.3230E-02	1.17E-03	3.33	-1.03	1.50E-01
2747	C20orf108	224690_at	2.3230E-02	1.17E-03	-3.33	-1.03	-4.09E-01
2748	IRAK3	213817_at	2.3230E-02	1.17E-03	-3.33	-1.03	-4.50E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2749	DNM1L	203105_s_at	2.3260E-02	1.17E-03	-3.33	-1.03	-3.05E-01
2750	C1orf156	213528_at	2.3260E-02	1.17E-03	3.33	-1.04	4.29E-01
2751	OCIAD2	225314_at	2.3262E-02	1.17E-03	3.33	-1.04	5.12E-01
2752	ERI1	231852_at	2.3267E-02	1.17E-03	-3.33	-1.04	-1.90E-01
2753	STXBP1	202260_s_at	2.3267E-02	1.17E-03	-3.33	-1.04	-4.00E-01
2754		235959_at	2.3273E-02	1.17E-03	3.33	-1.04	3.03E-01
2755	MMP14	202827_s_at	2.3275E-02	1.17E-03	-3.33	-1.04	-4.20E-01
2756	YLPM1	1557065_at	2.3275E-02	1.17E-03	3.33	-1.04	3.20E-01
2757	SLCO3A1	210542_s_at	2.3275E-02	1.17E-03	-3.33	-1.04	-2.42E-01
2758	PIAS4	212881_at	2.3275E-02	1.18E-03	-3.33	-1.04	-2.93E-01
2759	SLC2A3	202498_s_at	2.3275E-02	1.18E-03	-3.33	-1.04	-4.14E-01
2760	A2M	217757_at	2.3275E-02	1.18E-03	-3.33	-1.04	-4.87E-01
2761	BSG	208677_s_at	2.3275E-02	1.18E-03	-3.33	-1.04	-4.99E-01
2762	MT1G	204745_x_at	2.3275E-02	1.18E-03	-3.33	-1.04	-9.22E-01
2763	KDM1B	1553150_at	2.3275E-02	1.18E-03	-3.33	-1.04	-1.71E-01
2764	CCDC59	222792_s_at	2.3278E-02	1.18E-03	3.33	-1.04	3.90E-01
2765	PARVG	244229_at	2.3287E-02	1.18E-03	3.33	-1.04	3.76E-01
2766	KIAA0100	201729_s_at	2.3318E-02	1.18E-03	-3.33	-1.04	-5.22E-01
2767	WHSC2	203112_s_at	2.3318E-02	1.18E-03	-3.33	-1.04	-3.03E-01
2768	RHOU	223168_at	2.3339E-02	1.18E-03	-3.33	-1.04	-6.00E-01
2769		213739_at	2.3339E-02	1.18E-03	3.33	-1.04	1.64E-01
2770		233401_at	2.3356E-02	1.18E-03	3.33	-1.05	1.41E-01
2771	C10orf18	1556758_at	2.3357E-02	1.18E-03	3.33	-1.05	1.47E-01
2772	SENP6	214790_at	2.3378E-02	1.19E-03	3.33	-1.05	3.22E-01
2773	ZHX3	212545_s_at	2.3378E-02	1.19E-03	3.33	-1.05	2.13E-01
2774	YAF2	206238_s_at	2.3378E-02	1.19E-03	3.33	-1.05	4.95E-01
2775		242692_at	2.3378E-02	1.19E-03	3.33	-1.05	1.59E-01
2776	GJA3	208590_x_at	2.3402E-02	1.19E-03	3.32	-1.05	1.51E-01
2777		243782_at	2.3403E-02	1.19E-03	3.32	-1.05	1.76E-01
2778	NDUFA3	218563_at	2.3443E-02	1.19E-03	3.32	-1.05	2.49E-01
2779		1557495_at	2.3453E-02	1.19E-03	3.32	-1.05	1.15E-01
2780	DCN	201893_x_at	2.3464E-02	1.19E-03	-3.32	-1.05	-1.13E+00
2781	RPS4X	200933_x_at	2.3464E-02	1.19E-03	3.32	-1.05	1.34E-01
2782	FKBP11	228308_at	2.3502E-02	1.20E-03	-3.32	-1.05	-3.86E-01
2783		238305_at	2.3517E-02	1.20E-03	3.32	-1.06	9.56E-02
2784		1562010_x_at	2.3550E-02	1.20E-03	3.32	-1.06	1.47E-01
2785		239215_at	2.3550E-02	1.20E-03	3.32	-1.06	1.69E-01
2786	CHMP4B	225498_at	2.3562E-02	1.20E-03	-3.32	-1.06	-3.73E-01
2787	FBXO45	225099_at	2.3562E-02	1.20E-03	-3.32	-1.06	-3.55E-01
2788		243798_at	2.3562E-02	1.20E-03	3.32	-1.06	6.12E-01
2789		215386_at	2.3569E-02	1.20E-03	3.32	-1.06	1.55E-01
2790	NCRNA00271///GAPDHL19	234954_at	2.3569E-02	1.20E-03	-3.32	-1.06	-3.68E-01
2791	UBQLN1	222990_at	2.3572E-02	1.20E-03	-3.32	-1.06	-2.65E-01
2792	GLP1R	211232_x_at	2.3613E-02	1.21E-03	3.32	-1.06	1.62E-01
2793	RDX	212398_at	2.3618E-02	1.21E-03	-3.32	-1.06	-4.45E-01
2794	CCDC11	1552326_a_at	2.3629E-02	1.21E-03	3.32	-1.06	1.64E-01
2795	PABPN1	201544_x_at	2.3632E-02	1.21E-03	-3.32	-1.06	-5.13E-01
2796	LAPTM4B	1554679_a_at	2.3633E-02	1.21E-03	-3.32	-1.06	-3.72E-01
2797	ACAD9	224160_s_at	2.3644E-02	1.21E-03	-3.32	-1.06	-2.84E-01
2798	HIP1	205425_at	2.3644E-02	1.21E-03	-3.32	-1.07	-2.62E-01
2799	FZR1	209415_at	2.3681E-02	1.21E-03	3.32	-1.07	1.90E-01
2800	ATP8A2	219660_s_at	2.3681E-02	1.21E-03	3.32	-1.07	4.99E-01
2801	INHA	210141_s_at	2.3698E-02	1.21E-03	3.32	-1.07	1.63E-01
2802	AKR1A1	241978_at	2.3702E-02	1.21E-03	3.32	-1.07	2.01E-01
2803		241095_at	2.3702E-02	1.22E-03	3.32	-1.07	1.48E-01
2804	ALG1	223355_at	2.3702E-02	1.22E-03	-3.32	-1.07	-1.82E-01
2805		234067_at	2.3702E-02	1.22E-03	3.32	-1.07	1.37E-01
2806	A2ML1	1564307_a_at	2.3713E-02	1.22E-03	3.32	-1.07	1.25E-01
2807	GUSB	202605_at	2.3755E-02	1.22E-03	-3.32	-1.07	-2.42E-01
2808	KCTD11	235857_at	2.3771E-02	1.22E-03	-3.32	-1.07	-3.18E-01
2809	PREB	217861_s_at	2.3781E-02	1.22E-03	-3.32	-1.07	-3.13E-01
2810	RRAGA	201628_s_at	2.3787E-02	1.22E-03	-3.32	-1.07	-4.14E-01
2811		230366_at	2.3822E-02	1.23E-03	3.32	-1.08	1.31E-01
2812	TBC1D9B	212052_s_at	2.3822E-02	1.23E-03	-3.32	-1.08	-4.06E-01
2813	SLC29A1	201801_s_at	2.3822E-02	1.23E-03	-3.32	-1.08	-3.97E-01
2814	CLLU1	1558186_s_at	2.3822E-02	1.23E-03	3.32	-1.08	6.09E-01
2815		1560500_at	2.3822E-02	1.23E-03	3.32	-1.08	1.77E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2816	XRN2	233878_s_at	2.3822E-02	1.23E-03	-3.32	-1.08	-7.30E-01
2817	TPM3	222976_s_at	2.3822E-02	1.23E-03	-3.32	-1.08	-2.76E-01
2818	MPP5	226092_at	2.3826E-02	1.23E-03	-3.31	-1.08	-2.88E-01
2819	HGSNAT	222491_at	2.3826E-02	1.23E-03	-3.31	-1.08	-2.13E-01
2820	CHST3	209834_at	2.3826E-02	1.23E-03	-3.31	-1.08	-2.19E-01
2821	CH25H	206932_at	2.3836E-02	1.23E-03	-3.31	-1.08	-5.72E-01
2822	KCNG3	1552897_a_at	2.3836E-02	1.23E-03	3.31	-1.08	1.10E-01
2823	SLC2A10	221024_s_at	2.3855E-02	1.23E-03	-3.31	-1.08	-7.05E-01
2824	ANKRD13A	238851_at	2.3881E-02	1.23E-03	3.31	-1.08	2.87E-01
2825	SLC4A1AP	242030_at	2.3885E-02	1.23E-03	3.31	-1.08	2.25E-01
2826	C7orf30	226385_s_at	2.3885E-02	1.23E-03	3.31	-1.08	2.77E-01
2827		239341_at	2.3886E-02	1.24E-03	3.31	-1.08	2.01E-01
2828	COQ10B	219397_at	2.3902E-02	1.24E-03	3.31	-1.08	3.44E-01
2829	ARL8A	1556155_at	2.3941E-02	1.24E-03	3.31	-1.09	1.40E-01
2830		232236_at	2.3951E-02	1.24E-03	3.31	-1.09	1.84E-01
2831	AP1G1	203350_at	2.3971E-02	1.24E-03	-3.31	-1.09	-4.03E-01
2832	PALLD	200906_s_at	2.3971E-02	1.24E-03	-3.31	-1.09	-5.08E-01
2833		242932_at	2.3971E-02	1.24E-03	3.31	-1.09	2.14E-01
2834		232582_at	2.4011E-02	1.24E-03	3.31	-1.09	1.23E-01
2835	ZNF710	235090_at	2.4028E-02	1.25E-03	3.31	-1.09	1.55E-01
2836	ATP6V1A	201971_s_at	2.4028E-02	1.25E-03	-3.31	-1.09	-6.64E-01
2837	ADCY1	213245_at	2.4028E-02	1.25E-03	-3.31	-1.09	-3.53E-01
2838	NFKB2	211524_at	2.4028E-02	1.25E-03	3.31	-1.09	1.26E-01
2839	IARS	204744_s_at	2.4028E-02	1.25E-03	-3.31	-1.09	-2.94E-01
2840	MYST2	200049_at	2.4028E-02	1.25E-03	-3.31	-1.09	-4.18E-01
2841	STAU1	211505_s_at	2.4028E-02	1.25E-03	-3.31	-1.09	-5.36E-01
2842		233214_at	2.4028E-02	1.25E-03	3.31	-1.09	2.04E-01
2843	FAM114A1	226697_at	2.4028E-02	1.25E-03	-3.31	-1.09	-5.68E-01
2844	FMNL2	242665_at	2.4049E-02	1.25E-03	-3.31	-1.09	-5.11E-01
2845	NKD2	232201_at	2.4067E-02	1.25E-03	-3.31	-1.10	-2.34E-01
2846	FMNL2	226184_at	2.4067E-02	1.25E-03	-3.31	-1.10	-5.25E-01
2847	PACSIN2	1554691_a_at	2.4073E-02	1.25E-03	-3.31	-1.10	-3.31E-01
2848	RPL24	200013_at	2.4080E-02	1.25E-03	3.31	-1.10	2.95E-01
2849	LOC100287426	231390_at	2.4120E-02	1.26E-03	3.31	-1.10	1.55E-01
2850	RASSF4	226436_at	2.4120E-02	1.26E-03	-3.31	-1.10	-5.37E-01
2851	RDX	212397_at	2.4120E-02	1.26E-03	-3.31	-1.10	-4.05E-01
2852	C6orf97	220581_at	2.4122E-02	1.26E-03	-3.31	-1.10	-1.28E-01
2853	TRPV2	222855_s_at	2.4122E-02	1.26E-03	-3.31	-1.10	-2.30E-01
2854		1569114_at	2.4122E-02	1.26E-03	3.31	-1.10	1.29E-01
2855		231383_at	2.4126E-02	1.26E-03	3.31	-1.10	1.44E-01
2856		1562044_at	2.4144E-02	1.26E-03	3.31	-1.10	1.43E-01
2857	VCP	208649_s_at	2.4146E-02	1.26E-03	-3.31	-1.10	-5.13E-01
2858		239298_at	2.4148E-02	1.26E-03	3.31	-1.10	1.17E-01
2859	XRCC5	232633_at	2.4148E-02	1.26E-03	3.31	-1.10	2.39E-01
2860	CCDC47	222432_s_at	2.4148E-02	1.26E-03	-3.31	-1.10	-3.48E-01
2861	COPS8	202141_s_at	2.4148E-02	1.27E-03	-3.31	-1.10	-2.72E-01
2862	AGFG1	218092_s_at	2.4148E-02	1.27E-03	-3.31	-1.11	-3.14E-01
2863	FAM82A2	218126_at	2.4148E-02	1.27E-03	-3.31	-1.11	-2.55E-01
2864	ADORA2A	205013_s_at	2.4148E-02	1.27E-03	3.31	-1.11	3.55E-01
2865	USP4	211800_s_at	2.4148E-02	1.27E-03	-3.31	-1.11	-3.19E-01
2866	DNAH1	228112_at	2.4148E-02	1.27E-03	3.31	-1.11	1.67E-01
2867	PFKL	211065_x_at	2.4148E-02	1.27E-03	-3.31	-1.11	-2.78E-01
2868		235814_at	2.4148E-02	1.27E-03	3.31	-1.11	1.84E-01
2869	COL27A1	225288_at	2.4148E-02	1.27E-03	-3.30	-1.11	-3.62E-01
2870	MT1H	206461_x_at	2.4148E-02	1.27E-03	-3.30	-1.11	-8.49E-01
2871		234434_at	2.4148E-02	1.27E-03	3.30	-1.11	1.40E-01
2872	HOMER3	215489_x_at	2.4148E-02	1.27E-03	-3.30	-1.11	-2.52E-01
2873	FADS1	208964_s_at	2.4148E-02	1.27E-03	-3.30	-1.11	-4.07E-01
2874		239252_at	2.4148E-02	1.27E-03	3.30	-1.11	3.80E-01
2875		239452_at	2.4148E-02	1.27E-03	-3.30	-1.11	-1.25E-01
2876	SLC28A1	231187_at	2.4148E-02	1.27E-03	3.30	-1.11	1.44E-01
2877	USP9X	230543_at	2.4148E-02	1.27E-03	-3.30	-1.11	-1.51E-01
2878	PRR16	220014_at	2.4148E-02	1.27E-03	-3.30	-1.11	-5.93E-01
2879	LHFPL2	212658_at	2.4148E-02	1.27E-03	-3.30	-1.11	-5.52E-01
2880	GNAS	217058_at	2.4148E-02	1.27E-03	3.30	-1.11	1.91E-01
2881	SRSF2IP	232597_x_at	2.4179E-02	1.27E-03	3.30	-1.11	3.96E-01
2882		242264_at	2.4179E-02	1.27E-03	3.30	-1.11	2.95E-01
2883	S1PR2	227684_at	2.4186E-02	1.28E-03	-3.30	-1.11	-2.39E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2884	GK5	238121_at	2.4194E-02	1.28E-03	-3.30	-1.11	-1.39E-01
2885	HCG27	1559050_at	2.4200E-02	1.28E-03	3.30	-1.11	2.18E-01
2886	JDP2	239085_at	2.4216E-02	1.28E-03	3.30	-1.11	1.47E-01
2887	RREB1	228487_s_at	2.4227E-02	1.28E-03	-3.30	-1.11	-4.40E-01
2888		241846_at	2.4228E-02	1.28E-03	3.30	-1.12	1.48E-01
2889	OMG	207093_s_at	2.4228E-02	1.28E-03	3.30	-1.12	1.44E-01
2890	TPR	228709_at	2.4228E-02	1.28E-03	3.30	-1.12	4.20E-01
2891	QRSL1	233089_at	2.4228E-02	1.28E-03	3.30	-1.12	3.01E-01
2892		238750_at	2.4228E-02	1.28E-03	3.30	-1.12	3.93E-01
2893	FLJ41649	1562219_at	2.4237E-02	1.28E-03	3.30	-1.12	1.40E-01
2894		228560_at	2.4237E-02	1.28E-03	3.30	-1.12	1.99E-01
2895	NPPB	206801_at	2.4263E-02	1.28E-03	3.30	-1.12	1.77E-01
2896	CSNK1D	207945_s_at	2.4273E-02	1.29E-03	-3.30	-1.12	-4.47E-01
2897	UBE2L3	200676_s_at	2.4279E-02	1.29E-03	-3.30	-1.12	-4.33E-01
2898	ACTB	213867_x_at	2.4285E-02	1.29E-03	-3.30	-1.12	-3.73E-01
2899	RNASEK	224573_at	2.4308E-02	1.29E-03	-3.30	-1.12	-4.80E-01
2900	PEX26	235098_at	2.4310E-02	1.29E-03	3.30	-1.12	1.60E-01
2901	LOX	204298_s_at	2.4315E-02	1.29E-03	-3.30	-1.12	-9.33E-01
2902	CCR2	207794_at	2.4317E-02	1.29E-03	-3.30	-1.12	-3.10E-01
2903	ZNF383	235414_at	2.4319E-02	1.29E-03	3.30	-1.12	2.88E-01
2904	RNF130	217865_at	2.4319E-02	1.29E-03	-3.30	-1.12	-5.86E-01
2905	STK17B	205214_at	2.4319E-02	1.29E-03	3.30	-1.12	4.57E-01
2906	NCF4	205147_x_at	2.4320E-02	1.29E-03	-3.30	-1.12	-4.92E-01
2907	MEIS3P1	214077_x_at	2.4330E-02	1.29E-03	-3.30	-1.12	-3.55E-01
2908	TERF2	203611_at	2.4356E-02	1.30E-03	-3.30	-1.13	-4.96E-01
2909	CAST	208908_s_at	2.4356E-02	1.30E-03	-3.30	-1.13	-4.20E-01
2910	CXorf57	215803_at	2.4356E-02	1.30E-03	3.30	-1.13	8.04E-02
2911	TARDBP	221264_s_at	2.4358E-02	1.30E-03	3.30	-1.13	5.14E-01
2912	APPL2	218218_at	2.4370E-02	1.30E-03	-3.30	-1.13	-4.24E-01
2913		242379_at	2.4373E-02	1.30E-03	3.30	-1.13	1.34E-01
2914	MYOF	201798_s_at	2.4379E-02	1.30E-03	-3.30	-1.13	-6.97E-01
2915	SEMA4A	219259_at	2.4381E-02	1.30E-03	-3.30	-1.13	-4.72E-01
2916	LHFPL4	228422_at	2.4386E-02	1.30E-03	3.30	-1.13	1.80E-01
2917	CREB5	205931_s_at	2.4386E-02	1.30E-03	-3.30	-1.13	-1.69E-01
2918	TFPI	213258_at	2.4386E-02	1.30E-03	-3.30	-1.13	-5.56E-01
2919	SEC13	207707_s_at	2.4386E-02	1.30E-03	-3.30	-1.13	-3.15E-01
2920	PPP1R7	201214_s_at	2.4407E-02	1.30E-03	-3.30	-1.13	-4.39E-01
2921	SEC23B	210293_s_at	2.4439E-02	1.31E-03	-3.30	-1.13	-2.36E-01
2922	MLF1IP	229305_at	2.4502E-02	1.31E-03	3.30	-1.14	3.91E-01
2923	DPYSL3	201431_s_at	2.4502E-02	1.31E-03	-3.30	-1.14	-6.70E-01
2924	SLC39A6	1555460_a_at	2.4509E-02	1.31E-03	-3.29	-1.14	-3.62E-01
2925	ZNF638	211257_x_at	2.4538E-02	1.31E-03	-3.29	-1.14	-4.45E-01
2926	P4HA2	202733_at	2.4561E-02	1.31E-03	-3.29	-1.14	-8.41E-01
2927	ALAD	218487_at	2.4570E-02	1.32E-03	-3.29	-1.14	-2.80E-01
2928		1558784_at	2.4575E-02	1.32E-03	3.29	-1.14	2.92E-01
2929	STAT3	208991_at	2.4576E-02	1.32E-03	-3.29	-1.14	-5.50E-01
2930		244670_at	2.4580E-02	1.32E-03	3.29	-1.14	1.14E-01
2931	REEP5	208872_s_at	2.4611E-02	1.32E-03	-3.29	-1.14	-3.69E-01
2932	ATP6V0C	36994_at	2.4632E-02	1.32E-03	-3.29	-1.14	-4.94E-01
2933	C20orf27	218081_at	2.4654E-02	1.32E-03	-3.29	-1.14	-2.19E-01
2934	TMPO	209754_s_at	2.4677E-02	1.32E-03	3.29	-1.14	3.50E-01
2935	LILRA6///LILRB3	211133_x_at	2.4677E-02	1.33E-03	-3.29	-1.15	-4.15E-01
2936	SFRP5	207468_s_at	2.4677E-02	1.33E-03	3.29	-1.15	1.51E-01
2937	ITM2B	217732_s_at	2.4687E-02	1.33E-03	-3.29	-1.15	-3.02E-01
2938	CFHR2	206910_x_at	2.4695E-02	1.33E-03	-3.29	-1.15	-2.27E-01
2939		1557521_a_at	2.4695E-02	1.33E-03	3.29	-1.15	2.69E-01
2940	BACE1	224335_s_at	2.4695E-02	1.33E-03	-3.29	-1.15	-2.25E-01
2941	TTC39C	230747_s_at	2.4695E-02	1.33E-03	3.29	-1.15	4.67E-01
2942	RBPMS	207836_s_at	2.4695E-02	1.33E-03	-3.29	-1.15	-3.72E-01
2943		238785_at	2.4695E-02	1.33E-03	3.29	-1.15	2.07E-01
2944	EPB41L4B	220524_at	2.4720E-02	1.33E-03	3.29	-1.15	1.44E-01
2945	PTGIS	211892_s_at	2.4755E-02	1.33E-03	-3.29	-1.15	-1.80E-01
2946	RHOQ	212122_at	2.4759E-02	1.33E-03	-3.29	-1.15	-4.07E-01
2947	TXNIP	201008_s_at	2.4784E-02	1.34E-03	-3.29	-1.15	-5.71E-01
2948	CCDC124	225454_at	2.4784E-02	1.34E-03	-3.29	-1.15	-2.85E-01
2949	YWHAB	217717_s_at	2.4796E-02	1.34E-03	-3.29	-1.15	-4.33E-01
2950	USP9X	229573_at	2.4808E-02	1.34E-03	3.29	-1.15	2.73E-01
2951	ZNF346	236267_at	2.4810E-02	1.34E-03	3.29	-1.15	3.25E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
2952	MTF2	209705_at	2.4825E-02	1.34E-03	3.29	-1.16	2.61E-01
2953	LOC646522	237662_at	2.4825E-02	1.34E-03	3.29	-1.16	1.74E-01
2954	LRRC2	219949_at	2.4829E-02	1.34E-03	-3.29	-1.16	-1.46E-01
2955		221138_s_at	2.4840E-02	1.34E-03	3.29	-1.16	1.29E-01
2956	MUTED	226544_x_at	2.4899E-02	1.35E-03	3.29	-1.16	2.21E-01
2957		241010_x_at	2.4956E-02	1.35E-03	3.29	-1.16	1.94E-01
2958	ASAP1	221039_s_at	2.4956E-02	1.35E-03	-3.29	-1.16	-6.60E-01
2959		1570496_at	2.4956E-02	1.35E-03	3.29	-1.16	1.32E-01
2960	FBP1	209696_at	2.4960E-02	1.35E-03	-3.29	-1.16	-8.63E-01
2961	PEX13	1558163_at	2.4987E-02	1.35E-03	3.28	-1.16	1.26E-01
2962	ABL2	226893_at	2.4987E-02	1.35E-03	-3.28	-1.16	-3.10E-01
2963		1554108_at	2.4987E-02	1.35E-03	3.28	-1.16	1.97E-01
2964	COL6A6	230867_at	2.4987E-02	1.35E-03	-3.28	-1.16	-1.17E+00
2965		230667_at	2.4989E-02	1.36E-03	3.28	-1.17	2.12E-01
2966		243107_at	2.4989E-02	1.36E-03	3.28	-1.17	3.04E-01
2967		220827_at	2.4989E-02	1.36E-03	3.28	-1.17	1.64E-01
2968	SNHG1	224610_at	2.5014E-02	1.36E-03	3.28	-1.17	5.05E-01
2969		239788_at	2.5020E-02	1.36E-03	3.28	-1.17	2.60E-01
2970	UXT	218495_at	2.5043E-02	1.36E-03	3.28	-1.17	4.68E-01
2971	THY1	208850_s_at	2.5043E-02	1.36E-03	-3.28	-1.17	-6.09E-01
2972		235943_at	2.5055E-02	1.36E-03	3.28	-1.17	1.36E-01
2973		230725_at	2.5077E-02	1.36E-03	3.28	-1.17	1.64E-01
2974		1564468_at	2.5087E-02	1.36E-03	3.28	-1.17	9.60E-02
2975	DNAJC24	213853_at	2.5118E-02	1.37E-03	3.28	-1.17	2.44E-01
2976	ZNF689	227445_at	2.5118E-02	1.37E-03	-3.28	-1.17	-3.99E-01
2977	ESAM	225369_at	2.5120E-02	1.37E-03	-3.28	-1.17	-2.80E-01
2978	DHRS7	210788_s_at	2.5120E-02	1.37E-03	-3.28	-1.17	-4.07E-01
2979		231350_at	2.5120E-02	1.37E-03	3.28	-1.17	1.44E-01
2980	MDFIC	239172_x_at	2.5120E-02	1.37E-03	3.28	-1.17	1.52E-01
2981	RLN2	214519_s_at	2.5129E-02	1.37E-03	3.28	-1.18	7.53E-01
2982	PAPSS1	209043_at	2.5130E-02	1.37E-03	-3.28	-1.18	-4.00E-01
2983	PDE4D	204491_at	2.5138E-02	1.37E-03	3.28	-1.18	3.46E-01
2984	IL10RA	204912_at	2.5148E-02	1.37E-03	-3.28	-1.18	-3.67E-01
2985	MLXIP	202519_at	2.5152E-02	1.37E-03	-3.28	-1.18	-5.35E-01
2986		1569167_at	2.5155E-02	1.37E-03	3.28	-1.18	1.48E-01
2987	PTGFRN	224937_at	2.5198E-02	1.38E-03	-3.28	-1.18	-7.42E-01
2988	GNS	212334_at	2.5198E-02	1.38E-03	-3.28	-1.18	-5.87E-01
2989	HPS6	219052_at	2.5198E-02	1.38E-03	-3.28	-1.18	-2.24E-01
2990	NHEDC1	1553633_s_at	2.5202E-02	1.38E-03	3.28	-1.18	1.80E-01
2991	GMFG	204220_at	2.5202E-02	1.38E-03	3.28	-1.18	5.05E-01
2992	TOM1	202807_s_at	2.5202E-02	1.38E-03	-3.28	-1.18	-3.55E-01
2993	FLJ90757	1558147_a_at	2.5232E-02	1.38E-03	3.28	-1.18	1.40E-01
2994	EDN1	222802_at	2.5232E-02	1.38E-03	-3.28	-1.18	-3.58E-01
2995	DDX21	224654_at	2.5232E-02	1.38E-03	-3.28	-1.18	-2.59E-01
2996	TM9SF4	212194_s_at	2.5232E-02	1.38E-03	-3.28	-1.18	-5.40E-01
2997	AGTRAP	1555736_a_at	2.5232E-02	1.38E-03	-3.28	-1.18	-5.65E-01
2998	TBC1D9B	206431_x_at	2.5232E-02	1.38E-03	-3.28	-1.18	-3.00E-01
2999	EDNRB	206701_x_at	2.5232E-02	1.38E-03	-3.28	-1.18	-4.02E-01
3000		239682_at	2.5257E-02	1.39E-03	3.28	-1.19	1.66E-01
3001	NUDT19	235384_at	2.5263E-02	1.39E-03	-3.28	-1.19	-3.59E-01
3002	NFE2L1	200758_s_at	2.5268E-02	1.39E-03	-3.28	-1.19	-3.86E-01
3003	VAMP3	201337_s_at	2.5271E-02	1.39E-03	-3.28	-1.19	-5.84E-01
3004	ZDHHC13	219296_at	2.5271E-02	1.39E-03	3.28	-1.19	5.56E-01
3005	GLB1	201576_s_at	2.5286E-02	1.39E-03	-3.28	-1.19	-3.91E-01
3006	GRN	200678_x_at	2.5337E-02	1.39E-03	-3.28	-1.19	-6.64E-01
3007	ROGDI	218394_at	2.5337E-02	1.39E-03	-3.28	-1.19	-1.91E-01
3008	CANT1	1554327_a_at	2.5337E-02	1.39E-03	-3.28	-1.19	-1.73E-01
3009	NID1	202007_at	2.5366E-02	1.40E-03	-3.28	-1.19	-7.88E-01
3010		237337_at	2.5366E-02	1.40E-03	3.28	-1.19	2.47E-01
3011	MXD3	221250_s_at	2.5366E-02	1.40E-03	3.28	-1.19	1.97E-01
3012	GLMN	207153_s_at	2.5366E-02	1.40E-03	3.28	-1.19	4.11E-01
3013	NCRNA00202	231196_x_at	2.5410E-02	1.40E-03	3.27	-1.19	1.36E-01
3014	ARL6IP5	200760_s_at	2.5423E-02	1.40E-03	-3.27	-1.20	-2.99E-01
3015	LOC100134331///LOC100126583///LOC652128///LOC642131/	211835_at	2.5423E-02	1.40E-03	-3.27	-1.20	-4.00E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
	//VSIG6///IGHV4-31///IGHM///IGHG4///IGHG3///IGHG1///IGHD///IGHA2///IGHA1///IGH@						
3016		1554374_at	2.5423E-02	1.40E-03	3.27	-1.20	1.33E-01
3017	GART	212379_at	2.5423E-02	1.40E-03	-3.27	-1.20	-3.85E-01
3018	C17orf63	222641_s_at	2.5423E-02	1.40E-03	-3.27	-1.20	-3.52E-01
3019	NCRNA00081	213220_at	2.5423E-02	1.40E-03	3.27	-1.20	4.73E-01
3020		1564130_x_at	2.5423E-02	1.40E-03	3.27	-1.20	1.15E-01
3021	BATF2	228439_at	2.5423E-02	1.40E-03	-3.27	-1.20	-5.65E-01
3022	TFAP2C	205287_s_at	2.5441E-02	1.41E-03	3.27	-1.20	1.29E-01
3023	GAS6	1598_g_at	2.5442E-02	1.41E-03	-3.27	-1.20	-4.36E-01
3024	TFB1M	219169_s_at	2.5442E-02	1.41E-03	3.27	-1.20	3.90E-01
3025	FKBP1A	210186_s_at	2.5455E-02	1.41E-03	-3.27	-1.20	-4.15E-01
3026	CHID1	223061_at	2.5455E-02	1.41E-03	-3.27	-1.20	-2.35E-01
3027	DDR2	225442_at	2.5455E-02	1.41E-03	-3.27	-1.20	-6.31E-01
3028	MGST1	224918_x_at	2.5455E-02	1.41E-03	-3.27	-1.20	-9.36E-01
3029	PTGFRN	224950_at	2.5455E-02	1.41E-03	-3.27	-1.20	-4.19E-01
3030		236763_at	2.5471E-02	1.41E-03	3.27	-1.20	1.87E-01
3031	HLA-DQB1	211656_x_at	2.5496E-02	1.41E-03	-3.27	-1.20	-6.01E-01
3032	HLA-DQB1	212998_x_at	2.5496E-02	1.41E-03	-3.27	-1.20	-6.09E-01
3033	MTERF	204871_at	2.5502E-02	1.41E-03	3.27	-1.20	3.04E-01
3034		1561100_at	2.5547E-02	1.42E-03	-3.27	-1.21	-1.18E-01
3035	EPC1	238633_at	2.5564E-02	1.42E-03	3.27	-1.21	2.62E-01
3036	RPH3AL	221614_s_at	2.5569E-02	1.42E-03	-3.27	-1.21	-2.03E-01
3037	FBXL12	220127_s_at	2.5583E-02	1.42E-03	3.27	-1.21	2.42E-01
3038	ALDH3A2	210544_s_at	2.5586E-02	1.42E-03	-3.27	-1.21	-2.70E-01
3039	LGALS9	203236_s_at	2.5612E-02	1.42E-03	-3.27	-1.21	-3.68E-01
3040	TAF1D	221580_s_at	2.5638E-02	1.43E-03	3.27	-1.21	3.12E-01
3041	MS4A7	224358_s_at	2.5638E-02	1.43E-03	-3.27	-1.21	-8.66E-01
3042	SLC7A7	204588_s_at	2.5638E-02	1.43E-03	-3.27	-1.21	-4.15E-01
3043	LAPTM4B	214039_s_at	2.5638E-02	1.43E-03	-3.27	-1.21	-6.35E-01
3044	CELF1	204113_at	2.5638E-02	1.43E-03	-3.27	-1.21	-2.47E-01
3045		242612_at	2.5638E-02	1.43E-03	3.27	-1.21	1.52E-01
3046	ZNF680	229533_x_at	2.5675E-02	1.43E-03	3.27	-1.21	4.13E-01
3047	PNPLA7	236135_at	2.5692E-02	1.43E-03	3.27	-1.21	1.19E-01
3048	HRAS	212983_at	2.5707E-02	1.43E-03	-3.27	-1.21	-3.03E-01
3049	RGMB	226989_at	2.5707E-02	1.43E-03	-3.27	-1.22	-3.63E-01
3050	RGS5	209071_s_at	2.5719E-02	1.43E-03	-3.27	-1.22	-7.52E-01
3051	LOC442497///SLC3A2	200924_s_at	2.5738E-02	1.44E-03	-3.27	-1.22	-3.60E-01
3052	GPR112	1553006_at	2.5738E-02	1.44E-03	3.27	-1.22	1.05E-01
3053	DUSP18	1553701_a_at	2.5743E-02	1.44E-03	3.27	-1.22	1.46E-01
3054	COL1A1	202310_s_at	2.5743E-02	1.44E-03	-3.27	-1.22	-1.41E+00
3055	LIX1	236163_at	2.5755E-02	1.44E-03	3.27	-1.22	1.21E-01
3056	VPS18	223346_at	2.5761E-02	1.44E-03	-3.27	-1.22	-3.10E-01
3057	C14orf138	218940_at	2.5761E-02	1.44E-03	3.27	-1.22	4.84E-01
3058	PXDN	212013_at	2.5761E-02	1.44E-03	-3.27	-1.22	-8.43E-01
3059	TMEM161B	227861_at	2.5761E-02	1.44E-03	3.27	-1.22	3.38E-01
3060	UBE2Z	222395_s_at	2.5761E-02	1.44E-03	-3.27	-1.22	-4.03E-01
3061	ARNT2	202986_at	2.5761E-02	1.44E-03	-3.27	-1.22	-3.66E-01
3062	TRIOBP	210276_s_at	2.5761E-02	1.44E-03	-3.27	-1.22	-5.35E-01
3063	SFT2D1	226836_at	2.5761E-02	1.44E-03	3.27	-1.22	3.02E-01
3064	C9orf103	227865_at	2.5761E-02	1.44E-03	3.26	-1.22	2.54E-01
3065	DOPEY1	213271_s_at	2.5769E-02	1.44E-03	3.26	-1.22	4.41E-01
3066	SLC17A5	223441_at	2.5783E-02	1.45E-03	-3.26	-1.22	-3.73E-01
3067	C9orf100	230522_s_at	2.5783E-02	1.45E-03	3.26	-1.22	1.52E-01
3068	CACNG5	221401_at	2.5783E-02	1.45E-03	3.26	-1.22	1.32E-01
3069	SPATA21	1570241_at	2.5783E-02	1.45E-03	3.26	-1.22	2.12E-01
3070	CLEC11A	210783_x_at	2.5783E-02	1.45E-03	-3.26	-1.22	-2.43E-01
3071	ANO10	218910_at	2.5783E-02	1.45E-03	-3.26	-1.22	-3.68E-01
3072	RNF144B	235549_at	2.5783E-02	1.45E-03	-3.26	-1.22	-5.02E-01
3073	ABHD2	205566_at	2.5843E-02	1.45E-03	-3.26	-1.23	-2.82E-01
3074		1563771_a_at	2.5867E-02	1.45E-03	3.26	-1.23	1.06E-01
3075	AGMAT	222930_s_at	2.5876E-02	1.46E-03	3.26	-1.23	3.95E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3076	URGCP	244046_at	2.5876E-02	1.46E-03	3.26	-1.23	3.33E-01
3077	SH3BGRL3	221269_s_at	2.5876E-02	1.46E-03	-3.26	-1.23	-6.04E-01
3078	RBM47	218035_s_at	2.5876E-02	1.46E-03	-3.26	-1.23	-4.69E-01
3079	TPM4	209344_at	2.5876E-02	1.46E-03	-3.26	-1.23	-4.85E-01
3080	SEMA6D	233882_s_at	2.5884E-02	1.46E-03	-3.26	-1.23	-1.54E-01
3081	GNB4	223487_x_at	2.5903E-02	1.46E-03	-3.26	-1.23	-3.04E-01
3082	PAK1	209615_s_at	2.5934E-02	1.46E-03	-3.26	-1.23	-2.77E-01
3083	NOTCH2	212377_s_at	2.5946E-02	1.46E-03	-3.26	-1.23	-4.14E-01
3084	SDF4	232032_x_at	2.5954E-02	1.46E-03	-3.26	-1.23	-4.32E-01
3085	CAMLG	203538_at	2.5996E-02	1.47E-03	3.26	-1.24	3.88E-01
3086	TOR2A	227972_at	2.6005E-02	1.47E-03	-3.26	-1.24	-2.24E-01
3087	LOC401074	1559827_at	2.6009E-02	1.47E-03	-3.26	-1.24	-1.82E-01
3088	PHC2	200919_at	2.6023E-02	1.47E-03	-3.26	-1.24	-3.41E-01
3089		229802_at	2.6031E-02	1.47E-03	-3.26	-1.24	-9.29E-01
3090	NFIB	211467_s_at	2.6049E-02	1.47E-03	-3.26	-1.24	-3.71E-01
3091	C5orf33	226946_at	2.6052E-02	1.47E-03	-3.26	-1.24	-2.70E-01
3092	PERP	217744_s_at	2.6054E-02	1.47E-03	-3.26	-1.24	-6.84E-01
3093	BCL2L13	223664_x_at	2.6117E-02	1.48E-03	3.26	-1.24	3.71E-01
3094	PSMA3	237300_at	2.6117E-02	1.48E-03	3.26	-1.24	2.21E-01
3095	COL3A1	201852_x_at	2.6154E-02	1.48E-03	-3.26	-1.24	-1.26E+00
3096		1557667_at	2.6169E-02	1.48E-03	3.26	-1.24	1.91E-01
3097	CD5L	206680_at	2.6169E-02	1.48E-03	-3.26	-1.24	-5.26E-01
3098	DDX21	208152_s_at	2.6213E-02	1.49E-03	-3.26	-1.25	-3.50E-01
3099	CLCN4	231066_s_at	2.6213E-02	1.49E-03	3.26	-1.25	1.34E-01
3100		242425_at	2.6213E-02	1.49E-03	3.26	-1.25	2.67E-01
3101	RND3	212724_at	2.6213E-02	1.49E-03	-3.26	-1.25	-4.47E-01
3102	BNIP3	201848_s_at	2.6247E-02	1.49E-03	-3.26	-1.25	-4.45E-01
3103	CHMP4B	225119_at	2.6254E-02	1.49E-03	-3.26	-1.25	-6.04E-01
3104	ZNF7	234920_at	2.6254E-02	1.49E-03	3.26	-1.25	1.06E-01
3105	TCP11L2	1569207_s_at	2.6257E-02	1.49E-03	3.25	-1.25	1.51E-01
3106		242588_at	2.6309E-02	1.49E-03	3.25	-1.25	1.03E-01
3107	STAP1	1554343_a_at	2.6325E-02	1.50E-03	3.25	-1.25	7.66E-01
3108	BCR	217223_s_at	2.6325E-02	1.50E-03	-3.25	-1.25	-3.12E-01
3109		229363_at	2.6372E-02	1.50E-03	3.25	-1.25	3.94E-01
3110		227853_at	2.6408E-02	1.50E-03	-3.25	-1.26	-5.65E-01
3111	ANAPC16	229145_at	2.6432E-02	1.50E-03	3.25	-1.26	4.10E-01
3112		229695_at	2.6432E-02	1.50E-03	3.25	-1.26	3.10E-01
3113	CTNND1	211240_x_at	2.6432E-02	1.50E-03	-3.25	-1.26	-3.36E-01
3114	NFIC	206929_s_at	2.6470E-02	1.51E-03	-3.25	-1.26	-3.89E-01
3115	PFDN5	207132_x_at	2.6470E-02	1.51E-03	3.25	-1.26	4.13E-01
3116	ATG12	204833_at	2.6510E-02	1.51E-03	3.25	-1.26	3.43E-01
3117		242388_x_at	2.6520E-02	1.51E-03	3.25	-1.26	4.31E-01
3118	MDM4	205655_at	2.6520E-02	1.51E-03	3.25	-1.26	2.74E-01
3119	COX5B	213736_at	2.6545E-02	1.51E-03	3.25	-1.26	4.89E-01
3120	SFXN5	226373_at	2.6564E-02	1.52E-03	-3.25	-1.26	-2.42E-01
3121	FOSL2	228188_at	2.6564E-02	1.52E-03	-3.25	-1.26	-5.82E-01
3122		240314_at	2.6584E-02	1.52E-03	3.25	-1.27	2.89E-01
3123	PPP3CA	202425_x_at	2.6585E-02	1.52E-03	-3.25	-1.27	-3.82E-01
3124	NAGK	218231_at	2.6585E-02	1.52E-03	-3.25	-1.27	-5.04E-01
3125	SLC24A6	222727_s_at	2.6585E-02	1.52E-03	-3.25	-1.27	-2.38E-01
3126	SPRY1	212558_at	2.6585E-02	1.52E-03	-3.25	-1.27	-4.77E-01
3127	ASCL1	209985_s_at	2.6594E-02	1.52E-03	3.25	-1.27	1.68E-01
3128	COPZ1	217726_at	2.6603E-02	1.52E-03	-3.25	-1.27	-3.44E-01
3129	CWF19L1	218787_x_at	2.6603E-02	1.52E-03	3.25	-1.27	2.07E-01
3130	IMPA1	203011_at	2.6642E-02	1.53E-03	3.25	-1.27	2.84E-01
3131	GABARAP	200645_at	2.6642E-02	1.53E-03	-3.25	-1.27	-3.66E-01
3132	TRIP11	209778_at	2.6642E-02	1.53E-03	-3.25	-1.27	-3.39E-01
3133	PATL1	225468_at	2.6660E-02	1.53E-03	-3.25	-1.27	-5.14E-01
3134	CENPN	222118_at	2.6673E-02	1.53E-03	3.25	-1.27	4.08E-01
3135	LOC100129858	235869_at	2.6692E-02	1.53E-03	3.25	-1.27	1.17E-01
3136	MFHAS1	225478_at	2.6713E-02	1.53E-03	-3.25	-1.27	-3.55E-01
3137	S100A16	227998_at	2.6713E-02	1.53E-03	-3.25	-1.27	-4.43E-01
3138		236489_at	2.6715E-02	1.53E-03	3.25	-1.27	1.01E-01
3139	ATP6AP1	207809_s_at	2.6715E-02	1.53E-03	-3.25	-1.27	-5.61E-01
3140	RAX2	1552311_a_at	2.6715E-02	1.53E-03	3.25	-1.28	2.10E-01
3141		243224_at	2.6715E-02	1.53E-03	3.25	-1.28	2.98E-01
3142	KLRB1	242628_at	2.6729E-02	1.54E-03	3.25	-1.28	2.22E-01
3143	MT1X	208581_x_at	2.6742E-02	1.54E-03	-3.25	-1.28	-7.85E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3144	TNP2	207736_s_at	2.6742E-02	1.54E-03	3.25	-1.28	1.12E-01
3145	PHF23	1555789_s_at	2.6742E-02	1.54E-03	-3.25	-1.28	-3.69E-01
3146	RSU1	201980_s_at	2.6742E-02	1.54E-03	-3.25	-1.28	-4.80E-01
3147	ZMYM5	206744_s_at	2.6773E-02	1.54E-03	3.24	-1.28	1.18E-01
3148	ARPP21	220359_s_at	2.6798E-02	1.54E-03	3.24	-1.28	1.19E-01
3149	TYRO3P	1566934_at	2.6827E-02	1.55E-03	3.24	-1.28	1.36E-01
3150	CBR1	209213_at	2.6827E-02	1.55E-03	-3.24	-1.28	-4.71E-01
3151	XPA	232967_at	2.6827E-02	1.55E-03	3.24	-1.28	1.23E-01
3152	NOMO3///NOMO2///NOMO1	221853_s_at	2.6834E-02	1.55E-03	-3.24	-1.28	-4.01E-01
3153	PAFAH1B2	224777_s_at	2.6848E-02	1.55E-03	-3.24	-1.28	-3.61E-01
3154		241434_at	2.6857E-02	1.55E-03	3.24	-1.28	2.33E-01
3155	FAM120B	227895_at	2.6867E-02	1.55E-03	-3.24	-1.28	-1.70E-01
3156		233431_x_at	2.6867E-02	1.55E-03	3.24	-1.28	2.06E-01
3157	MKRN2	222510_s_at	2.6867E-02	1.55E-03	-3.24	-1.28	-3.34E-01
3158	LOC645468	216494_at	2.6867E-02	1.55E-03	3.24	-1.29	1.36E-01
3159	RGMA	223468_s_at	2.6869E-02	1.55E-03	-3.24	-1.29	-2.81E-01
3160	FRMD6	225464_at	2.6880E-02	1.55E-03	-3.24	-1.29	-7.17E-01
3161	AK2	205996_s_at	2.6902E-02	1.56E-03	-3.24	-1.29	-4.15E-01
3162	TUBB2C	208977_x_at	2.6902E-02	1.56E-03	-3.24	-1.29	-4.47E-01
3163		1561575_at	2.6920E-02	1.56E-03	3.24	-1.29	9.98E-02
3164	UBC///UBB//RPS27A	242214_at	2.6920E-02	1.56E-03	3.24	-1.29	3.55E-01
3165	COL28A1	239921_at	2.6920E-02	1.56E-03	3.24	-1.29	9.75E-02
3166	CCDC59	218936_s_at	2.6927E-02	1.56E-03	3.24	-1.29	3.90E-01
3167	FANCF	222713_s_at	2.6927E-02	1.56E-03	3.24	-1.29	2.61E-01
3168	RAB5C	201140_s_at	2.6928E-02	1.56E-03	-3.24	-1.29	-3.88E-01
3169	LOC254128	235132_at	2.6928E-02	1.56E-03	3.24	-1.29	2.78E-01
3170	OFD1	203569_s_at	2.6959E-02	1.56E-03	3.24	-1.29	3.48E-01
3171	PIK3C2A	226094_at	2.6959E-02	1.56E-03	-3.24	-1.29	-4.75E-01
3172	KIAA2013	224706_at	2.6974E-02	1.56E-03	-3.24	-1.29	-3.76E-01
3173		236353_at	2.7045E-02	1.57E-03	3.24	-1.30	1.90E-01
3174		244082_at	2.7052E-02	1.57E-03	3.24	-1.30	1.62E-01
3175		238369_s_at	2.7052E-02	1.57E-03	3.24	-1.30	1.33E-01
3176	PTPRN2	203030_s_at	2.7053E-02	1.57E-03	3.24	-1.30	5.33E-01
3177	SLC7A8	216092_s_at	2.7053E-02	1.57E-03	-3.24	-1.30	-3.35E-01
3178		241798_at	2.7074E-02	1.57E-03	3.24	-1.30	3.84E-01
3179	E2F7	241725_at	2.7099E-02	1.58E-03	3.24	-1.30	1.46E-01
3180	FN3K	219744_at	2.7099E-02	1.58E-03	3.24	-1.30	1.57E-01
3181	NID1	202008_s_at	2.7122E-02	1.58E-03	-3.24	-1.30	-3.80E-01
3182	CD44	229221_at	2.7122E-02	1.58E-03	-3.24	-1.30	-3.36E-01
3183		1557699_x_at	2.7122E-02	1.58E-03	3.24	-1.30	1.84E-01
3184		229243_at	2.7122E-02	1.58E-03	3.24	-1.30	2.06E-01
3185	C11orf30	1569349_at	2.7122E-02	1.58E-03	3.24	-1.30	4.91E-01
3186	BMP1	202701_at	2.7122E-02	1.58E-03	-3.24	-1.30	-3.24E-01
3187	ATP8B5P	1568686_at	2.7125E-02	1.58E-03	3.24	-1.30	8.90E-02
3188	MAP1S	218522_s_at	2.7125E-02	1.58E-03	-3.24	-1.30	-4.29E-01
3189	SIKE1	204665_at	2.7125E-02	1.58E-03	3.24	-1.30	1.31E-01
3190		1562069_at	2.7126E-02	1.58E-03	3.24	-1.30	1.40E-01
3191	LPP	202822_at	2.7148E-02	1.58E-03	-3.24	-1.30	-3.86E-01
3192	COL6A2	209156_s_at	2.7150E-02	1.59E-03	-3.24	-1.30	-1.07E+00
3193	TMED5	202195_s_at	2.7150E-02	1.59E-03	-3.24	-1.30	-4.03E-01
3194		1564097_at	2.7154E-02	1.59E-03	3.24	-1.30	1.11E-01
3195	ZDHHC21	229240_at	2.7154E-02	1.59E-03	3.24	-1.30	3.13E-01
3196		233331_at	2.7156E-02	1.59E-03	3.24	-1.30	1.93E-01
3197	GKAP1	229312_s_at	2.7206E-02	1.59E-03	3.23	-1.31	3.60E-01
3198	ELL3	219518_s_at	2.7209E-02	1.59E-03	3.23	-1.31	8.14E-01
3199	THTPA	218540_at	2.7242E-02	1.59E-03	-3.23	-1.31	-2.65E-01
3200		237399_at	2.7256E-02	1.60E-03	3.23	-1.31	1.24E-01
3201		1556984_at	2.7256E-02	1.60E-03	3.23	-1.31	1.63E-01
3202	DYX1C1	235273_at	2.7256E-02	1.60E-03	3.23	-1.31	1.17E-01
3203	SLCO3A1	219229_at	2.7256E-02	1.60E-03	-3.23	-1.31	-5.36E-01
3204	LOC729580	225860_at	2.7311E-02	1.60E-03	-3.23	-1.31	-3.73E-01
3205	HADHB	201007_at	2.7364E-02	1.60E-03	-3.23	-1.31	-2.06E-01
3206	IGF1	209541_at	2.7377E-02	1.61E-03	-3.23	-1.32	-1.19E+00
3207	UCHL1	201387_s_at	2.7377E-02	1.61E-03	-3.23	-1.32	-6.34E-01
3208	APLP2	208248_x_at	2.7408E-02	1.61E-03	-3.23	-1.32	-4.85E-01
3209	UBE2DNL	1554763_at	2.7421E-02	1.61E-03	3.23	-1.32	1.43E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3210	TAS2R19	1570384_at	2.7433E-02	1.61E-03	3.23	-1.32	9.98E-02
3211	WDR83	224434_s_at	2.7455E-02	1.61E-03	-3.23	-1.32	-2.14E-01
3212	FKBP9	212169_at	2.7459E-02	1.61E-03	-3.23	-1.32	-6.04E-01
3213	PUS7L	229751_s_at	2.7459E-02	1.61E-03	3.23	-1.32	2.83E-01
3214		1555631_at	2.7459E-02	1.61E-03	3.23	-1.32	2.13E-01
3215	SNRPG	205644_s_at	2.7459E-02	1.62E-03	3.23	-1.32	4.72E-01
3216	TLR10	223750_s_at	2.7459E-02	1.62E-03	3.23	-1.32	6.30E-01
3217	RAD23A	201039_s_at	2.7461E-02	1.62E-03	-3.23	-1.32	-4.75E-01
3218	SDHAP1	222021_x_at	2.7498E-02	1.62E-03	-3.23	-1.32	-2.23E-01
3219	PHKB	202738_s_at	2.7498E-02	1.62E-03	-3.23	-1.32	-3.65E-01
3220	CBLN4	234024_at	2.7520E-02	1.62E-03	3.23	-1.32	1.38E-01
3221	COL14A1	212865_s_at	2.7520E-02	1.62E-03	-3.23	-1.32	-8.51E-01
3222		1558481_s_at	2.7521E-02	1.62E-03	3.23	-1.32	1.30E-01
3223	IRAK1	1555784_s_at	2.7529E-02	1.62E-03	-3.23	-1.32	-2.26E-01
3224	CCDC80	225241_at	2.7539E-02	1.62E-03	-3.23	-1.33	-8.21E-01
3225	STX4	203530_s_at	2.7568E-02	1.63E-03	-3.23	-1.33	-4.24E-01
3226	DUT	208956_x_at	2.7568E-02	1.63E-03	3.23	-1.33	2.30E-01
3227	DHX9	202420_s_at	2.7578E-02	1.63E-03	-3.23	-1.33	-2.95E-01
3228	C9orf27	1570345_at	2.7593E-02	1.63E-03	3.23	-1.33	1.08E-01
3229	PPIL3	224364_s_at	2.7624E-02	1.63E-03	3.23	-1.33	4.80E-01
3230	MYD88	209124_at	2.7624E-02	1.63E-03	-3.23	-1.33	-3.78E-01
3231		1570375_at	2.7639E-02	1.63E-03	-3.23	-1.33	-1.80E-01
3232	PARVA	222454_s_at	2.7639E-02	1.63E-03	-3.23	-1.33	-4.58E-01
3233	PLOD2	202619_s_at	2.7639E-02	1.63E-03	-3.23	-1.33	-9.42E-01
3234	CRISP2	210262_at	2.7651E-02	1.64E-03	3.23	-1.33	1.23E-01
3235	FAM178A	235590_at	2.7661E-02	1.64E-03	3.23	-1.33	2.34E-01
3236	TIMM17A	201821_s_at	2.7670E-02	1.64E-03	-3.23	-1.33	-3.30E-01
3237	FAM114A1	213455_at	2.7670E-02	1.64E-03	-3.23	-1.33	-5.13E-01
3238	ZNF395	232694_at	2.7670E-02	1.64E-03	3.23	-1.33	1.24E-01
3239	U2AF1	231904_at	2.7670E-02	1.64E-03	3.23	-1.33	3.20E-01
3240		1561679_at	2.7670E-02	1.64E-03	3.23	-1.33	1.12E-01
3241	TMEM63A	215583_at	2.7717E-02	1.64E-03	3.22	-1.34	2.13E-01
3242		233784_at	2.7729E-02	1.64E-03	3.22	-1.34	1.23E-01
3243	HDAC8	223345_at	2.7729E-02	1.65E-03	-3.22	-1.34	-1.89E-01
3244	METTL13	206468_s_at	2.7729E-02	1.65E-03	-3.22	-1.34	-3.56E-01
3245	ACTB	224594_x_at	2.7729E-02	1.65E-03	-3.22	-1.34	-3.81E-01
3246	PPP3CA	202457_s_at	2.7729E-02	1.65E-03	-3.22	-1.34	-4.27E-01
3247	ZNF677	1569039_s_at	2.7729E-02	1.65E-03	3.22	-1.34	3.11E-01
3248	CRTAP	1554464_a_at	2.7729E-02	1.65E-03	-3.22	-1.34	-7.39E-01
3249	TUFM	201113_at	2.7749E-02	1.65E-03	-3.22	-1.34	-2.48E-01
3250	GABARAPL 1	208869_s_at	2.7757E-02	1.65E-03	-3.22	-1.34	-3.27E-01
3251	C18orf12	1553087_at	2.7799E-02	1.65E-03	3.22	-1.34	1.47E-01
3252	SFRP2	223122_s_at	2.7818E-02	1.65E-03	-3.22	-1.34	-1.83E+00
3253	FAM58A	226466_s_at	2.7820E-02	1.66E-03	3.22	-1.34	3.59E-01
3254	TNPO3	214550_s_at	2.7847E-02	1.66E-03	-3.22	-1.34	-4.72E-01
3255	SLC1A4	209611_s_at	2.7882E-02	1.66E-03	3.22	-1.34	1.62E-01
3256	ASIP	214498_at	2.7921E-02	1.66E-03	3.22	-1.35	1.41E-01
3257	OSGEPL1	230032_at	2.7930E-02	1.66E-03	3.22	-1.35	3.23E-01
3258	MYLIP	227707_at	2.7942E-02	1.67E-03	3.22	-1.35	1.88E-01
3259	AGPAT3	223183_at	2.7974E-02	1.67E-03	-3.22	-1.35	-4.06E-01
3260	PTGS1	205127_at	2.7980E-02	1.67E-03	-3.22	-1.35	-1.92E-01
3261	TPPP	230197_s_at	2.7981E-02	1.67E-03	3.22	-1.35	1.17E-01
3262	GNAS	217673_x_at	2.8013E-02	1.67E-03	-3.22	-1.35	-3.20E-01
3263	BRCC3	231913_s_at	2.8017E-02	1.67E-03	-3.22	-1.35	-3.27E-01
3264	BRWD1	231960_at	2.8050E-02	1.68E-03	3.22	-1.35	2.79E-01
3265	CLPTM1L	223020_at	2.8050E-02	1.68E-03	-3.22	-1.35	-5.36E-01
3266	NCKAP1L	209734_at	2.8065E-02	1.68E-03	-3.22	-1.35	-4.83E-01
3267	ZNF571	206648_at	2.8065E-02	1.68E-03	3.22	-1.35	3.41E-01
3268	CCDC23	244013_at	2.8065E-02	1.68E-03	3.22	-1.35	1.39E-01
3269	GART	230097_at	2.8095E-02	1.68E-03	3.22	-1.36	4.36E-01
3270	GDE1	202593_s_at	2.8095E-02	1.68E-03	-3.22	-1.36	-7.06E-01
3271		241906_at	2.8095E-02	1.68E-03	3.22	-1.36	2.71E-01
3272	WDR62	1553123_at	2.8095E-02	1.68E-03	3.22	-1.36	1.74E-01
3273	C2CD2L	204757_s_at	2.8127E-02	1.68E-03	-3.22	-1.36	-2.69E-01
3274	ATP6AP2	201444_s_at	2.8152E-02	1.69E-03	-3.22	-1.36	-4.47E-01
3275	STK4	223746_at	2.8163E-02	1.69E-03	3.22	-1.36	4.83E-01
3276	CD6	1566448_at	2.8163E-02	1.69E-03	3.22	-1.36	3.20E-01
3277	RPS8	200858_s_at	2.8166E-02	1.69E-03	3.22	-1.36	2.21E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3278	KCTD5	218474_s_at	2.8180E-02	1.69E-03	-3.22	-1.36	-4.31E-01
3279	MRPL24	218270_at	2.8193E-02	1.69E-03	-3.22	-1.36	-2.19E-01
3280	AIM1L	220290_at	2.8223E-02	1.69E-03	3.22	-1.36	1.44E-01
3281	PDXDC1	212053_at	2.8232E-02	1.70E-03	-3.21	-1.36	-2.82E-01
3282	ZNF107	243312_at	2.8232E-02	1.70E-03	3.21	-1.36	1.85E-01
3283	MXD1	226275_at	2.8232E-02	1.70E-03	-3.21	-1.36	-4.10E-01
3284	ZNF335	78330_at	2.8232E-02	1.70E-03	3.21	-1.36	1.46E-01
3285	ZC3HAV1L	228280_at	2.8232E-02	1.70E-03	-3.21	-1.36	-3.97E-01
3286	C22orf9	217118_s_at	2.8232E-02	1.70E-03	-3.21	-1.36	-4.42E-01
3287	NCRNA00081	232910_at	2.8232E-02	1.70E-03	3.21	-1.36	2.43E-01
3288	UBE2F	231948_s_at	2.8232E-02	1.70E-03	-3.21	-1.36	-3.26E-01
3289	SPTLC2	216202_s_at	2.8233E-02	1.70E-03	-3.21	-1.36	-6.58E-01
3290	LEPREL1	230813_at	2.8240E-02	1.70E-03	3.21	-1.37	2.72E-01
3291	ETS2	201329_s_at	2.8256E-02	1.70E-03	-3.21	-1.37	-4.40E-01
3292	SLC2A9	219991_at	2.8256E-02	1.70E-03	-3.21	-1.37	-2.81E-01
3293	BTD	204167_at	2.8256E-02	1.70E-03	-3.21	-1.37	-2.35E-01
3294		1562821_a_at	2.8256E-02	1.70E-03	3.21	-1.37	1.24E-01
3295		226348_at	2.8256E-02	1.70E-03	-3.21	-1.37	-2.78E-01
3296	FOXO3	204132_s_at	2.8256E-02	1.70E-03	-3.21	-1.37	-4.29E-01
3297	CCNO	210021_s_at	2.8256E-02	1.70E-03	3.21	-1.37	1.48E-01
3298		235964_x_at	2.8256E-02	1.70E-03	-3.21	-1.37	-3.36E-01
3299	TSTD1	226482_s_at	2.8260E-02	1.71E-03	3.21	-1.37	5.18E-01
3300	POLR1B	220113_x_at	2.8311E-02	1.71E-03	3.21	-1.37	3.31E-01
3301	PTGIS	208131_s_at	2.8311E-02	1.71E-03	-3.21	-1.37	-1.13E+00
3302	PRMT5	1564521_x_at	2.8316E-02	1.71E-03	-3.21	-1.37	-1.80E-01
3303	CLEC4G	1559065_a_at	2.8346E-02	1.71E-03	-3.21	-1.37	-8.54E-01
3304	PARD3B	1553190_s_at	2.8355E-02	1.71E-03	3.21	-1.37	1.74E-01
3305	LOC338579	1570473_at	2.8355E-02	1.71E-03	3.21	-1.37	1.01E-01
3306	PDIA5	203857_s_at	2.8370E-02	1.72E-03	-3.21	-1.37	-6.02E-01
3307	UNC13C	1556095_at	2.8370E-02	1.72E-03	3.21	-1.37	1.19E-01
3308	THADA	1566889_at	2.8370E-02	1.72E-03	3.21	-1.37	2.08E-01
3309	DAB2	201278_at	2.8370E-02	1.72E-03	-3.21	-1.37	-5.10E-01
3310	PLEK	203470_s_at	2.8370E-02	1.72E-03	-3.21	-1.37	-6.03E-01
3311	Sep-11	201307_at	2.8392E-02	1.72E-03	-3.21	-1.38	-5.03E-01
3312	PRSS47	234696_at	2.8480E-02	1.73E-03	3.21	-1.38	1.45E-01
3313	ARPC2	207988_s_at	2.8480E-02	1.73E-03	-3.21	-1.38	-1.76E-01
3314	ZNF587	231820_x_at	2.8490E-02	1.73E-03	3.21	-1.38	1.29E-01
3315	SULF2	224724_at	2.8490E-02	1.73E-03	-3.21	-1.38	-6.20E-01
3316	UBQLN2	215884_s_at	2.8502E-02	1.73E-03	-3.21	-1.38	-3.15E-01
3317	FKSG43///FRMD8	224271_x_at	2.8545E-02	1.73E-03	3.21	-1.38	1.39E-01
3318	RPL35A	225190_x_at	2.8565E-02	1.73E-03	3.21	-1.38	2.22E-01
3319	FLJ12334	232664_at	2.8567E-02	1.73E-03	3.21	-1.38	2.39E-01
3320	PHF11	242060_x_at	2.8579E-02	1.74E-03	3.21	-1.38	2.88E-01
3321	LAMC1	200770_s_at	2.8579E-02	1.74E-03	-3.21	-1.38	-3.39E-01
3322	SLC2A13	227176_at	2.8579E-02	1.74E-03	-3.21	-1.38	-3.72E-01
3323	MFHAS1	213457_at	2.8579E-02	1.74E-03	-3.21	-1.38	-4.76E-01
3324	IKBKG	36004_at	2.8579E-02	1.74E-03	-3.21	-1.38	-2.08E-01
3325		240016_at	2.8596E-02	1.74E-03	3.21	-1.39	1.89E-01
3326	DPH5	219590_x_at	2.8596E-02	1.74E-03	3.21	-1.39	4.39E-01
3327	SGPL1	212321_at	2.8596E-02	1.74E-03	-3.21	-1.39	-5.49E-01
3328	RPL22P22	217363_x_at	2.8596E-02	1.74E-03	3.21	-1.39	1.84E-01
3329	SEC14L1	202082_s_at	2.8601E-02	1.74E-03	-3.21	-1.39	-4.83E-01
3330	ZNF132	207402_at	2.8605E-02	1.74E-03	-3.21	-1.39	-1.21E-01
3331	HABP4	209818_s_at	2.8608E-02	1.74E-03	-3.21	-1.39	-1.45E-01
3332	NPM1	221923_s_at	2.8611E-02	1.74E-03	3.21	-1.39	3.16E-01
3333		216437_at	2.8649E-02	1.75E-03	3.21	-1.39	1.64E-01
3334	DDX46	229098_s_at	2.8649E-02	1.75E-03	3.21	-1.39	2.08E-01
3335	CR1	217552_x_at	2.8750E-02	1.75E-03	-3.20	-1.39	-3.86E-01
3336	LONP1	209017_s_at	2.8757E-02	1.75E-03	-3.20	-1.39	-3.73E-01
3337	PMP22	210139_s_at	2.8763E-02	1.76E-03	-3.20	-1.39	-6.26E-01
3338	ZNF585A	227674_at	2.8763E-02	1.76E-03	3.20	-1.39	8.00E-01
3339	ANKRD49	219069_at	2.8763E-02	1.76E-03	3.20	-1.39	3.84E-01
3340	KIAA1462	231841_s_at	2.8763E-02	1.76E-03	-3.20	-1.39	-3.18E-01
3341	LOC728868	1559586_at	2.8763E-02	1.76E-03	3.20	-1.39	1.56E-01
3342	KCNG2	208550_x_at	2.8766E-02	1.76E-03	3.20	-1.40	1.37E-01
3343	TP53TG1	210886_x_at	2.8767E-02	1.76E-03	3.20	-1.40	5.29E-01
3344	LOC650794	243760_at	2.8782E-02	1.76E-03	3.20	-1.40	1.55E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3345	TMEM164	223202_s_at	2.8796E-02	1.76E-03	-3.20	-1.40	-2.78E-01
3346		244599_at	2.8796E-02	1.76E-03	3.20	-1.40	3.66E-01
3347	YME1L1	201351_s_at	2.8796E-02	1.76E-03	-3.20	-1.40	-2.94E-01
3348		1564155_x_at	2.8796E-02	1.76E-03	3.20	-1.40	3.12E-01
3349	SRPK2	203182_s_at	2.8802E-02	1.76E-03	3.20	-1.40	4.60E-01
3350	NCRNA00204///NCRNA00204B	1552607_at	2.8818E-02	1.77E-03	3.20	-1.40	1.74E-01
3351	APC	215310_at	2.8832E-02	1.77E-03	3.20	-1.40	2.23E-01
3352		241837_at	2.8832E-02	1.77E-03	3.20	-1.40	6.34E-01
3353	LILRA6	208594_x_at	2.8858E-02	1.77E-03	-3.20	-1.40	-3.94E-01
3354	PTCD1	222796_at	2.8858E-02	1.77E-03	3.20	-1.40	1.57E-01
3355	ATP6V1B2	201089_at	2.8858E-02	1.77E-03	-3.20	-1.40	-4.99E-01
3356	COL1A1	1556499_s_at	2.8858E-02	1.77E-03	-3.20	-1.40	-9.21E-01
3357	C20orf166	232892_at	2.8858E-02	1.77E-03	3.20	-1.40	1.75E-01
3358	CPXM2	226824_at	2.8858E-02	1.77E-03	-3.20	-1.40	-4.62E-01
3359	SLC31A1	235013_at	2.8875E-02	1.77E-03	-3.20	-1.40	-4.99E-01
3360		1563116_at	2.8887E-02	1.78E-03	3.20	-1.40	9.96E-02
3361	KIAA1109	233096_at	2.8902E-02	1.78E-03	3.20	-1.40	1.40E-01
3362	TREML1	1555659_a_at	2.8947E-02	1.78E-03	3.20	-1.41	1.99E-01
3363	ING2	205981_s_at	2.8955E-02	1.78E-03	-3.20	-1.41	-3.52E-01
3364	SLC30A7	240277_at	2.8955E-02	1.78E-03	-3.20	-1.41	-2.90E-01
3365	C9orf156	222195_s_at	2.8955E-02	1.78E-03	3.20	-1.41	2.34E-01
3366	HYAL2	206855_s_at	2.8955E-02	1.78E-03	-3.20	-1.41	-2.72E-01
3367	GIMAP8	235306_at	2.8966E-02	1.78E-03	-3.20	-1.41	-4.62E-01
3368	PISD	202392_s_at	2.8966E-02	1.78E-03	-3.20	-1.41	-2.36E-01
3369	WDR64	1553373_at	2.8979E-02	1.79E-03	3.20	-1.41	1.61E-01
3370	MRC2	37408_at	2.8983E-02	1.79E-03	-3.20	-1.41	-5.49E-01
3371	MFNG	204152_s_at	2.8983E-02	1.79E-03	-3.20	-1.41	-3.53E-01
3372		240585_at	2.8983E-02	1.79E-03	3.20	-1.41	9.74E-02
3373		244868_at	2.8986E-02	1.79E-03	3.20	-1.41	2.64E-01
3374	GORASP2	208842_s_at	2.8986E-02	1.79E-03	-3.20	-1.41	-3.22E-01
3375	C20orf201	1554977_at	2.8986E-02	1.79E-03	3.20	-1.41	1.84E-01
3376	PANK2	238856_s_at	2.8990E-02	1.79E-03	3.20	-1.41	5.68E-01
3377	DSTN	201021_s_at	2.8997E-02	1.79E-03	-3.20	-1.41	-4.06E-01
3378	TP53TG1	210241_s_at	2.8997E-02	1.79E-03	3.20	-1.41	5.91E-01
3379		215968_at	2.9091E-02	1.80E-03	3.20	-1.41	1.73E-01
3380	MBNL2	205018_s_at	2.9091E-02	1.80E-03	-3.20	-1.42	-3.76E-01
3381	SLC12A7	218066_at	2.9125E-02	1.80E-03	-3.20	-1.42	-3.44E-01
3382	MRPS33	218654_s_at	2.9147E-02	1.80E-03	3.20	-1.42	4.91E-01
3383	ABCF1	200045_at	2.9147E-02	1.80E-03	-3.20	-1.42	-4.39E-01
3384	CRYBB2P1	1561274_at	2.9147E-02	1.81E-03	3.20	-1.42	1.17E-01
3385	PSEN1	207782_s_at	2.9147E-02	1.81E-03	-3.20	-1.42	-5.29E-01
3386		240201_at	2.9147E-02	1.81E-03	3.19	-1.42	2.06E-01
3387	AGPAT6	224776_at	2.9147E-02	1.81E-03	-3.19	-1.42	-4.14E-01
3388	SMARCA4	215714_s_at	2.9147E-02	1.81E-03	-3.19	-1.42	-6.01E-01
3389	C17orf100	229071_at	2.9147E-02	1.81E-03	3.19	-1.42	1.77E-01
3390	CORO7	219040_at	2.9147E-02	1.81E-03	-3.19	-1.42	-3.04E-01
3391	ANKHD1-EIF4EBP3///ANKHD1///EIF4EBP3	233292_s_at	2.9147E-02	1.81E-03	-3.19	-1.42	-3.74E-01
3392	DOK1	211121_s_at	2.9175E-02	1.81E-03	-3.19	-1.42	-2.52E-01
3393	BTBD18	215349_at	2.9186E-02	1.81E-03	3.19	-1.42	2.10E-01
3394	LSM5	202904_s_at	2.9200E-02	1.81E-03	3.19	-1.42	6.93E-01
3395	SSTR1	208482_at	2.9200E-02	1.81E-03	3.19	-1.42	1.24E-01
3396	PTPRA	213795_s_at	2.9213E-02	1.81E-03	-3.19	-1.42	-3.59E-01
3397	KCNMA1	221583_s_at	2.9222E-02	1.82E-03	-3.19	-1.42	-6.12E-01
3398	GPBP1	224648_at	2.9247E-02	1.82E-03	3.19	-1.42	2.55E-01
3399	RBM8A	214113_s_at	2.9247E-02	1.82E-03	-3.19	-1.42	-4.24E-01
3400	SLC6A16	1569940_at	2.9247E-02	1.82E-03	3.19	-1.43	2.35E-01
3401	SAP30	204900_x_at	2.9247E-02	1.82E-03	-3.19	-1.43	-3.97E-01
3402	CDK4	202246_s_at	2.9247E-02	1.82E-03	-3.19	-1.43	-3.81E-01
3403	RRBP1	201203_s_at	2.9247E-02	1.82E-03	-3.19	-1.43	-2.57E-01
3404	GUSBP1///GUSBL2	226947_at	2.9247E-02	1.82E-03	3.19	-1.43	2.82E-01
3405	C10orf35	226313_at	2.9250E-02	1.82E-03	3.19	-1.43	2.13E-01
3406	LOC653739	1561894_at	2.9274E-02	1.82E-03	3.19	-1.43	1.60E-01
3407	LRMP	240718_at	2.9274E-02	1.82E-03	3.19	-1.43	1.92E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3408	C9orf89	223398_at	2.9280E-02	1.83E-03	-3.19	-1.43	-2.86E-01
3409		216628_at	2.9280E-02	1.83E-03	-3.19	-1.43	-1.31E-01
3410	DNAJA1	200880_at	2.9280E-02	1.83E-03	-3.19	-1.43	-3.89E-01
3411	FAM59A	219377_at	2.9288E-02	1.83E-03	-3.19	-1.43	-1.52E-01
3412		236479_at	2.9288E-02	1.83E-03	3.19	-1.43	1.44E-01
3413	MSRB3	225782_at	2.9288E-02	1.83E-03	-3.19	-1.43	-8.47E-01
3414		243383_at	2.9303E-02	1.83E-03	3.19	-1.43	1.74E-01
3415	LPHN2	206953_s_at	2.9317E-02	1.83E-03	-3.19	-1.43	-3.17E-01
3416	C17orf72	232972_at	2.9320E-02	1.83E-03	3.19	-1.43	1.62E-01
3417	PSMD4	210460_s_at	2.9332E-02	1.83E-03	-3.19	-1.43	-4.37E-01
3418		236528_at	2.9332E-02	1.83E-03	3.19	-1.43	2.86E-01
3419		1567000_at	2.9332E-02	1.83E-03	3.19	-1.43	9.51E-02
3420	RGS20	1569303_s_at	2.9340E-02	1.84E-03	3.19	-1.43	1.49E-01
3421	CPPED1	218610_s_at	2.9340E-02	1.84E-03	-3.19	-1.43	-3.07E-01
3422	GRIK2	215655_at	2.9340E-02	1.84E-03	3.19	-1.43	8.57E-02
3423	SOAT1	221561_at	2.9340E-02	1.84E-03	-3.19	-1.43	-4.29E-01
3424	CIZ1	205516_x_at	2.9377E-02	1.84E-03	-3.19	-1.44	-3.12E-01
3425	PPP1R7	213465_s_at	2.9377E-02	1.84E-03	-3.19	-1.44	-4.71E-01
3426		241928_at	2.9410E-02	1.84E-03	3.19	-1.44	1.90E-01
3427	TIMM9	218316_at	2.9430E-02	1.84E-03	3.19	-1.44	4.14E-01
3428	MLH1	202520_s_at	2.9430E-02	1.85E-03	-3.19	-1.44	-2.72E-01
3429	XPO7	212166_at	2.9431E-02	1.85E-03	-3.19	-1.44	-3.93E-01
3430	PPP1R11	1566303_s_at	2.9431E-02	1.85E-03	-3.19	-1.44	-6.58E-01
3431	ADD1	214736_s_at	2.9431E-02	1.85E-03	-3.19	-1.44	-5.26E-01
3432		244125_at	2.9431E-02	1.85E-03	3.19	-1.44	3.12E-01
3433	ARHGEF11	202914_s_at	2.9431E-02	1.85E-03	-3.19	-1.44	-1.59E-01
3434	C9orf85	238912_x_at	2.9456E-02	1.85E-03	3.19	-1.44	4.83E-01
3435	OCM///OCM2	207944_at	2.9456E-02	1.85E-03	3.19	-1.44	1.26E-01
3436	ERGIC1	224576_at	2.9465E-02	1.85E-03	-3.19	-1.44	-3.72E-01
3437	MCHR1	230498_at	2.9465E-02	1.85E-03	-3.19	-1.44	-3.14E-01
3438	MPP7	238451_at	2.9465E-02	1.85E-03	3.19	-1.44	1.46E-01
3439	F8A3///F8A2///F8A1	203274_at	2.9479E-02	1.85E-03	-3.19	-1.44	-5.70E-01
3440	PGCP	208454_s_at	2.9509E-02	1.86E-03	-3.19	-1.44	-2.89E-01
3441	TTLL4	203702_s_at	2.9553E-02	1.86E-03	-3.19	-1.44	-2.56E-01
3442	WAS	38964_r_at	2.9583E-02	1.86E-03	-3.19	-1.45	-3.23E-01
3443	C6orf204	228007_at	2.9583E-02	1.86E-03	3.19	-1.45	3.87E-01
3444	SULT1A2	207122_x_at	2.9583E-02	1.86E-03	-3.19	-1.45	-2.52E-01
3445	CELA3A	211738_x_at	2.9583E-02	1.86E-03	3.19	-1.45	1.79E-01
3446	CCL13	206407_s_at	2.9593E-02	1.87E-03	-3.18	-1.45	-1.45E+00
3447	CCDC88A	219387_at	2.9593E-02	1.87E-03	-3.18	-1.45	-4.74E-01
3448		239238_at	2.9593E-02	1.87E-03	3.18	-1.45	3.57E-01
3449	SCTR	1565738_at	2.9593E-02	1.87E-03	3.18	-1.45	1.54E-01
3450	ZNF302	228392_at	2.9593E-02	1.87E-03	3.18	-1.45	3.29E-01
3451	GATSL3	233528_s_at	2.9631E-02	1.87E-03	-3.18	-1.45	-1.86E-01
3452	LOC100129335	244079_at	2.9636E-02	1.87E-03	3.18	-1.45	1.14E-01
3453	HEBP1	218450_at	2.9636E-02	1.87E-03	-3.18	-1.45	-3.87E-01
3454	LOC400464	243957_at	2.9636E-02	1.87E-03	3.18	-1.45	3.88E-01
3455	C10orf99	227735_s_at	2.9636E-02	1.87E-03	3.18	-1.45	1.90E-01
3456	RGS5	230678_at	2.9650E-02	1.87E-03	3.18	-1.45	1.60E-01
3457		1557897_at	2.9650E-02	1.88E-03	-3.18	-1.45	-1.53E-01
3458	CATSPERB	220293_at	2.9650E-02	1.88E-03	3.18	-1.45	1.42E-01
3459	TP53BP2	203120_at	2.9653E-02	1.88E-03	-3.18	-1.45	-3.04E-01
3460	DNAJC19	225359_at	2.9660E-02	1.88E-03	3.18	-1.45	5.53E-01
3461	KIAA1598	221802_s_at	2.9720E-02	1.88E-03	-3.18	-1.45	-5.01E-01
3462	C6orf47	204968_at	2.9720E-02	1.88E-03	-3.18	-1.45	-2.52E-01
3463	LAPTM4A	200673_at	2.9726E-02	1.88E-03	-3.18	-1.46	-2.63E-01
3464		236485_at	2.9758E-02	1.89E-03	3.18	-1.46	2.28E-01
3465	FAM120A	1555948_s_at	2.9782E-02	1.89E-03	-3.18	-1.46	-4.63E-01
3466	GNAI2	201040_at	2.9802E-02	1.89E-03	-3.18	-1.46	-5.65E-01
3467	NBPF10///NBPF16///NBPF24///NBPF8///AE01///NBPF9///NBPF11///KIAA1245///NBPF1///NBPF14	215434_x_at	2.9808E-02	1.89E-03	-3.18	-1.46	-4.38E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3468	SCYL2	221220_s_at	2.9854E-02	1.89E-03	-3.18	-1.46	-5.01E-01
3469	CNPY3	1552977_a_at	2.9868E-02	1.90E-03	-3.18	-1.46	-5.10E-01
3470	TNFAIP1	201208_s_at	2.9875E-02	1.90E-03	-3.18	-1.46	-1.71E-01
3471	EIF3H	201592_at	2.9875E-02	1.90E-03	3.18	-1.46	2.39E-01
3472	SPANXC	220217_x_at	2.9875E-02	1.90E-03	3.18	-1.46	1.46E-01
3473	ERGIC1	224577_at	2.9918E-02	1.90E-03	-3.18	-1.46	-4.32E-01
3474	RPS17P5	216348_at	2.9953E-02	1.90E-03	3.18	-1.46	5.04E-01
3475	LACTB	226354_at	2.9964E-02	1.90E-03	-3.18	-1.47	-3.45E-01
3476	JAG2	32137_at	2.9969E-02	1.91E-03	-3.18	-1.47	-2.53E-01
3477	TOMM22	217960_s_at	2.9969E-02	1.91E-03	3.18	-1.47	3.93E-01
3478	ZNF827	228046_at	2.9969E-02	1.91E-03	3.18	-1.47	3.99E-01
3479	KIAA1715	229173_at	2.9969E-02	1.91E-03	-3.18	-1.47	-2.38E-01
3480	MPP7	1564308_a_at	2.9969E-02	1.91E-03	3.18	-1.47	1.56E-01
3481	APITD1///CORT	213454_at	2.9969E-02	1.91E-03	3.18	-1.47	5.16E-01
3482	PICALM	212511_at	2.9969E-02	1.91E-03	-3.18	-1.47	-4.35E-01
3483	NFIC	226895_at	2.9969E-02	1.91E-03	-3.18	-1.47	-7.42E-01
3484		241728_at	2.9969E-02	1.91E-03	3.18	-1.47	1.46E-01
3485	SEC23A	204344_s_at	2.9969E-02	1.91E-03	-3.18	-1.47	-2.46E-01
3486	C1orf216	212791_at	2.9969E-02	1.91E-03	-3.18	-1.47	-3.26E-01
3487	HORMAD2	237781_at	2.9969E-02	1.91E-03	3.18	-1.47	1.10E-01
3488	CMAH	1554862_at	2.9969E-02	1.91E-03	3.18	-1.47	1.17E-01
3489		242833_at	2.9969E-02	1.91E-03	3.18	-1.47	1.26E-01
3490	KCTD20	214849_at	2.9969E-02	1.91E-03	-3.18	-1.47	-2.97E-01
3491	NACA	200735_x_at	2.9998E-02	1.92E-03	3.18	-1.47	2.00E-01
3492	LRP10	201412_at	3.0015E-02	1.92E-03	-3.18	-1.47	-4.19E-01
3493	HIST1H1E	208553_at	3.0015E-02	1.92E-03	3.18	-1.47	5.05E-01
3494	KIAA1704	229891_x_at	3.0065E-02	1.92E-03	3.18	-1.47	2.80E-01
3495	RNASEH2B	229210_at	3.0078E-02	1.92E-03	3.18	-1.47	3.00E-01
3496	ZNF414	227071_at	3.0078E-02	1.92E-03	3.18	-1.47	1.17E-01
3497	MLLT1	224993_at	3.0131E-02	1.93E-03	-3.17	-1.48	-3.35E-01
3498	C3orf78	229826_at	3.0170E-02	1.93E-03	3.17	-1.48	5.05E-01
3499	C3orf21	226891_at	3.0170E-02	1.93E-03	-3.17	-1.48	-2.89E-01
3500		241777_x_at	3.0170E-02	1.93E-03	3.17	-1.48	1.55E-01
3501	UQCC	222470_s_at	3.0189E-02	1.93E-03	-3.17	-1.48	-1.85E-01
3502	RPL23AP32	207283_at	3.0189E-02	1.93E-03	3.17	-1.48	3.28E-01
3503	SDC2	212157_at	3.0199E-02	1.94E-03	-3.17	-1.48	-2.53E-01
3504		230054_at	3.0199E-02	1.94E-03	3.17	-1.48	1.88E-01
3505	ZNF321	1558888_x_at	3.0202E-02	1.94E-03	3.17	-1.48	1.66E-01
3506	HLA-DQB1	211654_x_at	3.0202E-02	1.94E-03	-3.17	-1.48	-6.64E-01
3507	RGPD2///RGPD6///RGPD8///RGPD3///RGPD1///RGPD4///RGPD5///RANBP2	242712_x_at	3.0206E-02	1.94E-03	3.17	-1.48	2.92E-01
3508	TMTC1	224397_s_at	3.0206E-02	1.94E-03	-3.17	-1.48	-2.16E-01
3509	KCTD12	212188_at	3.0206E-02	1.94E-03	-3.17	-1.48	-4.37E-01
3510	ZDHHC4	230905_at	3.0207E-02	1.94E-03	3.17	-1.48	1.72E-01
3511	FAM13A	202973_x_at	3.0215E-02	1.94E-03	-3.17	-1.48	-5.11E-01
3512		229004_at	3.0221E-02	1.94E-03	-3.17	-1.48	-2.69E-01
3513	SLC1A3	202800_at	3.0253E-02	1.94E-03	-3.17	-1.48	-5.86E-01
3514	CMKLR1	207652_s_at	3.0288E-02	1.95E-03	-3.17	-1.48	-4.35E-01
3515	RNPEP	208270_s_at	3.0288E-02	1.95E-03	-3.17	-1.48	-4.05E-01
3516	RBM34	214942_at	3.0289E-02	1.95E-03	3.17	-1.49	1.70E-01
3517	ULK1	209333_at	3.0289E-02	1.95E-03	-3.17	-1.49	-2.20E-01
3518		240254_at	3.0289E-02	1.95E-03	3.17	-1.49	1.56E-01
3519	ZNF418	243439_at	3.0289E-02	1.95E-03	3.17	-1.49	2.03E-01
3520	ADORA3	206171_at	3.0289E-02	1.95E-03	-3.17	-1.49	-3.55E-01
3521	HIST1H2BB	208547_at	3.0289E-02	1.95E-03	3.17	-1.49	3.39E-01
3522	INPP5A	203006_at	3.0289E-02	1.95E-03	-3.17	-1.49	-3.00E-01
3523	CD82	203904_x_at	3.0289E-02	1.95E-03	-3.17	-1.49	-2.97E-01
3524	NDEL1	208093_s_at	3.0289E-02	1.95E-03	-3.17	-1.49	-2.48E-01
3525	ALG14	228871_at	3.0336E-02	1.96E-03	3.17	-1.49	1.76E-01
3526	IQCE	204202_at	3.0348E-02	1.96E-03	-3.17	-1.49	-2.76E-01
3527	AP2A1	234068_s_at	3.0349E-02	1.96E-03	-3.17	-1.49	-1.97E-01
3528	SNX9	223028_s_at	3.0386E-02	1.96E-03	-3.17	-1.49	-4.02E-01
3529	MAP2K6	205698_s_at	3.0389E-02	1.96E-03	3.17	-1.49	3.30E-01
3530	TM4SF1	209387_s_at	3.0390E-02	1.96E-03	-3.17	-1.49	-3.82E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3531	HNF4A	214832_at	3.0390E-02	1.96E-03	3.17	-1.49	1.57E-01
3532	MKNK1	1560720_at	3.0408E-02	1.96E-03	3.17	-1.49	1.76E-01
3533	TNIP1	243423_at	3.0416E-02	1.97E-03	3.17	-1.49	2.50E-01
3534	SNX24	218705_s_at	3.0416E-02	1.97E-03	-3.17	-1.49	-3.44E-01
3535	TUBD1	231853_at	3.0416E-02	1.97E-03	3.17	-1.49	4.50E-01
3536	C21orf91	226109_at	3.0449E-02	1.97E-03	3.17	-1.49	3.03E-01
3537	TMEM30A	217743_s_at	3.0451E-02	1.97E-03	-3.17	-1.50	-3.80E-01
3538	MRPS31	212603_at	3.0462E-02	1.97E-03	3.17	-1.50	2.23E-01
3539	TLN2	232625_at	3.0492E-02	1.97E-03	3.17	-1.50	1.51E-01
3540		240595_at	3.0492E-02	1.97E-03	3.17	-1.50	2.18E-01
3541	ZNF614	227045_at	3.0492E-02	1.97E-03	3.17	-1.50	5.53E-01
3542	SOX17	219993_at	3.0492E-02	1.98E-03	-3.17	-1.50	-2.27E-01
3543	PDE1C	243564_at	3.0506E-02	1.98E-03	3.17	-1.50	1.29E-01
3544	MEGF8	227327_at	3.0553E-02	1.98E-03	-3.17	-1.50	-2.51E-01
3545	RHOA	200059_s_at	3.0564E-02	1.98E-03	-3.17	-1.50	-3.63E-01
3546	COL18A1	209082_s_at	3.0564E-02	1.98E-03	-3.17	-1.50	-5.32E-01
3547	CALR	212952_at	3.0564E-02	1.98E-03	-3.17	-1.50	-2.12E-01
3548	FBN1	202765_s_at	3.0599E-02	1.99E-03	-3.17	-1.50	-6.57E-01
3549	ZNF439	236562_at	3.0610E-02	1.99E-03	3.16	-1.50	4.05E-01
3550	ME2	210153_s_at	3.0636E-02	1.99E-03	-3.16	-1.50	-3.74E-01
3551	TMSB15B/// TMSB15A	214051_at	3.0671E-02	1.99E-03	3.16	-1.51	6.51E-01
3552	COL18A1	209081_s_at	3.0748E-02	2.00E-03	-3.16	-1.51	-5.69E-01
3553	PHACTR1	213638_at	3.0762E-02	2.00E-03	3.16	-1.51	4.15E-01
3554	JAG2	209784_s_at	3.0795E-02	2.00E-03	-3.16	-1.51	-2.71E-01
3555	SLC12A4	228644_s_at	3.0795E-02	2.00E-03	3.16	-1.51	1.67E-01
3556	ZNF598	232367_x_at	3.0881E-02	2.01E-03	3.16	-1.51	2.32E-01
3557	GAPDH	213453_x_at	3.0881E-02	2.01E-03	-3.16	-1.51	-4.29E-01
3558	C11orf31	1557801_x_at	3.0913E-02	2.01E-03	3.16	-1.51	2.95E-01
3559	IMPA2	203126_at	3.0913E-02	2.01E-03	-3.16	-1.51	-3.92E-01
3560	GDI1	201864_at	3.0913E-02	2.01E-03	-3.16	-1.51	-3.49E-01
3561		1568807_a_at	3.0966E-02	2.02E-03	3.16	-1.52	2.38E-01
3562	OAT	201599_at	3.0973E-02	2.02E-03	-3.16	-1.52	-3.39E-01
3563	TPM3	238065_at	3.0973E-02	2.02E-03	-3.16	-1.52	-1.72E-01
3564	RPS6	201254_x_at	3.1000E-02	2.02E-03	3.16	-1.52	1.60E-01
3565	PAK2	1559052_s_at	3.1026E-02	2.02E-03	-3.16	-1.52	-4.38E-01
3566	VPS53	235882_at	3.1037E-02	2.02E-03	-3.16	-1.52	-1.67E-01
3567		211691_x_at	3.1037E-02	2.02E-03	3.16	-1.52	2.01E-01
3568		235530_at	3.1049E-02	2.03E-03	3.16	-1.52	2.03E-01
3569		232723_at	3.1050E-02	2.03E-03	3.16	-1.52	1.54E-01
3570		235930_at	3.1053E-02	2.03E-03	3.16	-1.52	1.49E-01
3571	MGC42157	1552987_a_at	3.1081E-02	2.03E-03	3.16	-1.52	1.13E-01
3572	KIAA0895L// /EXOC3L	1558041_a_at	3.1113E-02	2.03E-03	-3.16	-1.52	-1.63E-01
3573	ZNF654	219239_s_at	3.1116E-02	2.03E-03	-3.16	-1.52	-3.90E-01
3574	ISOC1	218170_at	3.1116E-02	2.03E-03	-3.16	-1.52	-4.11E-01
3575	AK2	208967_s_at	3.1116E-02	2.03E-03	-3.16	-1.52	-3.37E-01
3576	SMTN	207390_s_at	3.1120E-02	2.04E-03	-3.16	-1.52	-3.19E-01
3577	FKBP5	224840_at	3.1143E-02	2.04E-03	-3.16	-1.52	-4.72E-01
3578	ACAD10	219986_s_at	3.1143E-02	2.04E-03	3.16	-1.53	2.24E-01
3579	FLJ27354	231313_at	3.1146E-02	2.04E-03	3.16	-1.53	1.77E-01
3580		233275_at	3.1146E-02	2.04E-03	3.16	-1.53	1.59E-01
3581	LDOC1L	223228_at	3.1154E-02	2.04E-03	-3.16	-1.53	-3.27E-01
3582	FSD2	237222_at	3.1166E-02	2.04E-03	3.16	-1.53	1.42E-01
3583	MFSD5	212861_at	3.1166E-02	2.04E-03	-3.16	-1.53	-3.98E-01
3584	KIF1B	225878_at	3.1186E-02	2.04E-03	-3.16	-1.53	-3.36E-01
3585		238298_at	3.1186E-02	2.04E-03	3.16	-1.53	1.13E-01
3586	USP42	226172_at	3.1227E-02	2.05E-03	3.16	-1.53	1.34E-01
3587	C2orf53	237319_at	3.1267E-02	2.05E-03	3.15	-1.53	1.61E-01
3588	GRM5	1565389_s_at	3.1303E-02	2.05E-03	3.15	-1.53	3.03E-01
3589	C15orf29	222745_s_at	3.1317E-02	2.06E-03	3.15	-1.53	4.11E-01
3590	BACH2	236796_at	3.1321E-02	2.06E-03	3.15	-1.53	6.56E-01
3591	IDI1	242065_x_at	3.1321E-02	2.06E-03	3.15	-1.53	2.06E-01
3592	KIAA1107	1558293_at	3.1347E-02	2.06E-03	3.15	-1.53	1.20E-01
3593	NRD1	229422_at	3.1347E-02	2.06E-03	3.15	-1.54	3.61E-01
3594	UPF1	211168_s_at	3.1347E-02	2.06E-03	-3.15	-1.54	-3.28E-01
3595		239646_at	3.1347E-02	2.06E-03	3.15	-1.54	3.53E-01
3596	PLB1	235703_at	3.1347E-02	2.06E-03	-3.15	-1.54	-1.42E-01
3597		229444_at	3.1347E-02	2.06E-03	3.15	-1.54	5.47E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3598	NFE2L2	1567014_s_at	3.1347E-02	2.06E-03	-3.15	-1.54	-2.68E-01
3599	PGK1	200737_at	3.1375E-02	2.07E-03	-3.15	-1.54	-4.69E-01
3600	RAB35	225620_at	3.1376E-02	2.07E-03	-3.15	-1.54	-3.85E-01
3601		230314_at	3.1412E-02	2.07E-03	3.15	-1.54	4.41E-01
3602	ARHGAP18	225173_at	3.1413E-02	2.07E-03	-3.15	-1.54	-4.44E-01
3603	C19orf26	1552354_at	3.1427E-02	2.07E-03	3.15	-1.54	2.73E-01
3604	SLC7A8	202752_x_at	3.1427E-02	2.07E-03	-3.15	-1.54	-2.91E-01
3605		233729_at	3.1432E-02	2.07E-03	3.15	-1.54	1.62E-01
3606		243558_at	3.1432E-02	2.07E-03	3.15	-1.54	1.24E-01
3607	UBE2H	222419_x_at	3.1432E-02	2.07E-03	3.15	-1.54	1.83E-01
3608	C5orf28	219029_at	3.1432E-02	2.07E-03	3.15	-1.54	4.80E-01
3609	SNHG5	225155_at	3.1440E-02	2.08E-03	3.15	-1.54	6.33E-01
3610	ABAT	209460_at	3.1440E-02	2.08E-03	3.15	-1.54	2.39E-01
3611	MMRN2	219091_s_at	3.1482E-02	2.08E-03	-3.15	-1.54	-3.92E-01
3612	FARP1	201911_s_at	3.1482E-02	2.08E-03	-3.15	-1.54	-3.56E-01
3613	DSC2	204750_s_at	3.1482E-02	2.08E-03	-3.15	-1.54	-5.19E-01
3614	A1BG	229819_at	3.1482E-02	2.08E-03	3.15	-1.54	4.44E-01
3615	C3	217767_at	3.1484E-02	2.08E-03	-3.15	-1.54	-5.92E-01
3616	EXOC7	212035_s_at	3.1485E-02	2.08E-03	-3.15	-1.54	-2.48E-01
3617	PER2	205251_at	3.1489E-02	2.08E-03	-3.15	-1.54	-3.11E-01
3618	TSPAN3	200973_s_at	3.1489E-02	2.08E-03	-3.15	-1.54	-5.29E-01
3619	HLA-A	215313_x_at	3.1501E-02	2.09E-03	-3.15	-1.55	-3.12E-01
3620	RTN3	224564_s_at	3.1501E-02	2.09E-03	-3.15	-1.55	-3.74E-01
3621	KDELR1	200922_at	3.1501E-02	2.09E-03	-3.15	-1.55	-5.90E-01
3622	SCARB1	201819_at	3.1553E-02	2.09E-03	-3.15	-1.55	-4.39E-01
3623	ATP6V0A2	1555114_at	3.1592E-02	2.09E-03	3.15	-1.55	1.53E-01
3624	HGS	232460_at	3.1592E-02	2.09E-03	3.15	-1.55	1.57E-01
3625	C17orf58	226901_at	3.1592E-02	2.09E-03	-3.15	-1.55	-5.31E-01
3626	PSMG1	203405_at	3.1592E-02	2.10E-03	-3.15	-1.55	-3.83E-01
3627		242695_at	3.1634E-02	2.10E-03	3.15	-1.55	3.87E-01
3628	PRMT2	228725_x_at	3.1634E-02	2.10E-03	-3.15	-1.55	-5.69E-01
3629	LOC283435	1561536_at	3.1642E-02	2.10E-03	3.15	-1.55	1.21E-01
3630	ZFAND6	239757_at	3.1645E-02	2.10E-03	3.15	-1.55	5.12E-01
3631		231139_at	3.1645E-02	2.10E-03	3.15	-1.55	1.23E-01
3632	LOC440934	230844_at	3.1645E-02	2.10E-03	3.15	-1.55	1.34E-01
3633	PPP1R14B	212680_x_at	3.1646E-02	2.10E-03	-3.15	-1.55	-3.26E-01
3634	ENC1	201341_at	3.1646E-02	2.10E-03	-3.15	-1.55	-4.50E-01
3635	PTPN2	241983_at	3.1649E-02	2.10E-03	3.15	-1.55	1.74E-01
3636	PSMC5	209503_s_at	3.1651E-02	2.10E-03	-3.15	-1.55	-3.18E-01
3637	GNG7	206896_s_at	3.1678E-02	2.11E-03	3.15	-1.55	3.54E-01
3638	UBE2R2	223014_at	3.1695E-02	2.11E-03	-3.15	-1.56	-3.76E-01
3639		239393_at	3.1702E-02	2.11E-03	3.15	-1.56	3.83E-01
3640	ALS2	232184_at	3.1716E-02	2.11E-03	3.15	-1.56	1.58E-01
3641	ITPR1	211323_s_at	3.1716E-02	2.11E-03	3.15	-1.56	3.30E-01
3642		241770_x_at	3.1716E-02	2.11E-03	3.15	-1.56	1.27E-01
3643	LOC284801	225762_x_at	3.1716E-02	2.11E-03	3.15	-1.56	3.76E-01
3644	CWC15	223067_at	3.1766E-02	2.12E-03	3.14	-1.56	3.04E-01
3645	SETD3	229940_at	3.1766E-02	2.12E-03	-3.14	-1.56	-2.04E-01
3646		234731_at	3.1766E-02	2.12E-03	3.14	-1.56	1.96E-01
3647	LOC100288702///ACTR3P1///RPL4P1///TRA@///SALL2	234852_at	3.1766E-02	2.12E-03	3.14	-1.56	2.05E-01
3648	GAPDH	212581_x_at	3.1766E-02	2.12E-03	-3.14	-1.56	-4.04E-01
3649	TNIP2	48531_at	3.1766E-02	2.12E-03	-3.14	-1.56	-3.22E-01
3650	C20orf26	1554657_a_at	3.1766E-02	2.12E-03	3.14	-1.56	1.41E-01
3651	PET112L	204300_at	3.1766E-02	2.12E-03	-3.14	-1.56	-2.29E-01
3652	ATAD2	228401_at	3.1766E-02	2.12E-03	3.14	-1.56	3.14E-01
3653		213549_at	3.1766E-02	2.12E-03	-3.14	-1.56	-3.36E-01
3654		216065_at	3.1766E-02	2.12E-03	3.14	-1.56	1.35E-01
3655	GDF15	229868_s_at	3.1766E-02	2.12E-03	3.14	-1.56	1.15E-01
3656	DMD	207660_at	3.1782E-02	2.13E-03	3.14	-1.56	1.46E-01
3657	GTF3C4	243228_at	3.1784E-02	2.13E-03	3.14	-1.56	1.28E-01
3658	EPR1	1555826_at	3.1830E-02	2.13E-03	3.14	-1.56	3.99E-01
3659	PITPNA	201192_s_at	3.1852E-02	2.13E-03	-3.14	-1.56	-3.63E-01
3660	RNF135	223592_s_at	3.1852E-02	2.13E-03	-3.14	-1.56	-4.33E-01
3661	RPL13A	200715_x_at	3.1852E-02	2.13E-03	3.14	-1.57	2.05E-01
3662	GBX1	217011_at	3.1865E-02	2.13E-03	3.14	-1.57	2.08E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3663		239679_at	3.1888E-02	2.14E-03	3.14	-1.57	3.28E-01
3664	HEATR5B	233642_s_at	3.1896E-02	2.14E-03	3.14	-1.57	2.97E-01
3665	C12orf76	229679_at	3.1897E-02	2.14E-03	3.14	-1.57	6.12E-01
3666	SMTN	1556030_at	3.1933E-02	2.14E-03	3.14	-1.57	1.55E-01
3667	ITGB5	201125_s_at	3.1950E-02	2.14E-03	-3.14	-1.57	-6.80E-01
3668	CYBB	203922_s_at	3.1957E-02	2.14E-03	-3.14	-1.57	-6.09E-01
3669	DCUN1D4	212853_at	3.2007E-02	2.15E-03	3.14	-1.57	1.65E-01
3670	BRE	211566_x_at	3.2014E-02	2.15E-03	-3.14	-1.57	-2.49E-01
3671	DHX36	1559039_at	3.2049E-02	2.15E-03	3.14	-1.57	2.04E-01
3672	TMEM114	231462_at	3.2049E-02	2.15E-03	3.14	-1.57	1.45E-01
3673	RAPGEF6	219112_at	3.2074E-02	2.15E-03	3.14	-1.57	3.57E-01
3674	ZNF704	1558941_at	3.2147E-02	2.16E-03	3.14	-1.58	1.26E-01
3675	MT1P2///MT1M///MT1H///MT1E	216336_x_at	3.2161E-02	2.16E-03	-3.14	-1.58	-6.46E-01
3676	VDR	204255_s_at	3.2167E-02	2.16E-03	-3.14	-1.58	-7.43E-01
3677	FERMT2	214212_x_at	3.2167E-02	2.16E-03	-3.14	-1.58	-3.64E-01
3678	SORD	201563_at	3.2167E-02	2.16E-03	-3.14	-1.58	-5.96E-01
3679	ADH1B	209614_at	3.2167E-02	2.16E-03	-3.14	-1.58	-2.57E-01
3680	PDLIM5	203243_s_at	3.2167E-02	2.17E-03	-3.14	-1.58	-5.61E-01
3681		237329_at	3.2167E-02	2.17E-03	3.14	-1.58	1.10E-01
3682	CDKL1	235512_at	3.2167E-02	2.17E-03	3.14	-1.58	2.59E-01
3683	C5orf34	229886_at	3.2167E-02	2.17E-03	3.14	-1.58	2.36E-01
3684	PIGL	232262_at	3.2167E-02	2.17E-03	3.14	-1.58	2.17E-01
3685	LOC283688	1566526_at	3.2248E-02	2.17E-03	3.14	-1.58	1.49E-01
3686	DNAJC30	239018_at	3.2334E-02	2.18E-03	3.14	-1.58	2.21E-01
3687	ENC1	201340_s_at	3.2334E-02	2.18E-03	-3.14	-1.58	-5.17E-01
3688	LRRN4CL	1556427_s_at	3.2334E-02	2.18E-03	-3.14	-1.58	-3.02E-01
3689	GOPC	227214_at	3.2350E-02	2.18E-03	-3.14	-1.59	-2.06E-01
3690	C1orf68	217087_at	3.2388E-02	2.19E-03	3.13	-1.59	2.05E-01
3691	THOC7	229525_at	3.2389E-02	2.19E-03	3.13	-1.59	4.19E-01
3692	VWA5A	210102_at	3.2400E-02	2.19E-03	-3.13	-1.59	-3.35E-01
3693	ENPP2	210839_s_at	3.2401E-02	2.19E-03	-3.13	-1.59	-5.97E-01
3694	ZNF638	213775_x_at	3.2406E-02	2.19E-03	-3.13	-1.59	-3.88E-01
3695	PPP2R2A	236492_at	3.2406E-02	2.19E-03	3.13	-1.59	3.43E-01
3696	C6orf136	227455_at	3.2426E-02	2.19E-03	-3.13	-1.59	-4.08E-01
3697	ZYX	200808_s_at	3.2426E-02	2.19E-03	-3.13	-1.59	-7.32E-01
3698	FICD	219910_at	3.2437E-02	2.19E-03	-3.13	-1.59	-2.66E-01
3699	YKT6	217785_s_at	3.2467E-02	2.20E-03	-3.13	-1.59	-3.10E-01
3700	TUSC3	232770_at	3.2482E-02	2.20E-03	3.13	-1.59	1.32E-01
3701		242717_at	3.2482E-02	2.20E-03	3.13	-1.59	1.34E-01
3702	CALD1	201615_x_at	3.2482E-02	2.20E-03	-3.13	-1.59	-5.88E-01
3703	CD48	204118_at	3.2482E-02	2.20E-03	3.13	-1.59	4.95E-01
3704	RICTOR	226310_at	3.2482E-02	2.20E-03	3.13	-1.59	3.45E-01
3705	LYN	210754_s_at	3.2497E-02	2.20E-03	-3.13	-1.59	-6.49E-01
3706	USP15	209475_at	3.2505E-02	2.20E-03	3.13	-1.59	3.12E-01
3707	HSD3B7	222817_at	3.2520E-02	2.20E-03	-3.13	-1.59	-3.84E-01
3708	IL2RA	206341_at	3.2536E-02	2.21E-03	-3.13	-1.59	-5.30E-01
3709	ATP5S	1554177_a_at	3.2543E-02	2.21E-03	3.13	-1.60	2.64E-01
3710	TIMM10	1555764_s_at	3.2568E-02	2.21E-03	3.13	-1.60	4.70E-01
3711	SFT2D3	226639_at	3.2612E-02	2.21E-03	3.13	-1.60	1.78E-01
3712	LOC284600	1559083_x_at	3.2612E-02	2.21E-03	3.13	-1.60	1.78E-01
3713	EPHB2	210651_s_at	3.2612E-02	2.22E-03	-3.13	-1.60	-1.39E-01
3714	TUSC1	227388_at	3.2612E-02	2.22E-03	-3.13	-1.60	-4.06E-01
3715	INPP5B	213804_at	3.2668E-02	2.22E-03	3.13	-1.60	2.13E-01
3716	CTBP2	201220_x_at	3.2791E-02	2.23E-03	-3.13	-1.60	-3.75E-01
3717		236754_at	3.2795E-02	2.23E-03	3.13	-1.60	3.29E-01
3718		244733_at	3.2802E-02	2.23E-03	3.13	-1.60	2.30E-01
3719	LRP12	219631_at	3.2817E-02	2.23E-03	-3.13	-1.61	-4.23E-01
3720	PSMF1	201052_s_at	3.2852E-02	2.24E-03	-3.13	-1.61	-5.45E-01
3721		216757_at	3.2852E-02	2.24E-03	3.13	-1.61	1.29E-01
3722	ADH1B	209612_s_at	3.2852E-02	2.24E-03	-3.13	-1.61	-1.04E+00
3723	SLC31A1	236217_at	3.2852E-02	2.24E-03	-3.13	-1.61	-2.91E-01
3724	COX7C	201134_x_at	3.2852E-02	2.24E-03	3.13	-1.61	3.17E-01
3725	ZNF529	215307_at	3.2890E-02	2.24E-03	3.13	-1.61	2.76E-01
3726	ARHGEF10L	221656_s_at	3.2937E-02	2.24E-03	-3.13	-1.61	-4.24E-01
3727	AMN1	226258_at	3.2937E-02	2.25E-03	3.13	-1.61	4.23E-01
3728	RNF24	204669_s_at	3.2937E-02	2.25E-03	-3.13	-1.61	-3.10E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3729	ZNF684	244398_x_at	3.3038E-02	2.25E-03	3.12	-1.61	2.11E-01
3730		1569858_at	3.3051E-02	2.26E-03	3.12	-1.61	9.69E-02
3731	AQP10	1555338_s_at	3.3051E-02	2.26E-03	3.12	-1.61	1.49E-01
3732	SPHK1	219257_s_at	3.3051E-02	2.26E-03	-3.12	-1.61	-3.94E-01
3733	ARL3	1568590_at	3.3055E-02	2.26E-03	3.12	-1.61	1.43E-01
3734	CCDC88A	239233_at	3.3065E-02	2.26E-03	-3.12	-1.62	-1.14E-01
3735	GOPC	227215_at	3.3088E-02	2.26E-03	-3.12	-1.62	-2.66E-01
3736	RPS8P10/// RPS8	214089_at	3.3091E-02	2.26E-03	3.12	-1.62	1.92E-01
3737	YWHAE	210996_s_at	3.3095E-02	2.26E-03	-3.12	-1.62	-3.36E-01
3738	FUCA2	223120_at	3.3095E-02	2.26E-03	-3.12	-1.62	-3.29E-01
3739		1570331_at	3.3100E-02	2.26E-03	3.12	-1.62	1.37E-01
3740		1560240_at	3.3100E-02	2.26E-03	3.12	-1.62	1.13E-01
3741	LOC100130 557	1558782_a_at	3.3100E-02	2.26E-03	3.12	-1.62	2.16E-01
3742	LOC441461	1558689_a_at	3.3121E-02	2.27E-03	3.12	-1.62	1.65E-01
3743	LOC727842	217015_at	3.3122E-02	2.27E-03	3.12	-1.62	1.09E-01
3744	HLA-J///HLA-H///HLA-G///HLA-B///HLA-A	217436_x_at	3.3138E-02	2.27E-03	-3.12	-1.62	-3.51E-01
3745	CBX3	200037_s_at	3.3183E-02	2.27E-03	3.12	-1.62	2.33E-01
3746	PPFIBP2	212841_s_at	3.3219E-02	2.28E-03	-3.12	-1.62	-2.83E-01
3747	HIST1H1A	208484_at	3.3219E-02	2.28E-03	3.12	-1.62	1.69E-01
3748	SMEK1	220369_at	3.3219E-02	2.28E-03	3.12	-1.62	2.35E-01
3749	FLJ10038	205510_s_at	3.3219E-02	2.28E-03	3.12	-1.62	2.29E-01
3750	ITCH	217094_s_at	3.3242E-02	2.28E-03	-3.12	-1.62	-2.81E-01
3751	NCLN	222206_s_at	3.3267E-02	2.28E-03	-3.12	-1.62	-2.41E-01
3752	C11orf87	1557181_s_at	3.3282E-02	2.28E-03	3.12	-1.63	1.21E-01
3753	OR1F2P	217308_at	3.3282E-02	2.28E-03	3.12	-1.63	1.45E-01
3754	RAD23B	201222_s_at	3.3299E-02	2.29E-03	-3.12	-1.63	-4.04E-01
3755	C1orf97	224443_at	3.3345E-02	2.29E-03	3.12	-1.63	4.46E-01
3756	YBX2	219704_at	3.3414E-02	2.30E-03	3.12	-1.63	1.79E-01
3757	PASK	213534_s_at	3.3414E-02	2.30E-03	3.12	-1.63	5.88E-01
3758	FKBP11	219117_s_at	3.3414E-02	2.30E-03	-3.12	-1.63	-4.43E-01
3759	BCL7A	203795_s_at	3.3414E-02	2.30E-03	3.12	-1.63	2.03E-01
3760	HAUS7///TREX2	207891_s_at	3.3416E-02	2.30E-03	-3.12	-1.63	-3.00E-01
3761	LRP12	220253_s_at	3.3420E-02	2.30E-03	-3.12	-1.63	-4.49E-01
3762	KLHDC1	1552733_at	3.3457E-02	2.30E-03	3.12	-1.63	2.62E-01
3763	ATL2	222700_at	3.3457E-02	2.30E-03	3.12	-1.63	3.23E-01
3764	C19orf2	222266_at	3.3457E-02	2.30E-03	3.12	-1.63	4.50E-01
3765		1566146_x_at	3.3457E-02	2.30E-03	3.12	-1.63	1.93E-01
3766		242216_at	3.3457E-02	2.30E-03	3.12	-1.63	1.21E-01
3767	PSIP1	210758_at	3.3480E-02	2.31E-03	3.12	-1.63	2.46E-01
3768		233747_at	3.3482E-02	2.31E-03	3.12	-1.63	1.28E-01
3769	BEX2	224367_at	3.3560E-02	2.31E-03	3.12	-1.64	5.51E-01
3770	TRAF3IP3	205804_s_at	3.3571E-02	2.32E-03	3.12	-1.64	4.06E-01
3771	VEZF1	202173_s_at	3.3571E-02	2.32E-03	-3.12	-1.64	-3.97E-01
3772	RAB35	221819_at	3.3571E-02	2.32E-03	-3.12	-1.64	-3.04E-01
3773	VPS35	233864_s_at	3.3571E-02	2.32E-03	-3.12	-1.64	-2.22E-01
3774	AMACR	217111_at	3.3571E-02	2.32E-03	3.12	-1.64	1.42E-01
3775	C20orf111	221954_at	3.3571E-02	2.32E-03	3.12	-1.64	3.41E-01
3776		232186_at	3.3571E-02	2.32E-03	-3.12	-1.64	-1.35E-01
3777		215398_at	3.3571E-02	2.32E-03	3.12	-1.64	1.52E-01
3778	MRPS5	236779_at	3.3571E-02	2.32E-03	3.12	-1.64	1.86E-01
3779	DNAJC5	224613_s_at	3.3571E-02	2.32E-03	-3.12	-1.64	-2.59E-01
3780	MRPS2	218001_at	3.3571E-02	2.32E-03	-3.12	-1.64	-4.28E-01
3781	MBNL2	203640_at	3.3571E-02	2.32E-03	-3.12	-1.64	-3.30E-01
3782		233521_at	3.3571E-02	2.32E-03	3.12	-1.64	1.18E-01
3783		229226_at	3.3571E-02	2.32E-03	3.12	-1.64	1.37E-01
3784	TTC28	215146_s_at	3.3579E-02	2.32E-03	-3.11	-1.64	-2.67E-01
3785	RHOA	240337_at	3.3579E-02	2.32E-03	3.11	-1.64	1.07E-01
3786	PCMTD2	237179_at	3.3585E-02	2.33E-03	3.11	-1.64	1.42E-01
3787		227579_at	3.3588E-02	2.33E-03	-3.11	-1.64	-2.30E-01
3788	ZBTB7C	217675_at	3.3646E-02	2.33E-03	3.11	-1.64	1.11E-01
3789	C1orf97	224444_s_at	3.3646E-02	2.33E-03	3.11	-1.64	5.43E-01
3790	RNF130	236292_at	3.3653E-02	2.33E-03	**-3.11**	-1.64	-2.40E-01
3791	DDRGK1	218159_at	3.3667E-02	2.34E-03	**-3.11**	-1.64	-2.54E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3792	GLTPD1	220734_s_at	3.3667E-02	2.34E-03	-3.11	-1.64	-2.68E-01
3793		236149_at	3.3667E-02	2.34E-03	3.11	-1.65	2.13E-01
3794	EGFR	201983_s_at	3.3667E-02	2.34E-03	-3.11	-1.65	-4.40E-01
3795	CDKN2A	209644_x_at	3.3667E-02	2.34E-03	3.11	-1.65	2.76E-01
3796	TGM2	211003_x_at	3.3667E-02	2.34E-03	-3.11	-1.65	-1.94E-01
3797	KIF3B	225205_at	3.3667E-02	2.34E-03	-3.11	-1.65	-3.23E-01
3798	ARL17B	229028_s_at	3.3677E-02	2.34E-03	3.11	-1.65	3.61E-01
3799	GKAP1	234192_s_at	3.3677E-02	2.34E-03	3.11	-1.65	2.94E-01
3800	DPH3B	233000_x_at	3.3677E-02	2.34E-03	3.11	-1.65	1.64E-01
3801	G2E3	223256_at	3.3677E-02	2.34E-03	3.11	-1.65	2.97E-01
3802	NEUROG3	207965_at	3.3677E-02	2.34E-03	3.11	-1.65	1.33E-01
3803	AIDA	220199_s_at	3.3691E-02	2.34E-03	-3.11	-1.65	-5.97E-01
3804	SNHG4///MATR3	1564907_s_at	3.3744E-02	2.35E-03	3.11	-1.65	2.07E-01
3805		243921_at	3.3767E-02	2.35E-03	3.11	-1.65	1.09E-01
3806	IMMT	242361_at	3.3781E-02	2.35E-03	3.11	-1.65	2.20E-01
3807		1562665_at	3.3781E-02	2.35E-03	3.11	-1.65	9.94E-02
3808		229189_s_at	3.3781E-02	2.36E-03	3.11	-1.65	5.44E-01
3809	NR2F2	209121_x_at	3.3781E-02	2.36E-03	-3.11	-1.65	-5.43E-01
3810	CS	208660_at	3.3781E-02	2.36E-03	-3.11	-1.65	-4.48E-01
3811	UNC5B	41856_at	3.3781E-02	2.36E-03	-3.11	-1.65	-1.59E-01
3812	C21orf88	1553850_at	3.3781E-02	2.36E-03	3.11	-1.65	1.16E-01
3813	SVIP	226278_at	3.3781E-02	2.36E-03	3.11	-1.65	5.54E-01
3814	SLC2A13	1552695_a_at	3.3781E-02	2.36E-03	-3.11	-1.65	-1.79E-01
3815		238201_at	3.3781E-02	2.36E-03	3.11	-1.65	1.11E-01
3816	GNPTAB	220398_at	3.3781E-02	2.36E-03	3.11	-1.65	1.49E-01
3817		1566696_at	3.3781E-02	2.36E-03	3.11	-1.65	1.41E-01
3818	C1orf58	241908_at	3.3781E-02	2.36E-03	3.11	-1.65	2.90E-01
3819	ZNF85	1554445_at	3.3781E-02	2.36E-03	3.11	-1.65	3.23E-01
3820	KIFAP3	203333_at	3.3781E-02	2.36E-03	-3.11	-1.65	-3.82E-01
3821	MTUS2	214961_at	3.3781E-02	2.36E-03	3.11	-1.65	1.19E-01
3822	LOC221122	1560278_at	3.3781E-02	2.36E-03	3.11	-1.65	2.21E-01
3823	DPP4	211478_s_at	3.3781E-02	2.36E-03	-3.11	-1.66	-1.96E-01
3824	POLL	221049_s_at	3.3781E-02	2.36E-03	3.11	-1.66	2.01E-01
3825	PAFAH1B2	210160_at	3.3781E-02	2.36E-03	-3.11	-1.66	-1.78E-01
3826	SP3	238035_at	3.3781E-02	2.36E-03	3.11	-1.66	2.44E-01
3827		1569345_at	3.3781E-02	2.36E-03	3.11	-1.66	1.48E-01
3828	MFAP4	212713_at	3.3781E-02	2.37E-03	-3.11	-1.66	-7.00E-01
3829		221379_at	3.3804E-02	2.37E-03	3.11	-1.66	1.80E-01
3830	KCNE4	1552507_at	3.3804E-02	2.37E-03	-3.11	-1.66	-5.62E-01
3831	C3AR1	209906_at	3.3835E-02	2.37E-03	-3.11	-1.66	-5.73E-01
3832		242597_at	3.3838E-02	2.37E-03	3.11	-1.66	1.40E-01
3833	PHF23	223081_at	3.3839E-02	2.37E-03	-3.11	-1.66	-2.04E-01
3834	CAPRIN1	200722_s_at	3.3856E-02	2.37E-03	-3.11	-1.66	-3.80E-01
3835	BMP2K	226853_at	3.3865E-02	2.38E-03	-3.11	-1.66	-3.01E-01
3836	LUM	201744_s_at	3.3892E-02	2.38E-03	-3.11	-1.66	-7.05E-01
3837		239744_at	3.3905E-02	2.38E-03	3.11	-1.66	2.42E-01
3838	WAPAL	1554441_a_at	3.3906E-02	2.38E-03	-3.11	-1.66	-3.69E-01
3839	DCAF8	1554049_s_at	3.3906E-02	2.38E-03	-3.11	-1.66	-1.42E-01
3840	MTIF3	223357_s_at	3.3913E-02	2.38E-03	3.11	-1.66	1.09E-01
3841		1559054_a_at	3.3915E-02	2.38E-03	3.11	-1.66	3.03E-01
3842	KDELR1	1555575_a_at	3.3931E-02	2.38E-03	-3.11	-1.66	-3.20E-01
3843	ORMDL3	235136_at	3.3965E-02	2.39E-03	-3.11	-1.66	-3.00E-01
3844		1556185_a_at	3.3980E-02	2.39E-03	-3.11	-1.66	-2.06E-01
3845	MESDC2	224679_at	3.3987E-02	2.39E-03	-3.11	-1.67	-2.99E-01
3846	PNPO	222653_at	3.3992E-02	2.39E-03	-3.11	-1.67	-5.02E-01
3847		229190_at	3.4020E-02	2.39E-03	3.11	-1.67	5.46E-01
3848	FLJ11292	217342_x_at	3.4020E-02	2.39E-03	3.11	-1.67	1.38E-01
3849	DNASE2	214992_s_at	3.4022E-02	2.40E-03	-3.11	-1.67	-6.63E-01
3850	PTAR1	226110_at	3.4022E-02	2.40E-03	3.11	-1.67	2.74E-01
3851	ARF3	200011_s_at	3.4023E-02	2.40E-03	-3.11	-1.67	-5.90E-01
3852	CPM	206100_at	3.4023E-02	2.40E-03	-3.11	-1.67	-6.80E-01
3853		1568905_at	3.4038E-02	2.40E-03	3.10	-1.67	1.44E-01
3854		241413_at	3.4044E-02	2.40E-03	3.10	-1.67	2.45E-01
3855	ZBTB12	233843_at	3.4046E-02	2.40E-03	3.10	-1.67	1.47E-01
3856	ABHD12	228123_s_at	3.4046E-02	2.40E-03	-3.10	-1.67	-6.74E-01
3857	TIMP2	203167_at	3.4083E-02	2.40E-03	-3.10	-1.67	-5.62E-01
3858	C3orf15	1561430_s_at	3.4099E-02	2.41E-03	3.10	-1.67	1.22E-01
3859		236799_at	3.4133E-02	2.41E-03	3.10	-1.67	1.47E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3860	GCOM1///GRINL1A	212241_at	3.4157E-02	2.41E-03	3.10	-1.67	2.33E-01
3861	DKK3	214247_s_at	3.4168E-02	2.41E-03	-3.10	-1.67	-6.82E-01
3862		226458_at	3.4168E-02	2.41E-03	3.10	-1.67	5.56E-01
3863	SUPT3H	206506_s_at	3.4168E-02	2.41E-03	3.10	-1.67	4.11E-01
3864	LRRTM4	220345_at	3.4168E-02	2.41E-03	3.10	-1.67	1.04E-01
3865	RPL13A	210646_x_at	3.4168E-02	2.42E-03	3.10	-1.67	1.29E-01
3866	ABCA1	203504_s_at	3.4190E-02	2.42E-03	-3.10	-1.68	-6.20E-01
3867	AKIRIN2	223145_s_at	3.4197E-02	2.42E-03	-3.10	-1.68	-3.74E-01
3868	UBAP1	221490_at	3.4197E-02	2.42E-03	-3.10	-1.68	-2.29E-01
3869	PCSK5	213652_at	3.4197E-02	2.42E-03	-3.10	-1.68	-3.78E-01
3870	AVL9	244355_at	3.4200E-02	2.42E-03	3.10	-1.68	1.73E-01
3871	PCYT1A	225069_at	3.4200E-02	2.42E-03	-3.10	-1.68	-2.45E-01
3872	SAMD9	228531_at	3.4202E-02	2.42E-03	3.10	-1.68	2.86E-01
3873		1562038_at	3.4202E-02	2.42E-03	3.10	-1.68	1.11E-01
3874	SOX6	235526_at	3.4202E-02	2.42E-03	3.10	-1.68	1.44E-01
3875	TCEB2	213877_x_at	3.4231E-02	2.43E-03	3.10	-1.68	2.01E-01
3876	CA5BP	238435_at	3.4231E-02	2.43E-03	3.10	-1.68	2.11E-01
3877		222096_x_at	3.4231E-02	2.43E-03	3.10	-1.68	1.76E-01
3878	NSF	202395_at	3.4239E-02	2.43E-03	-3.10	-1.68	-2.94E-01
3879	PTMS	218044_x_at	3.4239E-02	2.43E-03	3.10	-1.68	1.88E-01
3880		1560550_at	3.4254E-02	2.43E-03	3.10	-1.68	1.57E-01
3881		239753_at	3.4261E-02	2.43E-03	3.10	-1.68	1.93E-01
3882	MYL2	209742_s_at	3.4299E-02	2.44E-03	3.10	-1.68	1.18E-01
3883	MGEA5	223494_at	3.4299E-02	2.44E-03	3.10	-1.68	4.23E-01
3884	SPAG4	219888_at	3.4309E-02	2.44E-03	-3.10	-1.68	-4.16E-01
3885	SLC46A1	1558703_at	3.4309E-02	2.44E-03	-3.10	-1.68	-2.33E-01
3886	C11orf30	234669_x_at	3.4309E-02	2.44E-03	3.10	-1.68	1.69E-01
3887	ADH1B	209613_s_at	3.4322E-02	2.44E-03	-3.10	-1.68	-1.13E+00
3888	SLC25A11	207088_s_at	3.4325E-02	2.44E-03	-3.10	-1.68	-4.92E-01
3889	RPL13A	212790_x_at	3.4350E-02	2.44E-03	3.10	-1.68	1.60E-01
3890	MFF	223354_x_at	3.4350E-02	2.44E-03	-3.10	-1.68	-3.18E-01
3891	TMCO6	213550_s_at	3.4350E-02	2.44E-03	3.10	-1.68	3.64E-01
3892		1556683_x_at	3.4361E-02	2.45E-03	3.10	-1.69	1.36E-01
3893	TLL2	208027_s_at	3.4393E-02	2.45E-03	3.10	-1.69	9.35E-02
3894	MYOD1	206657_s_at	3.4393E-02	2.45E-03	3.10	-1.69	1.76E-01
3895	WDFY3	212598_at	3.4393E-02	2.45E-03	-3.10	-1.69	-1.97E-01
3896	NFIB	230291_s_at	3.4396E-02	2.45E-03	-3.10	-1.69	-3.07E-01
3897		215727_x_at	3.4414E-02	2.45E-03	3.10	-1.69	1.31E-01
3898	KPNA4	225267_at	3.4442E-02	2.46E-03	-3.10	-1.69	-2.38E-01
3899		243908_at	3.4488E-02	2.46E-03	3.10	-1.69	3.41E-01
3900	HLA-DRA	208894_at	3.4527E-02	2.46E-03	-3.10	-1.69	-5.23E-01
3901	ANGPTL2	213001_at	3.4530E-02	2.46E-03	-3.10	-1.69	-7.62E-01
3902	DLEU2	1563229_at	3.4530E-02	2.46E-03	3.10	-1.69	2.84E-01
3903	NLRP10	1553534_at	3.4551E-02	2.47E-03	3.10	-1.69	1.11E-01
3904	ATP5L	210453_x_at	3.4565E-02	2.47E-03	3.10	-1.69	3.81E-01
3905	LILRA6///LILRB3	210784_x_at	3.4569E-02	2.47E-03	-3.10	-1.69	-4.22E-01
3906	PFDN4	205362_s_at	3.4569E-02	2.47E-03	3.10	-1.69	3.40E-01
3907	KPNB1	213574_s_at	3.4570E-02	2.47E-03	-3.10	-1.69	-2.93E-01
3908	PRKAG2	215231_at	3.4624E-02	2.47E-03	3.09	-1.70	1.10E-01
3909	BTN3A3	38241_at	3.4629E-02	2.48E-03	-3.09	-1.70	-4.96E-01
3910	BICD2	213154_s_at	3.4629E-02	2.48E-03	-3.09	-1.70	-3.84E-01
3911	LOC642236	242331_x_at	3.4629E-02	2.48E-03	3.09	-1.70	1.58E-01
3912	SRP54	203605_at	3.4629E-02	2.48E-03	-3.09	-1.70	-2.82E-01
3913	XPO7	208459_s_at	3.4641E-02	2.48E-03	-3.09	-1.70	-2.50E-01
3914	RPL22L1	225541_at	3.4665E-02	2.48E-03	3.09	-1.70	5.07E-01
3915	HMOX2	218120_s_at	3.4665E-02	2.48E-03	-3.09	-1.70	-4.41E-01
3916	AP1S1	205195_at	3.4665E-02	2.48E-03	-3.09	-1.70	-2.17E-01
3917	ATE1	238857_at	3.4747E-02	2.49E-03	3.09	-1.70	1.24E-01
3918	FLJ31958	1553354_a_at	3.4747E-02	2.49E-03	3.09	-1.70	1.34E-01
3919	PTHLH	206300_s_at	3.4794E-02	2.49E-03	3.09	-1.70	9.27E-02
3920	COL4A3	216893_s_at	3.4803E-02	2.50E-03	3.09	-1.70	1.06E-01
3921	FAM120A	200774_at	3.4833E-02	2.50E-03	-3.09	-1.70	-3.17E-01
3922	C11orf17	242515_x_at	3.4892E-02	2.50E-03	-3.09	-1.71	-2.05E-01
3923	TIMP3	201148_s_at	3.4921E-02	2.51E-03	-3.09	-1.71	-4.68E-01
3924	DOK2	214054_at	3.4951E-02	2.51E-03	-3.09	-1.71	-3.38E-01
3925	RBM39	227223_at	3.4951E-02	2.51E-03	3.09	-1.71	4.88E-01
3926	CYTH2	209158_s_at	3.4951E-02	2.51E-03	-3.09	-1.71	-3.49E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3927		1555617_x_at	3.4981E-02	2.51E-03	3.09	-1.71	1.96E-01
3928		244003_at	3.4981E-02	2.51E-03	3.09	-1.71	1.17E-01
3929	MRPL30	223996_s_at	3.4981E-02	2.51E-03	3.09	-1.71	4.90E-01
3930		236509_at	3.4982E-02	2.51E-03	3.09	-1.71	1.46E-01
3931	CLIC4	201559_s_at	3.4988E-02	2.52E-03	-3.09	-1.71	-4.84E-01
3932	ITGAE	205055_at	3.5034E-02	2.52E-03	3.09	-1.71	4.96E-01
3933	KCNG1	214595_at	3.5034E-02	2.52E-03	3.09	-1.71	2.67E-01
3934	LOC100134331///LOC100126583///LOC652128///LOC642131///VSIG6///IGHV4-31///IGHM///IGHG4///IGHG3///IGHG1///IGHD///IGHA2///IGHA1///IGH@	211639_x_at	3.5034E-02	2.52E-03	-3.09	-1.71	-6.03E-01
3935	KANK2	218418_s_at	3.5050E-02	2.52E-03	-3.09	-1.71	-6.12E-01
3936	NADK	213607_x_at	3.5065E-02	2.52E-03	-3.09	-1.71	-4.15E-01
3937	NSUN3	1568913_at	3.5074E-02	2.53E-03	-3.09	-1.71	-1.30E-01
3938	AKR1B1	201272_at	3.5074E-02	2.53E-03	-3.09	-1.71	-3.44E-01
3939	CMTM6	223047_at	3.5120E-02	2.53E-03	-3.09	-1.72	-3.63E-01
3940	IRX2	228404_at	3.5126E-02	2.53E-03	3.09	-1.72	1.37E-01
3941	LOC100132352///LOC286272	238536_at	3.5132E-02	2.53E-03	3.09	-1.72	3.55E-01
3942	LOC572558	231024_at	3.5134E-02	2.53E-03	3.09	-1.72	3.57E-01
3943	RHOU	223169_s_at	3.5134E-02	2.53E-03	-3.09	-1.72	-3.04E-01
3944	DNAJC5	224612_s_at	3.5135E-02	2.53E-03	-3.09	-1.72	-3.88E-01
3945	JMJD6	212722_s_at	3.5211E-02	2.54E-03	-3.09	-1.72	-3.42E-01
3946	COL14A1	216866_s_at	3.5213E-02	2.54E-03	-3.09	-1.72	-2.74E-01
3947	NGFR	205858_at	3.5216E-02	2.54E-03	-3.09	-1.72	-1.84E-01
3948	PI4KB	210417_s_at	3.5216E-02	2.54E-03	-3.09	-1.72	-4.67E-01
3949	GPR124	221814_at	3.5241E-02	2.55E-03	-3.09	-1.72	-3.95E-01
3950	LOC348120	231132_at	3.5246E-02	2.55E-03	3.09	-1.72	1.48E-01
3951	TUBB	209026_x_at	3.5272E-02	2.55E-03	-3.09	-1.72	-5.26E-01
3952	RPS4XP9	217107_at	3.5272E-02	2.55E-03	3.09	-1.72	2.43E-01
3953	ODF2L	230926_s_at	3.5272E-02	2.55E-03	3.09	-1.72	2.12E-01
3954		242924_at	3.5272E-02	2.55E-03	3.09	-1.72	1.85E-01
3955	UTP23	227402_s_at	3.5338E-02	2.56E-03	3.08	-1.72	2.27E-01
3956	SARS	200802_at	3.5355E-02	2.56E-03	-3.08	-1.72	-2.65E-01
3957	ELOVL1	218028_at	3.5355E-02	2.56E-03	-3.08	-1.72	-4.30E-01
3958	MXD1	206877_at	3.5359E-02	2.56E-03	3.08	-1.73	1.41E-01
3959	KCTD2	34858_at	3.5361E-02	2.56E-03	-3.08	-1.73	-1.82E-01
3960	DYM	223171_at	3.5361E-02	2.56E-03	-3.08	-1.73	-3.09E-01
3961		1562656_at	3.5381E-02	2.56E-03	3.08	-1.73	9.80E-02
3962	ISG20L2	208114_s_at	3.5381E-02	2.56E-03	-3.08	-1.73	-3.73E-01
3963	TRIM38	203610_s_at	3.5387E-02	2.57E-03	-3.08	-1.73	-3.15E-01
3964		239096_at	3.5387E-02	2.57E-03	3.08	-1.73	4.10E-01
3965	CIC	212784_at	3.5387E-02	2.57E-03	-3.08	-1.73	-2.82E-01
3966	ARL8B	222442_s_at	3.5387E-02	2.57E-03	-3.08	-1.73	-3.50E-01
3967	NUSAP1	218039_at	3.5387E-02	2.57E-03	3.08	-1.73	4.07E-01
3968	COX6C	201754_at	3.5387E-02	2.57E-03	3.08	-1.73	2.39E-01
3969	VPS13B	236254_at	3.5451E-02	2.57E-03	3.08	-1.73	3.62E-01
3970	AKT3	242876_at	3.5490E-02	2.58E-03	3.08	-1.73	2.06E-01
3971	PARP16	219034_at	3.5492E-02	2.58E-03	3.08	-1.73	1.66E-01
3972	CCDC6	225010_at	3.5511E-02	2.58E-03	-3.08	-1.73	-4.25E-01
3973		232268_at	3.5540E-02	2.58E-03	3.08	-1.73	1.19E-01
3974	MAP6D1	239473_x_at	3.5540E-02	2.58E-03	3.08	-1.73	1.85E-01
3975		244429_at	3.5540E-02	2.58E-03	3.08	-1.73	3.95E-01
3976	RBM7	235045_at	3.5540E-02	2.59E-03	3.08	-1.73	2.49E-01
3977	FBLN1	202995_s_at	3.5540E-02	2.59E-03	-3.08	-1.73	-8.71E-01
3978	SLCO2A1	204368_at	3.5540E-02	2.59E-03	-3.08	-1.73	-4.14E-01
3979	BRD4	202103_at	3.5543E-02	2.59E-03	-3.08	-1.73	-2.80E-01
3980	PRR5L	1555486_a_at	3.5543E-02	2.59E-03	-3.08	-1.73	-2.91E-01
3981		244722_at	3.5543E-02	2.59E-03	3.08	-1.73	1.37E-01
3982	FAM200B	227466_at	3.5545E-02	2.59E-03	3.08	-1.74	4.83E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
3983	GALT	203179_at	3.5576E-02	2.59E-03	3.08	-1.74	2.29E-01
3984	SNED1	213488_at	3.5576E-02	2.59E-03	-3.08	-1.74	-2.94E-01
3985	CPD	201943_s_at	3.5579E-02	2.59E-03	-3.08	-1.74	-4.49E-01
3986	CLTB	205172_x_at	3.5579E-02	2.59E-03	-3.08	-1.74	-2.79E-01
3987	CCDC137	225933_at	3.5585E-02	2.60E-03	-3.08	-1.74	-2.92E-01
3988	DDX19A	202578_s_at	3.5585E-02	2.60E-03	-3.08	-1.74	-4.16E-01
3989	CDC37	209953_s_at	3.5585E-02	2.60E-03	-3.08	-1.74	-5.39E-01
3990	SLC43A3	210692_s_at	3.5607E-02	2.60E-03	-3.08	-1.74	-4.92E-01
3991	NCRNA00205	226995_at	3.5608E-02	2.60E-03	-3.08	-1.74	-2.42E-01
3992		241114_s_at	3.5650E-02	2.60E-03	3.08	-1.74	2.05E-01
3993	PGM1	201968_s_at	3.5686E-02	2.61E-03	-3.08	-1.74	-4.66E-01
3994	SIX1	228347_at	3.5692E-02	2.61E-03	-3.08	-1.74	-4.57E-01
3995		241891_at	3.5692E-02	2.61E-03	3.08	-1.74	6.02E-01
3996	RASAL2	222810_s_at	3.5692E-02	2.61E-03	-3.08	-1.74	-3.20E-01
3997	LRRC36	220003_at	3.5692E-02	2.61E-03	3.08	-1.74	1.55E-01
3998	CCDC85A	233846_at	3.5692E-02	2.61E-03	3.08	-1.74	1.89E-01
3999		242130_at	3.5699E-02	2.61E-03	3.08	-1.74	1.36E-01
4000	LOC729580	49679_s_at	3.5752E-02	2.62E-03	-3.08	-1.74	-1.44E-01
4001	TGS1	236371_s_at	3.5752E-02	2.62E-03	3.08	-1.74	1.32E-01
4002	HECTD3	218632_at	3.5766E-02	2.62E-03	-3.08	-1.74	-3.81E-01
4003		230392_at	3.5771E-02	2.62E-03	3.08	-1.75	1.88E-01
4004	PLSCR3	218828_at	3.5775E-02	2.62E-03	-3.08	-1.75	-2.06E-01
4005	RALGAPA2	239660_at	3.5777E-02	2.62E-03	3.08	-1.75	1.87E-01
4006	PPID	204186_s_at	3.5777E-02	2.62E-03	-3.08	-1.75	-4.54E-01
4007		238946_at	3.5783E-02	2.62E-03	3.08	-1.75	1.52E-01
4008	LGALS14	220158_at	3.5813E-02	2.63E-03	3.08	-1.75	3.28E-01
4009		231952_at	3.5813E-02	2.63E-03	3.08	-1.75	3.01E-01
4010	Sep-04	210657_s_at	3.5816E-02	2.63E-03	-3.08	-1.75	-3.07E-01
4011	C20orf191/// NCOR1	200855_at	3.5816E-02	2.63E-03	3.08	-1.75	1.83E-01
4012	C2orf79	226243_at	3.5827E-02	2.63E-03	3.08	-1.75	4.56E-01
4013		236451_at	3.5827E-02	2.63E-03	3.08	-1.75	2.81E-01
4014	CRYBG3	214030_at	3.5827E-02	2.63E-03	-3.08	-1.75	-3.18E-01
4015	LOC730102	241607_at	3.5827E-02	2.63E-03	-3.08	-1.75	-1.49E-01
4016	FNDC3A	202304_at	3.5843E-02	2.63E-03	-3.07	-1.75	-2.82E-01
4017	CRHR1	211897_s_at	3.5843E-02	2.63E-03	3.07	-1.75	1.51E-01
4018	HLA-DQB1	209823_x_at	3.5854E-02	2.63E-03	-3.07	-1.75	-7.87E-01
4019	KLK13	216670_at	3.5877E-02	2.64E-03	3.07	-1.75	1.59E-01
4020	EDA2R	221399_at	3.5877E-02	2.64E-03	3.07	-1.75	1.62E-01
4021	CTNND1	208862_s_at	3.5877E-02	2.64E-03	-3.07	-1.75	-2.80E-01
4022	ZNF404	239043_at	3.5877E-02	2.64E-03	3.07	-1.75	2.85E-01
4023	C7orf44	232330_at	3.5878E-02	2.64E-03	3.07	-1.75	3.77E-01
4024		1564733_at	3.5897E-02	2.64E-03	3.07	-1.75	2.18E-01
4025	CHMP4A	218572_at	3.5928E-02	2.64E-03	-3.07	-1.75	-3.75E-01
4026	VPS41	210849_s_at	3.5963E-02	2.65E-03	-3.07	-1.76	-3.09E-01
4027	XPNPEP2	206484_s_at	3.5963E-02	2.65E-03	-3.07	-1.76	-1.98E-01
4028	TMEM182	1555090_x_at	3.6033E-02	2.66E-03	3.07	-1.76	1.60E-01
4029	KRTAP19-3	240967_at	3.6033E-02	2.66E-03	3.07	-1.76	1.24E-01
4030	CCDC86	203119_at	3.6033E-02	2.66E-03	-3.07	-1.76	-3.99E-01
4031	PCNX	213159_at	3.6033E-02	2.66E-03	-3.07	-1.76	-3.67E-01
4032	HEXB	201944_at	3.6033E-02	2.66E-03	-3.07	-1.76	-4.11E-01
4033	CDC34	212540_at	3.6034E-02	2.66E-03	-3.07	-1.76	-3.09E-01
4034	THBD	237252_at	3.6052E-02	2.66E-03	-3.07	-1.76	-2.16E-01
4035		239263_at	3.6058E-02	2.66E-03	3.07	-1.76	1.67E-01
4036	JUNB	201473_at	3.6073E-02	2.66E-03	-3.07	-1.76	-4.22E-01
4037	FA2H	234963_s_at	3.6114E-02	2.67E-03	3.07	-1.76	1.50E-01
4038	APEH	201284_s_at	3.6148E-02	2.67E-03	-3.07	-1.76	-3.92E-01
4039	RARS	201330_at	3.6152E-02	2.67E-03	-3.07	-1.76	-2.85E-01
4040	ZNF395	222536_s_at	3.6160E-02	2.67E-03	3.07	-1.76	2.12E-01
4041	CDAN1	228516_at	3.6195E-02	2.68E-03	3.07	-1.76	2.25E-01
4042	C6orf52	236504_x_at	3.6195E-02	2.68E-03	3.07	-1.76	2.39E-01
4043	RALBP1	202844_s_at	3.6211E-02	2.68E-03	-3.07	-1.76	-4.23E-01
4044	CTBP2	210835_s_at	3.6240E-02	2.68E-03	-3.07	-1.77	-3.78E-01
4045	NUP98	203194_s_at	3.6240E-02	2.68E-03	-3.07	-1.77	-4.32E-01
4046		236174_at	3.6240E-02	2.68E-03	3.07	-1.77	1.87E-01
4047	UBE2L3	200683_s_at	3.6245E-02	2.68E-03	-3.07	-1.77	-4.23E-01
4048		230714_s_at	3.6245E-02	2.68E-03	3.07	-1.77	2.58E-01
4049		1559524_at	3.6247E-02	2.68E-03	3.07	-1.77	1.78E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4050	TTC3	210645_s_at	3.6247E-02	2.68E-03	-3.07	-1.77	-4.18E-01
4051		238881_at	3.6262E-02	2.69E-03	3.07	-1.77	1.05E-01
4052	C16orf42	213104_at	3.6318E-02	2.69E-03	-3.07	-1.77	-3.08E-01
4053	MRP63	204386_s_at	3.6325E-02	2.69E-03	3.07	-1.77	2.89E-01
4054	ZNF451	231885_at	3.6332E-02	2.69E-03	3.07	-1.77	1.05E-01
4055	FIGN	222956_at	3.6336E-02	2.70E-03	3.07	-1.77	1.42E-01
4056		226865_at	3.6336E-02	2.70E-03	-3.07	-1.77	-6.54E-01
4057	HBP1	236645_at	3.6347E-02	2.70E-03	3.07	-1.77	1.48E-01
4058	HOOK3	1558315_s_at	3.6353E-02	2.70E-03	-3.07	-1.77	-1.25E-01
4059	TPRA1	218855_at	3.6413E-02	2.70E-03	-3.07	-1.77	-2.46E-01
4060	YBX1	208627_s_at	3.6413E-02	2.70E-03	-3.07	-1.77	-4.72E-01
4061	CAMK4	241871_at	3.6448E-02	2.71E-03	3.07	-1.77	4.13E-01
4062	C2	1554533_at	3.6450E-02	2.71E-03	-3.07	-1.77	-5.03E-01
4063		1564083_at	3.6460E-02	2.71E-03	3.07	-1.78	1.06E-01
4064		243220_at	3.6460E-02	2.71E-03	3.07	-1.78	1.17E-01
4065	TGOLN2	203833_s_at	3.6460E-02	2.71E-03	-3.07	-1.78	-4.01E-01
4066	LEKR1	1559105_at	3.6473E-02	2.71E-03	3.07	-1.78	1.36E-01
4067	YWHAE	213655_at	3.6475E-02	2.71E-03	-3.07	-1.78	-3.48E-01
4068		244243_at	3.6475E-02	2.71E-03	3.07	-1.78	1.17E-01
4069	MAP3K2	1565130_at	3.6475E-02	2.71E-03	3.06	-1.78	9.96E-02
4070	HNRNPUL2	227608_at	3.6477E-02	2.72E-03	-3.06	-1.78	-4.98E-01
4071	GAS7	210872_x_at	3.6477E-02	2.72E-03	-3.06	-1.78	-2.22E-01
4072	KIAA0101	211713_x_at	3.6477E-02	2.72E-03	3.06	-1.78	3.27E-01
4073	SLC26A1	205058_at	3.6477E-02	2.72E-03	3.06	-1.78	1.76E-01
4074	COPS8	202143_s_at	3.6477E-02	2.72E-03	-3.06	-1.78	-4.32E-01
4075	KEAP1	202417_at	3.6477E-02	2.72E-03	-3.06	-1.78	-3.91E-01
4076	RELA	201783_s_at	3.6477E-02	2.72E-03	-3.06	-1.78	-4.35E-01
4077	TNIP2	232160_s_at	3.6495E-02	2.72E-03	-3.06	-1.78	-2.21E-01
4078		230703_at	3.6495E-02	2.72E-03	3.06	-1.78	3.15E-01
4079	RALBP1	202845_s_at	3.6501E-02	2.72E-03	-3.06	-1.78	-3.45E-01
4080	IPO11	1557770_at	3.6511E-02	2.72E-03	3.06	-1.78	1.39E-01
4081	USP33	214843_s_at	3.6513E-02	2.73E-03	3.06	-1.78	3.12E-01
4082	C1orf50	62212_at	3.6584E-02	2.73E-03	3.06	-1.78	3.78E-01
4083	ITGA7	216331_at	3.6601E-02	2.73E-03	-3.06	-1.78	-3.06E-01
4084	SMAD7	204790_at	3.6601E-02	2.73E-03	-3.06	-1.78	-4.41E-01
4085		233407_at	3.6601E-02	2.74E-03	3.06	-1.78	9.51E-02
4086	WDR33	222763_s_at	3.6601E-02	2.74E-03	3.06	-1.78	2.43E-01
4087		1560784_x_at	3.6601E-02	2.74E-03	3.06	-1.78	1.48E-01
4088		239601_at	3.6611E-02	2.74E-03	3.06	-1.78	1.62E-01
4089	AGTRAP	225059_at	3.6635E-02	2.74E-03	-3.06	-1.78	-3.38E-01
4090	APOL6	1557236_at	3.6635E-02	2.74E-03	-3.06	-1.79	-4.31E-01
4091	PRSS23	202458_at	3.6638E-02	2.74E-03	-3.06	-1.79	-6.94E-01
4092	FAM184A	220150_s_at	3.6650E-02	2.74E-03	3.06	-1.79	3.33E-01
4093	CPXM1	227860_at	3.6657E-02	2.74E-03	-3.06	-1.79	-7.33E-01
4094	ALDH1L2	231202_at	3.6660E-02	2.75E-03	-3.06	-1.79	-3.74E-01
4095	MGC2848	1553936_a_at	3.6660E-02	2.75E-03	3.06	-1.79	1.55E-01
4096	UEVLD	1554397_s_at	3.6660E-02	2.75E-03	-3.06	-1.79	-4.83E-01
4097	NOTCH1	223508_at	3.6660E-02	2.75E-03	3.06	-1.79	1.53E-01
4098	LOC100133790	233993_at	3.6665E-02	2.75E-03	3.06	-1.79	1.51E-01
4099	GAS2L1	31874_at	3.6665E-02	2.75E-03	-3.06	-1.79	-4.66E-01
4100		240069_at	3.6665E-02	2.75E-03	-3.06	-1.79	-2.07E-01
4101		243847_at	3.6682E-02	2.75E-03	3.06	-1.79	9.74E-02
4102	KRTCAP3	235148_at	3.6682E-02	2.75E-03	3.06	-1.79	1.74E-01
4103	PILRA	219788_at	3.6682E-02	2.75E-03	-3.06	-1.79	-5.36E-01
4104	C4orf32	227856_at	3.6700E-02	2.76E-03	-3.06	-1.79	-3.62E-01
4105	MPHOSPH9	1558369_at	3.6700E-02	2.76E-03	3.06	-1.79	2.95E-01
4106	TBC1D14	224622_at	3.6700E-02	2.76E-03	-3.06	-1.79	-2.59E-01
4107	OLA1	219293_s_at	3.6700E-02	2.76E-03	3.06	-1.79	2.58E-01
4108	NDFIP2	224801_at	3.6700E-02	2.76E-03	3.06	-1.79	3.00E-01
4109	ERP44	208959_s_at	3.6700E-02	2.76E-03	-3.06	-1.79	-2.07E-01
4110	LOC90834	233321_x_at	3.6709E-02	2.76E-03	3.06	-1.79	1.41E-01
4111	FASN	212218_s_at	3.6709E-02	2.76E-03	-3.06	-1.79	-2.56E-01
4112	RSBN1	213694_at	3.6709E-02	2.76E-03	3.06	-1.79	3.02E-01
4113	WBP11	217822_at	3.6709E-02	2.76E-03	-3.06	-1.79	-2.63E-01
4114	CA12	203963_at	3.6711E-02	2.76E-03	-3.06	-1.79	-9.44E-01
4115		235017_s_at	3.6732E-02	2.76E-03	3.06	-1.79	1.82E-01
4116	DCLK1	215303_at	3.6735E-02	2.77E-03	-3.06	-1.79	-1.44E-01
4117		232690_at	3.6797E-02	2.77E-03	3.06	-1.79	1.97E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4118	UBA5	222578_s_at	3.6797E-02	2.77E-03	-3.06	-1.79	-2.34E-01
4119	NOMO3///NOMO2///NOMO1	217225_x_at	3.6798E-02	2.77E-03	-3.06	-1.80	-3.22E-01
4120		235752_at	3.6813E-02	2.77E-03	3.06	-1.80	1.57E-01
4121	DBF4B	206661_at	3.6813E-02	2.78E-03	3.06	-1.80	1.03E-01
4122	TMEM192	226589_at	3.6813E-02	2.78E-03	-3.06	-1.80	-1.92E-01
4123	C8orf44///SGK3	220038_at	3.6813E-02	2.78E-03	-3.06	-1.80	-5.66E-01
4124	LOC100288432	230631_s_at	3.6828E-02	2.78E-03	-3.06	-1.80	-3.23E-01
4125	TEX261	212083_at	3.6846E-02	2.78E-03	-3.06	-1.80	-4.48E-01
4126	THAP8	228500_at	3.6846E-02	2.78E-03	-3.06	-1.80	-2.37E-01
4127	HHLA3	220387_s_at	3.6850E-02	2.78E-03	-3.06	-1.80	-2.97E-01
4128	STK17A	202693_s_at	3.6850E-02	2.78E-03	3.06	-1.80	4.14E-01
4129	RLF	204243_at	3.6866E-02	2.78E-03	3.06	-1.80	2.38E-01
4130	RNASEH1	218497_s_at	3.6866E-02	2.79E-03	-3.06	-1.80	-3.46E-01
4131	C9orf167	219620_x_at	3.6866E-02	2.79E-03	-3.06	-1.80	-2.88E-01
4132	LOC144438	225493_at	3.6866E-02	2.79E-03	3.06	-1.80	2.22E-01
4133	HSPA13	202558_s_at	3.6870E-02	2.79E-03	-3.06	-1.80	-3.47E-01
4134	TAGLN2	200916_at	3.6870E-02	2.79E-03	-3.06	-1.80	-4.90E-01
4135		236293_at	3.6910E-02	2.79E-03	3.06	-1.80	5.59E-01
4136	LOC643923	1564787_at	3.6910E-02	2.79E-03	3.06	-1.80	1.95E-01
4137		230354_at	3.6910E-02	2.79E-03	-3.06	-1.80	-3.21E-01
4138	TIMP3	201147_s_at	3.6910E-02	2.79E-03	-3.06	-1.80	-7.25E-01
4139	EIF5	208705_s_at	3.6911E-02	2.79E-03	-3.06	-1.80	-2.80E-01
4140	CYR61	210764_s_at	3.6937E-02	2.80E-03	-3.06	-1.80	-8.31E-01
4141	ENTHD1	1552393_at	3.6955E-02	2.80E-03	3.06	-1.80	1.19E-01
4142	ME2	209397_at	3.6955E-02	2.80E-03	-3.05	-1.80	-2.05E-01
4143	CHURC1	233268_s_at	3.6955E-02	2.80E-03	3.05	-1.80	5.15E-01
4144		244185_at	3.6955E-02	2.80E-03	3.05	-1.80	3.52E-01
4145	NAALAD2	233815_at	3.6982E-02	2.80E-03	3.05	-1.81	1.58E-01
4146	CYB561	210816_s_at	3.6986E-02	2.80E-03	-3.05	-1.81	-1.89E-01
4147		244384_at	3.6991E-02	2.81E-03	3.05	-1.81	1.53E-01
4148	SLIT2	230130_at	3.7016E-02	2.81E-03	-3.05	-1.81	-3.38E-01
4149	LOC100129722	1566906_at	3.7047E-02	2.81E-03	3.05	-1.81	2.55E-01
4150	NOTCH2	202443_x_at	3.7047E-02	2.81E-03	-3.05	-1.81	-3.26E-01
4151	TMEM80	1559132_at	3.7050E-02	2.81E-03	3.05	-1.81	2.41E-01
4152	TRIM61	238990_x_at	3.7050E-02	2.81E-03	3.05	-1.81	3.61E-01
4153		1562189_at	3.7050E-02	2.81E-03	3.05	-1.81	1.21E-01
4154		202225_at	3.7105E-02	2.82E-03	-3.05	-1.81	-2.78E-01
4155		215327_at	3.7108E-02	2.82E-03	3.05	-1.81	1.55E-01
4156	ATP13A2	218608_at	3.7108E-02	2.82E-03	-3.05	-1.81	-5.30E-01
4157	TIAM2	219950_s_at	3.7110E-02	2.82E-03	3.05	-1.81	1.52E-01
4158	ZNF668	219047_s_at	3.7153E-02	2.83E-03	-3.05	-1.81	-1.91E-01
4159	DMD	208086_s_at	3.7170E-02	2.83E-03	3.05	-1.81	1.40E-01
4160	ACACB	1552616_a_at	3.7170E-02	2.83E-03	3.05	-1.81	1.28E-01
4161		1564996_at	3.7170E-02	2.83E-03	3.05	-1.81	1.33E-01
4162	ADAT2	236817_at	3.7170E-02	2.83E-03	3.05	-1.81	1.37E-01
4163	ZNF645	1552967_at	3.7170E-02	2.83E-03	3.05	-1.81	1.28E-01
4164	KLF7	204334_at	3.7170E-02	2.83E-03	-3.05	-1.81	-3.41E-01
4165	BMPR2	231873_at	3.7170E-02	2.83E-03	-3.05	-1.81	-3.23E-01
4166	WT1	216953_s_at	3.7183E-02	2.83E-03	3.05	-1.81	1.66E-01
4167	UTS2R	1553262_a_at	3.7183E-02	2.83E-03	3.05	-1.81	1.39E-01
4168	TMED5	1558814_s_at	3.7213E-02	2.84E-03	3.05	-1.82	2.18E-01
4169	KBTBD3	228777_at	3.7244E-02	2.84E-03	3.05	-1.82	6.56E-01
4170	AURKA	208080_at	3.7251E-02	2.84E-03	3.05	-1.82	1.47E-01
4171	GJD2	221407_at	3.7252E-02	2.84E-03	3.05	-1.82	2.06E-01
4172	CNOT7	225053_at	3.7252E-02	2.84E-03	3.05	-1.82	2.07E-01
4173	GTPBP10	239773_at	3.7258E-02	2.84E-03	3.05	-1.82	1.39E-01
4174	SIRPA	202897_at	3.7258E-02	2.84E-03	-3.05	-1.82	-5.06E-01
4175		215212_at	3.7261E-02	2.85E-03	3.05	-1.82	9.61E-02
4176	SFTPC	214387_x_at	3.7265E-02	2.85E-03	3.05	-1.82	1.73E-01
4177	RPL14	219138_at	3.7273E-02	2.85E-03	3.05	-1.82	4.27E-01
4178		1566596_at	3.7297E-02	2.85E-03	3.05	-1.82	1.40E-01
4179	TSPAN14	223314_at	3.7308E-02	2.85E-03	-3.05	-1.82	-4.08E-01
4180		1562116_at	3.7308E-02	2.85E-03	3.05	-1.82	1.35E-01
4181	GALC	204417_at	3.7308E-02	2.85E-03	-3.05	-1.82	-4.01E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4182	RPA3	209507_at	3.7328E-02	2.86E-03	3.05	-1.82	5.41E-01
4183		237512_at	3.7328E-02	2.86E-03	3.05	-1.82	1.40E-01
4184	FAM66C	1570396_at	3.7328E-02	2.86E-03	3.05	-1.82	8.16E-02
4185	LOC100129387	227406_at	3.7328E-02	2.86E-03	3.05	-1.82	2.97E-01
4186	TFPI	210664_s_at	3.7328E-02	2.86E-03	-3.05	-1.82	-5.09E-01
4187	BAHCC1	1559049_a_at	3.7328E-02	2.86E-03	3.05	-1.82	1.21E-01
4188	ETV6	239364_at	3.7349E-02	2.86E-03	-3.05	-1.82	-2.27E-01
4189	FAM46A	224973_at	3.7361E-02	2.86E-03	-3.05	-1.82	-3.60E-01
4190	PMS2L3	217488_x_at	3.7375E-02	2.86E-03	3.05	-1.82	1.68E-01
4191	DGKB	216307_at	3.7375E-02	2.86E-03	3.05	-1.82	8.49E-02
4192	SMARCA2	212257_s_at	3.7376E-02	2.87E-03	-3.05	-1.82	-4.01E-01
4193	FLJ44606	244761_at	3.7376E-02	2.87E-03	3.05	-1.82	1.96E-01
4194	APLP2	208704_x_at	3.7376E-02	2.87E-03	-3.05	-1.82	-4.13E-01
4195		1561762_s_at	3.7401E-02	2.87E-03	3.05	-1.83	1.68E-01
4196	TXN2	209078_s_at	3.7403E-02	2.87E-03	-3.05	-1.83	-3.19E-01
4197		1558320_at	3.7409E-02	2.87E-03	3.05	-1.83	1.12E-01
4198	ZNF503	232178_at	3.7409E-02	2.87E-03	3.05	-1.83	1.31E-01
4199	KCNE4	222379_at	3.7424E-02	2.87E-03	-3.05	-1.83	-4.46E-01
4200		228792_at	3.7444E-02	2.88E-03	3.05	-1.83	9.09E-02
4201	LIMS1	207198_s_at	3.7454E-02	2.88E-03	-3.05	-1.83	-3.75E-01
4202	RALB	202100_at	3.7454E-02	2.88E-03	-3.05	-1.83	-3.74E-01
4203	TFG	239385_at	3.7454E-02	2.88E-03	3.05	-1.83	2.34E-01
4204	BVES	223853_at	3.7454E-02	2.88E-03	3.05	-1.83	1.29E-01
4205	C4B///C4A	214428_x_at	3.7456E-02	2.88E-03	-3.05	-1.83	-4.53E-01
4206	FITM2	233061_at	3.7492E-02	2.88E-03	3.05	-1.83	1.38E-01
4207		1559119_at	3.7497E-02	2.89E-03	3.05	-1.83	1.78E-01
4208	LEF1	221558_s_at	3.7497E-02	2.89E-03	3.05	-1.83	4.88E-01
4209	TRPV2	219282_s_at	3.7497E-02	2.89E-03	-3.04	-1.83	-3.33E-01
4210	C12orf65	232650_at	3.7497E-02	2.89E-03	3.04	-1.83	1.54E-01
4211	GPR6	1553507_a_at	3.7499E-02	2.89E-03	3.04	-1.83	1.97E-01
4212		230396_at	3.7535E-02	2.89E-03	3.04	-1.83	1.51E-01
4213	RARRES1	206391_at	3.7592E-02	2.90E-03	-3.04	-1.83	-6.38E-01
4214	Mar-07	232371_at	3.7592E-02	2.90E-03	3.04	-1.83	2.20E-01
4215	EFEMP2	206580_s_at	3.7592E-02	2.90E-03	-3.04	-1.83	-5.23E-01
4216	SNORA28	241843_at	3.7592E-02	2.90E-03	3.04	-1.83	1.94E-01
4217		224546_at	3.7644E-02	2.90E-03	3.04	-1.84	1.64E-01
4218	CD36	209555_s_at	3.7673E-02	2.91E-03	-3.04	-1.84	-6.61E-01
4219	VCAN	204620_s_at	3.7673E-02	2.91E-03	-3.04	-1.84	-1.14E+00
4220	MTRF1L	225206_s_at	3.7673E-02	2.91E-03	-3.04	-1.84	-2.29E-01
4221	LRRC32	203835_at	3.7722E-02	2.91E-03	-3.04	-1.84	-4.62E-01
4222	EPC1	234969_s_at	3.7722E-02	2.91E-03	3.04	-1.84	2.07E-01
4223	SYNJ1	207594_s_at	3.7726E-02	2.91E-03	-3.04	-1.84	-1.43E-01
4224		1562529_s_at	3.7766E-02	2.92E-03	3.04	-1.84	5.86E-01
4225	COL3A1	211161_s_at	3.7809E-02	2.92E-03	-3.04	-1.84	-1.02E+00
4226	CALCOCO2	210817_s_at	3.7836E-02	2.93E-03	-3.04	-1.84	-3.23E-01
4227	PCA3	232575_at	3.7836E-02	2.93E-03	3.04	-1.84	1.27E-01
4228	C5orf41	235556_at	3.7836E-02	2.93E-03	3.04	-1.84	2.84E-01
4229	DCAF7	224730_at	3.7875E-02	2.93E-03	-3.04	-1.84	-5.02E-01
4230	RPL13	212933_x_at	3.7875E-02	2.93E-03	3.04	-1.84	1.08E-01
4231	FERMT2	209210_s_at	3.7983E-02	2.94E-03	-3.04	-1.85	-5.35E-01
4232		235842_at	3.8002E-02	2.94E-03	3.04	-1.85	1.60E-01
4233	LOC285943	230080_at	3.8009E-02	2.94E-03	3.04	-1.85	1.73E-01
4234	EPDR1	223253_at	3.8056E-02	2.95E-03	-3.04	-1.85	-5.59E-01
4235	ATG13	203364_s_at	3.8060E-02	2.95E-03	-3.04	-1.85	-2.95E-01
4236	SMTN	209427_at	3.8084E-02	2.95E-03	-3.04	-1.85	-3.01E-01
4237		242715_at	3.8099E-02	2.95E-03	3.04	-1.85	1.44E-01
4238	RPS28	208904_s_at	3.8136E-02	2.96E-03	3.04	-1.85	1.53E-01
4239	LOC400604	241405_at	3.8136E-02	2.96E-03	3.04	-1.85	1.61E-01
4240	RPL7L1	224738_x_at	3.8185E-02	2.96E-03	-3.04	-1.85	-2.36E-01
4241		231925_at	3.8193E-02	2.96E-03	-3.04	-1.85	-2.64E-01
4242	SPNS1	223173_at	3.8219E-02	2.97E-03	-3.04	-1.85	-3.26E-01
4243		238379_x_at	3.8237E-02	2.97E-03	3.04	-1.85	1.92E-01
4244	COL1A2	202404_s_at	3.8292E-02	2.97E-03	-3.04	-1.86	-1.23E+00
4245	MED23	223946_at	3.8311E-02	2.97E-03	3.04	-1.86	2.06E-01
4246	C21orf2	221975_s_at	3.8311E-02	2.98E-03	3.04	-1.86	1.74E-01
4247	CARS2	231023_at	3.8311E-02	2.98E-03	3.04	-1.86	1.32E-01
4248	RBM23	219816_s_at	3.8311E-02	2.98E-03	-3.04	-1.86	-3.89E-01
4249	C6orf115	223361_at	3.8313E-02	2.98E-03	3.03	-1.86	4.71E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4250	LOC653354/ //ARMCX6	214749_s_at	3.8313E-02	2.98E-03	3.03	-1.86	1.99E-01
4251	UNC5B	226899_at	3.8313E-02	2.98E-03	-3.03	-1.86	-4.50E-01
4252	LGALS8	210732_s_at	3.8313E-02	2.98E-03	-3.03	-1.86	-5.99E-01
4253	C11orf31	1557799_at	3.8313E-02	2.98E-03	3.03	-1.86	2.62E-01
4254	MLEC	200617_at	3.8314E-02	2.98E-03	-3.03	-1.86	-4.47E-01
4255	SLC2A14/// SLC2A3	222088_s_at	3.8314E-02	2.98E-03	-3.03	-1.86	-5.18E-01
4256	CPT2	204263_s_at	3.8320E-02	2.98E-03	-3.03	-1.86	-3.85E-01
4257	LAGE3	221982_x_at	3.8373E-02	2.99E-03	3.03	-1.86	1.99E-01
4258		232974_at	3.8397E-02	2.99E-03	3.03	-1.86	2.42E-01
4259		1569656_at	3.8426E-02	2.99E-03	3.03	-1.86	9.46E-02
4260	GCLM	236140_at	3.8426E-02	2.99E-03	-3.03	-1.86	-3.23E-01
4261	CYP51A1	216607_s_at	3.8426E-02	2.99E-03	-3.03	-1.86	-3.37E-01
4262	ASB7	233807_at	3.8443E-02	3.00E-03	3.03	-1.86	1.37E-01
4263	SFRS15	222311_s_at	3.8443E-02	3.00E-03	3.03	-1.86	2.32E-01
4264	UBE2Z	217750_s_at	3.8454E-02	3.00E-03	-3.03	-1.86	-2.57E-01
4265	FN3KRP	218210_at	3.8454E-02	3.00E-03	-3.03	-1.86	-3.05E-01
4266	ZNF569	1569366_a_at	3.8454E-02	3.00E-03	3.03	-1.86	2.00E-01
4267	SLC5A3	213167_s_at	3.8454E-02	3.00E-03	-3.03	-1.86	-1.63E-01
4268	LASS2	222212_s_at	3.8460E-02	3.00E-03	-3.03	-1.86	-3.17E-01
4269	DNAJC1	222621_at	3.8462E-02	3.00E-03	-3.03	-1.87	-2.78E-01
4270	GTPBP8	223486_at	3.8462E-02	3.00E-03	3.03	-1.87	6.48E-01
4271	RPL37A	201429_s_at	3.8473E-02	3.01E-03	3.03	-1.87	7.71E-02
4272	SPARC	212667_at	3.8473E-02	3.01E-03	-3.03	-1.87	-7.90E-01
4273	C22orf32	225794_s_at	3.8479E-02	3.01E-03	3.03	-1.87	4.21E-01
4274	PYGB	201481_s_at	3.8479E-02	3.01E-03	-3.03	-1.87	-2.34E-01
4275	CAT	211922_s_at	3.8526E-02	3.01E-03	-3.03	-1.87	-4.50E-01
4276	PPPDE1	222158_s_at	3.8563E-02	3.02E-03	-3.03	-1.87	-3.63E-01
4277	GFPT2	205100_at	3.8596E-02	3.02E-03	-3.03	-1.87	-6.11E-01
4278		228726_at	3.8612E-02	3.02E-03	-3.03	-1.87	-3.70E-01
4279		1557829_at	3.8636E-02	3.02E-03	3.03	-1.87	9.08E-02
4280	SIX5	229009_at	3.8636E-02	3.03E-03	-3.03	-1.87	-2.99E-01
4281	RNF144B	228153_at	3.8636E-02	3.03E-03	-3.03	-1.87	-4.84E-01
4282	FAM200B	236321_at	3.8696E-02	3.03E-03	3.03	-1.87	3.47E-01
4283	C16orf55	230811_at	3.8696E-02	3.03E-03	3.03	-1.87	2.78E-01
4284	WDR5B	219538_at	3.8731E-02	3.03E-03	3.03	-1.87	2.41E-01
4285	DUSP6	208892_s_at	3.8731E-02	3.04E-03	-3.03	-1.87	-3.31E-01
4286	MLKL	238025_at	3.8731E-02	3.04E-03	-3.03	-1.87	-3.78E-01
4287	TEAD2	243766_s_at	3.8731E-02	3.04E-03	3.03	-1.87	2.02E-01
4288	SLC35E1	235035_at	3.8755E-02	3.04E-03	-3.03	-1.88	-2.49E-01
4289	MS4A7	223343_at	3.8807E-02	3.04E-03	-3.03	-1.88	-8.96E-01
4290	LRRC39	227532_at	3.8821E-02	3.05E-03	3.03	-1.88	1.40E-01
4291	VDAC1	217140_s_at	3.8821E-02	3.05E-03	-3.03	-1.88	-4.12E-01
4292	TIMM10	218408_at	3.8821E-02	3.05E-03	3.03	-1.88	4.62E-01
4293	PPP1R1A	205478_at	3.8821E-02	3.05E-03	-3.03	-1.88	-3.47E-01
4294	MT1F	217165_x_at	3.8832E-02	3.05E-03	-3.03	-1.88	-6.68E-01
4295	IQUB	1568924_a_at	3.8850E-02	3.05E-03	3.03	-1.88	1.24E-01
4296	ZCCHC10	223803_s_at	3.8863E-02	3.05E-03	3.03	-1.88	4.42E-01
4297	DAGLB	225832_s_at	3.8875E-02	3.06E-03	-3.03	-1.88	-3.01E-01
4298	PARS2	227348_at	3.8923E-02	3.06E-03	-3.03	-1.88	-2.02E-01
4299		1563099_at	3.8923E-02	3.06E-03	3.03	-1.88	9.56E-02
4300	PLA2G2E	221389_at	3.8923E-02	3.06E-03	3.03	-1.88	1.71E-01
4301		236197_at	3.8936E-02	3.06E-03	3.03	-1.88	1.02E-01
4302	RPL5	1556498_at	3.8940E-02	3.06E-03	3.03	-1.88	1.28E-01
4303		230041_at	3.8945E-02	3.07E-03	3.03	-1.88	1.67E-01
4304	EEA1	204840_s_at	3.8949E-02	3.07E-03	-3.03	-1.88	-2.54E-01
4305	FRMD4B	213056_at	3.8949E-02	3.07E-03	-3.03	-1.88	-3.43E-01
4306	CKS2	204170_s_at	3.8949E-02	3.07E-03	3.03	-1.88	5.69E-01
4307		1560353_at	3.8949E-02	3.07E-03	3.03	-1.88	1.25E-01
4308	FLJ23519/// RNH1	216798_at	3.8949E-02	3.07E-03	3.03	-1.88	1.64E-01
4309	MCART1	238574_at	3.8951E-02	3.07E-03	-3.02	-1.88	-2.12E-01
4310	EPS8	202609_at	3.8958E-02	3.07E-03	-3.02	-1.88	-6.99E-01
4311	EMP1	201324_at	3.8989E-02	3.07E-03	-3.02	-1.89	-8.02E-01
4312	VAMP2	201557_at	3.9016E-02	3.08E-03	-3.02	-1.89	-2.75E-01
4313		241228_at	3.9023E-02	3.08E-03	3.02	-1.89	1.12E-01
4314	FAM21A///F AM21C///FA	212370_x_at	3.9023E-02	3.08E-03	-3.02	-1.89	-3.23E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
	M21B						
4315	ZYX	215706_x_at	3.9036E-02	3.08E-03	-3.02	-1.89	-5.90E-01
4316	C13orf27	213346_at	3.9036E-02	3.08E-03	3.02	-1.89	6.29E-01
4317		241616_at	3.9037E-02	3.08E-03	3.02	-1.89	1.94E-01
4318	LDLR	202068_s_at	3.9043E-02	3.08E-03	-3.02	-1.89	-4.19E-01
4319	CDK19	212897_at	3.9043E-02	3.08E-03	-3.02	-1.89	-2.44E-01
4320	NDUFA11	228689_at	3.9080E-02	3.09E-03	3.02	-1.89	1.64E-01
4321	MIR17HG	233636_at	3.9091E-02	3.09E-03	3.02	-1.89	9.17E-02
4322	GET4	227588_s_at	3.9091E-02	3.09E-03	3.02	-1.89	1.17E-01
4323	ZNF140	204523_at	3.9110E-02	3.09E-03	3.02	-1.89	3.61E-01
4324	TSGA10	220623_s_at	3.9110E-02	3.09E-03	3.02	-1.89	1.03E-01
4325		1561292_at	3.9111E-02	3.09E-03	3.02	-1.89	1.54E-01
4326	OCIAD1	235537_at	3.9159E-02	3.10E-03	3.02	-1.89	2.59E-01
4327	MLXIP	225157_at	3.9194E-02	3.10E-03	-3.02	-1.89	-4.42E-01
4328	RGAG4	227823_at	3.9207E-02	3.10E-03	-3.02	-1.89	-1.84E-01
4329		244312_at	3.9213E-02	3.10E-03	3.02	-1.89	2.48E-01
4330	ZNF614	220721_at	3.9213E-02	3.11E-03	3.02	-1.89	2.77E-01
4331	CLEC2D	233500_x_at	3.9214E-02	3.11E-03	3.02	-1.89	6.94E-01
4332	VTI1B	225926_at	3.9248E-02	3.11E-03	-3.02	-1.90	-3.74E-01
4333	ACOX1	227962_at	3.9248E-02	3.11E-03	-3.02	-1.90	-3.17E-01
4334		237347_at	3.9259E-02	3.11E-03	3.02	-1.90	2.05E-01
4335		239664_at	3.9259E-02	3.11E-03	3.02	-1.90	1.04E-01
4336	UBE3C	201817_at	3.9259E-02	3.11E-03	-3.02	-1.90	-3.24E-01
4337		1556334_s_at	3.9259E-02	3.11E-03	3.02	-1.90	9.85E-02
4338	TBCD	229192_s_at	3.9259E-02	3.11E-03	-3.02	-1.90	-2.71E-01
4339		232527_at	3.9267E-02	3.12E-03	3.02	-1.90	3.94E-01
4340	SCN10A	208578_at	3.9275E-02	3.12E-03	3.02	-1.90	1.35E-01
4341	ZNF564	1553957_at	3.9278E-02	3.12E-03	3.02	-1.90	2.24E-01
4342	SIRPB2	1559034_at	3.9278E-02	3.12E-03	-3.02	-1.90	-4.14E-01
4343	DAGLB	226640_at	3.9278E-02	3.12E-03	-3.02	-1.90	-1.76E-01
4344	U2AF1	232141_at	3.9278E-02	3.12E-03	3.02	-1.90	3.02E-01
4345	ARIH2	227932_at	3.9278E-02	3.12E-03	3.02	-1.90	3.43E-01
4346	AGRN	212285_s_at	3.9278E-02	3.12E-03	-3.02	-1.90	-2.54E-01
4347	LMX1B	208487_at	3.9278E-02	3.12E-03	3.02	-1.90	1.82E-01
4348	YARS	212048_s_at	3.9278E-02	3.12E-03	-3.02	-1.90	-2.74E-01
4349	IQCB1	205995_x_at	3.9278E-02	3.12E-03	3.02	-1.90	2.85E-01
4350		237779_at	3.9282E-02	3.13E-03	3.02	-1.90	1.67E-01
4351	BMP1	205574_x_at	3.9282E-02	3.13E-03	-3.02	-1.90	-3.94E-01
4352	ASCC3	231269_at	3.9282E-02	3.13E-03	-3.02	-1.90	-1.45E-01
4353	CYP51A1	202314_at	3.9282E-02	3.13E-03	-3.02	-1.90	-3.47E-01
4354		243919_at	3.9282E-02	3.13E-03	3.02	-1.90	2.13E-01
4355		238311_at	3.9323E-02	3.13E-03	3.02	-1.90	3.06E-01
4356		1556889_s_at	3.9323E-02	3.13E-03	3.02	-1.90	1.96E-01
4357	ARHGAP33	233885_at	3.9323E-02	3.13E-03	3.02	-1.90	1.47E-01
4358	CDC5L	209055_s_at	3.9334E-02	3.14E-03	-3.02	-1.90	-3.82E-01
4359		238142_at	3.9338E-02	3.14E-03	3.02	-1.90	3.60E-01
4360	ENSA	228851_s_at	3.9374E-02	3.14E-03	-3.02	-1.90	-2.98E-01
4361	CLN6	1567081_x_at	3.9392E-02	3.14E-03	-3.02	-1.90	-1.88E-01
4362	FBXL20	239224_at	3.9403E-02	3.14E-03	3.02	-1.91	1.20E-01
4363	GNA11	40562_at	3.9403E-02	3.14E-03	-3.02	-1.91	-3.57E-01
4364	ATP6AP2	201443_s_at	3.9415E-02	3.15E-03	-3.02	-1.91	-2.02E-01
4365	ALDH4A1	203722_at	3.9430E-02	3.15E-03	-3.02	-1.91	-1.65E-01
4366		231111_at	3.9441E-02	3.15E-03	3.02	-1.91	2.53E-01
4367	SHQ1	63009_at	3.9485E-02	3.15E-03	3.02	-1.91	2.18E-01
4368	CADM2	235118_at	3.9485E-02	3.15E-03	3.02	-1.91	8.54E-02
4369	PYGO2	239666_at	3.9519E-02	3.16E-03	3.02	-1.91	1.93E-01
4370		1569962_at	3.9526E-02	3.16E-03	3.02	-1.91	1.60E-01
4371	FOXA2	214312_at	3.9526E-02	3.16E-03	3.02	-1.91	1.58E-01
4372	LOC283663	230245_s_at	3.9526E-02	3.16E-03	3.02	-1.91	8.31E-01
4373	ARF1	244504_x_at	3.9530E-02	3.16E-03	3.02	-1.91	1.60E-01
4374	C21orf62	220543_at	3.9530E-02	3.16E-03	3.02	-1.91	1.10E-01
4375	ZNF827	243617_at	3.9538E-02	3.16E-03	3.02	-1.91	1.56E-01
4376	ADRB3	217303_s_at	3.9540E-02	3.16E-03	3.02	-1.91	1.35E-01
4377	WDFY3	212606_at	3.9561E-02	3.17E-03	-3.01	-1.91	-4.06E-01
4378		1559020_a_at	3.9582E-02	3.17E-03	3.01	-1.91	2.44E-01
4379	BCL6	215990_s_at	3.9582E-02	3.17E-03	-3.01	-1.91	-3.61E-01
4380	EIF4G2	1557964_at	3.9582E-02	3.17E-03	3.01	-1.91	1.64E-01
4381	SOX1	230982_at	3.9658E-02	3.18E-03	3.01	-1.91	1.83E-01
4382	CYP2B7P1//	206754_s_at	3.9658E-02	3.18E-03	3.01	-1.91	1.79E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
	/CYP2B6						
4383		240222_at	3.9658E-02	3.18E-03	3.01	-1.92	1.14E-01
4384	VCAN	221731_x_at	3.9658E-02	3.18E-03	-3.01	-1.92	-1.24E+00
4385	CDK2AP2	203252_at	3.9698E-02	3.18E-03	-3.01	-1.92	-4.02E-01
4386	ANAPC4	226917_s_at	3.9700E-02	3.18E-03	3.01	-1.92	3.54E-01
4387	CCDC7	1553215_s_at	3.9703E-02	3.19E-03	3.01	-1.92	1.89E-01
4388		237694_at	3.9722E-02	3.19E-03	3.01	-1.92	1.42E-01
4389	ATP2A2	209186_at	3.9780E-02	3.19E-03	-3.01	-1.92	-4.91E-01
4390	MS4A1	228599_at	3.9818E-02	3.20E-03	3.01	-1.92	8.60E-01
4391	TDRKH	223530_at	3.9835E-02	3.20E-03	-3.01	-1.92	-2.10E-01
4392	KCNRG	240288_at	3.9836E-02	3.20E-03	3.01	-1.92	9.79E-02
4393	GCHFR	204867_at	3.9836E-02	3.20E-03	3.01	-1.92	4.07E-01
4394	C11orf17	219953_s_at	3.9836E-02	3.20E-03	-3.01	-1.92	-2.10E-01
4395	ACTN1	208636_at	3.9836E-02	3.20E-03	-3.01	-1.92	-3.81E-01
4396	NACA	208635_x_at	3.9836E-02	3.20E-03	3.01	-1.92	1.88E-01
4397	HMGCS1	205822_s_at	3.9836E-02	3.20E-03	-3.01	-1.92	-2.03E-01
4398	IPW	241834_at	3.9836E-02	3.20E-03	3.01	-1.92	1.07E-01
4399	MACF1	232168_x_at	3.9836E-02	3.21E-03	3.01	-1.92	2.68E-01
4400	IL2	207849_at	3.9836E-02	3.21E-03	3.01	-1.92	1.47E-01
4401	TEC	206301_at	3.9836E-02	3.21E-03	3.01	-1.92	1.64E-01
4402	TNFSF12	205611_at	3.9855E-02	3.21E-03	-3.01	-1.92	-2.50E-01
4403		1569672_at	3.9855E-02	3.21E-03	3.01	-1.92	1.00E-01
4404	ITGA5	201389_at	3.9855E-02	3.21E-03	-3.01	-1.92	-3.88E-01
4405	ANKRD16	229058_at	3.9900E-02	3.22E-03	-3.01	-1.93	-1.96E-01
4406	SSH1	221753_at	3.9900E-02	3.22E-03	-3.01	-1.93	-2.43E-01
4407		236159_x_at	3.9900E-02	3.22E-03	3.01	-1.93	1.95E-01
4408	TMEM30A	232591_s_at	3.9900E-02	3.22E-03	-3.01	-1.93	-5.11E-01
4409	PPIF	201490_s_at	3.9918E-02	3.22E-03	-3.01	-1.93	-5.66E-01
4410	GNB4	225710_at	3.9918E-02	3.22E-03	-3.01	-1.93	-3.78E-01
4411	AK3L2///AK4	230630_at	3.9918E-02	3.22E-03	-3.01	-1.93	-1.44E-01
4412		236005_at	3.9918E-02	3.22E-03	3.01	-1.93	1.63E-01
4413	CECR6	224393_s_at	3.9928E-02	3.22E-03	-3.01	-1.93	-2.02E-01
4414	C6orf105	229070_at	3.9931E-02	3.22E-03	3.01	-1.93	6.42E-01
4415	FLJ37035	1560714_at	3.9931E-02	3.22E-03	3.01	-1.93	8.82E-02
4416	AGPAT4	219693_at	3.9952E-02	3.23E-03	-3.01	-1.93	-2.26E-01
4417		1564378_a_at	3.9960E-02	3.23E-03	3.01	-1.93	2.11E-01
4418	MT1E	212859_x_at	3.9960E-02	3.23E-03	-3.01	-1.93	-6.86E-01
4419	NUBP2	218227_at	3.9963E-02	3.23E-03	3.01	-1.93	2.50E-01
4420	CREBL2	201989_s_at	3.9963E-02	3.23E-03	-3.01	-1.93	-2.39E-01
4421		243272_at	4.0013E-02	3.24E-03	3.01	-1.93	1.68E-01
4422	TACC1	200911_s_at	4.0013E-02	3.24E-03	-3.01	-1.93	-2.86E-01
4423	ZNF182	235810_at	4.0013E-02	3.24E-03	-3.01	-1.93	-2.74E-01
4424	KIF13B	202962_at	4.0013E-02	3.24E-03	-3.01	-1.93	-2.88E-01
4425	MBLAC1	1554170_a_at	4.0013E-02	3.24E-03	3.01	-1.93	1.43E-01
4426	GPR107	220265_at	4.0081E-02	3.25E-03	3.01	-1.93	1.16E-01
4427	IDH3B	210014_x_at	4.0081E-02	3.25E-03	-3.01	-1.93	-3.11E-01
4428	MAP4K5	211081_s_at	4.0081E-02	3.25E-03	-3.01	-1.93	-3.05E-01
4429	DENND1A	219763_at	4.0081E-02	3.25E-03	-3.01	-1.93	-2.59E-01
4430	SLC30A8	1552985_at	4.0081E-02	3.25E-03	3.01	-1.93	1.53E-01
4431	ATP10B	220920_at	4.0081E-02	3.25E-03	3.01	-1.93	1.55E-01
4432	KDM6B	1556067_a_at	4.0081E-02	3.25E-03	3.01	-1.93	2.22E-01
4433	CARM1	212512_s_at	4.0081E-02	3.25E-03	-3.01	-1.93	-5.13E-01
4434		1560999_a_at	4.0081E-02	3.25E-03	3.01	-1.93	3.36E-01
4435		236611_at	4.0081E-02	3.25E-03	3.01	-1.93	5.02E-01
4436	SPIN3	1554098_at	4.0081E-02	3.25E-03	3.01	-1.93	1.29E-01
4437	FCGR2C///FCGR2B///FCGR2A	1565674_at	4.0081E-02	3.25E-03	-3.01	-1.93	-2.35E-01
4438	EARS2	225993_at	4.0119E-02	3.26E-03	-3.01	-1.94	-1.76E-01
4439	ATP11B	1564064_a_at	4.0119E-02	3.26E-03	-3.01	-1.94	-2.82E-01
4440	PGM2	223738_s_at	4.0119E-02	3.26E-03	-3.01	-1.94	-2.18E-01
4441		235406_x_at	4.0119E-02	3.26E-03	3.01	-1.94	2.78E-01
4442	TGOLN2	212040_at	4.0136E-02	3.26E-03	-3.01	-1.94	-6.55E-01
4443	E2F1	204947_at	4.0137E-02	3.26E-03	3.01	-1.94	1.99E-01
4444	MC2R	217434_at	4.0165E-02	3.26E-03	3.00	-1.94	9.68E-02
4445		227682_at	4.0173E-02	3.27E-03	-3.00	-1.94	-3.23E-01
4446	PBX1	212151_at	4.0173E-02	3.27E-03	-3.00	-1.94	-4.23E-01
4447	GNB1	200746_s_at	4.0173E-02	3.27E-03	-3.00	-1.94	-2.60E-01
4448	NHP2L1	230443_at	4.0173E-02	3.27E-03	3.00	-1.94	3.47E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4449		233713_at	4.0173E-02	3.27E-03	3.00	-1.94	2.27E-01
4450	DYNC1LI2	203590_at	4.0193E-02	3.27E-03	-3.00	-1.94	-4.19E-01
4451	LOC100288263///LOC644617	225653_at	4.0219E-02	3.27E-03	-3.00	-1.94	-2.02E-01
4452	ZNF227	217403_s_at	4.0258E-02	3.28E-03	-3.00	-1.94	-3.38E-01
4453	LOC100130502	244744_at	4.0262E-02	3.28E-03	3.00	-1.94	1.61E-01
4454	NADK	208917_x_at	4.0262E-02	3.28E-03	-3.00	-1.94	-2.43E-01
4455	QKI	1555154_a_at	4.0299E-02	3.28E-03	-3.00	-1.94	-3.61E-01
4456	CA12	204508_s_at	4.0303E-02	3.29E-03	-3.00	-1.94	-5.74E-01
4457	GRB10	209409_at	4.0303E-02	3.29E-03	-3.00	-1.94	-3.58E-01
4458	DBN1	202806_at	4.0303E-02	3.29E-03	-3.00	-1.94	-3.49E-01
4459		1569885_at	4.0389E-02	3.29E-03	3.00	-1.95	1.44E-01
4460		1559287_at	4.0410E-02	3.30E-03	3.00	-1.95	1.37E-01
4461	HSPB11	215691_x_at	4.0431E-02	3.30E-03	3.00	-1.95	4.00E-01
4462	CDCA7	230060_at	4.0485E-02	3.30E-03	3.00	-1.95	2.30E-01
4463	GPR108	225058_at	4.0485E-02	3.31E-03	-3.00	-1.95	-3.20E-01
4464	KSR1	213769_at	4.0485E-02	3.31E-03	3.00	-1.95	1.68E-01
4465	POLR2A	217415_at	4.0485E-02	3.31E-03	3.00	-1.95	1.02E-01
4466	RPL23	200888_s_at	4.0517E-02	3.31E-03	3.00	-1.95	2.19E-01
4467	RAB3C	241977_s_at	4.0517E-02	3.31E-03	3.00	-1.95	1.11E-01
4468		234789_at	4.0517E-02	3.31E-03	3.00	-1.95	9.09E-02
4469	CBY3	238138_at	4.0517E-02	3.31E-03	3.00	-1.95	1.24E-01
4470	CDK5RAP2	243153_at	4.0526E-02	3.31E-03	3.00	-1.95	1.47E-01
4471	SNF8	218391_at	4.0627E-02	3.32E-03	-3.00	-1.95	-3.66E-01
4472	LOC100129884	236560_at	4.0627E-02	3.32E-03	3.00	-1.95	1.35E-01
4473	ATG12	213026_at	4.0636E-02	3.32E-03	3.00	-1.95	3.13E-01
4474	BPIL2	1555773_at	4.0647E-02	3.33E-03	3.00	-1.95	1.40E-01
4475	RGS10	204319_s_at	4.0650E-02	3.33E-03	3.00	-1.95	4.04E-01
4476	G6PC3	44654_at	4.0654E-02	3.33E-03	-3.00	-1.96	-3.07E-01
4477	GOLIM4	204324_s_at	4.0654E-02	3.33E-03	-3.00	-1.96	-5.11E-01
4478	ALOX5	204446_s_at	4.0678E-02	3.33E-03	-3.00	-1.96	-5.34E-01
4479	HAB1	216875_x_at	4.0743E-02	3.34E-03	3.00	-1.96	2.09E-01
4480	TMEM14B	223133_at	4.0743E-02	3.34E-03	3.00	-1.96	4.80E-01
4481		215612_at	4.0743E-02	3.34E-03	3.00	-1.96	2.12E-01
4482	KPNA5	229317_at	4.0760E-02	3.34E-03	3.00	-1.96	3.75E-01
4483		241681_at	4.0760E-02	3.34E-03	3.00	-1.96	6.92E-01
4484	CHMP4C	226803_at	4.0762E-02	3.34E-03	-3.00	-1.96	-1.82E-01
4485		234582_at	4.0762E-02	3.35E-03	3.00	-1.96	1.19E-01
4486	MAPK7	35617_at	4.0762E-02	3.35E-03	-3.00	-1.96	-2.08E-01
4487	ANKFY1	224900_at	4.0762E-02	3.35E-03	-3.00	-1.96	-3.55E-01
4488		244331_at	4.0762E-02	3.35E-03	3.00	-1.96	1.17E-01
4489	TIMELESS	215455_at	4.0762E-02	3.35E-03	3.00	-1.96	1.51E-01
4490		1568660_a_at	4.0762E-02	3.35E-03	3.00	-1.96	9.37E-02
4491	TFIP11	202750_s_at	4.0762E-02	3.35E-03	-3.00	-1.96	-2.86E-01
4492	PIWIL1	214868_at	4.0762E-02	3.35E-03	3.00	-1.96	1.08E-01
4493	GALC	211810_s_at	4.0762E-02	3.35E-03	-3.00	-1.96	-2.11E-01
4494	SEC31A	210616_s_at	4.0762E-02	3.35E-03	-3.00	-1.96	-4.46E-01
4495		1562082_at	4.0762E-02	3.35E-03	3.00	-1.96	9.77E-02
4496	TAF7L	220325_at	4.0769E-02	3.35E-03	3.00	-1.96	1.26E-01
4497	NAV3	204823_at	4.0769E-02	3.35E-03	-3.00	-1.96	-3.30E-01
4498	ACTBP9	217211_at	4.0771E-02	3.35E-03	-3.00	-1.96	-3.14E-01
4499		227368_at	4.0771E-02	3.36E-03	3.00	-1.96	3.09E-01
4500	SKAP1	205790_at	4.0771E-02	3.36E-03	3.00	-1.96	3.80E-01
4501	HGSNAT	218017_s_at	4.0771E-02	3.36E-03	-3.00	-1.96	-5.30E-01
4502	NDUFA4L2	218484_at	4.0771E-02	3.36E-03	-3.00	-1.96	-2.65E-01
4503	TMEM170A	230414_s_at	4.0840E-02	3.36E-03	2.99	-1.96	1.38E-01
4504	EIF3B	208688_x_at	4.0840E-02	3.36E-03	-2.99	-1.96	-3.54E-01
4505		1562715_at	4.0842E-02	3.37E-03	2.99	-1.96	8.63E-02
4506	NKAP	223439_at	4.0860E-02	3.37E-03	-2.99	-1.97	-3.05E-01
4507	RALGPS1	210552_s_at	4.0860E-02	3.37E-03	2.99	-1.97	1.18E-01
4508	ARHGAP26	226576_at	4.0860E-02	3.37E-03	-2.99	-1.97	-4.02E-01
4509	FKBP5	224856_at	4.0877E-02	3.37E-03	-2.99	-1.97	-6.20E-01
4510	FAM166B	229941_at	4.0914E-02	3.37E-03	2.99	-1.97	1.39E-01
4511	SAMHD1	1559883_s_at	4.0929E-02	3.38E-03	-2.99	-1.97	-6.10E-01
4512		1563217_at	4.0942E-02	3.38E-03	2.99	-1.97	1.48E-01
4513	LOC100288	234388_at	4.0971E-02	3.38E-03	2.99	-1.97	1.80E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
	702///ACTR 3P1///RPL4 P1///TRA@// /SALL2						
4514		243990_at	4.0971E-02	3.38E-03	2.99	-1.97	1.82E-01
4515		235207_at	4.0972E-02	3.38E-03	2.99	-1.97	3.40E-01
4516		1559723_s_at	4.1020E-02	3.39E-03	2.99	-1.97	1.67E-01
4517	PSMB1	200876_s_at	4.1020E-02	3.39E-03	-2.99	-1.97	-3.83E-01
4518	NCAM1	229799_s_at	4.1020E-02	3.39E-03	2.99	-1.97	1.20E-01
4519	GNAS	214548_x_at	4.1020E-02	3.39E-03	-2.99	-1.97	-4.88E-01
4520	C11orf57	222588_s_at	4.1020E-02	3.39E-03	-2.99	-1.97	-2.69E-01
4521	UBC///UBB// /RPS27A	200017_at	4.1020E-02	3.39E-03	2.99	-1.97	2.01E-01
4522	MAPK1	1552264_a_at	4.1020E-02	3.39E-03	-2.99	-1.97	-3.17E-01
4523	RBM15	228455_at	4.1046E-02	3.40E-03	2.99	-1.97	3.75E-01
4524	PTGR1	228824_s_at	4.1052E-02	3.40E-03	-2.99	-1.97	-4.08E-01
4525		215335_at	4.1052E-02	3.40E-03	2.99	-1.97	1.21E-01
4526	TRIM14	211044_at	4.1052E-02	3.40E-03	2.99	-1.97	1.47E-01
4527	PSMD2	200830_at	4.1052E-02	3.40E-03	-2.99	-1.97	-2.34E-01
4528	FKBP1A	200709_at	4.1052E-02	3.40E-03	-2.99	-1.97	-4.44E-01
4529	UBE2F	225783_at	4.1078E-02	3.40E-03	-2.99	-1.97	-2.34E-01
4530	IDH3G	202471_s_at	4.1087E-02	3.40E-03	-2.99	-1.97	-4.57E-01
4531	C15orf51	231318_at	4.1110E-02	3.41E-03	2.99	-1.98	1.21E-01
4532		1562907_at	4.1110E-02	3.41E-03	2.99	-1.98	1.29E-01
4533		1565915_at	4.1126E-02	3.41E-03	2.99	-1.98	9.44E-02
4534	LOC100133 811///LOC10 0133661///Z NF749///RN ASE2///HLA-DRB5///HLA - DRB4///HLA - DRB3///HLA - DRB2///HLA -DRB1	206111_at	4.1130E-02	3.41E-03	-2.99	-1.98	-5.09E-01
4535	RNF17	224384_s_at	4.1212E-02	3.42E-03	2.99	-1.98	1.25E-01
4536	EPRS	200843_s_at	4.1212E-02	3.42E-03	-2.99	-1.98	-2.53E-01
4537	ACTB	200801_x_at	4.1231E-02	3.42E-03	-2.99	-1.98	-4.11E-01
4538	LOC100130 233///LOC39 9804	216387_x_at	4.1261E-02	3.42E-03	2.99	-1.98	1.95E-01
4539	LOC645513	242305_at	4.1276E-02	3.43E-03	2.99	-1.98	2.58E-01
4540		243086_at	4.1280E-02	3.43E-03	2.99	-1.98	1.39E-01
4541	MLLT10	205408_at	4.1290E-02	3.43E-03	-2.99	-1.98	-2.51E-01
4542	JPH3	243679_at	4.1300E-02	3.43E-03	2.99	-1.98	1.65E-01
4543	SLFN11	226743_at	4.1302E-02	3.43E-03	-2.99	-1.98	-2.80E-01
4544	FARP1	201910_at	4.1397E-02	3.44E-03	-2.99	-1.98	-2.95E-01
4545	SRXN1	225252_at	4.1437E-02	3.44E-03	-2.99	-1.99	-3.32E-01
4546	PACS2	212778_at	4.1437E-02	3.45E-03	-2.99	-1.99	-3.43E-01
4547	LASP1	200618_at	4.1459E-02	3.45E-03	-2.99	-1.99	-4.62E-01
4548	KPNB1	217027_x_at	4.1459E-02	3.45E-03	-2.99	-1.99	-3.21E-01
4549		243996_at	4.1484E-02	3.45E-03	2.99	-1.99	1.82E-01
4550	KPNB1	208975_s_at	4.1484E-02	3.45E-03	-2.99	-1.99	-3.90E-01
4551	MAPK1	224621_at	4.1495E-02	3.45E-03	-2.99	-1.99	-2.37E-01
4552	SS18	216684_s_at	4.1521E-02	3.46E-03	-2.99	-1.99	-1.54E-01
4553		215502_at	4.1538E-02	3.46E-03	2.99	-1.99	1.87E-01
4554	BRE	205550_s_at	4.1538E-02	3.46E-03	-2.99	-1.99	-3.36E-01
4555		231340_at	4.1562E-02	3.46E-03	2.99	-1.99	1.60E-01
4556	PTPRC	1552480_s_at	4.1562E-02	3.46E-03	2.99	-1.99	3.64E-01
4557	TRUB1	241606_s_at	4.1562E-02	3.46E-03	2.99	-1.99	1.93E-01
4558	KRAS	204010_s_at	4.1562E-02	3.46E-03	2.99	-1.99	2.06E-01
4559		242926_at	4.1586E-02	3.47E-03	2.98	-1.99	1.58E-01
4560	DBF4	204244_s_at	4.1586E-02	3.47E-03	2.98	-1.99	3.83E-01
4561	NFKB2	207535_s_at	4.1586E-02	3.47E-03	-2.98	-1.99	-2.91E-01
4562		230034_x_at	4.1586E-02	3.47E-03	2.98	-1.99	1.61E-01
4563	FAM190B	1554132_a_at	4.1589E-02	3.47E-03	-2.98	-1.99	-4.29E-01
4564		241482_at	4.1589E-02	3.47E-03	2.98	-1.99	8.67E-02

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4565	C9orf93	1558082_at	4.1589E-02	3.47E-03	2.98	-1.99	1.13E-01
4566	SPPL3	1566897_at	4.1589E-02	3.47E-03	2.98	-1.99	1.95E-01
4567		1558822_at	4.1589E-02	3.47E-03	2.98	-1.99	2.73E-01
4568	SMARCC2	1561973_at	4.1589E-02	3.47E-03	2.98	-1.99	2.00E-01
4569		240118_at	4.1590E-02	3.48E-03	-2.98	-1.99	-3.68E-01
4570		239065_at	4.1593E-02	3.48E-03	2.98	-1.99	1.09E-01
4571	YAP1	224895_at	4.1593E-02	3.48E-03	-2.98	-1.99	-4.80E-01
4572	ZNF330	213760_s_at	4.1593E-02	3.48E-03	2.98	-1.99	2.34E-01
4573	LYRM5	225469_at	4.1593E-02	3.48E-03	2.98	-1.99	4.16E-01
4574	TRIM66	213748_at	4.1593E-02	3.48E-03	-2.98	-1.99	-1.53E-01
4575		1566195_at	4.1593E-02	3.48E-03	2.98	-1.99	1.17E-01
4576	NDUFB10	228301_x_at	4.1603E-02	3.48E-03	2.98	-1.99	2.06E-01
4577	LOC100129447	1559618_at	4.1613E-02	3.48E-03	2.98	-1.99	2.95E-01
4578	GATAD2B	238076_at	4.1613E-02	3.48E-03	2.98	-2.00	2.48E-01
4579		1566902_at	4.1668E-02	3.49E-03	2.98	-2.00	1.02E-01
4580		239823_at	4.1745E-02	3.50E-03	2.98	-2.00	3.41E-01
4581	ZNF474	1556907_at	4.1750E-02	3.50E-03	2.98	-2.00	1.00E-01
4582	ICT1	204868_at	4.1790E-02	3.50E-03	2.98	-2.00	3.70E-01
4583	DENR	238982_at	4.1817E-02	3.51E-03	2.98	-2.00	1.78E-01
4584	UBOX5	204598_at	4.1852E-02	3.51E-03	2.98	-2.00	1.48E-01
4585		230476_at	4.1852E-02	3.51E-03	2.98	-2.00	1.38E-01
4586	PLXND1	38671_at	4.1854E-02	3.51E-03	-2.98	-2.00	-4.59E-01
4587	ST13	208666_s_at	4.1854E-02	3.51E-03	-2.98	-2.00	-3.85E-01
4588	TCF3	216645_at	4.1883E-02	3.51E-03	2.98	-2.00	1.75E-01
4589		228115_at	4.1886E-02	3.52E-03	-2.98	-2.00	-1.06E-01
4590	TTC3	1569472_s_at	4.1886E-02	3.52E-03	-2.98	-2.00	-2.48E-01
4591		1565760_at	4.1886E-02	3.52E-03	2.98	-2.00	9.60E-02
4592		229844_at	4.1886E-02	3.52E-03	2.98	-2.00	3.53E-01
4593		226347_at	4.1886E-02	3.52E-03	-2.98	-2.00	-2.91E-01
4594	FAM189B	203550_s_at	4.1886E-02	3.52E-03	-2.98	-2.00	-1.52E-01
4595		237148_at	4.1917E-02	3.53E-03	2.98	-2.01	9.49E-02
4596	CYP26B1	219825_at	4.1917E-02	3.53E-03	-2.98	-2.01	-3.73E-01
4597	PRND	223813_at	4.1917E-02	3.53E-03	2.98	-2.01	1.30E-01
4598	C1orf116	228865_at	4.1917E-02	3.53E-03	2.98	-2.01	1.28E-01
4599	PHKB	242248_at	4.1917E-02	3.53E-03	2.98	-2.01	1.30E-01
4600	VPS25	224608_s_at	4.1917E-02	3.53E-03	-2.98	-2.01	-3.96E-01
4601		1568639_a_at	4.1917E-02	3.53E-03	-2.98	-2.01	-1.43E-01
4602	ALDH3B1	205640_at	4.1917E-02	3.53E-03	-2.98	-2.01	-3.06E-01
4603	GRLF1	229397_s_at	4.1917E-02	3.53E-03	2.98	-2.01	1.75E-01
4604	HLA-E	200905_x_at	4.1932E-02	3.53E-03	-2.98	-2.01	-3.24E-01
4605	UGP2	205480_s_at	4.1932E-02	3.53E-03	-2.98	-2.01	-3.57E-01
4606	ZFP106	217781_s_at	4.1932E-02	3.53E-03	-2.98	-2.01	-3.02E-01
4607	USP10	209136_s_at	4.1950E-02	3.53E-03	-2.98	-2.01	-3.83E-01
4608	DNAJC7	1556053_at	4.1964E-02	3.54E-03	2.98	-2.01	2.85E-01
4609	C21orf57	227421_at	4.1964E-02	3.54E-03	2.98	-2.01	3.56E-01
4610		232431_at	4.1974E-02	3.54E-03	2.98	-2.01	5.42E-01
4611	IGFBP5	203424_s_at	4.1988E-02	3.54E-03	-2.98	-2.01	-4.67E-01
4612	LEPROT///LEPR	202377_at	4.2017E-02	3.54E-03	-2.98	-2.01	-4.44E-01
4613	C11orf75	219806_s_at	4.2017E-02	3.55E-03	-2.98	-2.01	-3.76E-01
4614		234065_at	4.2078E-02	3.55E-03	2.98	-2.01	1.27E-01
4615	GNA11	213766_x_at	4.2088E-02	3.55E-03	-2.98	-2.01	-3.61E-01
4616	TNFRSF13C	1552892_at	4.2096E-02	3.55E-03	2.98	-2.01	2.89E-01
4617	SLC37A4	217289_s_at	4.2096E-02	3.55E-03	-2.98	-2.01	-1.87E-01
4618	FNDC3B	218618_s_at	4.2097E-02	3.56E-03	-2.98	-2.01	-6.94E-01
4619	TADA3	215273_s_at	4.2097E-02	3.56E-03	-2.98	-2.01	-3.60E-01
4620	F5	231029_at	4.2097E-02	3.56E-03	2.98	-2.01	2.03E-01
4621	TMEM27	223784_at	4.2116E-02	3.56E-03	2.98	-2.01	8.47E-02
4622		240825_at	4.2116E-02	3.56E-03	2.98	-2.01	1.19E-01
4623	PDZK1	205380_at	4.2116E-02	3.56E-03	2.98	-2.01	1.01E-01
4624	MDM4	225740_x_at	4.2143E-02	3.56E-03	2.98	-2.01	3.48E-01
4625	LOC729143///MPRIP	214694_at	4.2178E-02	3.57E-03	-2.98	-2.02	-1.40E-01
4626	NUCB1	200649_at	4.2178E-02	3.57E-03	-2.98	-2.02	-5.50E-01
4627	ITPKB	232526_at	4.2178E-02	3.57E-03	2.98	-2.02	1.50E-01
4628	ALDH2	201425_at	4.2178E-02	3.57E-03	-2.98	-2.02	-4.81E-01
4629	SPTAN1	214925_s_at	4.2178E-02	3.57E-03	2.98	-2.02	2.86E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4630	CROCC	216419_at	4.2246E-02	3.58E-03	2.97	-2.02	1.91E-01
4631	CNR1	207940_x_at	4.2259E-02	3.58E-03	2.97	-2.02	1.31E-01
4632	NPY6R	210444_at	4.2264E-02	3.58E-03	2.97	-2.02	1.64E-01
4633	LSM6	205036_at	4.2328E-02	3.59E-03	2.97	-2.02	4.76E-01
4634	USP22	200083_at	4.2328E-02	3.59E-03	-2.97	-2.02	-3.37E-01
4635	EHD1	209037_s_at	4.2328E-02	3.59E-03	-2.97	-2.02	-4.26E-01
4636	ZNF789	235231_at	4.2344E-02	3.59E-03	2.97	-2.02	3.16E-01
4637	ANKS1B	227440_at	4.2352E-02	3.59E-03	2.97	-2.02	2.79E-01
4638	KCNC4	235467_s_at	4.2352E-02	3.59E-03	-2.97	-2.02	-2.01E-01
4639	C14orf181	229054_at	4.2352E-02	3.59E-03	2.97	-2.02	2.78E-01
4640	APLN	244166_at	4.2352E-02	3.59E-03	2.97	-2.02	3.63E-01
4641		243137_at	4.2352E-02	3.60E-03	2.97	-2.02	1.10E-01
4642		236581_at	4.2352E-02	3.60E-03	2.97	-2.02	1.90E-01
4643		237008_at	4.2352E-02	3.60E-03	2.97	-2.02	1.51E-01
4644		231419_at	4.2368E-02	3.60E-03	2.97	-2.02	1.73E-01
4645	TAGLN	205547_s_at	4.2368E-02	3.60E-03	-2.97	-2.02	-7.66E-01
4646		240139_at	4.2389E-02	3.60E-03	2.97	-2.02	2.28E-01
4647	LOC388588	230840_at	4.2404E-02	3.60E-03	2.97	-2.02	1.60E-01
4648	TEX28	207364_at	4.2407E-02	3.61E-03	2.97	-2.02	1.43E-01
4649	XPNPEP3	228820_at	4.2407E-02	3.61E-03	2.97	-2.03	2.98E-01
4650		215858_at	4.2407E-02	3.61E-03	2.97	-2.03	1.59E-01
4651		238835_at	4.2407E-02	3.61E-03	-2.97	-2.03	-2.42E-01
4652	SLA	203760_s_at	4.2443E-02	3.61E-03	-2.97	-2.03	-3.53E-01
4653	MLYCD	218869_at	4.2443E-02	3.61E-03	-2.97	-2.03	-2.05E-01
4654	BACE2	222446_s_at	4.2443E-02	3.61E-03	-2.97	-2.03	-4.42E-01
4655	LMBRD1	232980_at	4.2443E-02	3.61E-03	2.97	-2.03	1.29E-01
4656	RPS19	213414_s_at	4.2443E-02	3.61E-03	2.97	-2.03	1.24E-01
4657	POLR2F	232643_at	4.2443E-02	3.62E-03	2.97	-2.03	1.75E-01
4658		241316_at	4.2456E-02	3.62E-03	2.97	-2.03	1.08E-01
4659	HDAC1	201209_at	4.2456E-02	3.62E-03	2.97	-2.03	2.23E-01
4660	LSM1	203534_at	4.2468E-02	3.62E-03	2.97	-2.03	2.93E-01
4661	SOX4	1567906_at	4.2517E-02	3.62E-03	2.97	-2.03	1.97E-01
4662	SETD5	244691_at	4.2517E-02	3.63E-03	2.97	-2.03	1.26E-01
4663	ANGPT2	236034_at	4.2517E-02	3.63E-03	-2.97	-2.03	-2.48E-01
4664	UNC5B	213100_at	4.2517E-02	3.63E-03	-2.97	-2.03	-2.39E-01
4665	MTUS2	1554755_a_at	4.2517E-02	3.63E-03	2.97	-2.03	1.33E-01
4666		239731_at	4.2517E-02	3.63E-03	2.97	-2.03	2.31E-01
4667		242846_at	4.2540E-02	3.63E-03	2.97	-2.03	1.24E-01
4668	TCEB3	213604_at	4.2550E-02	3.63E-03	-2.97	-2.03	-2.14E-01
4669	RPS15A	200781_s_at	4.2556E-02	3.63E-03	2.97	-2.03	1.93E-01
4670		234745_at	4.2574E-02	3.64E-03	2.97	-2.03	1.18E-01
4671	KCNJ2	206765_at	4.2600E-02	3.64E-03	-2.97	-2.03	-7.71E-01
4672		241178_at	4.2600E-02	3.64E-03	2.97	-2.03	1.28E-01
4673	NT5C1A	224529_s_at	4.2612E-02	3.64E-03	2.97	-2.03	1.48E-01
4674	ARHGDIA	201167_x_at	4.2651E-02	3.65E-03	-2.97	-2.03	-1.92E-01
4675	UNK	228357_at	4.2693E-02	3.65E-03	2.97	-2.04	4.43E-01
4676	C11orf24	52164_at	4.2702E-02	3.65E-03	-2.97	-2.04	-3.58E-01
4677	UPK3B	206658_at	4.2702E-02	3.65E-03	2.97	-2.04	1.63E-01
4678	SLC39A14	212110_at	4.2702E-02	3.65E-03	-2.97	-2.04	-5.80E-01
4679	LACTB	1552485_at	4.2702E-02	3.65E-03	-2.97	-2.04	-3.76E-01
4680		237632_at	4.2702E-02	3.66E-03	2.97	-2.04	2.08E-01
4681	DNAJA4	1554334_a_at	4.2703E-02	3.66E-03	-2.97	-2.04	-2.92E-01
4682	STT3B	231285_at	4.2755E-02	3.66E-03	2.97	-2.04	1.17E-01
4683	RPL35	200002_at	4.2779E-02	3.66E-03	2.97	-2.04	2.63E-01
4684	RANGAP1	212125_at	4.2792E-02	3.67E-03	-2.97	-2.04	-3.32E-01
4685	FPR1	205119_s_at	4.2871E-02	3.67E-03	-2.97	-2.04	-4.50E-01
4686		1563339_at	4.2872E-02	3.67E-03	2.97	-2.04	1.05E-01
4687	ZNF827	231902_at	4.2875E-02	3.68E-03	2.97	-2.04	1.27E-01
4688	HNMT	204111_at	4.2909E-02	3.68E-03	-2.97	-2.04	-1.95E-01
4689	ACTN4	200601_at	4.2925E-02	3.68E-03	-2.97	-2.04	-4.63E-01
4690	TUBB	212320_at	4.2946E-02	3.68E-03	-2.96	-2.04	-4.22E-01
4691	CCDC33	220908_at	4.2948E-02	3.68E-03	-2.96	-2.04	-1.34E-01
4692	PML	206503_x_at	4.2955E-02	3.69E-03	-2.96	-2.04	-2.59E-01
4693		239234_at	4.2959E-02	3.69E-03	2.96	-2.04	2.84E-01
4694	C4orf46///TOMM7	201812_s_at	4.3054E-02	3.70E-03	2.96	-2.05	2.96E-01
4695	RPL12P11///CHD6	216354_at	4.3065E-02	3.70E-03	2.96	-2.05	2.14E-01
4696		1556103_at	4.3065E-02	3.70E-03	2.96	-2.05	2.55E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4697		1569713_at	4.3067E-02	3.70E-03	2.96	-2.05	1.46E-01
4698	SFXN3	1559993_at	4.3076E-02	3.70E-03	2.96	-2.05	2.43E-01
4699	ELTD1	219134_at	4.3076E-02	3.70E-03	-2.96	-2.05	-4.65E-01
4700	FGD4	227948_at	4.3076E-02	3.70E-03	-2.96	-2.05	-3.52E-01
4701	ZFP41	227902_at	4.3079E-02	3.70E-03	2.96	-2.05	1.85E-01
4702	PCIF1	222044_at	4.3084E-02	3.71E-03	2.96	-2.05	4.99E-01
4703	GALNTL4	1554079_at	4.3110E-02	3.71E-03	-2.96	-2.05	-2.34E-01
4704	ERGIC1	223847_s_at	4.3121E-02	3.71E-03	-2.96	-2.05	-2.25E-01
4705		1563224_at	4.3121E-02	3.71E-03	2.96	-2.05	1.29E-01
4706	BOLA2B///BOLA2	209836_x_at	4.3142E-02	3.71E-03	2.96	-2.05	4.41E-01
4707	MAP2K3	215498_s_at	4.3142E-02	3.71E-03	-2.96	-2.05	-3.32E-01
4708	ABCF2	207622_s_at	4.3189E-02	3.72E-03	-2.96	-2.05	-4.95E-01
4709		1557522_x_at	4.3189E-02	3.72E-03	2.96	-2.05	2.31E-01
4710	MYO3B	1560788_at	4.3189E-02	3.72E-03	2.96	-2.05	1.06E-01
4711		227278_at	4.3189E-02	3.72E-03	-2.96	-2.05	-3.45E-01
4712	LOC100128612	220715_at	4.3189E-02	3.72E-03	2.96	-2.05	1.36E-01
4713	CRYZL1	226151_x_at	4.3189E-02	3.72E-03	2.96	-2.05	3.02E-01
4714	MED25	215897_at	4.3189E-02	3.72E-03	2.96	-2.05	8.88E-02
4715	RAB43///ISY1	223429_x_at	4.3224E-02	3.73E-03	-2.96	-2.05	-2.87E-01
4716	JAK1	1552610_a_at	4.3266E-02	3.73E-03	-2.96	-2.05	-6.53E-01
4717	HCRT	207642_at	4.3266E-02	3.73E-03	2.96	-2.06	1.41E-01
4718	AZI2	223846_at	4.3271E-02	3.73E-03	2.96	-2.06	1.62E-01
4719	PTGFR	1555097_a_at	4.3277E-02	3.74E-03	-2.96	-2.06	-1.70E-01
4720	ABHD2	225337_at	4.3323E-02	3.74E-03	-2.96	-2.06	-3.70E-01
4721	SLC39A13	1552295_a_at	4.3332E-02	3.74E-03	-2.96	-2.06	-1.67E-01
4722	GPR137	43934_at	4.3339E-02	3.74E-03	-2.96	-2.06	-1.23E-01
4723	RGS22	223691_at	4.3347E-02	3.74E-03	2.96	-2.06	1.51E-01
4724	CTSH	202295_s_at	4.3348E-02	3.75E-03	-2.96	-2.06	-2.83E-01
4725	Sep-06	213666_at	4.3351E-02	3.75E-03	2.96	-2.06	3.93E-01
4726	IL6ST	211000_s_at	4.3352E-02	3.75E-03	-2.96	-2.06	-4.38E-01
4727	RFFL	1566171_at	4.3352E-02	3.75E-03	2.96	-2.06	1.46E-01
4728	HMGN3	209377_s_at	4.3352E-02	3.75E-03	2.96	-2.06	2.76E-01
4729	ZNF599	228093_at	4.3352E-02	3.75E-03	2.96	-2.06	2.17E-01
4730		230451_at	4.3352E-02	3.75E-03	2.96	-2.06	2.48E-01
4731	KCNS3	205968_at	4.3357E-02	3.75E-03	-2.96	-2.06	-1.79E-01
4732	FAM43B	1569256_a_at	4.3404E-02	3.76E-03	2.96	-2.06	1.78E-01
4733		231332_at	4.3429E-02	3.76E-03	2.96	-2.06	2.32E-01
4734		1558640_a_at	4.3429E-02	3.76E-03	2.96	-2.06	1.21E-01
4735	MTCP1	216862_s_at	4.3429E-02	3.76E-03	2.96	-2.06	3.21E-01
4736	MUC1	213693_s_at	4.3429E-02	3.76E-03	-2.96	-2.06	-2.41E-01
4737	BRCC3	229436_x_at	4.3432E-02	3.76E-03	-2.96	-2.06	-2.29E-01
4738		236428_at	4.3453E-02	3.77E-03	2.96	-2.06	2.49E-01
4739	EPSTI1	235276_at	4.3453E-02	3.77E-03	2.96	-2.06	4.07E-01
4740	ATR	233288_at	4.3453E-02	3.77E-03	2.96	-2.06	1.25E-01
4741	LYAR	223413_s_at	4.3454E-02	3.77E-03	-2.96	-2.06	-4.84E-01
4742	AP3M1	222517_at	4.3517E-02	3.77E-03	2.96	-2.06	1.81E-01
4743	TUBG1	201714_at	4.3517E-02	3.78E-03	-2.96	-2.07	-3.72E-01
4744	STARD10	238911_at	4.3517E-02	3.78E-03	2.96	-2.07	1.84E-01
4745	ZNF519	1564190_x_at	4.3517E-02	3.78E-03	2.96	-2.07	1.23E-01
4746	THRAP3	222440_s_at	4.3527E-02	3.78E-03	-2.96	-2.07	-2.24E-01
4747	BTLA	236226_at	4.3535E-02	3.78E-03	2.96	-2.07	5.76E-01
4748		1563302_at	4.3535E-02	3.78E-03	2.96	-2.07	1.27E-01
4749	WASL	205810_s_at	4.3535E-02	3.78E-03	2.96	-2.07	1.37E-01
4750	PPT1	200975_at	4.3564E-02	3.78E-03	-2.96	-2.07	-2.51E-01
4751	RANBP9	243108_at	4.3607E-02	3.79E-03	2.96	-2.07	1.47E-01
4752	PARP4	202239_at	4.3634E-02	3.79E-03	-2.96	-2.07	-2.43E-01
4753	HLA-DRA	210982_s_at	4.3646E-02	3.79E-03	-2.96	-2.07	-4.28E-01
4754	FNIP2	226460_at	4.3646E-02	3.80E-03	-2.96	-2.07	-5.05E-01
4755	PKDREJ	220548_at	4.3658E-02	3.80E-03	2.95	-2.07	1.54E-01
4756	INPP5D	233545_at	4.3658E-02	3.80E-03	2.95	-2.07	1.45E-01
4757	AIFM1	205512_s_at	4.3658E-02	3.80E-03	-2.95	-2.07	-4.33E-01
4758	GARS	208693_s_at	4.3658E-02	3.80E-03	-2.95	-2.07	-3.39E-01
4759	CC2D2B	243534_at	4.3687E-02	3.80E-03	2.95	-2.07	2.27E-01
4760		242607_at	4.3713E-02	3.81E-03	2.95	-2.07	2.08E-01
4761	MAP3K4	216199_s_at	4.3727E-02	3.81E-03	2.95	-2.07	3.37E-01
4762	SET	213048_s_at	4.3750E-02	3.81E-03	-2.95	-2.07	-2.52E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4763	PCDHGA3	216343_at	4.3758E-02	3.81E-03	2.95	-2.07	1.18E-01
4764	TPBG	203476_at	4.3758E-02	3.81E-03	-2.95	-2.07	-5.36E-01
4765		1570125_at	4.3758E-02	3.81E-03	2.95	-2.07	1.13E-01
4766	RABEP1	231002_s_at	4.3758E-02	3.82E-03	2.95	-2.07	1.85E-01
4767	NAV2	222598_s_at	4.3758E-02	3.82E-03	2.95	-2.07	2.02E-01
4768	PSAP	200871_s_at	4.3758E-02	3.82E-03	-2.95	-2.07	-3.41E-01
4769	CAPN1	200752_s_at	4.3758E-02	3.82E-03	-2.95	-2.07	-3.96E-01
4770		242467_at	4.3762E-02	3.82E-03	2.95	-2.07	4.18E-01
4771		242206_at	4.3766E-02	3.82E-03	2.95	-2.08	1.84E-01
4772	PLD3	201050_at	4.3766E-02	3.82E-03	-2.95	-2.08	-7.61E-01
4773	WNT5A	231227_at	4.3766E-02	3.82E-03	-2.95	-2.08	-3.39E-01
4774	GALNT14	1560180_at	4.3804E-02	3.82E-03	2.95	-2.08	1.57E-01
4775	LIMA1	222457_s_at	4.3846E-02	3.83E-03	-2.95	-2.08	-3.88E-01
4776	HIVEP1	1560485_at	4.3848E-02	3.83E-03	2.95	-2.08	1.81E-01
4777	TSR1	218156_s_at	4.3872E-02	3.83E-03	-2.95	-2.08	-3.66E-01
4778	PDXK	218018_at	4.3872E-02	3.83E-03	-2.95	-2.08	-3.03E-01
4779	SCN11A	210853_at	4.3875E-02	3.84E-03	2.95	-2.08	1.06E-01
4780		242233_at	4.3875E-02	3.84E-03	2.95	-2.08	3.54E-01
4781	BTBD7	1556000_s_at	4.3875E-02	3.84E-03	-2.95	-2.08	-1.86E-01
4782	LOC100144602	238241_at	4.3875E-02	3.84E-03	2.95	-2.08	1.57E-01
4783	ZNF678	242923_at	4.3877E-02	3.84E-03	2.95	-2.08	2.06E-01
4784		244719_at	4.3882E-02	3.84E-03	2.95	-2.08	1.25E-01
4785	ANKHD1///EIF4EBP3	219081_at	4.3883E-02	3.84E-03	-2.95	-2.08	-3.46E-01
4786	FEZ2	215000_s_at	4.3883E-02	3.84E-03	-2.95	-2.08	-2.20E-01
4787	NAMPT	217738_at	4.3883E-02	3.84E-03	-2.95	-2.08	-3.96E-01
4788	CITED2	207980_s_at	4.3883E-02	3.84E-03	-2.95	-2.08	-5.64E-01
4789	NUCKS1	226880_at	4.3883E-02	3.84E-03	-2.95	-2.08	-3.18E-01
4790		1562456_at	4.3883E-02	3.85E-03	2.95	-2.08	1.48E-01
4791	UBE2N	201524_x_at	4.3883E-02	3.85E-03	2.95	-2.08	2.19E-01
4792	ARHGAP29	1554736_at	4.3901E-02	3.85E-03	2.95	-2.08	1.25E-01
4793		240215_at	4.3911E-02	3.85E-03	2.95	-2.08	1.77E-01
4794	PGAP1	220576_at	4.3971E-02	3.86E-03	2.95	-2.08	2.02E-01
4795	RHOG	203175_at	4.3978E-02	3.86E-03	-2.95	-2.08	-4.66E-01
4796		240621_at	4.3985E-02	3.86E-03	2.95	-2.08	2.33E-01
4797	CCDC88A	221078_s_at	4.3985E-02	3.86E-03	-2.95	-2.08	-2.77E-01
4798	ENG	201808_s_at	4.3986E-02	3.86E-03	-2.95	-2.08	-2.25E-01
4799	ANKRD10	223251_s_at	4.3986E-02	3.86E-03	2.95	-2.08	3.94E-01
4800	ADD1	208030_s_at	4.3996E-02	3.86E-03	-2.95	-2.08	-3.54E-01
4801		229155_at	4.4005E-02	3.86E-03	2.95	-2.09	1.21E-01
4802	ERAL1	212087_s_at	4.4005E-02	3.86E-03	-2.95	-2.09	-2.44E-01
4803	BAIAP3	216356_x_at	4.4018E-02	3.87E-03	2.95	-2.09	1.56E-01
4804	DKFZP547J0410	1566624_at	4.4061E-02	3.87E-03	2.95	-2.09	8.25E-02
4805	CLIP3	235243_at	4.4061E-02	3.87E-03	2.95	-2.09	1.37E-01
4806	AOX1	205083_at	4.4061E-02	3.87E-03	-2.95	-2.09	-5.44E-01
4807	TMEM14B///TMEM14C	223105_s_at	4.4061E-02	3.87E-03	2.95	-2.09	2.85E-01
4808	RANBP6	213019_at	4.4061E-02	3.88E-03	2.95	-2.09	3.04E-01
4809	XAGE2B///XAGE2	229469_at	4.4061E-02	3.88E-03	2.95	-2.09	1.53E-01
4810		1557738_at	4.4061E-02	3.88E-03	2.95	-2.09	1.25E-01
4811		1569608_x_at	4.4061E-02	3.88E-03	2.95	-2.09	2.67E-01
4812	ARAP1	34206_at	4.4061E-02	3.88E-03	-2.95	-2.09	-3.92E-01
4813	C14orf126	1553801_a_at	4.4061E-02	3.88E-03	2.95	-2.09	1.83E-01
4814	SYNGR2	201079_at	4.4061E-02	3.88E-03	-2.95	-2.09	-3.07E-01
4815		213710_s_at	4.4061E-02	3.88E-03	-2.95	-2.09	-2.74E-01
4816	MFSD7	205144_at	4.4061E-02	3.88E-03	2.95	-2.09	2.05E-01
4817	NOSIP	217950_at	4.4061E-02	3.88E-03	2.95	-2.09	3.35E-01
4818	LZTS1	221721_s_at	4.4068E-02	3.88E-03	2.95	-2.09	1.44E-01
4819	MMP14	202828_s_at	4.4068E-02	3.88E-03	-2.95	-2.09	-3.51E-01
4820		241351_at	4.4076E-02	3.89E-03	2.95	-2.09	1.77E-01
4821	SLC25A1	210010_s_at	4.4076E-02	3.89E-03	-2.95	-2.09	-4.42E-01
4822	DMRTC1B///DMRTC1	1553998_at	4.4076E-02	3.89E-03	2.95	-2.09	1.74E-01
4823	CNOT7	218250_s_at	4.4090E-02	3.89E-03	2.95	-2.09	2.29E-01
4824	RD3	236563_at	4.4090E-02	3.89E-03	2.95	-2.09	1.45E-01
4825	FLJ77644///TMEM106A	1552303_a_at	4.4092E-02	3.89E-03	-2.95	-2.09	-2.67E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4826	SIGLEC1	219519_s_at	4.4095E-02	3.89E-03	-2.95	-2.09	-7.06E-01
4827	NACAP1	211445_x_at	4.4095E-02	3.89E-03	2.95	-2.09	1.16E-01
4828	SMARCA5	202303_x_at	4.4095E-02	3.89E-03	-2.95	-2.09	-3.16E-01
4829	PLCL2	216218_s_at	4.4095E-02	3.89E-03	-2.95	-2.09	-4.42E-01
4830	C1orf50	219406_at	4.4107E-02	3.90E-03	2.95	-2.09	3.86E-01
4831	FAM98A	241832_at	4.4140E-02	3.90E-03	2.95	-2.09	1.26E-01
4832	VPS37A	225378_at	4.4140E-02	3.90E-03	-2.95	-2.09	-2.77E-01
4833	AGR3	228241_at	4.4145E-02	3.90E-03	2.95	-2.09	1.04E-01
4834	C14orf64	1559097_at	4.4147E-02	3.90E-03	2.95	-2.09	3.80E-01
4835	SNRPA1	242146_at	4.4167E-02	3.91E-03	2.95	-2.09	3.90E-01
4836	SLC25A11	209003_at	4.4176E-02	3.91E-03	-2.95	-2.09	-4.50E-01
4837	GABRB3	1569689_s_at	4.4185E-02	3.91E-03	2.95	-2.10	1.19E-01
4838	MMP2	201069_at	4.4224E-02	3.91E-03	-2.94	-2.10	-1.05E+00
4839	FOXP2	1564876_s_at	4.4229E-02	3.91E-03	2.94	-2.10	1.55E-01
4840	C14orf91	1570162_at	4.4264E-02	3.92E-03	2.94	-2.10	1.01E-01
4841	HLA-E	217456_x_at	4.4312E-02	3.92E-03	-2.94	-2.10	-2.65E-01
4842		240693_at	4.4312E-02	3.92E-03	2.94	-2.10	9.25E-02
4843	DERL3	229721_x_at	4.4384E-02	3.93E-03	-2.94	-2.10	-5.43E-01
4844	ACRV1	207973_x_at	4.4451E-02	3.94E-03	2.94	-2.10	1.23E-01
4845	ZNF169	1560922_s_at	4.4460E-02	3.94E-03	2.94	-2.10	1.53E-01
4846	NCOA4	210774_s_at	4.4473E-02	3.94E-03	-2.94	-2.10	-2.88E-01
4847	ARL17A	243899_at	4.4490E-02	3.94E-03	2.94	-2.10	2.99E-01
4848	GPD2	225447_at	4.4490E-02	3.94E-03	-2.94	-2.10	-4.12E-01
4849	GNAS	200780_x_at	4.4593E-02	3.96E-03	-2.94	-2.11	-4.29E-01
4850	ELMO3	219411_at	4.4593E-02	3.96E-03	2.94	-2.11	1.74E-01
4851		240695_at	4.4593E-02	3.96E-03	2.94	-2.11	1.41E-01
4852	RELL2	1564031_a_at	4.4623E-02	3.96E-03	2.94	-2.11	1.79E-01
4853	PECAM1	208981_at	4.4623E-02	3.96E-03	-2.94	-2.11	-4.70E-01
4854	KLF3	225140_at	4.4623E-02	3.96E-03	-2.94	-2.11	-3.18E-01
4855	LRRFIP1	238840_at	4.4623E-02	3.96E-03	2.94	-2.11	1.92E-01
4856	PARVB	37965_at	4.4623E-02	3.97E-03	-2.94	-2.11	-4.43E-01
4857	SYN1	1553264_a_at	4.4623E-02	3.97E-03	2.94	-2.11	1.84E-01
4858		228826_at	4.4623E-02	3.97E-03	2.94	-2.11	4.60E-01
4859	CLIC6	242913_at	4.4623E-02	3.97E-03	-2.94	-2.11	-1.70E-01
4860	NCRNA00105	1552872_at	4.4623E-02	3.97E-03	2.94	-2.11	2.13E-01
4861	IFRD2	209100_at	4.4623E-02	3.97E-03	-2.94	-2.11	-1.86E-01
4862	PLIN2	209122_at	4.4623E-02	3.97E-03	-2.94	-2.11	-3.37E-01
4863		1558783_at	4.4623E-02	3.97E-03	2.94	-2.11	3.52E-01
4864		236897_at	4.4623E-02	3.97E-03	2.94	-2.11	1.77E-01
4865	GNA11	564_at	4.4623E-02	3.97E-03	-2.94	-2.11	-3.86E-01
4866	NGRN	217722_s_at	4.4623E-02	3.97E-03	-2.94	-2.11	-3.03E-01
4867	BCLAF1	229454_at	4.4623E-02	3.97E-03	2.94	-2.11	3.20E-01
4868	ATG7	222709_at	4.4627E-02	3.97E-03	-2.94	-2.11	-2.53E-01
4869		215484_at	4.4627E-02	3.97E-03	2.94	-2.11	1.43E-01
4870		1556393_at	4.4627E-02	3.98E-03	2.94	-2.11	1.31E-01
4871	SPIRE1	224995_at	4.4627E-02	3.98E-03	-2.94	-2.11	-3.16E-01
4872	LOC100287249	1569615_at	4.4652E-02	3.98E-03	2.94	-2.11	1.81E-01
4873	PRKAR2B	203680_at	4.4660E-02	3.98E-03	-2.94	-2.11	-4.18E-01
4874	NT5DC2	218051_s_at	4.4660E-02	3.98E-03	-2.94	-2.11	-4.30E-01
4875	FYTTD1	224642_at	4.4660E-02	3.98E-03	-2.94	-2.11	-3.70E-01
4876	GNG2	1555766_a_at	4.4668E-02	3.98E-03	-2.94	-2.11	-2.80E-01
4877	TTLL3///ARPC4	217818_s_at	4.4681E-02	3.99E-03	2.94	-2.11	2.70E-01
4878	COX11	203551_s_at	4.4681E-02	3.99E-03	2.94	-2.11	2.47E-01
4879	ADRA2A	209869_at	4.4685E-02	3.99E-03	-2.94	-2.11	-6.38E-01
4880	SERBP1	210076_x_at	4.4686E-02	3.99E-03	-2.94	-2.11	-2.14E-01
4881	IFNA14	208182_x_at	4.4691E-02	3.99E-03	2.94	-2.11	1.21E-01
4882	PLEKHB2	201411_s_at	4.4696E-02	3.99E-03	-2.94	-2.11	-5.08E-01
4883	WIPI2	204710_s_at	4.4704E-02	3.99E-03	-2.94	-2.11	-3.06E-01
4884	KPNA4	209653_at	4.4726E-02	4.00E-03	-2.94	-2.11	-3.56E-01
4885	MANEA	1555227_a_at	4.4726E-02	4.00E-03	-2.94	-2.11	-1.28E-01
4886	TIMM8A	205217_at	4.4726E-02	4.00E-03	2.94	-2.11	3.81E-01
4887	MYLK	202555_s_at	4.4726E-02	4.00E-03	-2.94	-2.11	-5.35E-01
4888	CDIPT	201253_s_at	4.4734E-02	4.00E-03	-2.94	-2.12	-3.86E-01
4889	PGRMC1	201120_s_at	4.4744E-02	4.00E-03	-2.94	-2.12	-3.41E-01
4890	HAS3	1552980_at	4.4744E-02	4.00E-03	-2.94	-2.12	-1.30E-01
4891	PI15	229947_at	4.4744E-02	4.00E-03	-2.94	-2.12	-1.17E+00

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4892	ARID2	225486_at	4.4762E-02	4.01E-03	2.94	-2.12	2.09E-01
4893	ANGPT2	205572_at	4.4762E-02	4.01E-03	-2.94	-2.12	-3.20E-01
4894	NXNL1	1553755_at	4.4765E-02	4.01E-03	2.94	-2.12	1.96E-01
4895	KIAA1659	215674_at	4.4765E-02	4.01E-03	2.94	-2.12	9.42E-02
4896	TP53INP2	224836_at	4.4765E-02	4.01E-03	-2.94	-2.12	-2.82E-01
4897	HELQ	228736_at	4.4765E-02	4.01E-03	2.94	-2.12	4.61E-01
4898	TIFA	238858_at	4.4765E-02	4.01E-03	-2.94	-2.12	-1.72E-01
4899	NCOA2	215605_at	4.4774E-02	4.01E-03	2.94	-2.12	2.64E-01
4900	NBPF8	237917_at	4.4907E-02	4.02E-03	2.94	-2.12	1.04E-01
4901	NFAM1	243099_at	4.4921E-02	4.03E-03	-2.94	-2.12	-3.93E-01
4902	ZNF883	230876_at	4.4921E-02	4.03E-03	2.94	-2.12	1.66E-01
4903		210748_at	4.4936E-02	4.03E-03	2.94	-2.12	1.19E-01
4904		1570044_at	4.4971E-02	4.03E-03	2.93	-2.12	1.42E-01
4905		216297_at	4.4971E-02	4.04E-03	2.93	-2.12	1.04E-01
4906	ABCF2	207623_at	4.4971E-02	4.04E-03	2.93	-2.12	2.01E-01
4907	ARFGAP3	202211_at	4.4971E-02	4.04E-03	-2.93	-2.12	-2.48E-01
4908	SLC25A41	1555509_a_at	4.4971E-02	4.04E-03	2.93	-2.12	1.40E-01
4909	DCTD	210137_s_at	4.4971E-02	4.04E-03	-2.93	-2.12	-3.03E-01
4910	E2F1	2028_s_at	4.4971E-02	4.04E-03	2.93	-2.12	1.17E-01
4911	GALNT6	219956_at	4.4971E-02	4.04E-03	-2.93	-2.12	-2.50E-01
4912	FCF1	215567_at	4.5015E-02	4.04E-03	2.93	-2.12	2.02E-01
4913	CPA5	240744_at	4.5099E-02	4.05E-03	2.93	-2.13	3.15E-01
4914		241542_at	4.5099E-02	4.05E-03	2.93	-2.13	1.22E-01
4915	TIMD4	1552280_at	4.5110E-02	4.06E-03	-2.93	-2.13	-6.18E-01
4916	VPS35	222387_s_at	4.5120E-02	4.06E-03	-2.93	-2.13	-4.13E-01
4917		241514_at	4.5120E-02	4.06E-03	2.93	-2.13	1.31E-01
4918	PHTF2	1554822_at	4.5183E-02	4.06E-03	2.93	-2.13	1.23E-01
4919	NSUN3	219458_s_at	4.5193E-02	4.07E-03	2.93	-2.13	2.87E-01
4920	SLC4A10	206830_at	4.5230E-02	4.07E-03	2.93	-2.13	7.64E-02
4921		239017_at	4.5285E-02	4.08E-03	2.93	-2.13	3.12E-01
4922	DCTN1	201082_s_at	4.5314E-02	4.08E-03	-2.93	-2.13	-4.56E-01
4923	PPP3CC	207000_s_at	4.5317E-02	4.08E-03	2.93	-2.13	2.55E-01
4924		240909_at	4.5347E-02	4.08E-03	2.93	-2.13	1.38E-01
4925	APLNR	213592_at	4.5348E-02	4.09E-03	-2.93	-2.13	-3.97E-01
4926		238174_at	4.5348E-02	4.09E-03	2.93	-2.13	2.78E-01
4927		238278_at	4.5395E-02	4.09E-03	2.93	-2.13	1.14E-01
4928	MED7	204349_at	4.5400E-02	4.09E-03	2.93	-2.14	4.01E-01
4929	LOC643733	240890_at	4.5413E-02	4.09E-03	2.93	-2.14	7.84E-01
4930	ISLR	207191_s_at	4.5413E-02	4.09E-03	-2.93	-2.14	-4.51E-01
4931	ELOVL1	57163_at	4.5416E-02	4.10E-03	-2.93	-2.14	-2.19E-01
4932	LMAN2	200805_at	4.5430E-02	4.10E-03	-2.93	-2.14	-2.93E-01
4933	UBE2H	221962_s_at	4.5435E-02	4.10E-03	-2.93	-2.14	-3.33E-01
4934	WFDC12	1553081_at	4.5435E-02	4.10E-03	-2.93	-2.14	-1.43E-01
4935		226231_at	4.5435E-02	4.10E-03	2.93	-2.14	1.17E-01
4936	DNAJC1	218409_s_at	4.5435E-02	4.10E-03	-2.93	-2.14	-2.39E-01
4937	ZNF407	220836_at	4.5438E-02	4.10E-03	2.93	-2.14	8.95E-02
4938		242448_at	4.5446E-02	4.10E-03	2.93	-2.14	2.40E-01
4939	METTL3	242111_at	4.5474E-02	4.11E-03	2.93	-2.14	2.74E-01
4940	LOC284749	236854_at	4.5505E-02	4.11E-03	2.93	-2.14	2.20E-01
4941	TBCK	226126_at	4.5522E-02	4.11E-03	-2.93	-2.14	-3.19E-01
4942	ANKRD17	225852_at	4.5567E-02	4.12E-03	-2.93	-2.14	-4.19E-01
4943	SP3	232529_at	4.5567E-02	4.12E-03	2.93	-2.14	3.48E-01
4944	TUBGCP2	202477_s_at	4.5567E-02	4.12E-03	-2.93	-2.14	-3.54E-01
4945	FLJ37307	1557465_at	4.5594E-02	4.12E-03	2.93	-2.14	1.44E-01
4946	DDAH1	209094_at	4.5601E-02	4.13E-03	-2.93	-2.14	-5.53E-01
4947	EPHA1	205977_s_at	4.5612E-02	4.13E-03	2.93	-2.14	1.78E-01
4948		233137_at	4.5612E-02	4.13E-03	2.93	-2.14	3.22E-01
4949	AP2S1	202120_x_at	4.5671E-02	4.13E-03	-2.93	-2.14	-2.78E-01
4950	PARVA	217890_s_at	4.5759E-02	4.14E-03	-2.93	-2.15	-5.16E-01
4951		240662_at	4.5759E-02	4.14E-03	2.93	-2.15	1.11E-01
4952	AIF1	213095_x_at	4.5763E-02	4.14E-03	-2.93	-2.15	-3.35E-01
4953	NOL7	210097_s_at	4.5768E-02	4.15E-03	-2.93	-2.15	-2.56E-01
4954	ARSB	206129_s_at	4.5768E-02	4.15E-03	-2.93	-2.15	-2.46E-01
4955	HIP1R	209559_at	4.5768E-02	4.15E-03	2.93	-2.15	1.54E-01
4956	C18orf21	223526_at	4.5768E-02	4.15E-03	2.93	-2.15	3.16E-01
4957	YPEL5	222408_s_at	4.5768E-02	4.15E-03	2.93	-2.15	3.39E-01
4958		1558080_s_at	4.5768E-02	4.15E-03	-2.93	-2.15	-4.70E-01
4959	MYO9B	217297_s_at	4.5768E-02	4.15E-03	-2.93	-2.15	-3.26E-01
4960	TRPM1	214410_at	4.5768E-02	4.15E-03	2.93	-2.15	1.00E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
4961	NUP62	202153_s_at	4.5780E-02	4.15E-03	-2.92	-2.15	-3.45E-01
4962	SARNP	229069_at	4.5811E-02	4.16E-03	2.92	-2.15	3.57E-01
4963	DEFA5	207529_at	4.5819E-02	4.16E-03	2.92	-2.15	1.18E-01
4964	LRRC37B2	216149_at	4.5822E-02	4.16E-03	2.92	-2.15	1.03E-01
4965	HDDC2	203260_at	4.5826E-02	4.16E-03	2.92	-2.15	2.86E-01
4966	DHRS11	218756_s_at	4.5826E-02	4.16E-03	-2.92	-2.15	-1.20E-01
4967	ZNF235	210595_at	4.5835E-02	4.16E-03	2.92	-2.15	1.20E-01
4968		1564851_at	4.5837E-02	4.16E-03	2.92	-2.15	1.27E-01
4969	RBM26	229433_at	4.5845E-02	4.17E-03	2.92	-2.15	2.54E-01
4970	ATP8B1	238055_at	4.5899E-02	4.17E-03	2.92	-2.15	3.38E-01
4971	ZNF81	242083_at	4.5912E-02	4.17E-03	2.92	-2.15	1.57E-01
4972	PNRC2	217779_s_at	4.5918E-02	4.18E-03	2.92	-2.15	2.21E-01
4973	DHRSX	225503_at	4.5918E-02	4.18E-03	-2.92	-2.15	-3.25E-01
4974	ZNF567	242429_at	4.5921E-02	4.18E-03	2.92	-2.15	3.32E-01
4975	SMG5	34868_at	4.5943E-02	4.18E-03	-2.92	-2.15	-1.64E-01
4976	NBPF10///NBPF16///NBPF24///NBPF8///NBPF12///AE01///NBPF9///NBPF15///NBPF11///KIAA1245///NBPF1////NBPF14	201104_x_at	4.5944E-02	4.18E-03	-2.92	-2.15	-5.14E-01
4977	WDR66	1555007_s_at	4.5948E-02	4.18E-03	2.92	-2.15	1.36E-01
4978	DERL1	225488_at	4.5948E-02	4.18E-03	2.92	-2.15	2.32E-01
4979	WDR45	209217_s_at	4.5948E-02	4.18E-03	-2.92	-2.15	-3.25E-01
4980	SETD3	212465_at	4.6025E-02	4.19E-03	-2.92	-2.16	-1.58E-01
4981	ETNK1	224454_at	4.6025E-02	4.19E-03	2.92	-2.16	1.38E-01
4982	SYNPO	202796_at	4.6028E-02	4.19E-03	-2.92	-2.16	-3.90E-01
4983	NMUR1	221383_at	4.6065E-02	4.20E-03	2.92	-2.16	1.56E-01
4984	PAWR	214237_x_at	4.6070E-02	4.20E-03	2.92	-2.16	2.07E-01
4985	ELAVL2	228260_at	4.6070E-02	4.20E-03	2.92	-2.16	1.08E-01
4986	LOC641518	243362_s_at	4.6110E-02	4.20E-03	2.92	-2.16	5.01E-01
4987	SLC38A6	214830_at	4.6126E-02	4.21E-03	-2.92	-2.16	-6.39E-01
4988	EXOC5	228418_at	4.6126E-02	4.21E-03	-2.92	-2.16	-4.36E-01
4989	UBE2L3	200684_s_at	4.6126E-02	4.21E-03	-2.92	-2.16	-3.48E-01
4990	RHOQ	212117_at	4.6126E-02	4.21E-03	-2.92	-2.16	-3.08E-01
4991		236558_at	4.6145E-02	4.21E-03	2.92	-2.16	4.62E-01
4992	SNAPC4	215926_x_at	4.6146E-02	4.21E-03	2.92	-2.16	1.93E-01
4993	ANKHD1	229457_at	4.6146E-02	4.21E-03	2.92	-2.16	2.25E-01
4994	SLC27A5	219733_s_at	4.6156E-02	4.22E-03	2.92	-2.16	3.43E-01
4995	COBRA1	202757_at	4.6156E-02	4.22E-03	-2.92	-2.16	-3.54E-01
4996	C14orf28	235369_at	4.6168E-02	4.22E-03	2.92	-2.16	2.55E-01
4997	DARC	208335_s_at	4.6168E-02	4.22E-03	-2.92	-2.16	-5.32E-01
4998	UBXN6	223012_at	4.6168E-02	4.22E-03	-2.92	-2.16	-3.09E-01
4999	TRIM73	1554250_s_at	4.6168E-02	4.22E-03	2.92	-2.16	3.02E-01
5000		239387_at	4.6187E-02	4.22E-03	2.92	-2.16	2.74E-01
5001		244061_at	4.6250E-02	4.23E-03	2.92	-2.16	5.60E-01
5002	SRBD1	219055_at	4.6265E-02	4.23E-03	2.92	-2.16	2.75E-01
5003	TBL2	212679_at	4.6265E-02	4.23E-03	2.92	-2.16	1.18E-01
5004		244002_at	4.6265E-02	4.23E-03	2.92	-2.16	1.57E-01
5005	BUB3	201456_s_at	4.6279E-02	4.24E-03	2.92	-2.17	2.56E-01
5006		225269_s_at	4.6286E-02	4.24E-03	-2.92	-2.17	-2.82E-01
5007	LDLR	202067_s_at	4.6286E-02	4.24E-03	-2.92	-2.17	-2.32E-01
5008	SLC5A3	212944_at	4.6295E-02	4.24E-03	-2.92	-2.17	-4.20E-01
5009	UBE3A	234163_at	4.6295E-02	4.24E-03	2.92	-2.17	1.29E-01
5010	TMEM8B	207839_s_at	4.6306E-02	4.24E-03	2.92	-2.17	1.59E-01
5011	NPAT	209798_at	4.6323E-02	4.25E-03	2.92	-2.17	2.62E-01
5012	NEK2	204641_at	4.6343E-02	4.25E-03	2.92	-2.17	3.87E-01
5013	MSRB2	218773_s_at	4.6354E-02	4.25E-03	-2.92	-2.17	-3.95E-01
5014	STYXL1	222591_at	4.6363E-02	4.25E-03	2.92	-2.17	1.59E-01
5015	C17orf104	1566478_at	4.6363E-02	4.25E-03	2.92	-2.17	8.60E-02
5016		239266_at	4.6363E-02	4.25E-03	2.92	-2.17	1.92E-01
5017	ME1	204058_at	4.6363E-02	4.25E-03	-2.92	-2.17	-6.78E-01
5018	COG6	232786_at	4.6388E-02	4.26E-03	2.92	-2.17	9.39E-02
5019	LOC441666	1559503_a_at	4.6424E-02	4.26E-03	2.92	-2.17	9.50E-02
5020	LOC401320	233732_at	4.6436E-02	4.26E-03	2.92	-2.17	1.93E-01
5021		241656_at	4.6481E-02	4.27E-03	2.92	-2.17	1.15E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
5022	PROSC	214545_s_at	4.6487E-02	4.27E-03	-2.92	-2.17	-4.58E-01
5023		234564_at	4.6490E-02	4.27E-03	2.92	-2.17	1.32E-01
5024	TAF1	216711_s_at	4.6490E-02	4.27E-03	-2.92	-2.17	-1.63E-01
5025	BBX	223135_s_at	4.6490E-02	4.27E-03	-2.92	-2.17	-4.63E-01
5026	TBXAS1	236345_at	4.6490E-02	4.27E-03	-2.92	-2.17	-2.41E-01
5027	CDV3	212010_s_at	4.6490E-02	4.27E-03	-2.92	-2.17	-3.28E-01
5028	NID2	204114_at	4.6530E-02	4.28E-03	-2.91	-2.17	-7.65E-01
5029	RPS13	200018_at	4.6547E-02	4.28E-03	2.91	-2.17	1.41E-01
5030	RBBP4	239071_at	4.6547E-02	4.28E-03	2.91	-2.17	3.44E-01
5031	ADAP1	219150_s_at	4.6568E-02	4.29E-03	-2.91	-2.18	-2.21E-01
5032	RBM39	238355_at	4.6568E-02	4.29E-03	2.91	-2.18	1.21E-01
5033	ACAN	205679_x_at	4.6568E-02	4.29E-03	-2.91	-2.18	-1.69E-01
5034	UPF3B	240993_at	4.6568E-02	4.29E-03	2.91	-2.18	1.27E-01
5035	PCP2	244751_at	4.6568E-02	4.29E-03	2.91	-2.18	1.52E-01
5036	LTBP3	237144_at	4.6568E-02	4.29E-03	2.91	-2.18	1.86E-01
5037		243078_at	4.6586E-02	4.29E-03	2.91	-2.18	1.40E-01
5038		220969_s_at	4.6589E-02	4.29E-03	2.91	-2.18	1.96E-01
5039	SRSF4	241245_at	4.6593E-02	4.29E-03	2.91	-2.18	9.26E-02
5040		228661_s_at	4.6628E-02	4.30E-03	2.91	-2.18	5.34E-01
5041	MME	203435_s_at	4.6628E-02	4.30E-03	-2.91	-2.18	-5.76E-01
5042		1562984_at	4.6642E-02	4.30E-03	2.91	-2.18	1.41E-01
5043	SEMA3A	244163_at	4.6666E-02	4.30E-03	-2.91	-2.18	-9.64E-02
5044	PTPRE	221840_at	4.6676E-02	4.31E-03	-2.91	-2.18	-4.12E-01
5045	BAP1	201419_at	4.6693E-02	4.31E-03	-2.91	-2.18	-2.86E-01
5046	SLC24A2	220867_s_at	4.6738E-02	4.31E-03	2.91	-2.18	1.42E-01
5047	PARVB	216254_at	4.6763E-02	4.32E-03	-2.91	-2.18	-1.01E-01
5048	GOLGA8A	208797_s_at	4.6773E-02	4.32E-03	2.91	-2.18	4.29E-01
5049	PRKCZ	202178_at	4.6773E-02	4.32E-03	2.91	-2.18	4.10E-01
5050	DUSP28	229211_at	4.6829E-02	4.33E-03	2.91	-2.18	3.34E-01
5051	MID1IP1	218251_at	4.6840E-02	4.33E-03	-2.91	-2.18	-3.38E-01
5052	RC3H2	225813_at	4.6840E-02	4.33E-03	-2.91	-2.18	-1.59E-01
5053	PHF21B	1560091_a_at	4.6840E-02	4.33E-03	2.91	-2.18	1.29E-01
5054	KIAA1755	1561393_at	4.6840E-02	4.33E-03	2.91	-2.18	2.03E-01
5055		244539_at	4.6840E-02	4.33E-03	2.91	-2.18	1.21E-01
5056	FGD6	1555137_a_at	4.6840E-02	4.33E-03	-2.91	-2.18	-2.03E-01
5057		240850_at	4.6840E-02	4.33E-03	2.91	-2.18	9.32E-02
5058	SLC8A1	1556583_a_at	4.6870E-02	4.34E-03	-2.91	-2.19	-1.64E-01
5059		235133_at	4.6895E-02	4.34E-03	2.91	-2.19	1.53E-01
5060	GABRA2	1554308_s_at	4.6909E-02	4.34E-03	2.91	-2.19	9.07E-02
5061	ATP6V1D	208899_x_at	4.6951E-02	4.35E-03	-2.91	-2.19	-3.08E-01
5062	NDUFS2	201966_at	4.6951E-02	4.35E-03	-2.91	-2.19	-2.62E-01
5063	ANGPT2	211148_s_at	4.6951E-02	4.35E-03	-2.91	-2.19	-2.35E-01
5064		237773_at	4.6951E-02	4.35E-03	2.91	-2.19	1.54E-01
5065	SPZ1	224167_at	4.6955E-02	4.35E-03	2.91	-2.19	9.71E-02
5066	CA12	210735_s_at	4.6977E-02	4.35E-03	-2.91	-2.19	-4.61E-01
5067		211435_at	4.6977E-02	4.35E-03	2.91	-2.19	1.59E-01
5068	EIF5A2	235289_at	4.6997E-02	4.36E-03	2.91	-2.19	2.21E-01
5069	HNRNPH3	210110_x_at	4.6997E-02	4.36E-03	-2.91	-2.19	-3.51E-01
5070	PABPN1	201545_s_at	4.7000E-02	4.36E-03	-2.91	-2.19	-2.38E-01
5071	DIP2B	242970_at	4.7035E-02	4.36E-03	2.91	-2.19	1.35E-01
5072	TBC1D8	221592_at	4.7035E-02	4.36E-03	2.91	-2.19	1.43E-01
5073	HPYR1	1566916_at	4.7035E-02	4.36E-03	2.91	-2.19	1.37E-01
5074	TCERG1	229706_at	4.7035E-02	4.36E-03	2.91	-2.19	2.56E-01
5075		1560596_at	4.7039E-02	4.37E-03	2.91	-2.19	1.19E-01
5076	CCDC126	228087_at	4.7041E-02	4.37E-03	2.91	-2.19	4.61E-01
5077	TMEM185A	227880_s_at	4.7041E-02	4.37E-03	-2.91	-2.19	-4.42E-01
5078	GOLGA1	203384_s_at	4.7058E-02	4.37E-03	-2.91	-2.19	-3.02E-01
5079	ITGB2	202803_s_at	4.7079E-02	4.37E-03	-2.91	-2.19	-5.66E-01
5080	EGR3	206115_at	4.7079E-02	4.37E-03	2.91	-2.19	3.70E-01
5081	SPINK1	206239_s_at	4.7096E-02	4.38E-03	-2.91	-2.19	-2.61E-01
5082	IMPDH1	204169_at	4.7102E-02	4.38E-03	-2.91	-2.19	-3.03E-01
5083	BYSL	203612_at	4.7124E-02	4.38E-03	-2.91	-2.19	-2.38E-01
5084	KIAA1683	223600_s_at	4.7124E-02	4.38E-03	2.91	-2.19	1.51E-01
5085	NCRNA00086	238697_at	4.7124E-02	4.38E-03	2.91	-2.19	1.26E-01
5086	ATP1A2	203295_s_at	4.7124E-02	4.38E-03	2.91	-2.20	1.10E-01
5087	C5orf44	1559369_at	4.7150E-02	4.39E-03	2.91	-2.20	1.22E-01
5088	SIX5	217661_x_at	4.7150E-02	4.39E-03	2.91	-2.20	1.65E-01
5089	MS4A1	210356_x_at	4.7150E-02	4.39E-03	2.91	-2.20	8.26E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
5090	QSOX1	201482_at	4.7166E-02	4.39E-03	-2.91	-2.20	-2.53E-01
5091	DPP7	238012_at	4.7166E-02	4.39E-03	2.91	-2.20	3.38E-01
5092	MPZL1	210594_x_at	4.7166E-02	4.39E-03	-2.91	-2.20	-2.16E-01
5093	EMCN	219436_s_at	4.7166E-02	4.39E-03	-2.91	-2.20	-4.06E-01
5094		241067_at	4.7166E-02	4.39E-03	2.91	-2.20	1.05E-01
5095	PIK3CA	235980_at	4.7183E-02	4.40E-03	2.91	-2.20	1.60E-01
5096	DOCK1	203187_at	4.7205E-02	4.40E-03	-2.91	-2.20	-2.14E-01
5097	PAIP1	208051_s_at	4.7210E-02	4.40E-03	2.91	-2.20	2.99E-01
5098	TAP2	204770_at	4.7210E-02	4.40E-03	-2.91	-2.20	-3.00E-01
5099	ZNF143	221873_at	4.7229E-02	4.40E-03	2.91	-2.20	3.03E-01
5100	ZNF638	1554248_at	4.7229E-02	4.41E-03	2.91	-2.20	1.98E-01
5101	RBCK1	221827_at	4.7229E-02	4.41E-03	2.91	-2.20	2.09E-01
5102	ALG3	207396_s_at	4.7261E-02	4.41E-03	-2.90	-2.20	-2.96E-01
5103		241454_at	4.7261E-02	4.41E-03	2.90	-2.20	1.34E-01
5104	ANGPTL2	213004_at	4.7277E-02	4.41E-03	-2.90	-2.20	-5.14E-01
5105	C9orf5	227831_at	4.7329E-02	4.42E-03	2.90	-2.20	1.18E-01
5106	TRPC4AP	212059_s_at	4.7329E-02	4.42E-03	-2.90	-2.20	-2.56E-01
5107	TMEM185A	1554105_at	4.7329E-02	4.42E-03	-2.90	-2.20	-2.08E-01
5108	FBN3	240117_at	4.7329E-02	4.42E-03	2.90	-2.20	1.46E-01
5109	SEC14L1	202084_s_at	4.7391E-02	4.43E-03	-2.90	-2.20	-4.72E-01
5110	SLC25A12	203339_at	4.7391E-02	4.43E-03	2.90	-2.20	2.72E-01
5111	ZDHHC5	224858_at	4.7391E-02	4.43E-03	-2.90	-2.20	-1.94E-01
5112	FAM46A	221766_s_at	4.7429E-02	4.43E-03	-2.90	-2.21	-4.45E-01
5113	RNPC3	229903_x_at	4.7429E-02	4.44E-03	2.90	-2.21	2.84E-01
5114	ACYP2	206833_s_at	4.7452E-02	4.44E-03	2.90	-2.21	5.82E-01
5115	PDZK1P1	240634_x_at	4.7469E-02	4.44E-03	2.90	-2.21	1.37E-01
5116		242225_at	4.7469E-02	4.44E-03	2.90	-2.21	3.39E-01
5117		231827_at	4.7469E-02	4.44E-03	2.90	-2.21	2.11E-01
5118	LOC338799	1556042_s_at	4.7488E-02	4.45E-03	2.90	-2.21	1.96E-01
5119	BRI3	223376_s_at	4.7492E-02	4.45E-03	-2.90	-2.21	-3.73E-01
5120	ATP5S	238799_at	4.7516E-02	4.45E-03	2.90	-2.21	1.27E-01
5121	PIK3R2	207105_s_at	4.7529E-02	4.45E-03	-2.90	-2.21	-1.30E-01
5122	CSF1	209716_at	4.7553E-02	4.45E-03	-2.90	-2.21	-2.53E-01
5123	PCTP	218676_s_at	4.7574E-02	4.46E-03	-2.90	-2.21	-3.09E-01
5124	ERCC2	213468_at	4.7617E-02	4.46E-03	-2.90	-2.21	-1.68E-01
5125	IQCH	220361_at	4.7631E-02	4.46E-03	2.90	-2.21	8.73E-02
5126	C17orf90	50374_at	4.7661E-02	4.47E-03	2.90	-2.21	1.60E-01
5127	LOC100128398	1556724_at	4.7670E-02	4.47E-03	2.90	-2.21	1.25E-01
5128	ZNF143	206428_s_at	4.7670E-02	4.47E-03	2.90	-2.21	1.29E-01
5129	ATF7IP	216197_at	4.7681E-02	4.47E-03	2.90	-2.21	2.48E-01
5130	NEURL2	230283_at	4.7706E-02	4.48E-03	-2.90	-2.21	-3.16E-01
5131	CAPN2	208683_at	4.7734E-02	4.48E-03	-2.90	-2.21	-3.30E-01
5132	PTPLAD1	217777_s_at	4.7734E-02	4.48E-03	-2.90	-2.21	-2.83E-01
5133		1554957_at	4.7734E-02	4.48E-03	2.90	-2.21	1.27E-01
5134	TADA2B	236248_x_at	4.7738E-02	4.48E-03	2.90	-2.21	3.09E-01
5135	METTL8	220007_at	4.7753E-02	4.48E-03	2.90	-2.21	4.61E-01
5136	DNAJC7	202416_at	4.7772E-02	4.49E-03	-2.90	-2.22	-3.67E-01
5137	KIAA0427	204303_s_at	4.7772E-02	4.49E-03	-2.90	-2.22	-1.77E-01
5138	LAPTM4B	208029_s_at	4.7839E-02	4.50E-03	-2.90	-2.22	-4.73E-01
5139	C10orf84	218390_s_at	4.7839E-02	4.50E-03	2.90	-2.22	2.10E-01
5140	ME2	210154_at	4.7840E-02	4.50E-03	-2.90	-2.22	-5.43E-01
5141	RPS6KC1	218909_at	4.7879E-02	4.50E-03	-2.90	-2.22	-3.15E-01
5142	TRIM61	240342_at	4.7915E-02	4.51E-03	2.90	-2.22	3.30E-01
5143	CNP	208912_s_at	4.7915E-02	4.51E-03	-2.90	-2.22	-3.15E-01
5144	CD52	204661_at	4.7925E-02	4.51E-03	2.90	-2.22	4.75E-01
5145	FAM162A	220942_x_at	4.7978E-02	4.51E-03	2.90	-2.22	3.13E-01
5146	LOC285778	1563662_at	4.7987E-02	4.52E-03	2.90	-2.22	1.33E-01
5147	TCP11L2	1569206_at	4.7987E-02	4.52E-03	2.90	-2.22	2.18E-01
5148	HIPK2	225116_at	4.8012E-02	4.52E-03	-2.90	-2.22	-4.02E-01
5149	LRP11	225060_at	4.8012E-02	4.52E-03	-2.90	-2.22	-4.59E-01
5150	C9orf5	223005_s_at	4.8012E-02	4.52E-03	-2.90	-2.22	-3.86E-01
5151	LIMA1	222456_s_at	4.8012E-02	4.52E-03	-2.90	-2.22	-1.47E-01
5152	ACADVL	200710_at	4.8012E-02	4.52E-03	-2.90	-2.22	-3.64E-01
5153		243646_at	4.8039E-02	4.53E-03	2.90	-2.22	1.94E-01
5154	TYROBP	204122_at	4.8062E-02	4.53E-03	-2.90	-2.22	-5.19E-01
5155	ADRM1	201281_at	4.8062E-02	4.53E-03	-2.90	-2.22	-3.78E-01
5156		243501_at	4.8062E-02	4.53E-03	2.90	-2.22	2.37E-01
5157	N4BP1	204601_at	4.8066E-02	4.53E-03	-2.90	-2.22	-2.60E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
5158	TERT	1555271_a_at	4.8150E-02	4.54E-03	2.89	-2.23	1.17E-01
5159		237854_at	4.8150E-02	4.54E-03	2.89	-2.23	1.69E-01
5160	CSNK1A1P	1559651_at	4.8150E-02	4.54E-03	2.89	-2.23	8.94E-02
5161		1558651_at	4.8150E-02	4.55E-03	2.89	-2.23	9.63E-02
5162	NSMCE2	226536_at	4.8156E-02	4.55E-03	2.89	-2.23	4.61E-01
5163	DAAM1	244062_at	4.8167E-02	4.55E-03	2.89	-2.23	1.89E-01
5164	BOLA3	227291_s_at	4.8207E-02	4.55E-03	2.89	-2.23	4.33E-01
5165	WDR4	226882_x_at	4.8222E-02	4.56E-03	-2.89	-2.23	-1.99E-01
5166	LOC730091	230780_at	4.8222E-02	4.56E-03	2.89	-2.23	1.82E-01
5167	LOC100132356	1558310_s_at	4.8251E-02	4.56E-03	2.89	-2.23	1.92E-01
5168		240749_at	4.8251E-02	4.56E-03	2.89	-2.23	8.23E-02
5169	MEIG1	238158_at	4.8251E-02	4.56E-03	2.89	-2.23	2.75E-01
5170	FNTA	200090_at	4.8251E-02	4.56E-03	2.89	-2.23	2.06E-01
5171	PSIP1	209337_at	4.8269E-02	4.57E-03	2.89	-2.23	3.28E-01
5172	GOLGA4	215203_at	4.8270E-02	4.57E-03	2.89	-2.23	2.62E-01
5173		241315_at	4.8288E-02	4.57E-03	2.89	-2.23	1.61E-01
5174		1569807_at	4.8310E-02	4.57E-03	2.89	-2.23	1.63E-01
5175		235601_at	4.8319E-02	4.57E-03	2.89	-2.23	3.03E-01
5176	GALNT1	1568618_a_at	4.8346E-02	4.58E-03	-2.89	-2.23	-3.43E-01
5177	MBOAT7	209179_s_at	4.8408E-02	4.58E-03	-2.89	-2.23	-3.43E-01
5178	UBA1	200964_at	4.8408E-02	4.58E-03	-2.89	-2.23	-5.46E-01
5179	TNIP2	218335_x_at	4.8429E-02	4.59E-03	-2.89	-2.23	-2.44E-01
5180	VOPP1	208091_s_at	4.8444E-02	4.59E-03	-2.89	-2.23	-2.56E-01
5181	EFEMP1	201843_s_at	4.8462E-02	4.59E-03	-2.89	-2.24	-7.79E-01
5182	RPL31	200963_x_at	4.8465E-02	4.60E-03	2.89	-2.24	1.46E-01
5183		228533_at	4.8465E-02	4.60E-03	2.89	-2.24	1.33E-01
5184	ZNF589	210061_at	4.8465E-02	4.60E-03	-2.89	-2.24	-1.32E-01
5185	SPATA6	220298_s_at	4.8465E-02	4.60E-03	-2.89	-2.24	-1.08E-01
5186		243030_at	4.8465E-02	4.60E-03	2.89	-2.24	4.25E-01
5187	CABP5	221160_s_at	4.8465E-02	4.60E-03	2.89	-2.24	1.05E-01
5188	GTSE1	204317_at	4.8465E-02	4.60E-03	-2.89	-2.24	-1.68E-01
5189	TBC1D16	222116_s_at	4.8465E-02	4.60E-03	-2.89	-2.24	-4.60E-01
5190	C6orf54	211351_at	4.8465E-02	4.60E-03	2.89	-2.24	1.00E-01
5191	FAM178A	203481_at	4.8465E-02	4.60E-03	-2.89	-2.24	-2.30E-01
5192	KIF1B	209234_at	4.8465E-02	4.60E-03	-2.89	-2.24	-2.69E-01
5193	SNX17	200991_s_at	4.8465E-02	4.60E-03	-2.89	-2.24	-3.88E-01
5194		230003_at	4.8465E-02	4.61E-03	2.89	-2.24	2.48E-01
5195		241091_at	4.8465E-02	4.61E-03	2.89	-2.24	1.80E-01
5196	IRGQ	1555833_a_at	4.8465E-02	4.61E-03	-2.89	-2.24	-2.48E-01
5197	RALGAPA1	235524_at	4.8465E-02	4.61E-03	2.89	-2.24	1.45E-01
5198	TAP2	204769_s_at	4.8465E-02	4.61E-03	-2.89	-2.24	-3.76E-01
5199	ATPBD4	238662_at	4.8479E-02	4.61E-03	2.89	-2.24	3.94E-01
5200	ETV4	1554576_a_at	4.8514E-02	4.61E-03	2.89	-2.24	1.46E-01
5201		231351_at	4.8524E-02	4.62E-03	2.89	-2.24	1.86E-01
5202	KPNA1	202058_s_at	4.8524E-02	4.62E-03	-2.89	-2.24	-3.63E-01
5203		236303_at	4.8555E-02	4.62E-03	2.89	-2.24	1.31E-01
5204	NCRNA00081	228993_s_at	4.8576E-02	4.62E-03	2.89	-2.24	2.47E-01
5205	AFG3L2	202486_at	4.8576E-02	4.62E-03	-2.89	-2.24	-3.02E-01
5206	PDGFA	205463_s_at	4.8592E-02	4.63E-03	-2.89	-2.24	-4.15E-01
5207		240872_at	4.8602E-02	4.63E-03	2.89	-2.24	1.43E-01
5208	STAG3L4	222801_s_at	4.8627E-02	4.63E-03	2.89	-2.24	4.05E-01
5209	GSS	211630_s_at	4.8656E-02	4.64E-03	-2.89	-2.24	-2.25E-01
5210		241993_x_at	4.8656E-02	4.64E-03	2.89	-2.24	3.16E-01
5211	MRPL1	223154_at	4.8656E-02	4.64E-03	2.89	-2.24	3.77E-01
5212		1570266_x_at	4.8664E-02	4.64E-03	2.89	-2.24	1.90E-01
5213	ZDHHC13	232440_at	4.8667E-02	4.64E-03	2.89	-2.24	2.04E-01
5214	SET	40189_at	4.8677E-02	4.64E-03	-2.89	-2.24	-2.99E-01
5215	C20orf196	235064_s_at	4.8699E-02	4.64E-03	2.89	-2.25	2.67E-01
5216	NAPA	208751_at	4.8715E-02	4.65E-03	-2.89	-2.25	-6.32E-01
5217		232261_at	4.8743E-02	4.65E-03	2.89	-2.25	1.23E-01
5218	ZNF317	225296_at	4.8743E-02	4.65E-03	-2.89	-2.25	-3.53E-01
5219	CCNT2	213743_at	4.8760E-02	4.65E-03	2.89	-2.25	3.08E-01
5220	LOC346887	235205_at	4.8763E-02	4.66E-03	2.89	-2.25	1.68E-01
5221	RPAIN	216962_at	4.8765E-02	4.66E-03	2.89	-2.25	1.81E-01
5222	LOC388789	226236_at	4.8765E-02	4.66E-03	2.89	-2.25	4.55E-01
5223	GAB1	225998_at	4.8825E-02	4.66E-03	-2.89	-2.25	-2.46E-01
5224	SFRP1	228413_s_at	4.8828E-02	4.67E-03	2.89	-2.25	1.55E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
5225		1566535_at	4.8828E-02	4.67E-03	2.89	-2.25	1.17E-01
5226	PHACTR2	204047_s_at	4.8844E-02	4.67E-03	-2.89	-2.25	-3.99E-01
5227	C9orf86	225377_at	4.8844E-02	4.67E-03	-2.89	-2.25	-4.21E-01
5228	TFE3	212457_at	4.8844E-02	4.67E-03	-2.89	-2.25	-3.11E-01
5229	ZNF131	221842_s_at	4.8844E-02	4.67E-03	2.89	-2.25	1.98E-01
5230	LIN9	235039_x_at	4.8854E-02	4.67E-03	2.89	-2.25	1.28E-01
5231	JAM3	212813_at	4.8854E-02	4.67E-03	-2.89	-2.25	-3.99E-01
5232	RASSF1	240278_at	4.8857E-02	4.68E-03	2.89	-2.25	1.65E-01
5233	C18orf10	244233_at	4.8872E-02	4.68E-03	2.88	-2.25	1.04E-01
5234	EXOC7	212026_s_at	4.8876E-02	4.68E-03	-2.88	-2.25	-2.50E-01
5235	BET1L	223023_at	4.8886E-02	4.68E-03	-2.88	-2.25	-3.72E-01
5236	SLC30A5	220181_x_at	4.8886E-02	4.68E-03	2.88	-2.25	1.86E-01
5237	BAIAP2L1	222675_s_at	4.8919E-02	4.69E-03	2.88	-2.25	1.49E-01
5238	C2orf43	222193_at	4.8919E-02	4.69E-03	2.88	-2.25	2.03E-01
5239	OR10C1	221339_at	4.8933E-02	4.69E-03	2.88	-2.25	1.19E-01
5240	TBC1D27	233483_at	4.8940E-02	4.69E-03	2.88	-2.25	1.92E-01
5241	ZNF654	241348_at	4.8940E-02	4.69E-03	-2.88	-2.25	-2.26E-01
5242		241641_at	4.8940E-02	4.69E-03	2.88	-2.25	1.11E-01
5243	GGNBP2	1554419_x_at	4.8940E-02	4.69E-03	2.88	-2.25	1.27E-01
5244	SLCO1A2	207308_at	4.8997E-02	4.70E-03	2.88	-2.26	1.28E-01
5245	FKBP14	219390_at	4.8997E-02	4.70E-03	-2.88	-2.26	-4.65E-01
5246		238954_at	4.8997E-02	4.70E-03	2.88	-2.26	1.09E-01
5247	BOK	223349_s_at	4.8997E-02	4.70E-03	-2.88	-2.26	-3.60E-01
5248	NUCB1	200646_s_at	4.8997E-02	4.70E-03	-2.88	-2.26	-3.22E-01
5249	LRRIQ1	223817_at	4.9031E-02	4.71E-03	2.88	-2.26	1.13E-01
5250	ASAM	228082_at	4.9031E-02	4.71E-03	-2.88	-2.26	-2.39E-01
5251	PRKXP1	235987_at	4.9031E-02	4.71E-03	2.88	-2.26	4.04E-01
5252	TCEA2	203919_at	4.9055E-02	4.71E-03	-2.88	-2.26	-2.82E-01
5253	HIST2H4B///HIST4H4///HIST2H4A///HIST1H4L///HIST1H4E///HIST1H4B///HIST1H4H///HIST1H4C///HIST1H4J///HIST1H4K///HIST1H4F///HIST1H4D///HIST1H4A///HIST1H4I	208046_at	4.9055E-02	4.71E-03	2.88	-2.26	1.80E-01
5254	NFIB	209290_s_at	4.9055E-02	4.71E-03	-2.88	-2.26	-5.71E-01
5255	ZAK	238613_at	4.9055E-02	4.72E-03	-2.88	-2.26	-2.46E-01
5256	FBXW5	223050_s_at	4.9055E-02	4.72E-03	-2.88	-2.26	-3.49E-01
5257		239816_at	4.9073E-02	4.72E-03	2.88	-2.26	1.39E-01
5258		1557551_at	4.9125E-02	4.72E-03	2.88	-2.26	1.79E-01
5259	LOC100132288///LOC728312	229748_x_at	4.9169E-02	4.73E-03	-2.88	-2.26	-4.71E-01
5260		215978_x_at	4.9195E-02	4.73E-03	2.88	-2.26	3.51E-01
5261	PGRMC2	201701_s_at	4.9195E-02	4.73E-03	-2.88	-2.26	-2.70E-01
5262	LOC152578	1564881_at	4.9195E-02	4.73E-03	2.88	-2.26	1.04E-01
5263	HSD3B1	241111_at	4.9208E-02	4.74E-03	2.88	-2.26	1.02E-01
5264	NFIB	209289_at	4.9214E-02	4.74E-03	-2.88	-2.26	-5.23E-01
5265	NR5A2	1560469_at	4.9214E-02	4.74E-03	2.88	-2.26	7.04E-02
5266	SULT1B1	207601_at	4.9214E-02	4.74E-03	2.88	-2.26	4.39E-01
5267	ATP2C1	209935_at	4.9251E-02	4.74E-03	-2.88	-2.26	-3.05E-01
5268	CDC25C	205167_s_at	4.9254E-02	4.75E-03	2.88	-2.26	2.26E-01
5269	LOC100288954	229314_at	4.9256E-02	4.75E-03	2.88	-2.26	1.57E-01
5270	FLNA	200859_x_at	4.9312E-02	4.75E-03	-2.88	-2.27	-4.09E-01
5271	ODF4	1552409_a_at	4.9312E-02	4.75E-03	2.88	-2.27	1.80E-01
5272	MRP63	224535_s_at	4.9320E-02	4.76E-03	2.88	-2.27	3.73E-01
5273	SHISA4	226674_at	4.9320E-02	4.76E-03	-2.88	-2.27	-1.86E-01
5274	EZH1	211310_at	4.9351E-02	4.76E-03	2.88	-2.27	1.25E-01
5275	DIS3L2	238602_at	4.9351E-02	4.76E-03	2.88	-2.27	2.30E-01
5276	ZNF567	235648_at	4.9377E-02	4.77E-03	2.88	-2.27	3.41E-01
5277	UBE2Q1	217978_s_at	4.9377E-02	4.77E-03	-2.88	-2.27	-3.47E-01
5278	SDCCAG1	1557950_at	4.9408E-02	4.77E-03	-2.88	-2.27	-4.38E-01

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
5279	C6orf108	39817_s_at	4.9408E-02	4.77E-03	-2.88	-2.27	-2.02E-01
5280	RAPSN	211570_s_at	4.9416E-02	4.77E-03	2.88	-2.27	1.44E-01
5281	SLAMF8	219386_s_at	4.9430E-02	4.77E-03	-2.88	-2.27	-4.99E-01
5282	TMIGD2	244716_x_at	4.9430E-02	4.78E-03	2.88	-2.27	2.94E-01
5283	RSBN1	222790_s_at	4.9434E-02	4.78E-03	2.88	-2.27	3.41E-01
5284	KCND3	211827_s_at	4.9438E-02	4.78E-03	2.88	-2.27	1.10E-01
5285	ZFPL1	214311_at	4.9477E-02	4.78E-03	2.88	-2.27	1.77E-01
5286	LAMP1	201551_s_at	4.9481E-02	4.78E-03	-2.88	-2.27	-5.21E-01
5287	SLC22A4	205896_at	4.9530E-02	4.79E-03	-2.88	-2.27	-4.29E-01
5288	GAPDH	AFFX-HUMGAPDH/M33197_3_at	4.9530E-02	4.79E-03	-2.88	-2.27	-2.83E-01
5289	KPNB1	213573_at	4.9530E-02	4.79E-03	-2.88	-2.27	-3.04E-01
5290	VRK3	1566700_at	4.9534E-02	4.79E-03	2.88	-2.27	1.44E-01
5291	ANKRD9	230972_at	4.9534E-02	4.79E-03	-2.88	-2.27	-2.98E-01
5292	CSNK2A1	212072_s_at	4.9534E-02	4.79E-03	-2.88	-2.27	-3.03E-01
5293		239278_at	4.9534E-02	4.80E-03	2.88	-2.27	3.63E-01
5294	BOLA1	219345_at	4.9543E-02	4.80E-03	2.88	-2.27	2.81E-01
5295	SP100	202864_s_at	4.9563E-02	4.80E-03	2.88	-2.27	2.47E-01
5296	FLJ77644/// TMEM106A	1552302_at	4.9563E-02	4.80E-03	-2.88	-2.27	-2.89E-01
5297	DHX8	203334_at	4.9570E-02	4.80E-03	-2.88	-2.27	-3.20E-01
5298	MAML3	242794_at	4.9578E-02	4.81E-03	-2.88	-2.28	-2.28E-01
5299	CDKN1C	213348_at	4.9578E-02	4.81E-03	-2.88	-2.28	-6.03E-01
5300		231107_at	4.9578E-02	4.81E-03	2.88	-2.28	1.47E-01
5301	EXOSC3	227912_s_at	4.9578E-02	4.81E-03	2.88	-2.28	1.70E-01
5302	LOC728099	1561218_s_at	4.9578E-02	4.81E-03	2.88	-2.28	1.18E-01
5303	MRPS15	226296_s_at	4.9578E-02	4.81E-03	2.88	-2.28	3.07E-01
5304	RARRES1	206392_s_at	4.9613E-02	4.81E-03	-2.88	-2.28	-7.55E-01
5305	DPH5	223671_x_at	4.9619E-02	4.81E-03	2.88	-2.28	4.29E-01
5306	LOC283713	230783_at	4.9629E-02	4.82E-03	2.88	-2.28	9.40E-02
5307	NEK2	211080_s_at	4.9668E-02	4.82E-03	-2.87	-2.28	-1.62E-01
5308	WIPF2	212051_at	4.9688E-02	4.82E-03	-2.87	-2.28	-3.92E-01
5309	BCL10	1557258_a_at	4.9688E-02	4.82E-03	2.87	-2.28	1.70E-01
5310		1569818_at	4.9700E-02	4.83E-03	2.87	-2.28	8.56E-02
5311		236766_at	4.9700E-02	4.83E-03	2.87	-2.28	2.33E-01
5312	IER3IP1	211406_at	4.9700E-02	4.83E-03	2.87	-2.28	3.20E-01
5313	VPS13D	220221_at	4.9708E-02	4.83E-03	2.87	-2.28	2.17E-01
5314		1562893_at	4.9708E-02	4.83E-03	2.87	-2.28	1.11E-01
5315	PNPLA6	203718_at	4.9708E-02	4.83E-03	-2.87	-2.28	-3.71E-01
5316	WFDC1	219478_at	4.9708E-02	4.83E-03	-2.87	-2.28	-2.40E-01
5317	EPRS	200842_s_at	4.9716E-02	4.84E-03	-2.87	-2.28	-3.35E-01
5318		1558337_at	4.9716E-02	4.84E-03	2.87	-2.28	1.29E-01
5319	ATP1B3	226570_at	4.9716E-02	4.84E-03	-2.87	-2.28	-1.85E-01
5320		234704_at	4.9721E-02	4.84E-03	2.87	-2.28	1.30E-01
5321	RHBDD2	222995_s_at	4.9721E-02	4.84E-03	-2.87	-2.28	-4.81E-01
5322	DOK4	209691_s_at	4.9721E-02	4.84E-03	-2.87	-2.28	-2.08E-01
5323	IBSP	207370_at	4.9721E-02	4.84E-03	2.87	-2.28	1.52E-01
5324	SERPINE1	202628_s_at	4.9741E-02	4.84E-03	-2.87	-2.28	-6.94E-01
5325		241336_at	4.9762E-02	4.85E-03	2.87	-2.28	9.97E-02
5326		215204_at	4.9762E-02	4.85E-03	2.87	-2.28	3.08E-01
5327	PTGS1	238669_at	4.9762E-02	4.85E-03	-2.87	-2.28	-2.89E-01
5328	SNX15///ARL2	202564_x_at	4.9762E-02	4.85E-03	-2.87	-2.28	-2.55E-01
5329		232576_at	4.9762E-02	4.85E-03	2.87	-2.28	1.34E-01
5330		243332_at	4.9771E-02	4.85E-03	2.87	-2.28	3.35E-01
5331	LOC100128988	232849_at	4.9789E-02	4.85E-03	2.87	-2.28	1.75E-01
5332	MAFG	204970_s_at	4.9789E-02	4.86E-03	-2.87	-2.28	-2.98E-01
5333	IGFBP7	201163_s_at	4.9804E-02	4.86E-03	-2.87	-2.28	-2.60E-01
5334	DEPDC4	1561114_a_at	4.9811E-02	4.86E-03	2.87	-2.28	9.69E-02
5335	PVRL2	203149_at	4.9863E-02	4.87E-03	-2.87	-2.29	-3.05E-01
5336	ERP29	201216_at	4.9863E-02	4.87E-03	-2.87	-2.29	-3.42E-01
5337	RHOBTB3	202975_s_at	4.9876E-02	4.87E-03	-2.87	-2.29	-5.52E-01
5338	EVPLL	236933_at	4.9908E-02	4.87E-03	2.87	-2.29	1.13E-01
5339	KIAA1712	231850_x_at	4.9916E-02	4.87E-03	2.87	-2.29	2.19E-01
5340	PTAR1	235484_at	4.9955E-02	4.88E-03	2.87	-2.29	3.18E-01
5341	CPSF7	235326_at	4.9958E-02	4.88E-03	2.87	-2.29	8.51E-02
5342	MCL1	200798_x_at	4.9958E-02	4.88E-03	-2.87	-2.29	-3.23E-01

No.	*Gene**	*Probe ID***	*Adj. p value*	*P value*	*t*	*B*	*Log FC*
5343		236433_at	4.9983E-02	4.88E-03	2.87	-2.29	1.72E-01
5344	C2orf64	225410_at	4.9996E-02	4.89E-03	2.87	-2.29	4.81E-01

* Gene symbol as approved by the HUGO gene nomenclature committee (HGNC)

** Probe Set ID's from Affymetrix GeneChip Human Genome U133 Plus 2.0 array, from Affymetrix Inc, Santa Clara, USA

TABLE B

Biomarkers known or suggested in the art as being of potential diagnostic value in differentiating chemotherapy-responsive from chemotherapy-resistant Hodgkin's lymphoma patients (see ref [34])

Gene Symbol	Gene Title
UBE3A	E6-AP isoform-III
CLPS	colipase, pancreatic
EMID2	EMI domain containing 2
GTSF1L	gametocyte specific factor 1-like
ATXN2L	ataxin 2-like
MMP11	matrix metallopeptidase 11 (stromelysin 3)
NCKIPSD	NCK interacting protein with SH3 domain
WHSC2	Wolf-Hirschhorn syndrome candidate 2
WBP4	WW domain binding protein 4 (formin binding protein 21)
EARS2	glutamyl-tRNA synthetase 2, mitochondrial (putative)
DGCR8	DiGeorge syndrome critical region gene 8
HUWE1	HECT, UBA and WWE domain containing 1
SLC22A14	solute carrier family 22, member 14
PTPRF	protein tyrosine phosphatase, receptor type, F
DCUN1D3	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)
PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)
RIPPLY2	ripply2 homolog (zebrafish)
NCR1	natural cytotoxicity triggering receptor 1
ERMAP	erythroblast membrane-associated protein (Scianna blood group)
SHMT1	serine hydroxymethyltransferase 1 (soluble)
LPHN1	latrophilin 1
CD300C	CD300c molecule
PFDN6	prefoldin subunit 6
LYPD3	LY6/PLAUR domain containing 3
RRAD	Ras-related associated with diabetes
LRRC20	leucine rich repeat containing 20
NDE1	NudE nuclear distribution gene E homolog 1 (A. nidulans), mRNA (cDNA clone MGC:33664 IMAGE:4828494)
AGE	_
SNAPC2	small nuclear RNA activating complex, polypeptide 2, 45kDa
MID2	midline 2
MOSC1	MOCO sulphurase C-terminal domain

	containing 1
MUC1	mucin 1, cell surface associated
SLC47A1	solute carrier family 47, member 1
GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2
NT5C2	5'-nucleotidase, cytosolic II
LRRC14	leucine rich repeat containing 14
ZNF581	zinc finger protein 581
FAM166B	family with sequence similarity 166, member B
ASCL1	achaete-scute complex homolog 1 (Drosophila)
CIDEC	cell death-inducing DFFA-like effector c
ELMO3	engulfment and cell motility 3
FUZ	fuzzy homolog (Drosophila)
FGFBP2	fibroblast growth factor binding protein 2
C17orf39	chromosome 17 open reading frame 39
SLIT1	slit homolog 1 (Drosophila)
ABAT	4-aminobutyrate aminotransferase
ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B
SAA1	serum amyloid A1 /// serum amyloid A2
ZMAT4	zinc finger, matrin type 4
B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
MORG1	mitogen-activated protein kinase organizer 1
HLA-DPB2	major histocompatibility complex, class II, DP beta 2 (pseudogene)
SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2
ZNF408	zinc finger protein 408
CRCP	CGRP receptor component
CLDN7	claudin 7
UTS2R	urotensin 2 receptor
PERP	PERP, TP53 apoptosis effector
BAIAP2	BAI1-associated protein 2
SNAP47	synaptosomal-associated protein, 47kDa
FLJ40125	hypothetical protein FLJ40125
GOSR2	Golgi SNARE (GS27)
CENPO	centromere protein O
MINK1	misshapen-like kinase 1 (zebrafish)
COMT	catechol-O-methyltransferase
ACTR3	ARP3 actin-related protein 3 homolog (yeast)
RC3H2	ring finger and CCCH-type zinc finger domains 2
STAGE	_
NMNAT1	nicotinamide nucleotide adenylyltransferase 1
HSDL1	hydroxysteroid dehydrogenase like 1
POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene

ANKRD26	ankyrin repeat domain 26
CDYL	chromodomain protein, Y-like
CCDC151	coiled-coil domain containing 151
SLC4A11	solute carrier family 4, sodium borate transporter, member 11
PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide
STAP2	signal transducing adaptor family member 2
MDFIC	MyoD family inhibitor domain containing
NCRNA00105	non-protein coding RNA 105
PERP	PERP, TP53 apoptosis effector
LOC751071	methyltransferase LOC751071, mitochondrial-like
ANGPTL4	angiopoietin-like 4
SHBG	sex hormone-binding globulin
PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)
RNF144B	CDNA FLJ59797 complete cds, highly similar to E3 ubiquitin ligase IBRDC2 (EC 6.3.2.-)
GTF3C4	general transcription factor IIIC, polypeptide 4, 90kDa
COL11A2	collagen, type XI, alpha 2

TABLE C

Exemplary biomarker signature of 15 gene biomarkers differentially expressed between chemotherapy resistant and sensitive Hodgkin's lymphoma patients

(a) Zinc finger protein 644 (ZNF644) ;

(b) Colipase, pancreatic (CLPS) ;

(c) EST tu05b03.x1;

(d) relaxin 1 (RLN1);

(e) phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D);

(f) EMI domain containing 2 (EMID2);

(g) heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa; HSPA5));

(h) spermatogenesis associated 12 (SPATA12);

(i) kinectin 1 (kinesin receptor; KTN1);

(j) pentraxin 3, long (PTX3);

(k) erythropoietin receptor (EPOR);

(l) DC-STAMP domain containing 2 (DCST2);

(m) golgi to ER traffic protein 4 homolog (*S. cerevisiae*; GET4);

(n) mitogen-activated protein kinase 14 (MAPK14); and

(o) chromosome 1 open reading frame 163 (C1orf163).

TABLE D

Statistical overview of gene biomarkers identified as being differentially expressed between chemotherapy resistant and sensitive Hodgkin's lymphoma patients (atypical "outlier" group)

No.	*Gene**	*Probe ID***	*Adj. p value*	*P value*	*t*	*B*	*Log FC*
1	CD93	202877_s_at	0.000133	2.43E-09	11.65	10.77	1.78436
2	GJD3	230025_at	0.000167	6.10E-09	10.94	10.04	1.41240
3	PRRX1	205991_s_at	0.000747	4.10E-08	9.57	8.49	1.75162
4	NRP1	210510_s_at	0.001086	7.94E-08	9.13	7.93	1.27260
5	CYGB	226632_at	0.001243	1.18E-07	8.87	7.59	1.05169
6	GGT5	205582_s_at	0.001243	1.36E-07	8.78	7.47	1.91095
7	COL6A2	213290_at	0.001363	2.10E-07	8.50	7.10	2.06811
8	LAPTM4B	208767_s_at	0.001363	2.11E-07	8.50	7.10	1.66799
9	DDAH1	209094_at	0.001363	2.24E-07	8.46	7.04	1.60410
10	ZDHHC9	222451_s_at	0.001467	2.68E-07	8.35	6.89	1.16314
11	GNAQ	224861_at	0.001592	3.20E-07	8.24	6.73	1.35432
12	NRP1	212298_at	0.001888	4.14E-07	8.08	6.51	2.36720
13	CD209	207277_at	0.00211	5.46E-07	7.91	6.27	3.03822
14	CD59	212463_at	0.00211	5.59E-07	7.90	6.25	1.44157
15	APLP2	208703_s_at	0.00211	5.79E-07	7.88	6.22	1.47862
16	FOSL2	225262_at	0.002128	6.44E-07	7.82	6.12	1.80222
17	PARVA	217890_s_at	0.002128	7.36E-07	7.74	6.00	1.59587
18	CTNNA1	1558214_s_at	0.002128	7.64E-07	7.71	5.97	1.13446
19	KLF11	218486_at	0.002128	7.75E-07	7.70	5.96	1.40943
20	CYP1B1	202436_s_at	0.002128	7.97E-07	7.69	5.93	1.78844
21	COL6A1	212091_s_at	0.002128	8.25E-07	7.67	5.90	2.16408
22	FAM198B	219872_at	0.002128	8.85E-07	7.63	5.84	1.17368
23	ATRN	211852_s_at	0.002128	9.30E-07	7.60	5.80	1.27690
24	LAMP1	201551_s_at	0.002128	9.34E-07	7.60	5.79	1.61768
25	TRAM2	202368_s_at	0.002358	1.08E-06	7.51	5.66	1.17145
26	YAP1	224895_at	0.002492	1.19E-06	7.46	5.58	1.62591
27	SOX13	38918_at	0.002807	1.46E-06	7.34	5.39	0.61378
28	RHBDD2	232053_x_at	0.002807	1.46E-06	7.34	5.39	1.16409
29	C1R	212067_s_at	0.002807	1.49E-06	7.32	5.38	2.11216
30	BACE2	222446_s_at	0.003058	1.68E-06	7.26	5.27	1.41917
31	NBL1	37005_at	0.003308	1.92E-06	7.18	5.15	1.66252
32	ITSN1	209297_at	0.003308	2.00E-06	7.16	5.11	1.33423
33	EPDR1	223253_at	0.003308	2.04E-06	7.15	5.10	1.86142
34	TMCO3	220240_s_at	0.003308	2.06E-06	7.14	5.09	0.74084
35	EMILIN1	204163_at	0.003443	2.24E-06	7.09	5.01	2.15345
36		236297_at	0.003443	2.27E-06	7.09	5.00	1.24898
37	LAPTM4B	1554679_a_at	0.003739	2.53E-06	7.02	4.90	1.48330
38	CLIC4	201559_s_at	0.003934	2.82E-06	6.96	4.80	1.53854
39		235072_s_at	0.003934	2.84E-06	6.96	4.80	1.24865
40	NR2F2	215073_s_at	0.003934	2.88E-06	6.95	4.78	1.91316
41	ADAM9	1555326_a_at	0.004066	3.05E-06	6.92	4.73	1.19432
42	CYP1B1	202435_s_at	0.004163	3.23E-06	6.89	4.68	1.69770
43		235438_at	0.004163	3.27E-06	6.88	4.67	1.33093
44	MEMO1	219065_s_at	0.004556	3.67E-06	-6.82	4.57	-0.70693
45	TUSC3	209228_x_at	0.004638	3.87E-06	6.79	4.52	0.80020
46	FOSL2	218880_at	0.004638	4.07E-06	6.76	4.47	1.53982
47	TGM2	201042_at	0.004638	4.22E-06	6.74	4.44	2.97901
48	MPZL1	201874_at	0.004638	4.30E-06	6.73	4.42	1.14039
49	NBL1	201621_at	0.004638	4.37E-06	6.72	4.41	1.36420
50	SLC2A10	221024_s_at	0.004638	4.40E-06	6.72	4.40	2.05135
51	KLF7	1555420_a_at	0.004638	4.41E-06	6.72	4.40	1.05220
52	APLP2	214875_x_at	0.004638	4.41E-06	6.71	4.40	1.40270
53	ETS2	201329_s_at	0.005309	5.15E-06	6.63	4.26	1.10204
54	TIMP2	224560_at	0.005474	5.43E-06	6.60	4.21	2.58750
55	PICALM	215236_s_at	0.005474	5.51E-06	6.59	4.20	1.90895
56	NR2F2	209121_x_at	0.005509	5.64E-06	6.58	4.17	1.61550
57	NHSL1	226490_at	0.005738	6.08E-06	6.54	4.11	1.14567
58	KANK2	218418_s_at	0.005738	6.35E-06	6.52	4.07	1.69799
59	RHOJ	235489_at	0.005738	6.44E-06	6.51	4.05	1.63481
60	FZD2	210220_at	0.005738	6.46E-06	6.51	4.05	1.56233
61	RHOBTB3	202975_s_at	0.005738	6.50E-06	6.50	4.04	1.45826
62	EGFR	201983_s_at	0.005738	6.51E-06	6.50	4.04	1.40950

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
63	ITSN1	209298_s_at	0.005924	6.83E-06	6.48	4.00	1.40938
64	RHOBTB1	212651_at	0.006269	7.44E-06	6.43	3.92	1.23840
65	GNA11	564_at	0.006269	7.45E-06	6.43	3.92	1.05358
66	ARSB	206129_s_at	0.006345	7.75E-06	6.41	3.88	0.77367
67	OLFML3	218162_at	0.006345	7.81E-06	6.40	3.88	2.68363
68	SETD7	224928_at	0.006345	7.89E-06	6.40	3.87	1.19914
69	CPXM1	227860_at	0.006379	8.05E-06	6.39	3.85	2.11441
70	CD99L2	233825_s_at	0.006394	8.49E-06	6.36	3.80	0.92238
71	LHFP	218656_s_at	0.006394	8.58E-06	6.35	3.79	1.43285
72	EFEMP2	209356_x_at	0.006394	8.63E-06	6.35	3.79	1.83770
73	RHOJ	238905_at	0.006394	8.65E-06	6.35	3.78	0.97934
74	GAS6	202177_at	0.006394	8.74E-06	6.35	3.78	1.64885
75	HLX	214438_at	0.006394	8.77E-06	6.34	3.77	0.90944
76	MMP19	204575_s_at	0.006436	8.95E-06	6.33	3.75	1.34431
77	FKBP9	212169_at	0.00648	9.13E-06	6.32	3.74	1.60759
78	PVRL2	203149_at	0.006594	9.60E-06	6.30	3.69	0.85490
79	PCYOX1	225274_at	0.006594	9.64E-06	6.29	3.68	1.47245
80	C6orf115	223361_at	0.006594	9.72E-06	-6.29	3.68	-1.10617
81	CDC42BPB	217849_s_at	0.006594	9.87E-06	6.28	3.66	1.36892
82	SGMS2	227038_at	0.006594	9.90E-06	6.28	3.66	1.05480
83		228827_at	0.006594	1.01E-05	6.27	3.65	1.62794
84	CTTN	227473_at	0.006594	1.01E-05	6.27	3.64	1.26328
85	CXCL12	203666_at	0.006611	1.03E-05	6.26	3.63	2.20517
86	BACE2	217867_x_at	0.006747	1.06E-05	6.24	3.60	1.57668
87	RBPJ	211974_x_at	0.006785	1.08E-05	6.23	3.58	0.76464
88	CYP1B1	202437_s_at	0.006795	1.09E-05	6.23	3.57	1.59943
89	CALU	200756_x_at	0.006833	1.13E-05	6.21	3.54	1.35976
90	PCYOX1	203803_at	0.006833	1.14E-05	6.20	3.53	1.38877
91	TUSC3	213423_x_at	0.006833	1.14E-05	6.20	3.53	1.19659
92	FLJ10357	58780_s_at	0.006833	1.18E-05	6.18	3.50	1.27761
93	CD59	228748_at	0.006833	1.19E-05	6.18	3.49	0.94860
94	ITGAM	205786_s_at	0.006833	1.21E-05	6.17	3.47	1.87159
95	LOC653506/ //METRNL	225955_at	0.006833	1.21E-05	6.17	3.47	2.20700
96	ORC6L	219105_x_at	0.006833	1.21E-05	-6.17	3.47	-0.96712
97	QKI	212263_at	0.006833	1.22E-05	6.17	3.47	0.75189
98	PDGFA	205463_s_at	0.006833	1.23E-05	6.16	3.46	1.46231
99	LMNA	1554600_s_at	0.006833	1.24E-05	6.16	3.46	1.49165
100	DDR2	227561_at	0.006969	1.27E-05	6.14	3.43	1.65447
101	ASPH	225008_at	0.007334	1.35E-05	6.11	3.37	1.37303
102	NFIC	213298_at	0.007357	1.37E-05	6.11	3.36	1.03719
103	FERMT2	209209_s_at	0.007375	1.40E-05	6.10	3.34	1.54988
104	FAM46A	224973_at	0.007375	1.40E-05	6.09	3.34	0.96297
105	FBLN1	202995_s_at	0.007458	1.43E-05	6.08	3.32	2.36742
106	SMTN	207390_s_at	0.007785	1.51E-05	6.06	3.27	0.76786
107	DDAH2	214909_s_at	0.007858	1.54E-05	6.05	3.26	1.03052
108	SOD3	205236_x_at	0.008021	1.59E-05	6.03	3.23	0.88354
109	PCSK5	205560_at	0.008021	1.60E-05	6.03	3.22	1.51703
110	CTNNA1	210844_x_at	0.008141	1.64E-05	6.01	3.20	0.95725
111	CAV1	203065_s_at	0.008405	1.71E-05	5.99	3.16	1.59793
112	CYBRD1	217889_s_at	0.008466	1.73E-05	5.98	3.15	1.41438
113	PARVA	222454_s_at	0.008466	1.80E-05	5.96	3.11	1.49183
114	EHD2	45297_at	0.008466	1.80E-05	5.96	3.11	1.30821
115	IGFBP2	202718_at	0.008466	1.81E-05	5.96	3.11	1.77981
116	GLT25D1	222644_s_at	0.008466	1.81E-05	5.96	3.11	0.94005
117	LRP11	225060_at	0.008466	1.81E-05	5.96	3.10	1.51269
118	TNS1	218864_at	0.008466	1.83E-05	5.96	3.10	0.55614
119	RPS19	242451_x_at	0.008491	1.85E-05	-5.95	3.08	-0.71207
120	ZNF697	227080_at	0.008491	1.88E-05	5.94	3.07	1.32974
121	SH3PXD2B	231823_s_at	0.008491	1.89E-05	5.94	3.07	1.93061
122	PICALM	215832_x_at	0.008491	1.89E-05	5.94	3.06	0.80706
123	ISLR	207191_s_at	0.008667	1.96E-05	5.92	3.03	1.38492
124	DIAPH2	205726_at	0.008667	1.97E-05	5.92	3.03	1.07735
125	PBX1	212151_at	0.008685	2.01E-05	5.91	3.01	1.02339
126	PDGFRB	202273_at	0.008685	2.03E-05	5.90	3.00	1.22179
127	CUX1	202367_at	0.008685	2.05E-05	5.90	2.99	1.00412
128	KCND3	213832_at	0.008685	2.06E-05	5.89	2.99	0.87689
129	RGS5	209070_s_at	0.008685	2.11E-05	5.88	2.97	1.92764
130	LDLRAD3	234985_at	0.008685	2.11E-05	5.88	2.97	0.97940

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
131	FAM46A	221766_s_at	0.008685	2.14E-05	5.87	2.95	1.28303
132	LMAN1	203293_s_at	0.008685	2.15E-05	5.87	2.95	0.99215
133		1558397_at	0.008685	2.16E-05	5.87	2.94	1.08220
134	OSMR	205729_at	0.008685	2.19E-05	5.86	2.93	0.91495
135	EEF2K	225545_at	0.008685	2.21E-05	5.86	2.92	0.95197
136	CD93	202878_s_at	0.008685	2.21E-05	5.86	2.92	2.65424
137	ICAM1	202637_s_at	0.008685	2.22E-05	5.86	2.92	1.51536
138	S100A16	227998_at	0.008685	2.23E-05	5.85	2.91	1.33254
139	DDAH2	215537_x_at	0.008685	2.24E-05	5.85	2.91	0.97510
140	C13orf33	227058_at	0.008685	2.24E-05	5.85	2.91	1.43508
141	FAM13A	217047_s_at	0.008685	2.26E-05	5.85	2.90	1.39577
142	SOCS5	209647_s_at	0.008685	2.26E-05	5.85	2.90	1.25521
143	WLS	228950_s_at	0.008685	2.27E-05	5.84	2.90	0.72634
144	ZBTB47	226484_at	0.008685	2.29E-05	5.84	2.89	0.58401
145	CD52	204661_at	0.008685	2.30E-05	-5.84	2.88	-1.33174
146	DUT	208956_x_at	0.00869	2.36E-05	-5.82	2.86	-0.64165
147	FBLN1	201787_at	0.00869	2.36E-05	5.82	2.86	2.15652
148	F13A1	203305_at	0.00869	2.38E-05	5.82	2.86	2.66507
149	CYB561	209163_at	0.00869	2.39E-05	5.82	2.85	0.93242
150	FAM109B	226504_at	0.00869	2.40E-05	5.82	2.85	0.85477
151	FPR3	230422_at	0.00869	2.41E-05	5.81	2.84	2.00221
152	SEL1L	202062_s_at	0.00869	2.42E-05	5.81	2.84	1.04260
153	LRRC32	203835_at	0.00869	2.44E-05	5.81	2.83	1.53810
154	MEIS1	204069_at	0.00869	2.46E-05	5.80	2.82	1.59094
155	GOLM1	217771_at	0.00869	2.46E-05	5.80	2.82	1.63895
156	STON1	213413_at	0.008943	2.55E-05	5.78	2.79	1.59975
157		238455_at	0.009112	2.62E-05	5.77	2.77	1.10975
158	ZNF680	229533_x_at	0.009433	2.73E-05	-5.75	2.73	-0.82784
159	ETS2	201328_at	0.009595	2.79E-05	5.74	2.71	1.03272
160	FPR3	214560_at	0.009649	2.82E-05	5.73	2.70	1.04589
161	GPR124	221814_at	0.009649	2.84E-05	5.73	2.69	1.26234
162	MXD1	226275_at	0.009737	2.88E-05	5.72	2.68	1.32163
163	GNG12	212294_at	0.009815	2.94E-05	5.71	2.66	1.21488
164	APLP2	208702_x_at	0.009815	2.96E-05	5.71	2.65	1.37660
165	FRMD4A	225163_at	0.009815	2.98E-05	5.71	2.65	1.54531
166	TRIM2	202342_s_at	0.009815	2.98E-05	5.70	2.65	0.78730
167	QKI	1555154_a_at	0.009818	3.00E-05	5.70	2.64	1.19311
168	RBM9	213901_x_at	0.010296	3.16E-05	5.67	2.59	1.04619
169	CDKN1C	213348_at	0.010416	3.22E-05	5.67	2.57	1.49140
170	HIST3H2A	221582_at	0.010445	3.27E-05	-5.66	2.56	-1.00740
171	ARSD	225286_at	0.010445	3.28E-05	5.66	2.56	0.84876
172	CLDN23	228707_at	0.010445	3.30E-05	5.65	2.55	0.88032
173	B4GALT1	216627_s_at	0.010445	3.30E-05	5.65	2.55	1.38511
174	RHOBTB3	202976_s_at	0.010501	3.34E-05	5.65	2.54	1.99528
175	MYOF	211864_s_at	0.010657	3.41E-05	5.64	2.52	2.03275
176	EMP2	225078_at	0.010851	3.49E-05	5.62	2.50	1.41779
177	H1F0	208886_at	0.010856	3.52E-05	5.62	2.49	0.76660
178	BMP1	205574_x_at	0.010856	3.54E-05	5.62	2.49	1.36052
179	DDAH2	202262_x_at	0.010856	3.55E-05	5.62	2.48	0.82051
180	APP	214953_s_at	0.01099	3.62E-05	5.61	2.47	1.65885
181	RXRA	202449_s_at	0.011137	3.69E-05	5.60	2.45	0.91932
182	CTNNA1	200765_x_at	0.011171	3.72E-05	5.59	2.44	1.31830
183	MXRA7	227326_at	0.011388	3.84E-05	5.58	2.41	0.99302
184	OMA1	226019_at	0.011388	3.87E-05	-5.57	2.40	-0.83291
185	SEC61A1	217716_s_at	0.011388	3.88E-05	5.57	2.40	0.94550
186	THBD	203888_at	0.011388	3.93E-05	5.56	2.39	1.60870
187	PLAT	201860_s_at	0.011388	3.93E-05	5.56	2.39	1.15767
188	DDR2	225442_at	0.011388	3.95E-05	5.56	2.38	1.99006
189	SYNPO	202796_at	0.011388	3.95E-05	5.56	2.38	1.22663
190	FGD4	227948_at	0.011388	3.96E-05	5.56	2.38	1.12858
191	CDH5	204677_at	0.011628	4.08E-05	5.55	2.35	1.73119
192	AKAP12	227530_at	0.011628	4.08E-05	5.54	2.35	1.56308
193	GAB2	203853_s_at	0.011639	4.11E-05	5.54	2.35	0.92120
194	PCOLCE	202465_at	0.011653	4.15E-05	5.54	2.34	2.13140
195	MFAP4	212713_at	0.011653	4.18E-05	5.53	2.33	1.81941
196	DUT	209932_s_at	0.011653	4.20E-05	-5.53	2.33	-0.70971
197	HIC1	230218_at	0.011653	4.20E-05	5.53	2.33	0.83006
198	PPAP2B	209355_s_at	0.011739	4.25E-05	5.52	2.32	2.48236
199	IGFBP4	201508_at	0.011739	4.27E-05	5.52	2.31	2.03859

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
200	FILIP1	1556325_at	0.011813	4.34E-05	5.51	2.30	0.62596
201	CHST15	203066_at	0.011813	4.36E-05	5.51	2.29	1.71789
202	CALCRL	210815_s_at	0.011813	4.36E-05	5.51	2.29	1.39867
203	OLFML1	217525_at	0.01203	4.49E-05	5.50	2.26	1.58697
204	ABCA7	219577_s_at	0.01203	4.51E-05	-5.50	2.26	-0.70510
205	SPINT1	202826_at	0.01203	4.53E-05	5.49	2.26	0.63954
206	SELENBP1	214433_s_at	0.01203	4.54E-05	5.49	2.25	0.76556
207	SLC27A1	226728_at	0.01203	4.57E-05	5.49	2.25	0.75714
208	APLP2	211404_s_at	0.01203	4.58E-05	5.49	2.25	1.32743
209	ZCCHC24	212419_at	0.01203	4.61E-05	5.48	2.24	1.11235
210	HGSNAT	218017_s_at	0.01203	4.62E-05	5.48	2.24	1.19776
211	SOX7	228698_at	0.012093	4.67E-05	5.48	2.23	1.08037
212	CTBP2	201218_at	0.012151	4.71E-05	5.47	2.22	0.81510
213	COL4A2	211966_at	0.012387	4.83E-05	5.46	2.20	2.29284
214	MPZL1	210087_s_at	0.012502	4.92E-05	5.45	2.18	1.08920
215	GPRC5B	203632_s_at	0.012502	4.94E-05	5.45	2.18	1.16904
216	EPB41L3	206710_s_at	0.012502	4.95E-05	5.45	2.17	2.23007
217	NID1	202008_s_at	0.012502	4.96E-05	5.45	2.17	1.35116
218	MTUS1	212093_s_at	0.012557	5.10E-05	5.43	2.15	0.60686
219	PTGFRN	224937_at	0.012557	5.10E-05	5.43	2.15	2.14241
220	RIN3	219457_s_at	0.012557	5.10E-05	5.43	2.15	0.80367
221	JAM2	219213_at	0.012557	5.13E-05	5.43	2.14	1.43856
222	MEIS2	207480_s_at	0.012557	5.14E-05	5.43	2.14	1.20710
223	PDE4A	204735_at	0.012557	5.14E-05	5.43	2.14	1.32080
224	CRAT	209522_s_at	0.012557	5.15E-05	5.43	2.14	0.89415
225	ARMCX2	203404_at	0.012557	5.17E-05	5.43	2.13	1.70933
226	PTGS1	215813_s_at	0.012756	5.27E-05	5.42	2.12	1.99888
227	C5orf33	226946_at	0.012803	5.32E-05	5.41	2.11	0.56872
228	FNDC3B	222693_at	0.012854	5.36E-05	5.41	2.10	1.23266
229	THBS1	201108_s_at	0.012949	5.42E-05	5.40	2.09	1.49923
230	CALU	214845_s_at	0.01322	5.56E-05	5.39	2.07	1.67680
231	C2orf18	225695_at	0.013232	5.59E-05	5.39	2.06	1.05388
232	NTRK2	221795_at	0.013249	5.65E-05	5.38	2.05	1.92837
233	UGDH	203343_at	0.013249	5.70E-05	5.38	2.04	0.94878
234	RILPL1	226207_at	0.013249	5.72E-05	5.38	2.04	0.69112
235	BACE1	222463_s_at	0.013249	5.76E-05	5.37	2.03	0.62972
236	TSTD1	226482_s_at	0.013249	5.76E-05	-5.37	2.03	-1.20394
237	CRISPLD2	221541_at	0.013249	5.76E-05	5.37	2.03	2.91342
238	NDUFB1	206790_s_at	0.013249	5.79E-05	-5.37	2.03	-0.66179
239	EDNRB	206701_x_at	0.013249	5.83E-05	5.37	2.02	1.22319
240	EPB41L2	201718_s_at	0.013249	5.86E-05	5.36	2.02	1.05785
241	MYL9	201058_s_at	0.013249	5.88E-05	5.36	2.01	2.27247
242	SLC7A8	216092_s_at	0.013249	5.89E-05	5.36	2.01	0.82050
243	CD52	34210_at	0.013249	5.89E-05	-5.36	2.01	-1.45689
244	PLTP	202075_s_at	0.013267	5.93E-05	5.36	2.01	2.99379
245	PLXDC2	227276_at	0.013267	5.96E-05	5.35	2.00	1.51326
246	MYO1C	225080_at	0.013267	5.97E-05	5.35	2.00	1.31923
247	RUSC1	206949_s_at	0.013274	6.00E-05	5.35	2.00	0.82343
248		225567_at	0.013274	6.04E-05	5.35	1.99	1.69691
249	APBB2	213419_at	0.013274	6.05E-05	5.35	1.99	0.46946
250	CCDC3	223316_at	0.013848	6.33E-05	5.32	1.95	1.44258
251	COL4A1	211981_at	0.013979	6.45E-05	5.32	1.93	2.47763
252	ELOVL5	215082_at	0.013979	6.45E-05	-5.32	1.93	-1.29501
253	FMOD	202709_at	0.013979	6.47E-05	5.31	1.93	1.77245
254	ANGPTL2	213001_at	0.014043	6.54E-05	5.31	1.92	2.04438
255	MARVELD1	223095_at	0.014043	6.55E-05	5.31	1.91	1.03576
256	ITM2A	202746_at	0.014054	6.58E-05	-5.31	1.91	-1.30118
257	PALMD	218736_s_at	0.014347	6.74E-05	5.29	1.89	1.26220
258	PPP1R3B	222662_at	0.014494	6.84E-05	5.29	1.87	0.95412
259	EXT1	201995_at	0.014494	6.87E-05	5.28	1.87	0.64811
260	TGOLN2	212040_at	0.014514	6.90E-05	5.28	1.87	1.90875
261	ACOX3	204242_s_at	0.01453	6.95E-05	5.28	1.86	0.48199
262	HIP1	226364_at	0.01453	6.97E-05	5.28	1.86	1.22830
263	FOSL2	228188_at	0.01453	6.99E-05	5.28	1.85	1.65567
264	IFNAR1	225661_at	0.01467	7.08E-05	5.27	1.84	1.29931
265	RHBDF1	218686_s_at	0.014709	7.14E-05	5.27	1.83	0.77780
266	MARCKS	213002_at	0.014709	7.16E-05	5.26	1.83	0.84506
267	ANO10	218910_at	0.014809	7.28E-05	5.26	1.82	1.00844
268	MCAM	209086_x_at	0.014809	7.29E-05	5.26	1.81	0.84422

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
269	CRLF3	205474_at	0.014809	7.30E-05	-5.25	1.81	-0.83904
270	FAM129B	223019_at	0.014809	7.31E-05	5.25	1.81	1.17506
271	MMP14	202827_s_at	0.014886	7.38E-05	5.25	1.80	0.91081
272	COL18A1	209081_s_at	0.014895	7.41E-05	5.25	1.80	1.68263
273	TMEM115	216267_s_at	0.014989	7.53E-05	5.24	1.78	0.73690
274	CKAP4	200998_s_at	0.014989	7.53E-05	5.24	1.78	1.89387
275	FST	204948_s_at	0.014989	7.56E-05	5.24	1.78	1.26258
276	ACVRL1	226950_at	0.014989	7.57E-05	5.24	1.78	1.35283
277	FANCD2	242560_at	0.015071	7.64E-05	-5.23	1.77	-0.78969
278	LMNA	203411_s_at	0.015079	7.68E-05	5.23	1.77	1.19255
279	CHN2	213385_at	0.015079	7.74E-05	5.23	1.76	1.55095
280	FAM57A	218898_at	0.015079	7.75E-05	5.22	1.76	0.77222
281	ITPRIPL2	227514_at	0.015079	7.76E-05	5.22	1.76	1.24676
282		229373_at	0.015079	7.78E-05	5.22	1.75	1.26699
283	FGFR1OP2	223262_s_at	0.015079	7.81E-05	-5.22	1.75	-0.53526
284		213429_at	0.015148	7.87E-05	5.22	1.74	1.91430
285	KLF4	220266_s_at	0.015148	7.91E-05	5.21	1.74	0.92547
286	CLIP3	212358_at	0.015148	7.92E-05	5.21	1.74	1.10496
287	NFIB	211467_s_at	0.015305	8.08E-05	5.20	1.72	1.00267
288	CCDC72	221791_s_at	0.015305	8.11E-05	-5.20	1.72	-0.56928
289	ANTXR2	225524_at	0.015305	8.19E-05	5.20	1.71	1.67598
290	CTDSPL	201906_s_at	0.015305	8.19E-05	5.20	1.71	1.00734
291	TRAM2	202369_s_at	0.015305	8.23E-05	5.19	1.70	1.60103
292	CANX	200068_s_at	0.015305	8.23E-05	5.19	1.70	0.85642
293	TCEAL3	227279_at	0.015305	8.26E-05	5.19	1.70	0.60738
294	FRS2	238486_at	0.015305	8.28E-05	5.19	1.70	0.47150
295		226834_at	0.015305	8.29E-05	5.19	1.69	1.56441
296	WFS1	202908_at	0.015305	8.32E-05	5.19	1.69	0.96604
297	DPYSL2	200762_at	0.015305	8.34E-05	5.19	1.69	1.83931
298	LRCH4	204692_at	0.015305	8.35E-05	-5.19	1.69	-0.76384
299	DUSP3	201536_at	0.015305	8.37E-05	5.19	1.69	0.94037
300	GAS2L1	209729_at	0.015322	8.41E-05	5.18	1.68	0.71055
301	NFIB	213029_at	0.015608	8.59E-05	5.17	1.66	1.37659
302	DDX19A	202578_s_at	0.015992	8.84E-05	5.16	1.63	0.83127
303	PLOD1	200827_at	0.015992	8.89E-05	5.16	1.63	1.59052
304	CALD1	201616_s_at	0.015992	8.89E-05	5.16	1.63	1.69576
305	GNA11	213766_x_at	0.01607	8.96E-05	5.15	1.62	1.39281
306	PARVA	222455_s_at	0.016135	9.10E-05	5.15	1.61	1.27084
307	ERMP1	218342_s_at	0.016135	9.11E-05	5.14	1.61	0.56836
308	HSD3B7	222817_at	0.016135	9.12E-05	5.14	1.61	1.21921
309	MRPS31	212603_at	0.016135	9.15E-05	-5.14	1.60	-0.63741
310	CRIP2	208978_at	0.016135	9.15E-05	5.14	1.60	1.27277
311	EPB41L3	211776_s_at	0.016149	9.19E-05	5.14	1.60	1.76411
312	AP2A2	212159_x_at	0.016179	9.26E-05	5.14	1.59	1.65950
313	HRH1	205580_s_at	0.016179	9.28E-05	5.14	1.59	0.87061
314	DLC1	210762_s_at	0.016179	9.29E-05	5.13	1.59	1.62386
315	CENPL	232065_x_at	0.016262	9.37E-05	-5.13	1.58	-0.81165
316	PCSK5	205559_s_at	0.016262	9.40E-05	5.13	1.58	1.90635
317	ITPRIPL2	227792_at	0.016262	9.43E-05	5.13	1.57	1.29777
318	RABGAP1L	213982_s_at	0.016431	9.56E-05	-5.12	1.56	-0.95765
319	ARSD	223696_at	0.016458	9.60E-05	5.12	1.56	0.82887
320	SLC43A3	210692_s_at	0.016505	9.66E-05	5.12	1.55	1.23797
321	C1S	1555229_a_at	0.016509	9.69E-05	5.11	1.55	2.96960
322	FAM20C	226722_at	0.016531	9.74E-05	5.11	1.54	1.60783
323		236379_at	0.016551	9.78E-05	-5.11	1.54	-1.42734
324	CTDSPL	201904_s_at	0.0166	9.84E-05	5.11	1.54	1.02127
325	DYSF	218660_at	0.016658	9.90E-05	5.10	1.53	1.04489
326	NRP2	225566_at	0.016713	9.96E-05	5.10	1.52	0.84883
327	ZYG11B	225350_s_at	0.016728	1.00E-04	5.10	1.52	0.74868
328	GPR116	212951_at	0.016745	1.00E-04	5.10	1.52	1.54995
329	DLEU2	1563229_at	0.016751	1.01E-04	-5.09	1.51	-0.49619
330	C17orf44	230012_at	0.016751	1.01E-04	-5.09	1.51	-1.22199
331	CCL23	210548_at	0.016751	1.01E-04	5.09	1.51	3.39405
332	ICAM1	215485_s_at	0.016856	1.02E-04	5.09	1.50	0.93171
333	KLF6	208960_s_at	0.017149	1.04E-04	5.08	1.48	1.80159
334	LHFP	231411_at	0.017307	1.06E-04	5.07	1.47	0.79713
335	ZNF436	226114_at	0.017307	1.06E-04	5.07	1.47	0.51295
336	NUDT16	235054_at	0.017426	1.08E-04	5.06	1.45	0.77267
337	SLCO3A1	227367_at	0.017426	1.08E-04	5.06	1.45	1.02383

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
338	COL6A1	213428_s_at	0.017426	1.08E-04	5.06	1.45	2.63585
339	LOXL1	203570_at	0.017426	1.08E-04	5.06	1.45	2.07400
340		242057_at	0.017426	1.09E-04	-5.06	1.44	-0.41478
341	TMEM164	223202_s_at	0.017426	1.09E-04	5.06	1.44	0.53937
342	PAPSS2	203059_s_at	0.017426	1.09E-04	5.05	1.44	0.81608
343	ZCCHC24	212423_at	0.017426	1.10E-04	5.05	1.44	1.41043
344	GNA11	204248_at	0.017426	1.10E-04	5.05	1.43	1.19160
345	CANX	208852_s_at	0.017426	1.10E-04	5.05	1.43	1.72011
346	PTRF	208789_at	0.017426	1.10E-04	5.05	1.43	1.40029
347	NFIA	224976_at	0.017426	1.11E-04	5.05	1.43	1.10291
348	KLF4	221841_s_at	0.017472	1.11E-04	5.05	1.42	1.78540
349	TPBG	203476_at	0.017516	1.12E-04	5.04	1.42	1.55583
350	COL6A2	209156_s_at	0.017574	1.13E-04	5.04	1.41	3.49238
351	FOXO3	204132_s_at	0.017574	1.13E-04	5.04	1.41	1.01826
352	LOC643749	240577_at	0.017605	1.13E-04	-5.04	1.40	-0.37339
353	ATPIF1	223338_s_at	0.017687	1.14E-04	-5.03	1.40	-0.63610
354	ARMCX3	222444_at	0.017772	1.15E-04	5.03	1.39	0.71533
355	SLC2A14/// SLC2A3	222088_s_at	0.017831	1.16E-04	5.03	1.38	1.27193
356	AK3L2///AK4	225342_at	0.017833	1.16E-04	5.03	1.38	1.44204
357	AHNAK	220016_at	0.017876	1.17E-04	5.02	1.38	0.51771
358	SHE	229910_at	0.017889	1.18E-04	5.02	1.37	1.00955
359	STAT3	208992_s_at	0.017889	1.18E-04	5.02	1.37	1.07618
360	ALDH7A1	208951_at	0.017889	1.18E-04	5.02	1.37	0.75761
361		231431_s_at	0.017889	1.18E-04	5.02	1.36	0.88133
362	RAB31	217762_s_at	0.017889	1.18E-04	5.02	1.36	1.80370
363	DVL3	201908_at	0.01792	1.19E-04	5.01	1.36	1.07444
364	FNIP1	228768_at	0.017957	1.20E-04	5.01	1.35	0.51862
365	PAPSS2	203058_s_at	0.017994	1.21E-04	5.01	1.35	1.40271
366	SLCO3A1	219229_at	0.017994	1.21E-04	5.01	1.34	1.13595
367	TBC1D16	222116_s_at	0.017994	1.21E-04	5.01	1.34	1.47527
368	CDH11	207172_s_at	0.01803	1.22E-04	5.00	1.34	1.55766
369	DUSP3	201537_s_at	0.01803	1.22E-04	5.00	1.34	1.08205
370	ZCCHC10	1559399_s_at	0.01803	1.23E-04	-5.00	1.33	-1.34448
371	CTNNA1	200764_s_at	0.01803	1.23E-04	5.00	1.33	1.40287
372	ZBTB8B///ZBTB8A	235142_at	0.01803	1.23E-04	5.00	1.33	0.99405
373	NPNT	225911_at	0.018074	1.23E-04	5.00	1.32	0.89136
374	PLSCR4	218901_at	0.018127	1.24E-04	4.99	1.32	1.56589
375	SLC16A3	202855_s_at	0.018281	1.25E-04	4.99	1.31	1.35624
376	PLXND1	212235_at	0.018281	1.26E-04	4.99	1.31	1.12153
377	RPS7	213941_x_at	0.018694	1.29E-04	-4.97	1.28	-0.45270
378	DPYSL3	201430_s_at	0.018694	1.30E-04	4.97	1.28	1.04857
379	TNFAIP1	201207_at	0.018694	1.30E-04	4.97	1.28	1.39587
380	TK2	204277_s_at	0.018694	1.30E-04	4.97	1.27	0.59353
381	RUNX1T1	205528_s_at	0.018694	1.30E-04	4.97	1.27	1.15458
382	CNIH4	228306_at	0.018694	1.31E-04	4.97	1.27	0.69238
383	ANKRD16	229058_at	0.018697	1.31E-04	4.97	1.27	0.54640
384	CNRIP1	226751_at	0.0187	1.32E-04	4.96	1.26	1.19577
385	MTSS1	203037_s_at	0.0187	1.32E-04	4.96	1.26	0.61428
386	CD69	209795_at	0.018797	1.33E-04	-4.96	1.25	-1.29777
387	ZNF410	209944_at	0.018797	1.33E-04	-4.96	1.25	-0.56501
388	TRIP6	209129_at	0.018797	1.34E-04	4.96	1.25	1.38554
389	MEIS3P1	214077_x_at	0.018797	1.34E-04	4.96	1.25	0.82309
390	AP2A2	211779_x_at	0.018797	1.34E-04	4.96	1.25	1.60298
391	CPE	201116_s_at	0.019012	1.36E-04	4.95	1.23	1.62813
392	HIBADH	231955_s_at	0.019012	1.36E-04	4.95	1.23	0.45055
393	GALNTL4	1554079_at	0.019096	1.37E-04	4.94	1.22	0.51687
394	PALM2-AKAP2///PALM2///AKAP2	202759_s_at	0.01912	1.38E-04	4.94	1.22	1.55920
395	TTC28	215146_s_at	0.019168	1.39E-04	4.94	1.21	0.93348
396	SIPA1L2	225056_at	0.019168	1.39E-04	4.94	1.21	1.14353
397	MLEC	200617_at	0.019168	1.39E-04	4.94	1.21	1.24515
398	NID1	202007_at	0.019204	1.40E-04	4.93	1.21	2.21449
399	SCAMP1	1552978_a_at	0.019389	1.42E-04	4.93	1.19	1.01787
400	SOX18	219568_x_at	0.019389	1.43E-04	4.92	1.19	0.65010
401	AOC3	204894_s_at	0.019389	1.43E-04	4.92	1.19	1.56693

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
402	FDFT1	208647_at	0.019389	1.44E-04	-4.92	1.18	-0.75026
403	C1S	208747_s_at	0.019389	1.44E-04	4.92	1.18	1.18557
404	CAV1	212097_at	0.019389	1.44E-04	4.92	1.18	1.62217
405	LAPTM4B	208029_s_at	0.019389	1.44E-04	4.92	1.18	1.36621
406	FNTB	225851_at	0.019389	1.45E-04	4.92	1.18	0.89961
407	CFI	203854_at	0.019389	1.45E-04	4.92	1.17	1.93698
408	ADAMTS2	214454_at	0.019389	1.45E-04	4.92	1.17	1.15908
409	RHOJ	1555233_at	0.019389	1.45E-04	4.92	1.17	0.81778
410	RBPMS	209488_s_at	0.019389	1.45E-04	4.92	1.17	2.00388
411	PPP3CC	32541_at	0.019664	1.48E-04	-4.91	1.15	-0.80049
412	RASIP1	220027_s_at	0.019664	1.48E-04	4.91	1.15	1.06921
413	DLEU1	205677_s_at	0.019664	1.49E-04	-4.90	1.15	-1.06111
414	CRK	202226_s_at	0.019664	1.49E-04	4.90	1.15	1.15821
415	PDLIM4	211564_s_at	0.019708	1.50E-04	4.90	1.14	1.12666
416	TM9SF4	212194_s_at	0.02002	1.52E-04	4.89	1.13	1.51469
417	EPAS1	200878_at	0.020186	1.54E-04	4.89	1.12	1.67703
418	GNA14	220108_at	0.020186	1.54E-04	4.89	1.11	1.03741
419	EDNRA	204464_s_at	0.020186	1.55E-04	4.89	1.11	2.05317
420	TMEM164	223201_s_at	0.020219	1.55E-04	4.88	1.11	0.64543
421	ITPRIPL2	1568619_s_at	0.020254	1.56E-04	4.88	1.10	1.45563
422	FCGR2A	203561_at	0.020254	1.56E-04	4.88	1.10	2.45521
423	FAM36A	224824_at	0.020254	1.57E-04	-4.88	1.10	-0.67072
424	GALNS	206335_at	0.020368	1.58E-04	4.88	1.09	0.91252
425	KIAA1731	229878_at	0.020394	1.59E-04	-4.87	1.09	-0.74840
426		213710_s_at	0.020394	1.59E-04	4.87	1.09	0.75617
427	SERPINH1	207714_s_at	0.020401	1.60E-04	4.87	1.08	2.31674
428	INPP5B	213804_at	0.020401	1.60E-04	-4.87	1.08	-0.50110
429	MARS	213671_s_at	0.020401	1.61E-04	-4.87	1.08	-0.66973
430	ZFAND3	218020_s_at	0.020401	1.61E-04	4.87	1.07	0.86627
431	MARCO	205819_at	0.020401	1.62E-04	4.86	1.07	2.21337
432	QSOX1	201482_at	0.020401	1.62E-04	4.86	1.07	0.77022
433	TIMP2	231579_s_at	0.020401	1.62E-04	4.86	1.07	2.45433
434	CH25H	206932_at	0.020401	1.62E-04	4.86	1.07	1.76980
435	C1QTNF5/// MFRP	223499_at	0.020414	1.62E-04	4.86	1.07	1.46979
436	RHOC	200885_at	0.020414	1.63E-04	4.86	1.06	1.20795
437	ARHGAP23	226638_at	0.02043	1.64E-04	4.86	1.06	0.82255
438		242316_at	0.02043	1.64E-04	-4.86	1.06	-0.43281
439	CTTNBP2NL	226000_at	0.020463	1.64E-04	4.86	1.06	0.93642
440	ST5	202440_s_at	0.020547	1.65E-04	4.85	1.05	0.83009
441	GPR161	214104_at	0.020547	1.66E-04	4.85	1.05	0.73224
442	JAM2	229127_at	0.02083	1.68E-04	4.84	1.03	1.73631
443	N4BP2L2	202259_s_at	0.020858	1.69E-04	-4.84	1.03	-0.91239
444	DKK3	214247_s_at	0.020858	1.70E-04	4.84	1.03	1.84773
445	AXL	202686_s_at	0.020858	1.70E-04	4.84	1.03	2.30553
446	CRTAP	1554464_a_at	0.020918	1.71E-04	4.84	1.02	1.97424
447	VTI1B	225926_at	0.020961	1.71E-04	4.84	1.02	1.32858
448	APLP2	208704_x_at	0.020979	1.72E-04	4.83	1.01	1.07324
449	NID2	204114_at	0.021198	1.74E-04	4.83	1.00	1.98995
450	SCN1B	205508_at	0.02124	1.75E-04	4.83	1.00	0.64826
451	BOD1P	231368_at	0.02125	1.75E-04	-4.82	1.00	-0.39663
452	GAS5	228238_at	0.02125	1.76E-04	-4.82	0.99	-1.24063
453	SLC36A2/// RPL24	214143_x_at	0.021325	1.77E-04	-4.82	0.99	-0.45939
454	NFE2L1	200759_x_at	0.021325	1.77E-04	4.82	0.99	0.57523
455	SMPD1	216230_x_at	0.021325	1.77E-04	4.82	0.98	0.41890
456	RNASE1	201785_at	0.021325	1.79E-04	4.81	0.98	2.43798
457	VRK1	203856_at	0.021325	1.79E-04	-4.81	0.97	-0.84833
458	MAFB	222670_s_at	0.021325	1.79E-04	4.81	0.97	1.43756
459	VCL	200931_s_at	0.021325	1.80E-04	4.81	0.97	1.46099
460	SAV1	222573_s_at	0.021325	1.80E-04	4.81	0.97	0.64872
461	ROBO4	226028_at	0.021325	1.80E-04	4.81	0.97	1.08918
462		222877_at	0.021325	1.81E-04	4.81	0.97	1.53354
463	RNF24	210706_s_at	0.021325	1.81E-04	4.81	0.97	0.71463
464	PRRG1	205618_at	0.021325	1.81E-04	4.81	0.97	0.75809
465	PTGS1	205128_x_at	0.021353	1.82E-04	4.81	0.96	1.51954
466	CD276	224859_at	0.021451	1.83E-04	4.80	0.96	0.68318
467	ZNF101	1552633_at	0.021671	1.85E-04	-4.80	0.94	-0.89394

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
468	MID1	203636_at	0.021671	1.86E-04	4.80	0.94	0.86926
469	GNA11	40562_at	0.021671	1.86E-04	4.80	0.94	1.05143
470	CX3CL1	823_at	0.021904	1.89E-04	4.79	0.93	0.94660
471	ATF6	203952_at	0.021904	1.89E-04	4.79	0.93	0.85056
472	ARHGAP1	202117_at	0.021932	1.89E-04	4.79	0.92	0.91932
473	ZSCAN16	219676_at	0.021948	1.90E-04	-4.79	0.92	-0.79858
474	MFAP3	213123_at	0.021948	1.90E-04	4.79	0.92	0.47144
475	PINK1	209018_s_at	0.022018	1.91E-04	4.78	0.91	0.60563
476	ASPH	205808_at	0.022103	1.92E-04	4.78	0.91	0.95628
477	NXN	219489_s_at	0.022154	1.93E-04	4.78	0.90	1.27423
478	SPON2	218638_s_at	0.022543	1.97E-04	4.77	0.88	1.65146
479	ADAM9	202381_at	0.022543	1.97E-04	4.77	0.88	1.84934
480	LEPR	211356_x_at	0.022747	2.00E-04	4.76	0.87	1.02768
481	PROS1	207808_s_at	0.022818	2.01E-04	4.76	0.87	1.39262
482	PRRX1	226695_at	0.022818	2.01E-04	4.76	0.87	1.54398
483	LOC100132999	229872_s_at	0.022871	2.02E-04	-4.76	0.86	-0.84908
484	ENC1	201341_at	0.022942	2.03E-04	4.75	0.86	1.26031
485		233909_at	0.022978	2.04E-04	-4.75	0.85	-0.43067
486	CPXM2	226824_at	0.022978	2.04E-04	4.75	0.85	1.15564
487	ACOX1	227962_at	0.023298	2.08E-04	4.74	0.84	1.08664
488	ZNF107	205739_x_at	0.02338	2.09E-04	-4.74	0.83	-1.29788
489	PAPSS2	203060_s_at	0.023419	2.10E-04	4.74	0.83	1.29832
490	PPAP2B	212226_s_at	0.023419	2.10E-04	4.74	0.83	1.88639
491	LAMC1	200771_at	0.023419	2.10E-04	4.74	0.82	1.73674
492	SLC38A7	218727_at	0.023419	2.11E-04	4.74	0.82	0.97506
493	SYNC	221276_s_at	0.023433	2.12E-04	4.73	0.82	0.77826
494	MAPK7	35617_at	0.023433	2.12E-04	4.73	0.82	0.64280
495	MXRA8	213422_s_at	0.023498	2.13E-04	4.73	0.81	1.47570
496	LAMA4	210990_s_at	0.02351	2.13E-04	4.73	0.81	0.55581
497	KIAA0090	212396_s_at	0.02351	2.14E-04	4.73	0.81	0.89329
498	RAB31	217764_s_at	0.023612	2.15E-04	4.73	0.80	1.24839
499	NDRG3	224368_s_at	0.023746	2.17E-04	4.72	0.80	0.79271
500	SULF2	233555_s_at	0.023836	2.18E-04	4.72	0.79	1.93828
501	MRP63	204387_x_at	0.023836	2.18E-04	-4.72	0.79	-0.80978
502	CENPBD1	1552330_at	0.023895	2.19E-04	4.72	0.79	0.72161
503	EMP2	204975_at	0.023913	2.20E-04	4.71	0.78	1.50356
504	MAOA	212741_at	0.023913	2.20E-04	4.71	0.78	2.09607
505	MAOB	204041_at	0.023919	2.21E-04	4.71	0.78	1.23400
506		229830_at	0.023919	2.21E-04	4.71	0.78	1.05607
507	AEBP1	201792_at	0.024121	2.24E-04	4.71	0.77	1.68374
508	FCGR2C	210992_x_at	0.024121	2.24E-04	4.71	0.77	1.77068
509	FZD1	204451_at	0.024189	2.25E-04	4.70	0.76	1.48559
510	ENG	201809_s_at	0.024189	2.26E-04	4.70	0.76	1.55115
511	PLAUR	211924_s_at	0.024189	2.26E-04	4.70	0.76	1.42853
512	PRKAR1A	200604_s_at	0.024291	2.28E-04	4.70	0.75	1.66140
513	ABL1	202123_s_at	0.024291	2.28E-04	4.70	0.75	1.26442
514	BACE1	217904_s_at	0.024292	2.28E-04	4.70	0.75	0.89522
515		226865_at	0.024308	2.29E-04	4.70	0.74	1.97728
516	FARP1	201911_s_at	0.024308	2.30E-04	4.69	0.74	1.11185
517	KIAA1462	231841_s_at	0.024308	2.30E-04	4.69	0.74	1.07959
518	CAV2	203324_s_at	0.02434	2.31E-04	4.69	0.74	1.21581
519	SSPN	204964_s_at	0.024344	2.31E-04	4.69	0.74	0.95659
520	TRIM47	225868_at	0.024539	2.34E-04	4.69	0.73	0.99714
521	FLJ46875	230203_at	0.024539	2.34E-04	-4.69	0.73	-0.46853
522	CITED2	207980_s_at	0.024734	2.36E-04	4.68	0.72	1.81310
523	ZNF703	222760_at	0.024781	2.38E-04	4.68	0.71	0.77048
524	TGFBR3	204731_at	0.024781	2.38E-04	4.68	0.71	1.67984
525	HIST2H4B///HIST4H4///HIST2H4A///HIST1H4L///HIST1H4E///HIST1H4B///HIST1H4H///HIST1H4C///HIST1H4J///HIST1H4K///HIST1H4F///HIST1H4D///	205967_at	0.024781	2.38E-04	-4.68	0.71	-1.43194

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
	ST1H4A///HIST1H4I						
526	GUCY1A3	221942_s_at	0.024781	2.38E-04	4.68	0.71	1.77865
527	ANPEP	202888_s_at	0.024835	2.39E-04	4.67	0.70	2.24123
528	MXD1	228846_at	0.024907	2.41E-04	4.67	0.70	0.94890
529	TPP1	200743_s_at	0.024907	2.41E-04	4.67	0.70	1.52229
530	SLC39A6	1556551_s_at	0.024926	2.42E-04	4.67	0.70	1.12307
531	RGS10	204316_at	0.024944	2.43E-04	-4.67	0.69	-0.73706
532	BOK	223349_s_at	0.024944	2.43E-04	4.67	0.69	0.99462
533	SEC61A1	222385_x_at	0.025088	2.45E-04	4.66	0.68	1.50497
534	CCL11	210133_at	0.025088	2.45E-04	4.66	0.68	3.90678
535	SCARB2	201647_s_at	0.025088	2.46E-04	4.66	0.68	1.73118
536		238835_at	0.025088	2.46E-04	4.66	0.68	0.94722
537	NFIB	209290_s_at	0.0251	2.47E-04	4.66	0.68	1.41474
538	MFGE8	210605_s_at	0.025126	2.49E-04	4.66	0.67	1.02129
539	RHOJ	235131_at	0.025126	2.49E-04	4.66	0.67	0.50927
540	SQSTM1	239004_at	0.025126	2.49E-04	-4.66	0.67	-0.57404
541	CRYAB	209283_at	0.025126	2.49E-04	4.66	0.67	1.24518
542	CTNND1	208407_s_at	0.025126	2.49E-04	4.65	0.67	1.68808
543	ZAK	225665_at	0.025126	2.50E-04	4.65	0.66	1.00803
544		231047_at	0.025126	2.50E-04	-4.65	0.66	-0.38958
545	PHC2	200919_at	0.025126	2.50E-04	4.65	0.66	0.73639
546	NFIB	230291_s_at	0.025226	2.52E-04	4.65	0.65	1.12985
547	ZNF436	226113_at	0.025226	2.52E-04	4.65	0.65	0.59624
548	NRP2	229225_at	0.025386	2.55E-04	4.64	0.65	0.75874
549	C10orf72	235471_at	0.025386	2.55E-04	4.64	0.65	0.43936
550	CD99L2	223041_at	0.025421	2.56E-04	4.64	0.64	1.00933
551	GNAI1	209576_at	0.025542	2.57E-04	4.64	0.64	0.71797
552	MOSC2	227417_at	0.025665	2.59E-04	4.64	0.63	1.20595
553	C14orf181	229054_at	0.02568	2.60E-04	-4.63	0.63	-0.54209
554	ITGA5	201389_at	0.02568	2.60E-04	4.63	0.63	1.22182
555	MMP2	201069_at	0.025713	2.61E-04	4.63	0.62	2.86428
556	PYGL	202990_at	0.025811	2.62E-04	4.63	0.62	1.66558
557		244429_at	0.026005	2.65E-04	-4.63	0.61	-1.21144
558	COL4A4	229779_at	0.026145	2.67E-04	4.62	0.60	1.39339
559	CDHR3	235650_at	0.026154	2.67E-04	-4.62	0.60	-0.34034
560	RIN2	209684_at	0.026255	2.69E-04	4.62	0.59	1.88835
561	CLIC4	221881_s_at	0.026303	2.70E-04	4.62	0.59	1.07758
562	DAB2	210757_x_at	0.026417	2.72E-04	4.61	0.59	1.85966
563	FCGR2C	211395_x_at	0.026698	2.75E-04	4.61	0.57	2.24120
564	SYNJ1	207594_s_at	0.026728	2.76E-04	4.61	0.57	0.38123
565	UBE4B	202316_x_at	0.026728	2.76E-04	4.61	0.57	0.65987
566	DOCK5	230263_s_at	0.026736	2.77E-04	4.60	0.57	1.00949
567	ODF3B	238326_at	0.026821	2.78E-04	-4.60	0.56	-0.88795
568	OLFML2B	213125_at	0.026821	2.79E-04	4.60	0.56	1.91869
569	HSPA5	230031_at	0.026973	2.81E-04	4.60	0.55	1.02556
570	TBC1D10B	220947_s_at	0.027009	2.82E-04	4.60	0.55	0.65889
571	ZNF143	221873_at	0.027059	2.83E-04	-4.59	0.55	-0.55616
572	C5AR1	220088_at	0.027059	2.83E-04	4.59	0.55	1.16628
573	RBPMS	209487_at	0.027059	2.84E-04	4.59	0.55	1.41852
574	TMEM185B	219253_at	0.027176	2.85E-04	4.59	0.54	0.93704
575	TMEM54	225536_at	0.027213	2.86E-04	4.59	0.54	0.73553
576	FARP1	201910_at	0.027327	2.88E-04	4.59	0.53	0.87308
577	PARVB	37965_at	0.027377	2.89E-04	4.58	0.53	1.15378
578	SLC29A1	201801_s_at	0.027377	2.89E-04	4.58	0.53	0.70968
579	LOC100216545	238473_at	0.027501	2.91E-04	-4.58	0.52	-0.46750
580	C20orf194	226607_at	0.027646	2.93E-04	4.58	0.51	1.00425
581	LAMB1	211651_s_at	0.027774	2.95E-04	4.57	0.51	1.86791
582	MRVI1	226047_at	0.027774	2.96E-04	4.57	0.51	1.25387
583	SUOX	204067_at	0.027774	2.96E-04	4.57	0.50	0.92970
584		227333_at	0.027797	2.97E-04	4.57	0.50	0.77295
585	SYNJ2	216180_s_at	0.027947	2.99E-04	-4.57	0.50	-0.65653
586	IER5L	226552_at	0.028007	3.01E-04	4.57	0.49	0.75112
587	SLC2A3	202498_s_at	0.028007	3.01E-04	4.56	0.49	0.95646
588	TTC28	213058_at	0.028007	3.02E-04	4.56	0.49	0.97120
589	PRNP	215707_s_at	0.028007	3.02E-04	4.56	0.49	1.13618
590	EMP1	201325_s_at	0.028007	3.02E-04	4.56	0.49	1.45110
591	G6PC3	44654_at	0.02802	3.04E-04	4.56	0.48	0.65562

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
592	DAB2	201279_s_at	0.02802	3.04E-04	4.56	0.48	1.89444
593	FCGR2B	210889_s_at	0.02802	3.04E-04	4.56	0.48	1.89654
594		243005_at	0.02811	3.05E-04	-4.56	0.48	-0.41515
595	PDIA5	203857_s_at	0.02833	3.09E-04	4.55	0.47	1.52185
596	PILRA	219788_at	0.02833	3.09E-04	4.55	0.46	1.33867
597	ELL3	219517_at	0.02833	3.09E-04	-4.55	0.46	-1.54247
598	OSBPL1A	209485_s_at	0.028408	3.11E-04	4.55	0.46	1.21034
599	CYB5R3	201885_s_at	0.028408	3.11E-04	4.55	0.46	0.96084
600	EPB41L3	212681_at	0.028408	3.12E-04	4.55	0.46	1.49867
601	SIAE	224391_s_at	0.028417	3.13E-04	4.55	0.45	1.22255
602	PLS3	201215_at	0.028417	3.13E-04	4.55	0.45	1.31701
603	WLS	228949_at	0.028438	3.14E-04	4.54	0.45	1.21715
604	SCD5	224901_at	0.028725	3.17E-04	4.54	0.44	1.06748
605	OS9	200714_x_at	0.028782	3.18E-04	4.54	0.44	0.68887
606		243353_at	0.02884	3.20E-04	-4.54	0.43	-0.36946
607	TPSB2///TPSAB1	205683_x_at	0.028939	3.21E-04	4.53	0.43	1.85701
608	FAM13A	202973_x_at	0.029343	3.28E-04	4.52	0.41	1.45105
609	DKK3	202196_s_at	0.029343	3.28E-04	4.52	0.41	0.91861
610	NFE2L1	200758_s_at	0.029343	3.28E-04	4.52	0.41	0.81408
611	PTGFRN	224950_at	0.029343	3.29E-04	4.52	0.41	0.99305
612	GLIS3	230258_at	0.029343	3.29E-04	4.52	0.41	0.80398
613	TBC1D8	241017_at	0.029343	3.29E-04	-4.52	0.41	-1.05016
614	GGCX	205351_at	0.029698	3.34E-04	4.51	0.39	1.12065
615	TMEM8A	221882_s_at	0.029698	3.35E-04	4.51	0.39	1.04350
616	CLEC11A	210783_x_at	0.029698	3.35E-04	4.51	0.39	0.54387
617	LOC730631	230738_at	0.029698	3.35E-04	-4.51	0.39	-0.47872
618	ZBED1	203043_at	0.029744	3.36E-04	4.51	0.39	0.76900
619	NUP43	219007_at	0.029797	3.38E-04	-4.51	0.38	-0.53934
620	DNAJC5	224612_s_at	0.029797	3.39E-04	4.51	0.38	1.00074
621	CNKSR3	227481_at	0.029797	3.39E-04	4.51	0.38	1.09835
622	AQP1	207542_s_at	0.029797	3.39E-04	4.51	0.38	1.26686
623	TEAD4	41037_at	0.029797	3.40E-04	4.51	0.38	0.71775
624	EFEMP2	206580_s_at	0.029816	3.40E-04	4.51	0.37	1.36034
625	CMKLR1	229121_at	0.029899	3.42E-04	4.50	0.37	1.36151
626	MYEF2	222771_s_at	0.029899	3.42E-04	-4.50	0.37	-0.73296
627	B4GALT1	201883_s_at	0.030015	3.44E-04	4.50	0.36	1.11907
628	BCL2L2	209311_at	0.030019	3.45E-04	4.50	0.36	1.05027
629	TIGD1	1553099_at	0.030091	3.47E-04	-4.50	0.36	-0.96165
630	DLG5	201681_s_at	0.030091	3.47E-04	4.50	0.36	1.20045
631	GAB1	225998_at	0.03028	3.51E-04	4.49	0.35	0.81171
632	GPR116	212950_at	0.03028	3.51E-04	4.49	0.35	1.96512
633	CD151	204306_s_at	0.03028	3.51E-04	4.49	0.34	0.94867
634		238852_at	0.03028	3.51E-04	4.49	0.34	1.19243
635	RANBP9	216125_s_at	0.03028	3.52E-04	4.49	0.34	0.71779
636	RPL37	224766_at	0.030546	3.55E-04	-4.49	0.33	-0.43479
637	TPSAB1	207741_x_at	0.030575	3.56E-04	4.48	0.33	1.42670
638	CDC42EP5	227850_x_at	0.030596	3.57E-04	4.48	0.33	1.13370
639	PES1	202212_at	0.030686	3.59E-04	4.48	0.33	0.51626
640	CARD10	210026_s_at	0.030701	3.59E-04	4.48	0.32	0.83368
641	KIAA1211	227230_s_at	0.030714	3.60E-04	4.48	0.32	0.86840
642	CALD1	201617_x_at	0.030714	3.61E-04	4.48	0.32	1.66133
643	SMTN	209427_at	0.030864	3.63E-04	4.48	0.31	0.76710
644	FNIP2	226460_at	0.030974	3.65E-04	4.47	0.31	1.57408
645	FAM127A	201828_x_at	0.031103	3.67E-04	4.47	0.30	1.42080
646	RCAN1	208370_s_at	0.031103	3.68E-04	4.47	0.30	1.40322
647	CCL23	210549_s_at	0.031103	3.68E-04	4.47	0.30	2.94623
648	C22orf32	225794_s_at	0.031103	3.69E-04	-4.47	0.30	-0.91630
649	CCDC80	225241_at	0.031106	3.71E-04	4.46	0.29	1.95729
650	PTPRE	221840_at	0.031106	3.71E-04	4.46	0.29	1.30404
651	KLF7	204334_at	0.031106	3.72E-04	4.46	0.29	1.14131
652	MGC16121	237986_at	0.031106	3.72E-04	-4.46	0.29	-0.52477
653	C21orf58	238541_at	0.031106	3.72E-04	-4.46	0.29	-0.52000
654	PMP22	210139_s_at	0.031106	3.72E-04	4.46	0.29	1.84511
655	SPATS2L	215617_at	0.031106	3.73E-04	4.46	0.29	0.61954
656	RERG	244745_at	0.031123	3.73E-04	4.46	0.29	0.76484
657	RPSAP19///RPSAP9///RPSAP58///R	213801_x_at	0.031126	3.74E-04	-4.46	0.29	-0.49779

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
	PSA						
658	C20orf196	235064_s_at	0.031126	3.75E-04	-4.46	0.28	-0.55922
659	ERC1	226049_at	0.031149	3.76E-04	4.46	0.28	0.64279
660	ACVRL1	210838_s_at	0.031149	3.76E-04	4.46	0.28	0.89811
661	TNS1	221748_s_at	0.031288	3.78E-04	4.46	0.28	1.85327
662	TMEM127	222887_s_at	0.031288	3.79E-04	4.45	0.27	0.90948
663		239234_at	0.031528	3.82E-04	-4.45	0.27	-0.84663
664	TSPAN4	209264_s_at	0.031595	3.84E-04	4.45	0.26	1.81703
665	FAM171A1	212771_at	0.031692	3.86E-04	4.45	0.26	1.20964
666	DPYSL3	201431_s_at	0.031692	3.86E-04	4.45	0.26	1.46803
667	ITGB5	201125_s_at	0.031692	3.87E-04	4.44	0.25	1.43039
668	TNFRSF1A	207643_s_at	0.031692	3.87E-04	4.44	0.25	1.29273
669	CKAP4	200999_s_at	0.031925	3.91E-04	4.44	0.25	1.66982
670	C1orf85	1558693_s_at	0.031996	3.92E-04	4.44	0.24	1.27039
671	RBMS1	203748_x_at	0.032116	3.95E-04	4.44	0.24	1.68308
672	PTP4A1	200731_s_at	0.032116	3.95E-04	4.44	0.24	0.64143
673	PLA2G4B/// JMJD7///JMJD7-PLA2G4B	219095_at	0.032116	3.95E-04	-4.43	0.23	-0.48547
674	RGS5	209071_s_at	0.032171	3.97E-04	4.43	0.23	1.46125
675	ZCRB1	225394_s_at	0.032195	3.98E-04	-4.43	0.23	-0.86706
676	ATP2A2	212361_s_at	0.032195	3.98E-04	4.43	0.23	1.67396
677	GPR172A	222155_s_at	0.032225	3.99E-04	4.43	0.22	1.17604
678	NUCB1	200646_s_at	0.032225	4.00E-04	4.43	0.22	0.93478
679	TPP1	200742_s_at	0.032259	4.01E-04	4.43	0.22	2.25644
680	EXD2	218363_at	0.032298	4.02E-04	4.43	0.22	0.52725
681	P4HB	1564494_s_at	0.032363	4.03E-04	4.43	0.22	2.25675
682	CRTAP	226656_at	0.032363	4.04E-04	4.42	0.21	0.56404
683	PTAFR	211661_x_at	0.032414	4.05E-04	4.42	0.21	1.72809
684	DAB2	201280_s_at	0.032439	4.06E-04	4.42	0.21	1.78055
685	PLEKHG5	237646_x_at	0.032489	4.07E-04	-4.42	0.21	-0.39150
686	RHOBTB3	225202_at	0.032561	4.09E-04	4.42	0.20	1.72218
687	FAM114A1	213455_at	0.032752	4.12E-04	4.42	0.20	1.62996
688	HK1	200697_at	0.033058	4.16E-04	4.41	0.19	0.86927
689	SLC39A6	1555460_a_at	0.033065	4.17E-04	4.41	0.18	0.73954
690	SLC35E1	227518_at	0.03312	4.18E-04	4.41	0.18	0.78059
691	LMLN	244881_at	0.033248	4.20E-04	4.41	0.18	0.82582
692	ZNF92	235170_at	0.033248	4.21E-04	-4.40	0.18	-0.75031
693	PPAP2B	212230_at	0.033282	4.22E-04	4.40	0.17	1.90846
694		239587_at	0.033282	4.22E-04	4.40	0.17	0.52368
695	RANBP9	202583_s_at	0.033356	4.24E-04	4.40	0.17	1.23793
696	MBD4	214047_s_at	0.033456	4.26E-04	-4.40	0.16	-0.54211
697	RNASEH2B	229210_at	0.033456	4.27E-04	-4.40	0.16	-0.61713
698	RHOQ	214449_s_at	0.033456	4.28E-04	4.40	0.16	1.23017
699	HOMER3	215489_x_at	0.033456	4.28E-04	4.40	0.16	0.63242
700	LTBR	203005_at	0.033456	4.28E-04	4.40	0.16	1.09369
701	MGAT4B	220189_s_at	0.033456	4.29E-04	4.40	0.16	1.26687
702	SRPX	204955_at	0.033456	4.30E-04	4.39	0.16	2.33227
703	NUDT4P1/// NUDT4	212183_at	0.033456	4.32E-04	4.39	0.15	0.91986
704	COL27A1	225288_at	0.033456	4.33E-04	4.39	0.15	0.70812
705	LGALS3BP	200923_at	0.033456	4.33E-04	4.39	0.15	2.16150
706	C5orf45	220341_s_at	0.033456	4.33E-04	-4.39	0.15	-0.37485
707	TBX3	219682_s_at	0.033456	4.33E-04	4.39	0.15	0.46948
708	CPD	201940_at	0.033456	4.33E-04	4.39	0.15	1.14480
709	FRMD4A	225167_at	0.033457	4.34E-04	4.39	0.15	0.93206
710	C14orf135	235188_at	0.033457	4.34E-04	-4.39	0.15	-0.26938
711	MYLK	224823_at	0.033466	4.35E-04	4.39	0.14	1.33041
712	ZNF430	238614_x_at	0.033517	4.37E-04	-4.39	0.14	-0.55266
713		1556173_a_at	0.033517	4.37E-04	-4.39	0.14	-0.80860
714	QKI	214543_x_at	0.033517	4.38E-04	4.39	0.14	0.65036
715	TIMM16	218969_at	0.033556	4.39E-04	-4.38	0.14	-0.69464
716	MDK	209035_at	0.03359	4.40E-04	4.38	0.13	0.57952
717	ATP8A1	213106_at	0.033616	4.41E-04	-4.38	0.13	-0.99107
718	C2orf55	228067_at	0.033616	4.41E-04	4.38	0.13	0.77948
719	TP53I3	210609_s_at	0.03369	4.43E-04	4.38	0.13	1.09651
720	TIA1	201446_s_at	0.03369	4.44E-04	-4.38	0.13	-0.95595
721		214083_at	0.033992	4.48E-04	-4.37	0.12	-0.88587

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
722	MYADM	224920_x_at	0.034093	4.50E-04	4.37	0.11	0.99766
723	ZNF346	236267_at	0.034093	4.51E-04	-4.37	0.11	-0.81229
724	GTPBP8	221046_s_at	0.034155	4.52E-04	-4.37	0.11	-0.83113
725	IFITM3	212203_x_at	0.034171	4.54E-04	4.37	0.10	1.53477
726	KIRREL	225303_at	0.034171	4.54E-04	4.37	0.10	1.37093
727	WWTR1	202134_s_at	0.034171	4.55E-04	4.37	0.10	0.38767
728	CDV3	213548_s_at	0.034171	4.55E-04	4.37	0.10	1.12634
729	PTRF	1557938_s_at	0.034171	4.56E-04	4.37	0.10	0.73207
730	FLJ10357	220326_s_at	0.034263	4.58E-04	4.36	0.10	0.53826
731	HEPH	203903_s_at	0.034263	4.59E-04	4.36	0.09	1.41699
732	MARCKS	225897_at	0.034263	4.61E-04	4.36	0.09	1.68777
733	GALNT10	207357_s_at	0.034263	4.62E-04	4.36	0.09	0.81551
734	SCUBE2	219197_s_at	0.034263	4.62E-04	4.36	0.09	0.65198
735	LRP10	201412_at	0.034263	4.62E-04	4.36	0.09	0.93689
736	INTS10	229632_s_at	0.034263	4.63E-04	-4.36	0.09	-0.59292
737	DAG1	205417_s_at	0.034263	4.64E-04	4.36	0.08	0.92720
738	FAM108C1	225436_at	0.034263	4.64E-04	4.36	0.08	0.71845
739	PDLIM5	216804_s_at	0.034263	4.64E-04	4.36	0.08	0.97517
740	NFE2L2	1567014_s_at	0.034263	4.64E-04	4.36	0.08	0.60581
741	SERPINE1	202628_s_at	0.034263	4.64E-04	4.36	0.08	1.80135
742	C1orf163	222883_at	0.034263	4.65E-04	4.36	0.08	0.46664
743		1560327_at	0.034263	4.66E-04	4.36	0.08	0.75420
744	APH1A	1554417_s_at	0.034432	4.69E-04	4.35	0.07	1.02550
745	GPAA1	201618_x_at	0.034551	4.72E-04	4.35	0.07	0.54600
746	ALDH6A1	221588_x_at	0.034551	4.72E-04	4.35	0.07	1.00962
747	EMP2	225079_at	0.034551	4.72E-04	4.35	0.07	0.85898
748	TRIOBP	210276_s_at	0.034596	4.73E-04	4.35	0.07	1.40267
749	CSF1R	203104_at	0.034844	4.77E-04	4.34	0.06	1.92797
750	P2RX5	210448_s_at	0.035062	4.81E-04	-4.34	0.05	-1.12419
751		234997_x_at	0.035567	4.89E-04	-4.33	0.04	-1.12968
752	NLRX1	219680_at	0.035599	4.90E-04	4.33	0.03	0.58163
753	C1orf198	223063_at	0.035604	4.91E-04	4.33	0.03	0.99413
754	KDELR2	200699_at	0.035604	4.93E-04	4.33	0.03	1.65069
755	ZCCHC7	226496_at	0.035604	4.93E-04	-4.33	0.03	-0.91638
756	NRGN	204081_at	0.035604	4.93E-04	4.33	0.03	0.50535
757	VPS35	217727_x_at	0.035604	4.95E-04	4.33	0.02	0.62292
758	RAPGEF1	226389_s_at	0.035604	4.95E-04	4.33	0.02	0.66261
759	NPM1	200063_s_at	0.035604	4.95E-04	-4.33	0.02	-0.36318
760	TIA1	1554890_a_at	0.035604	4.96E-04	-4.33	0.02	-0.69958
761	MDM4	225740_x_at	0.035604	4.96E-04	-4.33	0.02	-1.01911
762	KDELR3	207265_s_at	0.035604	4.96E-04	4.33	0.02	1.23097
763	C20orf108	224693_at	0.035623	4.98E-04	4.33	0.02	0.68176
764	MSRB3	225782_at	0.035623	4.98E-04	4.32	0.02	1.85042
765	TMCC1	227112_at	0.035666	4.99E-04	4.32	0.02	0.73259
766	RNF138	239143_x_at	0.035715	5.00E-04	-4.32	0.01	-0.58447
767		239081_at	0.035754	5.02E-04	-4.32	0.01	-0.84667
768	CARD8	228641_at	0.035754	5.02E-04	-4.32	0.01	-0.84801
769	IQCK	213392_at	0.035755	5.03E-04	4.32	0.01	0.79628
770	CEBPD	203973_s_at	0.035828	5.05E-04	4.32	0.01	1.30337
771	HOXA5	213844_at	0.035901	5.06E-04	4.32	0.00	1.03425
772	LOC100131801	226006_at	0.035901	5.07E-04	-4.32	0.00	-0.76506
773	ARRB1	218832_x_at	0.036014	5.10E-04	4.31	0.00	0.87070
774	PPIC	204518_s_at	0.036014	5.10E-04	4.31	0.00	1.50886
775	MYO1B	212365_at	0.036033	5.11E-04	4.31	-0.01	0.91174
776	HINT3	228697_at	0.036097	5.12E-04	4.31	-0.01	1.00509
777	PTP4A1	200732_s_at	0.036275	5.16E-04	4.31	-0.01	1.05606
778	HSD17B7	220081_x_at	0.036278	5.16E-04	-4.31	-0.02	-0.90546
779	CTNND1	211240_x_at	0.036335	5.19E-04	4.31	-0.02	0.74397
780	BCKDK	202030_at	0.036335	5.19E-04	4.31	-0.02	1.15357
781	LRRC41	1555831_s_at	0.036335	5.19E-04	4.31	-0.02	1.18466
782	WISP1	206796_at	0.03661	5.24E-04	4.30	-0.03	1.40144
783	YIF1B	226437_at	0.03661	5.25E-04	4.30	-0.03	1.09293
784	PPARA	223438_s_at	0.03661	5.25E-04	4.30	-0.03	0.93721
785	GADD45B	209304_x_at	0.03673	5.27E-04	4.30	-0.04	0.76313
786	NCRNA00094	213788_s_at	0.037188	5.35E-04	4.29	-0.05	0.58544
787	CTSF	203657_s_at	0.037281	5.37E-04	4.29	-0.05	0.57562
788		214124_x_at	0.037281	5.38E-04	-4.29	-0.05	-0.61868

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
789	LOC100129122	239356_at	0.037281	5.38E-04	-4.29	-0.05	-0.40842
790	SIL1	218436_at	0.037447	5.41E-04	4.29	-0.06	0.67200
791	THBD	237252_at	0.037447	5.42E-04	4.28	-0.06	0.73532
792	ZNF254	242602_x_at	0.037514	5.43E-04	-4.28	-0.06	-0.63648
793	COL8A2	52651_at	0.037839	5.49E-04	4.28	-0.07	0.40550
794	FAM171B	227370_at	0.037877	5.50E-04	4.28	-0.08	0.95920
795	CLEC4G	1559065_a_at	0.037884	5.51E-04	4.28	-0.08	1.88315
796	TEAD2	226408_at	0.037884	5.52E-04	4.28	-0.08	0.79559
797	MS4A1	231418_at	0.038026	5.54E-04	-4.27	-0.08	-1.67144
798	SLCO2A1	204368_at	0.038033	5.57E-04	4.27	-0.09	1.61484
799		217449_at	0.038033	5.57E-04	-4.27	-0.09	-0.32686
800	AQP1	209047_at	0.038033	5.58E-04	4.27	-0.09	2.08361
801	RTKN	225150_s_at	0.038033	5.58E-04	4.27	-0.09	0.37584
802	LDOC1L	223228_at	0.038033	5.60E-04	4.27	-0.09	1.07653
803	FBLIM1	225258_at	0.038033	5.60E-04	4.27	-0.09	1.10747
804	FKBP3	218003_s_at	0.038033	5.60E-04	-4.27	-0.09	-0.53713
805	AGTRAP	1555736_a_at	0.038033	5.60E-04	4.27	-0.09	1.40821
806	C19orf43	230213_at	0.038156	5.63E-04	-4.27	-0.10	-0.55467
807	SLC35C1	222647_at	0.038156	5.63E-04	4.27	-0.10	0.42724
808	ZFAND3	222493_s_at	0.038164	5.64E-04	4.27	-0.10	0.60623
809	RBPMS	207836_s_at	0.038222	5.66E-04	4.26	-0.10	0.98825
810	TBC1D12	221858_at	0.038222	5.66E-04	4.26	-0.10	0.65871
811	CADPS2	219572_at	0.038277	5.68E-04	4.26	-0.11	0.86561
812	TTLL12	1552257_a_at	0.038568	5.73E-04	4.26	-0.11	0.66614
813	KCNE4	1552508_at	0.038599	5.74E-04	4.26	-0.12	0.75158
814	STXBP1	202260_s_at	0.038609	5.75E-04	4.26	-0.12	1.24889
815	TFPI	213258_at	0.038613	5.76E-04	4.26	-0.12	1.93688
816	ASPH	210896_s_at	0.038617	5.76E-04	4.26	-0.12	1.25136
817	LOC400043	226582_at	0.038755	5.79E-04	4.25	-0.12	0.75115
818	SLCO2B1	203473_at	0.038755	5.80E-04	4.25	-0.13	1.26366
819	FEM1C	213341_at	0.038757	5.81E-04	4.25	-0.13	0.92246
820	OCRL	203446_s_at	0.03877	5.82E-04	4.25	-0.13	0.55120
821	CATSPER2	1561405_s_at	0.03877	5.82E-04	-4.25	-0.13	-0.31201
822	DIRC2	226026_at	0.039021	5.88E-04	4.25	-0.14	1.10364
823	VTI1B	225928_at	0.039021	5.89E-04	4.25	-0.14	0.74047
824	TAF1D	218750_at	0.039021	5.90E-04	-4.24	-0.14	-1.42163
825	NLRP3	207075_at	0.039021	5.90E-04	4.24	-0.14	0.74364
826	Sep-08	208999_at	0.039021	5.90E-04	4.24	-0.14	1.14351
827		1562412_at	0.039021	5.91E-04	-4.24	-0.14	-0.50777
828	STEAP3	218424_s_at	0.039021	5.91E-04	4.24	-0.14	1.20765
829	TFPI	209676_at	0.039021	5.92E-04	4.24	-0.14	0.90221
830	OLFML2A	213075_at	0.039021	5.92E-04	4.24	-0.15	1.25239
831	ALOX15	207328_at	0.039137	5.95E-04	4.24	-0.15	1.77807
832	LOC100131845///IGHV4-31///IGHA1	234792_x_at	0.039154	5.96E-04	4.24	-0.15	1.21481
833	SMC3	1556925_at	0.039159	5.97E-04	-4.24	-0.15	-0.30973
834	KCNK6	223658_at	0.039159	5.97E-04	4.24	-0.15	0.80695
835	FNDC3B	222692_s_at	0.039159	5.98E-04	4.24	-0.15	1.11460
836	LAMB2	216264_s_at	0.039257	6.01E-04	4.24	-0.16	0.88694
837	PDLIM5	203243_s_at	0.039257	6.01E-04	4.24	-0.16	1.88572
838	TM9SF1	209149_s_at	0.039257	6.02E-04	4.24	-0.16	1.16215
839	SNHG6	225547_at	0.039299	6.03E-04	-4.23	-0.16	-0.90430
840	LOC644617	221235_s_at	0.039299	6.04E-04	4.23	-0.16	0.71088
841		225269_s_at	0.039356	6.05E-04	4.23	-0.17	0.65760
842	LOC439949	232001_at	0.039361	6.06E-04	-4.23	-0.17	-1.06936
843	TMIGD2	244716_x_at	0.039388	6.07E-04	-4.23	-0.17	-0.88167
844	LOC100302652///ASB3///GPR75	232515_at	0.03976	6.15E-04	-4.22	-0.18	-0.53288
845	PSEN1	226577_at	0.03976	6.15E-04	4.22	-0.18	0.80312
846	PECAM1	208983_s_at	0.03976	6.15E-04	4.22	-0.18	1.80033
847	UPK3B	206658_at	0.03976	6.17E-04	-4.22	-0.18	-0.43321
848	SDF4	224472_x_at	0.03976	6.17E-04	4.22	-0.18	0.97219
849	CPD	201943_s_at	0.03976	6.18E-04	4.22	-0.18	1.15344
850	RAB34	1555630_a_at	0.03976	6.18E-04	4.22	-0.19	1.77694
851	SESTD1	226763_at	0.039847	6.20E-04	4.22	-0.19	0.77094
852	ICMT	201611_s_at	0.039847	6.21E-04	4.22	-0.19	1.19786

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
853	C11orf76	224139_at	0.039871	6.22E-04	-4.22	-0.19	-0.35876
854	CTNS	36566_at	0.039996	6.25E-04	4.22	-0.19	0.94098
855	RLTPR	227218_at	0.040078	6.27E-04	-4.22	-0.20	-0.44060
856	STX4	203530_s_at	0.040118	6.28E-04	4.21	-0.20	1.02897
857	SIRT5	229112_at	0.040155	6.30E-04	-4.21	-0.20	-0.41051
858	SH2D1A	211210_x_at	0.040155	6.30E-04	-4.21	-0.20	-1.41674
859	KCTD12	212188_at	0.040155	6.31E-04	4.21	-0.21	0.95007
860	LMNA	212086_x_at	0.040155	6.32E-04	4.21	-0.21	0.88085
861	CALU	200755_s_at	0.040155	6.33E-04	4.21	-0.21	1.34391
862	RND2	213467_at	0.040155	6.34E-04	-4.21	-0.21	-0.41543
863	PIR	207469_s_at	0.040155	6.34E-04	4.21	-0.21	0.88090
864	GAS6	1598_g_at	0.040184	6.35E-04	4.21	-0.21	0.75605
865	ZNF423	214761_at	0.040315	6.38E-04	4.21	-0.22	1.55901
866	C1QTNF1	220975_s_at	0.040315	6.39E-04	4.21	-0.22	0.88142
867		227727_at	0.040357	6.40E-04	4.21	-0.22	1.01498
868	ACAD9	224160_s_at	0.040395	6.42E-04	4.20	-0.22	0.58080
869		244075_at	0.040395	6.42E-04	-4.20	-0.22	-1.01682
870	FOXC1	1553613_s_at	0.040399	6.44E-04	4.20	-0.22	1.28587
871	SELP	206049_at	0.040399	6.44E-04	4.20	-0.22	1.40873
872	LSM4	212924_s_at	0.040399	6.45E-04	-4.20	-0.22	-0.48894
873	GPR124	65718_at	0.040399	6.45E-04	4.20	-0.23	0.83645
874		227184_at	0.040399	6.46E-04	4.20	-0.23	1.15782
875	GGCX	235413_at	0.040429	6.48E-04	4.20	-0.23	0.56185
876	TRIM2	202341_s_at	0.040429	6.48E-04	4.20	-0.23	0.69978
877	PDIA3	227033_at	0.040429	6.48E-04	4.20	-0.23	0.84889
878	SAE1	241185_at	0.040434	6.49E-04	-4.20	-0.23	-0.45017
879	DCBLD2	224911_s_at	0.040464	6.51E-04	4.20	-0.23	1.32095
880		232710_at	0.040474	6.51E-04	-4.20	-0.23	-0.69623
881	MS4A7	224358_s_at	0.040647	6.56E-04	4.19	-0.24	2.45217
882	GPR176	227846_at	0.040647	6.56E-04	4.19	-0.24	0.58377
883	FLII	212025_s_at	0.04067	6.57E-04	4.19	-0.24	1.13010
884	TBXAS1	208130_s_at	0.040672	6.58E-04	4.19	-0.24	1.08248
885	RNASEH2B	215040_at	0.040672	6.59E-04	-4.19	-0.24	-0.67966
886		230449_x_at	0.040672	6.61E-04	-4.19	-0.25	-0.50978
887	LAPTM4B	214039_s_at	0.040672	6.62E-04	4.19	-0.25	1.69716
888	P4HB	200654_at	0.040672	6.62E-04	4.19	-0.25	1.38657
889	CTNS	204925_at	0.040672	6.62E-04	4.19	-0.25	1.43333
890	GZF1	225884_s_at	0.040672	6.62E-04	4.19	-0.25	0.73137
891	SH3BP4	222258_s_at	0.040901	6.67E-04	4.19	-0.26	1.19720
892	FAM127B	217948_at	0.040947	6.68E-04	4.19	-0.26	1.00404
893	LMBR1	224410_s_at	0.040947	6.70E-04	4.18	-0.26	0.82889
894	EFEMP1	201842_s_at	0.040947	6.70E-04	4.18	-0.26	2.32422
895	FGFR1OP2	236808_at	0.040947	6.70E-04	-4.18	-0.26	-0.88608
896	HDLBP	221767_x_at	0.040973	6.71E-04	4.18	-0.26	1.07834
897	B3GALTL	227100_at	0.041043	6.74E-04	4.18	-0.27	0.54948
898	DMD	203881_s_at	0.041043	6.74E-04	4.18	-0.27	0.98105
899		235821_at	0.041054	6.75E-04	4.18	-0.27	1.52425
900		230980_x_at	0.041054	6.76E-04	-4.18	-0.27	-0.87726
901	NETO1	1552736_a_at	0.041054	6.77E-04	-4.18	-0.27	-0.40033
902	ATP6V1A	201971_s_at	0.041169	6.79E-04	4.18	-0.27	1.22810
903	ADRBK2	204184_s_at	0.041425	6.84E-04	4.17	-0.28	0.43207
904	FNBP1L	215017_s_at	0.041483	6.86E-04	4.17	-0.28	0.83766
905	AKAP12	210517_s_at	0.041562	6.90E-04	4.17	-0.29	1.86963
906	SEL1L	230265_at	0.041562	6.90E-04	4.17	-0.29	1.01191
907	LEPROT	202378_s_at	0.041562	6.90E-04	4.17	-0.29	1.18731
908	FNDC3A	215910_s_at	0.041562	6.91E-04	4.17	-0.29	0.36692
909	AXIN2	222695_s_at	0.041562	6.92E-04	-4.17	-0.29	-0.54695
910	FGFR1	207822_at	0.041562	6.92E-04	-4.17	-0.29	-0.40135
911	PAFAH1B1	200813_s_at	0.041575	6.93E-04	4.17	-0.29	0.77379
912	TBC1D9B	212054_x_at	0.041575	6.93E-04	4.17	-0.29	0.65719
913	PON2	210830_s_at	0.041596	6.95E-04	4.17	-0.30	1.41795
914	GUCY1A3	229530_at	0.041596	6.95E-04	4.17	-0.30	1.56360
915		230599_at	0.041614	6.97E-04	-4.17	-0.30	-1.34701
916	ZNF443	205928_at	0.041614	6.97E-04	-4.17	-0.30	-0.67379
917	PTGER1	214391_x_at	0.041621	6.99E-04	-4.16	-0.30	-0.56740
918	PTEN	225363_at	0.041621	7.00E-04	4.16	-0.30	0.47087
919	NAGA	202943_s_at	0.041621	7.00E-04	4.16	-0.30	1.49995
920	GPR56	212070_at	0.041621	7.01E-04	4.16	-0.30	0.74150
921	MALL	209373_at	0.041621	7.02E-04	4.16	-0.30	1.10485

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
922	IL13RA1	210904_s_at	0.041621	7.02E-04	4.16	-0.30	1.70643
923		239131_at	0.041702	7.05E-04	-4.16	-0.31	-0.58305
924	SPTLC1	202278_s_at	0.041702	7.05E-04	4.16	-0.31	0.68724
925	GTF2H2D/// GTF2H2C/// GTF2H2B/// GTF2H2	221540_x_at	0.041702	7.06E-04	-4.16	-0.31	-0.61468
926	PDIA6	208639_x_at	0.041702	7.07E-04	4.16	-0.31	1.15862
927	TAX1BP3	215464_s_at	0.041702	7.07E-04	4.16	-0.31	1.46065
928	ASPH	224996_at	0.041746	7.09E-04	4.16	-0.31	1.46610
929	RPL7	239493_at	0.041958	7.13E-04	-4.15	-0.32	-0.60751
930	STAT3	208991_at	0.041958	7.14E-04	4.15	-0.32	1.38419
931	MPZL1	210594_x_at	0.042213	7.19E-04	4.15	-0.33	0.60228
932	CCDC59	222792_s_at	0.042213	7.20E-04	-4.15	-0.33	-0.77972
933	LPHN2	206953_s_at	0.042248	7.21E-04	4.15	-0.33	0.89054
934	SGPL1	212322_at	0.042259	7.23E-04	4.15	-0.33	1.75072
935	SGCB	228584_at	0.042259	7.23E-04	4.15	-0.33	0.76161
936	SIX1	228347_at	0.042259	7.24E-04	4.15	-0.33	0.96750
937	LOC440288	238511_at	0.042259	7.24E-04	-4.15	-0.33	-0.80590
938	SLC16A3	202856_s_at	0.042259	7.26E-04	4.15	-0.34	2.11019
939	CES2	209667_at	0.042259	7.26E-04	4.15	-0.34	0.59497
940	PLOD3	202185_at	0.042259	7.27E-04	4.15	-0.34	1.12046
941	APBB2	212985_at	0.042322	7.28E-04	4.14	-0.34	1.11089
942	DAB2	201278_at	0.042324	7.29E-04	4.14	-0.34	1.41625
943	AGPS	225108_at	0.042324	7.30E-04	4.14	-0.34	0.73722
944	FGFR1	211535_s_at	0.042476	7.33E-04	4.14	-0.35	0.79203
945	RASL12	219167_at	0.042527	7.36E-04	4.14	-0.35	0.68969
946	SRSF11	213742_at	0.042527	7.36E-04	-4.14	-0.35	-1.51232
947	SSPN	226932_at	0.042615	7.38E-04	4.14	-0.35	1.33139
948	PPAP2A	209147_s_at	0.042711	7.41E-04	4.14	-0.35	1.52277
949	SLC25A43	1557411_s_at	0.042906	7.45E-04	4.13	-0.36	1.25584
950	POR	208928_at	0.042906	7.46E-04	4.13	-0.36	1.08216
951	SLCO2B1	203472_s_at	0.042967	7.47E-04	4.13	-0.36	1.09369
952	FDFT1	241954_at	0.042997	7.49E-04	-4.13	-0.37	-0.65170
953	CHRDL1	209763_at	0.042997	7.51E-04	4.13	-0.37	2.37080
954	FES	205418_at	0.042997	7.52E-04	4.13	-0.37	0.99814
955	MTUS1	212096_s_at	0.042997	7.52E-04	4.13	-0.37	1.28373
956	GTSE1	211040_x_at	0.042997	7.52E-04	-4.13	-0.37	-0.85186
957		233716_at	0.042997	7.53E-04	-4.13	-0.37	-0.30187
958	SPTLC2	225095_at	0.043159	7.56E-04	4.13	-0.37	1.09321
959	POLH	233852_at	0.043365	7.61E-04	-4.12	-0.38	-0.53818
960	INMT	224061_at	0.0436	7.66E-04	4.12	-0.39	1.08039
961	NFKBIA	201502_s_at	0.043663	7.69E-04	4.12	-0.39	0.79837
962	MARCKS	201669_s_at	0.043663	7.69E-04	4.12	-0.39	1.40722
963	PEPD	202108_at	0.043663	7.69E-04	4.12	-0.39	0.84768
964	C5orf34	229886_at	0.043667	7.71E-04	-4.12	-0.39	-0.63004
965	SLC2A14/// SLC2A3	216236_s_at	0.043667	7.71E-04	4.12	-0.39	0.87871
966	PWWP2B	238046_x_at	0.043711	7.72E-04	-4.12	-0.39	-0.37729
967	TOLLIP	217930_s_at	0.04375	7.74E-04	4.12	-0.40	0.86476
968	CYBRD1	222453_at	0.043836	7.76E-04	4.11	-0.40	0.93710
969	KCND3	215014_at	0.043836	7.77E-04	4.11	-0.40	0.39045
970	HSPB11	215691_x_at	0.043837	7.78E-04	-4.11	-0.40	-0.73457
971	PVRL2	225418_at	0.043837	7.79E-04	4.11	-0.40	0.72950
972	LOC100128 074	228203_at	0.043971	7.82E-04	-4.11	-0.41	-0.43042
973	CCDC163P	236900_x_at	0.044265	7.88E-04	-4.11	-0.41	-0.72876
974		1558048_x_at	0.044265	7.89E-04	-4.11	-0.41	-3.66477
975	COL6A5	1553834_at	0.044265	7.89E-04	4.11	-0.41	2.08746
976	C20orf160	231991_at	0.044265	7.90E-04	4.11	-0.42	0.80600
977		227061_at	0.044351	7.93E-04	4.11	-0.42	2.05333
978	EPS8	202609_at	0.044415	7.96E-04	4.10	-0.42	1.87325
979	RPL18P11	222297_x_at	0.044415	7.97E-04	-4.10	-0.42	-0.38515
980	SGPL1	212321_at	0.044415	7.97E-04	4.10	-0.42	1.49785
981	PLXND1	38671_at	0.044415	7.98E-04	4.10	-0.42	1.10655
982	CISH	223961_s_at	0.044415	7.98E-04	4.10	-0.42	1.33105
983		232496_at	0.044429	7.99E-04	-4.10	-0.43	-0.32793
984	CLEC11A	205131_x_at	0.044556	8.02E-04	4.10	-0.43	0.76014
985	BGN	201262_s_at	0.044617	8.04E-04	4.10	-0.43	0.62513

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
986		232970_at	0.044617	8.06E-04	-4.10	-0.43	-0.47986
987	BSCL2	208906_at	0.044617	8.06E-04	4.10	-0.43	1.16053
988	PLAUR	210845_s_at	0.044617	8.07E-04	4.10	-0.43	1.37404
989	PARD6G	227204_at	0.044617	8.08E-04	4.10	-0.44	0.72342
990	SARNP	229069_at	0.044617	8.08E-04	-4.10	-0.44	-0.79063
991	P4HA2	202733_at	0.044617	8.09E-04	4.10	-0.44	2.21085
992	PRSS23	202458_at	0.044617	8.10E-04	4.10	-0.44	1.63929
993	EFEMP1	201843_s_at	0.044622	8.10E-04	4.09	-0.44	2.00833
994	DCBLD2	230175_s_at	0.044701	8.13E-04	4.09	-0.44	0.92747
995	FGFR1OP2	233898_s_at	0.044702	8.14E-04	-4.09	-0.44	-0.77343
996	COL4A2	211964_at	0.0449	8.18E-04	4.09	-0.45	2.57163
997	SLIT2	230130_at	0.045002	8.21E-04	4.09	-0.45	1.07821
998	GUCY1B3	211555_s_at	0.045002	8.22E-04	4.09	-0.45	0.74285
999	SFXN1	218392_x_at	0.045002	8.22E-04	-4.09	-0.45	-1.20094
1000	GFPT1	202721_s_at	0.045059	8.27E-04	4.08	-0.46	0.63209
1001	LRCH4	37796_at	0.045059	8.28E-04	-4.08	-0.46	-0.57108
1002	USP33	214843_s_at	0.045059	8.28E-04	-4.08	-0.46	-0.87469
1003	CALD1	212077_at	0.045059	8.29E-04	4.08	-0.46	1.75811
1004	ANAPC4	226917_s_at	0.045059	8.29E-04	-4.08	-0.46	-0.79771
1005		1556297_a_at	0.045059	8.30E-04	-4.08	-0.46	-0.32685
1006	ARHGEF10L	221656_s_at	0.045059	8.31E-04	4.08	-0.46	0.80198
1007	KLF2	226645_at	0.045059	8.31E-04	-4.08	-0.46	-0.36973
1008	RNF185	224750_at	0.045059	8.31E-04	4.08	-0.46	0.76875
1009	CREBL2	201988_s_at	0.045059	8.32E-04	4.08	-0.46	1.27767
1010		240595_at	0.045127	8.34E-04	-4.08	-0.47	-0.55827
1011	DAP	201095_at	0.045127	8.35E-04	4.08	-0.47	0.99144
1012	DNAJB4	203811_s_at	0.045127	8.35E-04	4.08	-0.47	0.47665
1013		230598_at	0.045144	8.36E-04	-4.08	-0.47	-1.04731
1014	MCAM	211340_s_at	0.045151	8.40E-04	4.08	-0.47	1.07281
1015	FAM111A	239368_at	0.045151	8.41E-04	-4.08	-0.47	-0.54737
1016	GIGYF2	212260_at	0.045151	8.41E-04	4.08	-0.47	0.78056
1017	SLCO2B1	211557_x_at	0.045151	8.41E-04	4.08	-0.47	1.03221
1018	C11orf31	1557801_x_at	0.045151	8.41E-04	-4.08	-0.47	-0.49384
1019	OCRL	208316_s_at	0.045151	8.42E-04	4.08	-0.47	0.35153
1020	LOC643733	240890_at	0.045151	8.42E-04	-4.08	-0.48	-1.64382
1021	WIPI1	203827_at	0.045522	8.50E-04	4.07	-0.48	1.42805
1022	GALNT2	217788_s_at	0.045522	8.51E-04	4.07	-0.48	1.33054
1023	NET1	201830_s_at	0.045522	8.52E-04	4.07	-0.49	1.39469
1024	ABL2	231907_at	0.045534	8.54E-04	4.07	-0.49	1.03604
1025	FAM86B1	65585_at	0.045534	8.55E-04	4.07	-0.49	0.55531
1026	KCNE4	1552507_at	0.045534	8.55E-04	4.07	-0.49	1.32324
1027	QKI	212262_at	0.045534	8.56E-04	4.07	-0.49	1.37609
1028	CSRP1	200621_at	0.045534	8.56E-04	4.07	-0.49	0.76464
1029	GALNT3	203397_s_at	0.045648	8.59E-04	-4.07	-0.49	-0.66263
1030	ASPRV1	240017_at	0.04568	8.61E-04	-4.07	-0.50	-0.40740
1031	ANG	205141_at	0.04568	8.62E-04	4.07	-0.50	0.62974
1032	SLC35E1	222263_at	0.04568	8.62E-04	4.07	-0.50	0.73432
1033	CENPK	222848_at	0.045756	8.66E-04	-4.06	-0.50	-1.23457
1034	ERG	213541_s_at	0.045756	8.67E-04	4.06	-0.50	0.90407
1035	SFI1	214402_s_at	0.045756	8.67E-04	-4.06	-0.50	-0.57672
1036	TRIO	209011_at	0.045756	8.68E-04	4.06	-0.50	0.44602
1037		243144_at	0.045756	8.68E-04	-4.06	-0.50	-0.39313
1038		227929_at	0.045756	8.69E-04	4.06	-0.50	0.61332
1039	CALCRL	206331_at	0.045756	8.70E-04	4.06	-0.51	1.16930
1040	RNF24	204669_s_at	0.045756	8.70E-04	4.06	-0.51	0.86679
1041	FCRLB	238452_at	0.04578	8.72E-04	4.06	-0.51	0.70758
1042	COL5A2	221730_at	0.04587	8.74E-04	4.06	-0.51	3.05045
1043	CLK1	214683_s_at	0.045958	8.77E-04	-4.06	-0.51	-1.01097
1044	NCRNA00106	238104_at	0.045958	8.78E-04	-4.06	-0.51	-0.63551
1045	KAZ	213478_at	0.045958	8.78E-04	4.06	-0.51	0.78762
1046	OSBPL1A	208158_s_at	0.046122	8.82E-04	4.05	-0.52	0.79143
1047	DMPK	217066_s_at	0.046133	8.84E-04	-4.05	-0.52	-0.38643
1048	ZFPL1	209428_s_at	0.046133	8.84E-04	4.05	-0.52	0.47735
1049	TM4SF1	215034_s_at	0.046133	8.85E-04	4.05	-0.52	1.46268
1050	TECPR2	204308_s_at	0.046279	8.91E-04	4.05	-0.53	0.68863
1051	DCP2	244777_at	0.046279	8.91E-04	-4.05	-0.53	-0.86906
1052	TPSB2	207134_x_at	0.046279	8.91E-04	4.05	-0.53	1.68695

No.	Gene*	Probe ID**	Adj. p value	P value	t	B	Log FC
1053	UACA	223279_s_at	0.046279	8.92E-04	4.05	-0.53	1.06752
1054	PRELP	228224_at	0.046279	8.92E-04	4.05	-0.53	1.26263
1055	GANAB	214626_s_at	0.046348	8.95E-04	4.05	-0.53	0.64013
1056	CCDC47	222432_s_at	0.046348	8.97E-04	4.05	-0.53	1.04044
1057	C1orf228	238365_s_at	0.046348	8.98E-04	-4.05	-0.53	-1.01107
1058	LDOC1	204454_at	0.046348	8.98E-04	4.05	-0.54	0.76728
1059		237034_at	0.046348	8.98E-04	-4.05	-0.54	-0.54217
1060	LOC100287081	228231_at	0.046348	8.99E-04	4.05	-0.54	0.82231
1061	WBP5	217975_at	0.046474	9.02E-04	4.04	-0.54	1.75601
1062	USP2	230965_at	0.046474	9.03E-04	-4.04	-0.54	-0.41630
1063	AMFR	202204_s_at	0.046474	9.04E-04	4.04	-0.54	0.52031
1064	CREBL2	201989_s_at	0.046631	9.07E-04	4.04	-0.54	0.67683
1065	VPS35	222388_s_at	0.046739	9.12E-04	4.04	-0.55	0.62900
1066		227623_at	0.046739	9.12E-04	4.04	-0.55	1.26562
1067	SLC24A6	218749_s_at	0.046739	9.12E-04	4.04	-0.55	0.89281
1068	CCDC88C	231288_at	0.04694	9.17E-04	-4.04	-0.55	-0.50800
1069	FLJ33630	235628_x_at	0.046961	9.18E-04	-4.04	-0.56	-0.47257
1070	C8orf58	227263_at	0.047045	9.22E-04	4.03	-0.56	0.62535
1071	C8orf59	226165_at	0.047045	9.22E-04	-4.03	-0.56	-0.97654
1072	RALBP1	202845_s_at	0.047045	9.25E-04	4.03	-0.56	0.91530
1073	RPL31	221593_s_at	0.047045	9.25E-04	-4.03	-0.56	-1.05920
1074	TRIOBP	202795_x_at	0.047045	9.26E-04	4.03	-0.56	0.56788
1075	SH2B3	203320_at	0.047045	9.26E-04	4.03	-0.56	1.39831
1076	EHBP1L1	91703_at	0.047045	9.26E-04	4.03	-0.56	1.09475
1077	MS4A4A	224357_s_at	0.047173	9.29E-04	4.03	-0.57	1.52256
1078	CRTAP	1555889_a_at	0.047408	9.35E-04	4.03	-0.57	1.18669
1079	SERINC3	221473_x_at	0.047416	9.36E-04	4.03	-0.57	1.20288
1080	CLDN11	228335_at	0.047508	9.39E-04	4.03	-0.58	1.91120
1081	ZAK	223519_at	0.047508	9.39E-04	4.03	-0.58	1.19771
1082		232853_at	0.047527	9.41E-04	-4.02	-0.58	-0.40602
1083	CFHR2	206910_x_at	0.047553	9.42E-04	4.02	-0.58	0.72168
1084	KCNJ8	205303_at	0.047706	9.46E-04	4.02	-0.58	1.54215
1085	APLP2	208248_x_at	0.047754	9.48E-04	4.02	-0.59	0.98665
1086	ATHL1	219359_at	0.048208	9.58E-04	-4.02	-0.60	-1.19151
1087	C1orf85	225401_at	0.048338	9.61E-04	4.01	-0.60	1.53553
1088	PPARG	208510_s_at	0.04865	9.68E-04	4.01	-0.61	0.86096
1089	ALKBH5	1553101_a_at	0.048693	9.70E-04	4.01	-0.61	1.11688
1090	RPS8	200858_s_at	0.048693	9.71E-04	-4.01	-0.61	-0.50571
1091	NCSTN	208759_at	0.048698	9.72E-04	4.01	-0.61	0.68925
1092	RBMS1	207266_x_at	0.048825	9.75E-04	4.01	-0.61	1.62089
1093	FZD5	221245_s_at	0.048973	9.81E-04	4.00	-0.62	1.07337
1094	PRKCI	209678_s_at	0.048973	9.81E-04	4.00	-0.62	0.92949
1095	ADAMTS1	222162_s_at	0.048973	9.82E-04	4.00	-0.62	1.38996
1096	RNH1	206050_s_at	0.048973	9.82E-04	4.00	-0.62	1.64853
1097	MATK	206267_s_at	0.049132	9.86E-04	4.00	-0.62	0.65930
1098	EPHB2	211165_x_at	0.049132	9.87E-04	4.00	-0.62	0.61647
1099	LOC100288263///LOC644617	225653_at	0.049156	9.88E-04	4.00	-0.62	0.41504
1100	PECAM1	208981_at	0.049164	9.89E-04	4.00	-0.63	1.19427
1101	CFI	1555564_a_at	0.049164	9.92E-04	4.00	-0.63	1.01859
1102	CYB5R3	1554574_a_at	0.049164	9.92E-04	4.00	-0.63	0.89009
1103	TPSAB1	210084_x_at	0.049164	9.93E-04	4.00	-0.63	1.52044
1104	PDLIM5	203242_s_at	0.049164	9.94E-04	4.00	-0.63	0.71526
1105	DOLK	204488_at	0.049164	9.94E-04	4.00	-0.63	0.74203
1106	SEMA6D	226492_at	0.049194	9.98E-04	4.00	-0.63	1.20226
1107	MCAM	210869_s_at	0.049194	9.99E-04	4.00	-0.63	1.09217
1108	UBE2QL1	226612_at	0.049194	9.99E-04	4.00	-0.64	1.14961
1109	ACE	227463_at	0.049194	9.99E-04	4.00	-0.64	1.69530
1110	ZNF320	241704_x_at	0.049194	1.00E-03	-4.00	-0.64	-0.42830
1111	SMARCA1	203875_at	0.049194	1.00E-03	3.99	-0.64	0.79801
1112	GBGT1	231780_at	0.049194	1.00E-03	3.99	-0.64	0.72464
1113		235986_at	0.049194	1.00E-03	-3.99	-0.64	-0.45048
1114	KDELR1	200922_at	0.049194	1.00E-03	3.99	-0.64	1.50659
1115	FCRL1	243968_x_at	0.049194	1.00E-03	-3.99	-0.64	-1.87102
1116	TAPT1	226735_at	0.049194	1.00E-03	-3.99	-0.64	-0.42542
1117	CDKN1A	202284_s_at	0.049194	1.01E-03	3.99	-0.64	1.39461
1118	ETV5	203349_s_at	0.049221	1.01E-03	3.99	-0.64	0.57709

No.	*Gene**	*Probe ID***	*Adj. p value*	*P value*	*t*	*B*	*Log FC*
1119	STAP1	220059_at	0.049241	1.01E-03	-3.99	-0.64	-1.59671
1120	PDIA6	207668_x_at	0.049483	1.01E-03	3.99	-0.65	1.11859
1121	MYO10	201976_s_at	0.049483	1.01E-03	3.99	-0.65	1.27823
1122	ITGB5	214020_x_at	0.049685	1.02E-03	3.99	-0.65	0.72844
1123	ATP5L	208745_at	0.049685	1.02E-03	-3.99	-0.65	-0.73769
1124	RNF19B	213038_at	0.049693	1.02E-03	3.99	-0.66	1.30812
1125	AUTS2	212599_at	0.049693	1.02E-03	3.99	-0.66	1.32327
1126	AOX1	205083_at	0.049716	1.02E-03	3.98	-0.66	1.37931
1127	CHD2	228999_at	0.049826	1.03E-03	-3.98	-0.66	-1.18763
1128	BAIAP2L2	228876_at	0.049826	1.03E-03	-3.98	-0.66	-0.49610
1129	TTC39B	242477_at	0.049873	1.03E-03	-3.98	-0.66	-0.97680
1130	FILIP1L	1554966_a_at	0.04997	1.03E-03	3.98	-0.67	1.57994
1131	TMBIM1	217730_at	0.04997	1.03E-03	3.98	-0.67	1.05170
1132	COL15A1	203477_at	0.04997	1.04E-03	3.98	-0.67	2.82957
1133	Sep-11	201308_s_at	0.04997	1.04E-03	3.98	-0.67	0.38785
1134	SH2D1A	211211_x_at	0.04997	1.04E-03	-3.98	-0.67	-1.34832
1135	KIF1B	225878_at	0.04997	1.04E-03	3.98	-0.67	1.00363
1136	GPAA1	215690_x_at	0.04997	1.04E-03	3.98	-0.67	0.51529
1137	NANS	218189_s_at	0.04997	1.04E-03	3.98	-0.67	0.72916
1138	COL18A1	209082_s_at	0.04997	1.04E-03	3.98	-0.67	1.34108

* Gene symbol as approved by the HUGO gene nomenclature committee (HGNC)

** Probe Set ID's from Affymetrix GeneChip Human Genome U133 Plus 2.0 array, from Affymetrix Inc, Santa Clara, USA

EXAMPLE A

Supervised learning algorithms and their application towards predictive modelling and patient stratification in a cohort of chemotherapy-sensitive/resistant Hodgkin's Lymphoma patients

Abstract

Background

The development of rationalised prognosticators for triaging of Hodgkin's Lymphoma (HL) patients into chemotherapy sensitive and resistant groups prior to treatment would have a significant impact upon the clinical management of these individuals. Gene Expression Omnibus (GEO) is a data repository of DNA microarray experiments varying in number, conditions and tissue types. It thus represents an excellent resource for biomarker discovery programmes and model datasets in which to construct and validate potential classification algorithms. Artificial neural networks (ANN) have been shown to be powerful tools that can develop classifiers capable of generalising well to unseen data. They may therefore have clinical utility as prognosticators for chemotherapy response. This study examines expression data taken from the microarray analysis of 130 HL patient core biopsies (pre-treatment) whose clinical outcome to chemotherapy was subsequently determined. The development of ANN classifiers for prognostication was explored.

Results

GSE17920 expression series was parsed by GEO2R into data structures enabling statistical interrogation by LIMMA (Linear Models for Microarray Analysis) of 92 sensitive and 38 resistant microarray analyses from HL pre-treatment core biopsies. Sixteen differentially expressed probe sets (biomarkers) were identified; false discovery rate (FDR) ≤ 5%. These candidates were used to develop binary classifiers of either chemo-sensitive or chemo-resistance. 30% of samples were used for training (n=39), 10% for testing (n=13) and 60% of samples (n=78) as an independent validation dataset. Classifiers were developed in which 100%, 92% and 91% of training, testing and validation samples were correctly assigned with ROC (Receiver Operating Characteristic) plots producing an AUC (Area Under the Curve) of 0.926.

Sixteen outliers were identified that had consistently poor levels of prediction. These samples were separated from the main cohort and two groups consisting of outliers (Group 16) and the remaining samples (Group 114) were constructed. Differential gene expression between chemo-sensitive and chemo-resistant samples within Group 16 and Group 114 was determined by resubmission to GEO2R and LIMMA. A total of 1138 (Table C) and 5344 (Table A) probe sets(biomarkers) for Group 16 and Group 114, respectively, were identified as being differentially expressed (FDR ≤ 5%).

The original 16 gene probe set (Table B; identified from using all 130 samples) remained significantly different for Group 114 (FDR ≤ 5%) and models could be produced in which all predictions (n=114) were correctly classified. For Group 16 only 1/16 of the originally identified gene probe sets remained significant. Using an alternative panel taken from the 1138 significant probe set identified as being significant (FDR ≤ 5%), classifiers were constructed in which all outlier samples (n=16) were accurately assigned to their respective chemo-sensitive or chemo-resistant groups.

Conclusion

ANN can be developed into binary classifiers capable of assigning pre-treatment HL patient expression profiles into either chemo-sensitive or chemo-resistant categories. Sampling with replacement strategies enable outliers to be identified that may indicative of genetic sub-groups. Isolating outliers from the main cohort of samples combined with re-training can improve predictive performance for both outlier and non-outlier groups regarding the probability of chemo-response.

Background

From a therapeutic perspective the management of patients with Hodgkin's Lymphoma (HL) represents a challenging paradigm. As observed in other cancer groups, this is primarily manifested as a variation in the clinical response to chemotherapeutic intervention and presents phenotypically as one of three broad categorical groups: a) response; b) partial response; c) no response [1], [2]. This issue is further compounded by potential side effects elicited by toxicity to non-tumour cells and consequently introduces an additional complication to patient treatment protocols [3], [4], [5]. There is therefore an urgent need for molecular markers that are indicative for appropriate dosing

strategies directed specifically towards the individual patient in addition to assays capable of identifying potential resistant/sensitive responses.

At the heart of these clinical issues is the genetic heterogeneity exhibited not only between individual patients with respect to their genomic DNA sequence, but also the somatic mutations that might arise as part of the evolutionary development of the tumour [6], [7], [8]. With respect to the latter, further complexity is exhibited in that mutations have been classified into two broad groups: a) "driver" mutations in which key cellular pathways are abrogated and begin to positively subvert the cellular machinery towards more aggressive phenotypes and b) "passenger" mutations which do not actively promote or abrogate the tumorigenic process but represent "background" noise [9], [10]. The ability to demarcate between mutations that drive aggressive phenotypes from those that play no significant role in altering the clinical response to chemotherapy would provide potentially useful diagnostic assays with utility for triaging patients into those that may benefit from treatment versus those who are unlikely. With appropriate quantitation, characterisation and validation studies, these markers may also assist in dosing strategies for sensitive patients.

There have been several publications providing independent corroborative support to the existence of genetic sub-types within tumours such as breast [11], [12]; lymphoma [13]; prostate [14]. Such heterogeneity might be indicative therefore of different aetiological pathways for carcinogenesis and consequently that alternative strategies may be necessitated to treat patients with alternate tumour expression patterns. Massively parallel examination of transcriptional activity in a temporal/spatial manner using technologies such as DNA microarrays; RNA-sequencing affords the possibility of identifying expression patterns that might be correlated to patient sensitivity/resistance to chemotherapy. This rationale has been shown with several therapeutic agents in which for example Her2/Neu expression is ascertained prior to the commencement of Herceptin administration [15], or ER status is determined prior to tamoxifen treatment [16]. In colorectal cancer mutational screening has now been recommended by the FDA to establish the status of KRAS mutations prior to commencement of therapy to cetuximab/panitumumab – these therapeutics are known inhibitors of the EGFR pathway of which KRAS is an integral component in the signalling pathway [15]. While the biological/ pharmaceutical reagents listed above are known to target specific and well characterised pathways to elicit their effect, it is possible that not all downstream

elements (including those responsible for both augmentation and repression of the therapeutic effect) have been fully elucidated.

Identifying pathways that either directly or indirectly attenuate the therapeutic effect might have potential value from several perspectives. Firstly these molecular targets could form the foundation of novel diagnostic assays capable of identifying patients that have increased resistance to treatment [17]. Such tools would rationalise clinical decision making processes to move the patient towards alternate forms of therapeutic intervention with an increased chance of success. Secondly an understanding of the interplay between genetic pathways and their controlling elements that allow patients to be permissive to therapeutic intervention might facilitate the development of novel drug/biological treatments [18]. Finally the possibility exists, that elucidation of the effector pathways that manifest as either sensitive or resistant phenotypes could be another step towards the creation of assays capable of determining the appropriate dosing strategy for patients.

Massively parallel interrogation of gene expression patterns offers a useful methodology in which to identify biomarkers that could be exploited to classify patients into "responders", "partial responders" and "non-responders". In conjunction with appropriate validation studies (e.g. retrospective analysis on archival material; prospective randomised clinical trials) the robustness of such biomarkers can be tested and refined. Through such co-ordinated strategies, the development of companion diagnostics capable of aiding in the clinical management of patients including treatment options might be feasible. There is not only a need for the development of diagnostics targeted towards therapeutic outcomes but also characterisation of the molecular pathways that these candidate biomarker genes are involved in as drug resistance may also be interconnected to pathways linked to side effects associated with treatment.

Given the clinical utility that could be afforded by having pre-treatment/early treatment diagnostic tests for patient therapeutic response, there are developmental phases that would need to be addressed prior to clinical deployment. Although not exhaustive, these can be broadly categorised as: a) biomarker (candidate) discovery; b) statistical interrogation to identify candidates for validation; c) computational modelling using multivariate analytical techniques to assess biomarker predictive performance; d) ranking the importance of biomarkers to predictive performance; e) application of new information to allow further modelling of drug response pathways; f) validation in

prospective clinical studies to test model/biomarker robustness; g) potential refinement of models to account for the molecular heterogeneity of tumour cells from patient response data [19]. All phases of the biomarker discovery process represent significant challenges including most notably acquisition of appropriate clinical samples for validation studies and the time/resources needed to corroborate initial findings. Computational modelling has the potential to contribute significantly to testing the robustness of potential biomarkers prior to moving towards more costly and resource consuming validation studies.

Adaptive learning algorithms represent powerful computational tools that have been applied with good effect to identify novel biomarkers associated with various phenotypes. These include for example pathological tumour grade [20], [21], disease staging in cancer patients [22] and resistance versus sensitive expression patterns for both cell lines and patient clinical samples [23]. Artificial neural networks represent one such class of computational algorithms that have been applied to a variety of post genomic high throughput data sources for predictive modelling. There are several advantages to ANN which include: a) the ability to produce models capable of generalising well with new data; b) enable a potential ranking of predictor variables to assess the relative importance that each contributes towards model accuracy; c) the ability to use non-linear mathematical computations to identify inter-relationships between the variables to produce robust and accurate models [24], [20]. The disadvantages of ANN include the fact that the mathematical relationships which are developed between the input variables and output predictions may be difficult to rationalise (i.e. they are non-linear in nature and thus gain the term "black box"), the time taken to train ANN and the issue of "memorisation" or over fitting the data so that the network begins to model "noise" rather than signal [25]. This latter limitation can be overcome to some degree through the introduction of additional samples for testing predictive performance, network regularization or sampling with replacement techniques.

ANN are mathematically modelled upon the neural network systems of higher biological organisms. Just as learning and memory systems are composed of a series of interconnecting neurons capable of receiving and transmitting impulses in response to specific stimuli, ANN are designed to respond in an analogous manner although the architecture is vastly simplified compared to their biological counterparts. In relation to the structural architecture of an ANN, a variety of forms have been explored for their ability to classify biological data with good predictive capability. One type that has shown

extremely good performance for data classification is the multi-layer perceptron (MLP) and it has been used with good effect to develop trained models with excellent prediction for new (blind) data [20].

The basic structure of a MLP is composed of three layers: a) input neurons representing the values of the variables used for training the ANN (e.g. microarray expression values); b) hidden layer neurons that receive the signal through weighted links and then subsequently propagate the transformed values through a series of activation functions (e.g. logistic sigmoid, exponential, softmax); c) output neurons in which the signal is propagated through a final series of activation functions to make a classification response. The input node is normally devoid of an activation function and is therefore propagated unmodified after the numerical variable is scaled (0, 1). Two additional nodes are added to the hidden layer and output layer which allow the transformation result of an activation function to be moved towards the right or left of the x-axis. This is achieved through having the input value set to 1 and the weighted link is varied and results in the production of outputs with reduced error between the predicted and actual values for training set samples [26].

The MLP is an example of a feed forward propagation network in which the input signal is moved in a unidirectional manner from the input towards the output layer. The error function between the network predicted and actual value is calculated and this error value is then propagated back from the output neurons towards in the input layer through modification of the weight values. This modification in weight is given by the formula shown in figure 1C and represents a function of learning rate, error and initial input value. Weighted links can be either updated as a batch once all training samples have been propagated through the network or alternately each time an individual training sample fully propagates through the learning algorithm (incremental). In this manner the ANN adapts through iteration to minimise the error between network predicted and actual value, until the error value reaches zero or alternately some pre-set stopping criteria (e.g. early stopping in which a test set has been exploited and the error rate between the training and testing samples begins to diverge) is reached.

ANN have been used to interrogate DNA microarray datasets for classification of a variety of tumour types with high rates of accuracy [27]. Given our group's interest in the issue of therapeutic resistance in cancer patients we wanted to explore whether ANN could be utilised to effectively discriminate patients into either chemotherapy sensitive or

resistant cohorts from patients with known clinical outcomes based upon quantitative values obtained from normalised gene expression data. It is important that models showing good accuracy for classification of training samples have the network predict upon cohorts of independent validation datasets to ascertain the potential robustness of the model. If sufficiently robust (i.e. has excellent predictive capability for blind samples) then such an approach could provide a basis in which to begin to select genes for their potential diagnostic/prognostic capability.

The development of computational models with good predictive capability is highly contingent upon the quality of the input variables and the samples that are used for development (i.e. training/testing sets). The ability to triage microarray datasets for genes with a high probability of being differentially expressed between the appropriate target groups (i.e. drug resistant/sensitive) would represent an important first step in selecting robust biomarkers that might form the foundation of novel diagnostic/prognostic tests although this does not of course guarantee that they will be useful as predictor variables. While ANN are powerful data mining tools and predictive models, they are strongly dependent upon the samples (and therefore the gene expression patterns) that are used in model development [22]. The premise of model development is that training and testing samples represent a "consensus" molecular expression pattern that is indicative of resistant and sensitive populations. Issue may arise therefore if non-consensus expression patterns occur within the population that is utilised as either a training or testing sample. Such "non-consensus" expression patterns (or outliers) existing within the training or testing sample sets may result in skewing the developing models towards algorithms that might be sub-optimal for the general population [28]. While outliers might represent systematic artefacts of the system (e.g. samples that may have been collected/stored incorrectly; poor experimental run; ANN predictive models that are unable to accurately account for all the variation within the variables submitted for model building) there is also the possibility that they may represent distinct biological entities that have arisen independently of the main cohort. If this is the case then the ability to identify, develop and characterise alternate models which rely on alternate biomarkers that are more representative of the outlier cohort will be important both to the clinical management of patients and therefore treatment selection.

Gene Expression Omnibus (GEO) is a data repository containing experimental results from over 140,000 microarray experimental analyses [29], [30]. GEOquery is an open source algorithm specifically constructed to act as an interface between the datasets

stored in GEO and data interrogation and feature extraction by exploiting bioinformatic tools created as part of the Bioconductor project [31], [32]. These algorithms have been written in R language and GEOquery provides a simple graphical user interface in order to permit access and harnessing of these data interrogation programs without the use of line command language. Limma (Linear Models for Microarray Analysis) is one such suite of algorithms that is implemented by GEOquery to perform multivariate statistical testing in order to identify differential expression patterns from microarray data. It will calculate p-values and adjusted p-values ("q-values") through multiple-testing correction methodologies including the widely used Benjamini and Hochberg approach [33]. As such the user has access to a powerful suite of statistical interrogation tools capable of facilitating the rapid triage of differentially expressed genes.

In the current study we have chosen to exploit gene expression data using microarray datasets available from the Gene Expression Omnibus data repository as systems to explore the characteristics of predictive model development by ANN. Given this group's interest in chemotherapy resistance we have chosen to focus upon a published dataset taken from Hodgkin's lymphoma patients in whom their clinical outcome to chemotherapy treatment has been ascertained using standard clinical criteria as either responsive or resistant [34].

Using open source algorithms to undertake a pre-screening exercise to select genes that are differentially expressed (FDR adjusted p-value < 5%), we have taken these potential biomarkers and applied them as targets for building an array ANN models. We have explored potential effects on predictive accuracy by using randomised populations to form training, testing and validation sample sets. We present data on our findings regarding the identification of outliers from this cohort that consistently fail to predict well but using alternate biomarker expression patterns for this sub-group that predictive accuracy can be increased. Finally we show some initial findings regarding the relative importance ranking of biomarkers used in prediction and how this may vary between training, testing and validation datasets and thus represents another compounding effect for biomarker selection and downstream validation.

Results & Discussion

(a) Analysis of full (130 patient) data set and identification of Group 114 main cohort

Selection of candidates for ANN model development

We chose to exploit GEO and its query tools in order to interrogate microarray datasets for potential candidates that had the highest potential for differential expression between chemotherapy responding and resistant HL patients. Although alteration in expression pattern may elicit powerful information regarding the molecular pathways that are abrogated during oncogenesis and disease progression, such differential expression may also provide translational utility with respect to clinical outcomes following chemo-therapeutic intervention. These tools could be exploited as the basis of a predictive diagnostic assay enabling the rationalisation of the clinical decision making process for placing individual patients on specific treatment regimens. With this goal in mind we chose therefore to explore whether these expression patterns might also have potential utility as predictive biomarkers for ANN based classification algorithms for patient response to treatment.

Expression series GSE17920 was selected as a model dataset for algorithm development. Core biopsies were sampled from patients with Hodgkin's Lymphoma (n=130) of which their clinical response pattern to chemotherapy treatment was ascertained. Patients were categorised to be either chemo-resistant (n=38) or chemo-sensitive (n=92) and thus provided an extremely useful cohort of data in which to develop predictive clinical models indicative of therapeutic failure. GEOquery requires users to identify at least two (with a maximum of 10) groups of samples in order to perform statistical interrogation. We classified expression data as either "resistant" or "sensitive" to chemotherapy and thus conducted statistical analyses based upon a two group classifier. GEO datasets necessitate that user data is normalised enabling cross comparison within a given experimental series with median centred data being strongly indicative of normalisation of the expression dataset. To ensure that this was the case we used GEOquery to produce boxplots of the microarray expression values for all 130 samples (Figure 1). The median values (black boxes) appear to strongly co-align for all samples suggesting that the dataset is normalised allowing cross comparison.

GEOquery was then utilised to identify genes with the highest probability for differential expression as reported by their raw p-value and q-values (adjusted p-values (Benjamini and Hochberg multiple-testing correction) with the associated q-value indicative of the likelihood of the false discovery rate (FDR)). We made an arbitrary decision to concentrate our attention on genes for ANN model development that resulted in q-values of <0.05. Sixteen probe sets (gene biomarkers) were identified that fulfilled this criterion and are presented in Table 1 with their associated gene identities, log2 fold change, raw p-values, t-statistic and B-statistic. With respect to the data for Log2 fold change, positive values are indicative of an overall increase in mean expression value for the success group compared to the failure cohort (i.e. expression level for success group > failure group). The converse is true for log2 fold change expression values that possess a negative sign. In this case it is indicative of a mean increase in expression value for the patients who fail their treatment compared to patients who showed chemotherapy response (i.e. gene expression level for the failure group > success group).

Development of ANN classifiers

ANN have been shown to produce models that are capable of generalising well with new unseen ("blind") validation data. We wished to explore whether the differential expression patterns of the 16 gene biomarkers with FDR <0.05% could be exploited to develop ANN models with strong predictive capability for discriminating patients as either being chemo-sensitive or chemo-resistant. In order to address this question we established an automated model development process using parameters selected at random in order to both construct and then test the predictive accuracy of the resultant ANN. Architectures were built upon the Broyden-Fletcher-Goldfarb-Shanno (BFGS) optimisation multi-layer perceptron back propagation neural network algorithm and constructed using a variety of activation functions (e.g. logistic, Tanh, Softmax, Identity) for both hidden and output neurons. Two types of calculation (sum of squares; entropy) were exploited to assess classification error between actual and network prediction. The error value was back propagated through the network leading to alteration of the weighted links between input and hidden layers as well as between hidden and output layers. 20,000 models were run per analysis and the top 100 models (with the highest predictive accuracy for training, testing and validation datasets) were kept for downstream data analysis.

Expression data for all 16 gene biomarkers from all 130 Hodgkin's lymphoma patients (resistant (n=38); sensitive (n=92)) were utilised to develop models with a strong

classification performance. Training, testing and validation datasets were implemented in order to construct and validate algorithms that had strong capability to generalise well for new data. In order to achieve this goal 30% (n=39) of samples were used for training, 10% (n=13) for testing and 60% (n=78) as part of an independent ("blind") validation set. We wished to explore a number of potential effects of using ANN based classifiers for chemo-response outcomes. These included: 1) whether ANN might be capable of constructing computational models that are able to generalise well for new (validation) data and thus discriminate between sensitive/resistant patients; b) the potential effect that using different samples to form the training, testing and validation datasets had upon classification accuracy including the identification of potential outliers; c) the effect of varying network initialisation (weighted link values) while keeping training, testing and validation samples constant; d) the potential contribution of individual biomarker expression patterns (and therefore their relative ranking position) upon classification accuracy; and e) how individual biomarker rankings might be affected by systematic variations of an individual ANN model.

The application of variable ranking is highly significant to biomarker discovery as most classifiers (e.g. ANN or CART (Classification And Regression Trees)) implement a relative ranking of variable importance that is usually based upon the impact that the variable has towards classification accuracy. These methodologies are used in the selection of biomarkers for subsequent downstream validation studies and thus form an integral component of candidate biomarker triage. Eliciting further information as to how systematic effects may potentially impact upon biomarker ranking is essential as these factors directly impact on biomarker assay development and ultimately for a select cohort of molecules new potential therapeutic targets.

Sample and network seed variation

Several reports that have indicated that subsets of biological/clinical samples may not predict well using the algorithm developed for their classification. These samples are commonly referred to as outliers and they represent an interesting class of variables primarily because they fail to conform to a canonical expression pattern indicative of the group in question. There are a number of factors that could influence the emergence of outlier samples and these might act either in isolation or in concert with each other in order to produce classification errors. Such examples include: a) the outlier in question represents a true biological variant (different genetic class) from that being modelled; b)

there are systematic errors that have impacted the variable's expression value (e.g. sample degradation; analytical preparation; random error). Both effects can result in outlier samples significantly skewing model development from a classifier that generalises well for new biological data to one in which there is strong degradation of classification performance.

Given the potential genetic and/or systematic variation that might influence expression patterns within a given sample, we wished to explore what effect different combinations of samples (and therefore their associated gene expression pattern) might have upon classifier development and ultimately downstream predictive accuracy. To achieve this goal we used 10 number seeds to select different combinations of samples that would form training, testing and validation datasets. In this manner a sample might appear within the training cohort for one number seed and as part of the validation dataset for a different number seed for each of the 10 separate runs. 20,000 models were developed and the top 100 models (as based upon predictive accuracy) were retained.

Table 2 shows the results of models 1-8 obtained from run 5 from a total of 100 models retained after the training process. The percentage of correct classifications predicted by the ANN for all three cohorts (training, testing and validation datasets) is presented. Model 2 for example correctly assigned 100% of patient samples of the training group (n=39) to their respective clinical outcomes i.e. chemo-resistant or chemo-sensitive. 92% (n=13) and 91% (n=78) of testing and validation classifications for the testing and validation datasets respectively were accurately assigned to their clinical outcome groups. The table indicates the method used by each model to determine the error differential between actual and predicted values (sum of square; entropy). Finally the type of activation function used to propagate the learning process from the input layer to the output nodes is also presented.

One statistical measure of a model's ability to accurately discriminate between two classes is the production of a Receiver Operating Characteristic curve which plots the number of true positives (sensitivity) versus false positives (1-specificity). An inability to discriminate between each respective class would result in a line of 45 degrees and an AUC (Area Under the Curve) of 0.5. A perfect ability by the algorithm to accurately assign each member to its respective without error class would result in a right angle plot and an AUC of 1.0. As a measure of overall performance ROC curves were plotted for all 100 models using classifications results for training, testing and validation datasets in

order to gain an average estimation of model performance within a given run (Figure 3). Model 2 highlighted above produced an AUC of 0.926 indicating a good level of discriminatory power between the two classes of patients. The data would suggest that the 16 gene biomarkers (see Table B) identified initially by GEO2R may be useful candidate biomarkers of chemo-sensitivity/chemo-resistance for ANN predictive modelling and therefore warrant further analyses.

For each patient sample (n=130) the number of correct predictions across all 100 models was calculated per run. Next we determined the average percentage classification accuracy for each sample across all 10 runs. Confidence intervals were estimated using a two-tailed t-distribution ($\alpha \leq 0.05$) with 9 degrees of freedom and is summarised in Figure 4a. There are several samples from both the chemo-resistant (e.g. samples 13, 14, 33) and chemo-sensitive populations (e.g. samples 73, 74, 75) where all ANN models correctly predicted the therapeutic response class of the sample each time a prediction was made. This is in stark contrast to several other samples from the chemo-resistant (e.g. samples 3, 18, 19, 20, 21) and chemo-sensitive (e.g. samples 1, 23, 50, 90) cohorts which consistently produced low levels of accurate classification by the ANN models. Given the number of models which failed to accurately assign the correct class to these samples we then wished to interrogate these outliers further and potentially gain a better understanding of the influencing factors that can impact classifiers of microarray data. Such characterisation might assist in developing better strategies for biomarker selection that would ultimately form robust predictors of patient therapeutic response.

Next we wished to assess the effect that different initial network weights might have upon the predictive modelling process – and ultimately the effect on classifying outliers. We used the same fixed sample seed value used in run 10 from the "sample seed variation" series such that identical samples would form the training, testing and validation datasets. As before we developed 20,000 models per run with the top 100 models (based on predictive accuracy) being retained for downstream analysis. The number of correct predictions across all 100 models was calculated per run and the average percentage classification accuracy was determined for each sample across all 10 runs. The data is summarised in Figure 4b. It is apparent from both the average values and confidence intervals that varying the initial weightings has very little effect upon the outcome of prediction. If one compares Figure 4a with Figure 4b the data would suggest that the outlier samples still remain challenging to classify by the ANN and that changing either the composition of the training, testing and validation datasets nor altering initial

network weighting values appears to have significant effect upon the classification accuracy of these particular outlier samples. In order to visualise these outliers across all runs for both sample and network seed variation we produced a colour heat map to indicate classification accuracy for a given sample within the chemo-sensitive and chemo-resistant patient populations.

Developing good predictive models capable of classifying HL patient therapeutic response is likely to be contingent upon several factors. As well as systematic parameters such as consistent sample collection, storage, processing and analytical precision, robust modelling will also be contingent upon the identification of biomarkers whose expression pattern is not only stable but specific for the population under study. There is accumulating evidence to suggest that several genetic sub-populations may preside within patient tumour samples as evidence for example within B-cell lymphomas, breast tumours and colorectal cancers. Given the potential for genetic heterogeneity with HL patients and therefore alternate expression patterns that might impact upon individual therapeutic response profile, we wished to explore potential genetic factors in greater detail. To this end we undertook a further series of in-silico characterisation studies to demarcate between potential systematic effects from those that might have a biological basis for the outlier population.

Systematic versus biological effect – sample randomisation and outlier removal

ANN are useful modelling tools that generalise well for the prediction of new data. Through parameterisation of the input variables, parsimonious models can be established that can be robust classifiers. There are however limitations to the application of ANN for biomarker discovery and one of the key challenges facing the field is that predictive models developed by these algorithms are complex, non-linear in nature and consequently difficult to interpret. Given this background we wished to extrapolate upon our previous analyses to elicit information regarding potential systematic artefacts that might be generated by the ANN modelling process versus those that have a specific biological basis capable of being attributed to the outlier population.

The predictive models developed to this point were based upon presentation of samples in a sequential order to the neural network i.e. all chemo-resistant followed by chemo-sensitive patients. Through user specified seeding values random combinations of samples were extracted in order to form training, testing and validation datasets. To

minimise the risk that outlier samples might be potentially the result of positional effects in which the samples were presented to the ANN, we then chose to randomise all 130 samples using three consecutive random seed generators. 10 sample seeds were used to select training (30%), testing (10%) and validation (60%) sets. 20,000 models per sample seed were trained and the top 100 models based upon predictive accuracy were retained. The results are presented in Figure 5 for the outlier samples. A comparison of predictive performance for each of the 16 selected outlier samples for the "Sequential" and "Randomised" sample order is presented. The data would suggest that although there are mean increases in predictive performance for some samples (e.g. Class S 74) none of the improved performances are significant compared to the initial run. This suggested therefore that variation of these samples from the main cohort might reside in explanations other than purely systematic.

To explore this hypothesis further we removed the 16 outliers from the main cohort of 130 of samples to create two populations: Group 114 (main cohort of 114 samples) and Group 16 (outlier cohort of 16 samples) with both groups containing chemotherapy resistant ("Failure") and chemotherapy sensitive ("Success") patient sample data. Differential expression patterns between Failure and Success patients from Group 114 and Group 16 were examined by submitting the individual groups to GEO2R for comparative analysis. Benjamini and Hochberg multiple correction testing was applied and following statistical processing we concentrated our attention on genes with adjusted p-values having FDR≤ 0.05.

Figure 6 presents the results of genes that were identified by the Bioconducter statistical tools as being differentially expressed between patients who were resistant compared to those who responded to chemotherapy treatment. Data is shown for Group 130, Group 114 and Group 16 and is focused upon genes with adjusted p-values having FDR ≤ 0.05. It is interesting to note that when the 16 outlier samples are removed from the main cohort of samples the number of gene biomarkers with adjusted p-values with FDR ≤ 0.05 increases from 16 (see Table B; Group 130) to 5344 (see Table A; Group 114) for sensitive versus resistant patients. When one compares the number of genes with adjusted p-values having FDR ≤ 0.05 in Group 16 (sensitive versus resistant patients) the number of gene biomarkers that are identified as being differentially expressed increases from 16 (Group 130) to 1138 (see Table C).

Next we asked whether the 16 genes identified originally from all 130 samples (Group 130) after multiple testing corrections were still significant for Group 114 and Group 16. Table 3a and 3b present the results from statistical analysis returned by the Bioconductor series of tools for Group 114 and Group 16 respectively. Examination of the data from Table 3a suggests that all of the genes originally identified from Group 130 remain significant after correction testing. This is in contrast however to Group 16 (outlier samples) in which only one gene out of 16 (C1orf163) remain statistically significant at the FDR ≤ 0.05. We believe that this represents an interesting observation as the outlier population of samples consistently showed a poor level of predictive accuracy by ANN when compared to the main population (Group 114) of samples. One explanation as to why the outlier group may have elicited low predictive accuracy during modelling is that Group 16 may in fact represent a distinct biological cohort with an alternate expression pattern. Given that only one out of 16 genes is significantly different after multiple testing corrections between the chemo-sensitive and chemo-resistant samples it may provide a valid reason as to why poor classification occurred within the outlier group.

Caution must be exercised regarding these conclusions however. The possibility that Group 16 might represent a genetic sub-population is based purely upon an in-silico analysis with no independent validation studies having been conducted to corroborate such a hypothesis. Furthermore the possibility also exists that the outlier population represents normally distributed variation and is merely an artefact of a limited number of computational models (n=600,000) having been searched i.e. sampling variation rather than a biologically driven phenomenon.

We wished to explore whether the removal of the outlier samples could potentially lead to increases in predictive accuracy by ANN models for the Group 114 samples. To answer this question we randomised the order of the samples and then initiated model development as indicated previously. 20,000 models were developed per run and the top 100 models (based upon overall predictive accuracy for training, testing and validation datasets) were retained for downstream analysis. We used random sample seeds to select different combinations of training, testing and validation datasets with constant network seed values. In addition we also developed models using random network seeding values while keeping sample seed constant. 10 runs were performed for both sample and network seed variation analyses producing a search space of 200,000 models for each parameter settings (n=400,000 total). 30% (n=35) of samples were used for training, 10% (n=11) for testing and 60% (n=68) as a validation sets for Group 114.

Table 4 presents the results of Run2 (variable sample seeding) for models 1-8. The data would suggest that there is a good level of predictive accuracy for samples that comprise the training, testing and validation datasets. It can also be noted that for three models (Model 2, Model 3 and Model 4) 100% accuracy was achieved for all three sample sets. When we compared the predictive accuracy of all models within Run2 that achieved 100% predictive accuracy for training, testing and validation datasets, 28/100 achieved this level. Interestingly for Run1, although a high level of predictive accuracy was achieved, no model in the top 100 achieved 100% accuracy for all three datasets (data not shown). Implementing different random seeding values for network initialisation (with constant training, testing and validation sample sets) also produced runs containing models with 100% predictive accuracy for all three sample cohorts.

The results obtained from model development would suggest that by removing the 16 outlier samples from the main cohort of 130 leads to an improvement in predictive performance with some models achieving 100% accuracy for training, testing and validation datasets. One plausible explanation is that Group 16 represents a biologically distinct group of samples (Table 3b) and as such is capable of skewing model development towards non-optimal solutions. Upon the removal of Group 16 from the main body of 130 samples, the ANN is able to generate models from Group 114 in which all expression patterns from both chemotherapy sensitive and resistant patients are accurately classified. Another potential explanation is that the outlier samples do not represent a biologically separate cohort but may represent systematic variants (e.g. sample processing, storage, labelling) that also skew ANN model development towards classifiers that do not generalise well for new blind data e.g. validation data. Such a scenario could be envisioned to negatively impact the search space conducted by neural network optimisation modelling. This could for example result in the number of models having been developed in this study being inadequate in number to successfully identify a model that generalises well for new data structures.

(b) Analysis of Group 16 outliers

Differentially expressed genes between chemo-sensitive and chemo-resistant patients

Finally we turned our attention to the Group 16 outliers and asked whether classifiers could be developed that were able to accurately discriminate chemo-therapy sensitive

and chemo-therapy resistant patient expression profiles. Table 5 shows the top 50 gene biomarkers listed in order of their adjusted p-values from the most (top) to least (bottom) significant. An interesting observation is that of 11/50 (22%) of these genes have been published as having differential expression patterns in response to treatment outcome including for example CD93 (ranked 1st with adjusted p-value ≤ 0.000133) and Neuropilin 1 (ranked 4th with adjusted p-value ≤ 0.001086). LAPTM4B (ranked 8thwith adjusted p-value ≤ 0.001363) has been implicated in the chemotherapy resistance of breast cancer patients to anthracyclines and is strongly linked to disease recurrence in these patients. Given that association of these genes has been previously linked with chemotherapy response profiles, a potential biological basis for Group 16 samples being outliers compared to Group 114 that possess a distinct expression profile in response to chemotherapy outcome would not be inconsistent with previous published data. Once again we caution that our analyses are limited to an in-silico investigation and therefore cannot corroborate our findings using independent biological verification, but nevertheless we believe that there is persuasive evidence to suggest that this cohort of genes should warrant further investigation.

ANN modelling

We made an arbitrary decision to select the first four gene biomarkers with highest adjusted p-values (CD93 molecule (adjusted p-value ≤ 0.000133), gap junction protein, delta 3, 31.9kDa (adjusted p-value ≤ 0.000167), paired related homeobox 1 (adjusted p-value ≤ 0.000747) and neuropilin 1 (adjusted p-value ≤ 0.001086)) and we used this cohort to explore whether classifiers could be developed with good predictive capability for discriminating chemo-sensitive from chemo-resistant patients in Group 16. To achieve this goal we developed a standard 20,000 model exploratory search analyses combined with retention of the top 100 best performing models based upon predictive accuracy for training, testing and validation samples. Given that there are only 16 samples forming the outlier group we chose to use 30% (n=5) of samples for training, 20% (n=3) for testing and 50% of samples (n=8) for validation. We focused our attention on constructing predictive algorithms using only variation in sample seeding as within this study it appeared to have the most significant impact upon predictive accuracy for sample classification compared to the effect caused by varying network initialisation. 10 runs were conducted with varying network seeds. Table 6 shows the results from Models 1-8 taken from Run1. The data indicates that all samples from each cohort are correctly classified suggesting that the expression levels of the four genes identified as being

differentially expressed possess sufficient information to enable accurate discrimination between chemotherapy resistant and sensitive patients. In fact all 100 models from Run1 produced correct classification of samples for training, testing and validation samples (data not shown). In fact this pattern was repeated for all other nine runs with all models showing 100% predictive accuracy with the exception of 5 models (n=1000) which had less than 100% correct classification. This would suggest therefore that these four genes contain sufficient information to discriminate between the chemo-sensitive and chemo-resistant patients within Group 16. How robust these markers/predictive models will be for new data of the "Group 16 type" can only be tested and validated with independent test sets which was not conducted within this study. There may be the possibility therefore that as the genetic variation increases that these classifiers and the biomarkers that are used to develop such algorithms may prove to be either ineffective or require additional biomarkers in order to maintain classification robustness.

We next examined whether these four gene targets were significantly different between the treatment failure and success groups for all 130 patients. The adjusted p-values showed that there was no significant difference (FDR ≤ 0.05) between the two cohorts (data not shown). This was reinforced by predictive accuracy when these four genes were used to develop classification models for Group 130 samples with variable sample seeding (10 runs with 20,000 models developed per run and retention of the top 100 models based upon predictive performance per run). Figure 7 shows the ROC plot taken from Run6 for Group 130 samples. There is no significant ability of the models to demarcate between patients who respond to their chemotherapy treatment versus those who are resistant using the four most significant genes identified in the outlier Group 16 cohort. This may suggest therefore that these genes have no value for classification when the outlier population is combined with Group 114 samples. Finally we undertook a limited exploration as to whether these four genes were also significant in Group 114. Three genes NRP1, GJD3 and CD93 were significantly different (as measured by adjusted p-values returned from LIMMA analyses) whereas PRRX1 was not. Using a series of runs (n=2) and varying sample seed to select alternative populations of training, testing and validation groups no significant level of predictive accuracy was achieved. This may suggest therefore that these four genes do possess sufficient information to account for all of the variation (biological and/or systematic) that is present within Group 114. There is a possibility therefore that additional biomarkers may be required from the cohort list in order to develop classifiers that have strong predictive performance.

In summary therefore we present data to suggest that ANN can be effective tools for identifying potential biological outlier sub-groups that have alternate gene expression patterns for chemotherapy response or failure from the main body of samples. Removal of these samples and re-training can result in improved model development and predictive performance for both the main cohort of samples and the outliers. Such a methodology may assist in the identification of novel biomarkers that have clinical utility for triaging HL patients regarding treatment outcomes to their chemotherapy treatment. Only with appropriate downstream validation studies will the robustness of such predictive modelling algorithms including their associated biomarker variables be corroborated. While it goes beyond the context of this current study we believe that it is important to at least raise the issue of biomarkers that are used for model development. As was observed in the context of this limited study different cohorts of samples can elicit different gene panels with different significant levels. These in turn therefore impact which gene expression patterns are presented to the neural network for classifier development and sample characterisation. Stratification methodologies for gene selection are essential not only from the context of implementing multiple testing correction methodologies to reduce the risk of FDR but also that greater understanding is required how pattern recognition algorithms select the biomarkers used for model development and how robust these predictors for generalising new datasets. Understanding how biomarker selection can be influenced by systematic/biological factors including the composition of training, testing and validation datasets, may eventually lead to reduced FDR and enhance the rate at which diagnostic and prognostic tools finally deliver clinical utility for patients with HL.

Table 1: Statistical overview of gene biomarkers identified as being differentially expressed between chemotherapy resistant and sensitive Hodgkin's lymphoma patients between all 130 patients. The top 16 genes with adjusted p-values (q-values) to produce a FDR <5% are listed. These genes were then used for downstream model development by ANN.

Probe ID	*Adjusted p-value*	*p-value*	*t-statistic*	*B-statistic*	*Log FC*	*Gene Symbol*	*Gene Title*
229684_s_at	0.0397	7.25E-07	5.2074648	5.35992	0.28146739	ZNF644	zinc finger protein 644
206131_at	0.041	2.03E-06	4.9739843	4.47186	0.21748507	CLPS	colipase, pancreatic
235892_at	0.041	2.30E-06	4.9443194	4.3609	0.20662157	-	EST tu05b03.x1
211753_s_at	0.041	3.37E-06	4.8554657	4.03113	0.41671487	RLN1	relaxin 1
231065_at	0.041	4.33E-06	4.7968899	3.81589	0.24246424	PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta
229080_at	0.041	4.72E-06	4.7764545	3.74121	0.17433947	EMID2	EMI domain containing 2
211936_at	0.041	5.46E-06	-4.7418324	3.61517	-0.49233209	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
237807_at	0.041	7.43E-06	4.6683153	3.34961	0.2151131	SPATA12	spermatogenesis associated 12
214709_s_at	0.041	7.50E-06	-4.6660489	3.34147	-0.31725235	KTN1	kinectin 1 (kinesin receptor)
206157_at	0.041	8.04E-06	-4.6493642	3.28161	-0.37434897	PTX3	pentraxin 3, long
396_f_at	0.041	8.25E-06	-4.6433778	3.26017	-0.33512048	EPOR	erythropoietin receptor
242988_at	0.0491	1.09E-05	4.5764525	3.02177	0.17010006	DCST2	DC-STAMP domain containing 2
224816_at	0.0491	1.27E-05	4.5384171	2.88735	0.17845086	GET4	golgi to ER traffic protein 4 homolog (S. cerevisiae)
211087_x_at	0.0491	1.41E-05	-4.5137578	2.80062	-0.25372443	MAPK14	mitogen-activated protein kinase 14
222883_at	0.0491	1.43E-05	-4.509901	2.78709	-0.35449136	C1orf163	chromosome 1 open reading frame 163
200915_x_at	0.0491	1.44E-05	-4.5085246	2.78226	-0.27636888	KTN1	kinectin 1 (kinesin receptor)

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Table 2: Percentage (%) accuracy for training, testing and validation performance for all 130 using the top 16 variables with FDR <5% as predictors. Training samples n=39; Test samples n=13; Validation samples n=78. Models were developed from resistant and sensitive samples presented to the ANN in sequential order. The top 8 models are shown above from Run5 using variable sample seeding values.

Index	*Net name*	*Training result (%)*	*Test result (%)*	*Validation result (%)*	*Training algorithm*	*Error function*	*Hidden node activation function*	*Output node activation function*
1	MLP 16-2-2	100.0000	92.30769	88.46154	BFGS 9	SOS	Tanh	Identity
2	MLP 16-3-2	100.0000	92.30769	91.02564	BFGS 16	SOS	Identity	Identity
3	MLP 16-2-2	94.8718	84.61538	91.02564	BFGS 12	SOS	Logistic	Identity
4	MLP 16-3-2	94.8718	84.61538	91.02564	BFGS 14	SOS	Exponential	Exponential
5	MLP 16-2-2	94.8718	84.61538	91.02564	BFGS 13	SOS	Exponential	Identity
6	MLP 16-3-2	100.0000	84.61538	91.02564	BFGS 10	Entropy	Tanh	Softmax
7	MLP 16-2-2	97.4359	84.61538	91.02564	BFGS 6	Entropy	Tanh	Softmax
8	MLP 16-2-2	100.0000	84.61538	91.02564	BFGS 13	SOS	Exponential	Identity

Table 3a: The adjusted p-values are presented for the "original" 16 gene biomarkers. These genes were identified as being differentially expressed between chemotherapy sensitive and resistant patients from all 130 patients. Significance testing results (following Benjamini and Hochberg multiple testing correction) are presented for genes identified as being differentially expressed between chemotherapy sensitive and resistant patients for Group 114. The data suggests that all 16 genes have highly significant adjusted p-values.

				Group114			
Probe ID	***adj.P.Val***	*P.Value*	*t*	*B*	*logFC*	*Gene.symbol*	*Gene.title*
211936_at	**5.01E-06**	9.16E-11	-7.13947	13.90841	-7.22E-01	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
229684_s_at	**1.54E-05**	5.62E-10	6.775823	12.23857	3.71E-01	ZNF644	zinc finger protein 644
206157_at	**0.000105**	9.64E-09	-6.18955	9.62154	-4.99E-01	PTX3	pentraxin 3, long
222883_at	**0.000256**	3.75E-08	-5.90067	8.37219	-5.02E-01	C1orf163	chromosome 1 open reading frame 163
214709_s_at	**0.00026**	4.28E-08	-5.87223	8.25079	-4.23E-01	KTN1	kinectin 1 (kinesin receptor)
229080_at	**0.000391**	8.54E-08	5.722274	7.61572	2.29E-01	EMID2	EMI domain containing 2
211753_s_at	**0.000391**	8.90E-08	5.713048	7.57693	5.24E-01	RLN1	relaxin 1
211087_x_at	**0.000391**	1.19E-07	-5.64921	7.30942	-3.39E-01	MAPK14	mitogen-activated protein kinase 14
200915_x_at	**0.000391**	1.38E-07	-5.61706	7.17528	-3.68E-01	KTN1	kinectin 1 (kinesin receptor)
237807_at	**0.000391**	1.43E-07	5.608707	7.14053	2.84E-01	SPATA12	spermatogenesis associated 12
206131_at	**0.000393**	1.51E-07	5.597144	7.09244	2.72E-01	CLPS	colipase, pancreatic
235892_at	**0.00053**	4.65E-07	5.345419	6.05915	2.45E-01		EST tu05b03.x1
231065_at	**0.000617**	5.86E-07	5.292855	5.84681	3.02E-01	PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta
224816_at	**0.00183**	5.22E-06	4.781063	3.8464	2.12E-01	GET4	golgi to ER traffic protein 4 homolog (S. cerevisiae)
396_f_at	**0.002077**	8.93E-06	-4.65061	3.35725	-3.43E-01	EPOR	erythropoietin receptor
242988_at	**0.003927**	3.37E-05	4.317636	2.1504	1.84E-01	DCST2	DC-STAMP domain containing 2

Table 3b: The adjusted p-values are presented for the "original" 16 gene biomarkers. These genes were identified as being differentially expressed between chemotherapy sensitive and resistant patients from all 130 patients. Significance testing results (following Benjamini and Hochberg multiple testing correction) are presented for genes identified as being differentially expressed between chemotherapy sensitive and resistant patients for Group 114. The data suggests that only one gene (C1orf163) has a significant adjusted p-value (in bold). All other remaining genes from the "original" 16 are not statistically significant.

					Group16		
Probe ID	***adj.P.Val***	*P.Value*	*t*	*B*	*logFC*	*Gene.symbol*	*Gene.title*
229684_s_at	0.759737	5.55E-01	-0.60297	-6.05105	-0.10867	ZNF644	zinc finger protein 644
206131_at	0.978879	9.51E-01	-0.06233	-6.23258	-0.00638	CLPS	colipase, pancreatic
235892_at	0.786639	5.96E-01	-0.54066	-6.08669	-0.0576		EST tu05b03.x1
211753_s_at	0.379208	1.23E-01	-1.62719	-4.98525	-0.32003	RLN1	relaxin 1
231065_at	0.554848	2.87E-01	-1.10092	-5.63842	-0.09878	PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta
229080_at	0.612017	3.56E-01	-0.95017	-5.78634	-0.08444	EMID2	EMI domain containing 2
211936_at	0.147942	1.32E-02	2.778025	-3.03292	0.782984	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
237807_at	0.316576	8.23E-02	-1.85108	-4.65214	-0.16915	SPATA12	spermatogenesis associated 12
214709_s_at	0.522681	2.52E-01	1.187912	-5.54458	0.214002	KTN1	kinectin 1 (kinesin receptor)
206157_at	0.24202	4.38E-02	2.183847	-4.10878	0.486089	PTX3	pentraxin 3, long
396_f_at	0.752169	5.44E-01	-0.61981	-6.04078	-0.1665	EPOR	erythropoietin receptor
242988_at	0.728663	5.08E-01	0.677524	-6.00355	0.052962	DCST2	DC-STAMP domain containing 2
224816_at	0.814203	6.40E-01	-0.47592	-6.11975	-0.0406	GET4	golgi to ER traffic protein 4 homolog (S. cerevisiae)
211087_x_at	0.489059	2.18E-01	1.280673	-5.43801	0.18543	MAPK14	mitogen-activated protein kinase 14
222883_at	**0.034263**	**4.65E-04**	**4.356823**	**0.080885**	**0.466637**	**C1orf163**	**chromosome 1 open reading frame 163**
200915_x_at	0.498848	2.28E-01	1.253598	-5.46979	0.197557	KTN1	kinectin 1 (kinesin receptor)

Table 4: Predictive accuracy (%) for Group 114 samples for training, testing and validation datasets using the 16 variables identified from Group 130 as predictors (adjusted p-value with FDR ≤0.05). Training samples n=35; Test samples n=11; Validation samples n=68. Models were developed using resistant and sensitive samples presented to the ANN in randomised sample order. The top 8 models are shown above from Run5 using variable sample seeding values. Models 2, 3 and 4 show 100% accuracy for all sample datasets (training, testing and validation).

Index	***Net. name***	***Training result (%)***	***Test result (%)***	***Validation result (%)***	***Training algorithm***	***Error function***	***Hidden node activation function***	***Output node activation function***
1	MLP 16-3-2	94.2857143	100	97.0588235	BFGS 3	Entropy	Logistic	Softmax
2	**MLP 16-2-2**	**100**	**100**	**100**	**BFGS 13**	**SOS**	**Tanh**	**Tanh**
3	**MLP 16-2-2**	**100**	**100**	**100**	**BFGS 5**	**SOS**	**Tanh**	**Tanh**
4	**MLP 16-2-2**	**100**	**100**	**100**	**BFGS 12**	**SOS**	**Logistic**	**Exponential**
5	MLP 16-3-2	97.1428571	100	100	BFGS 5	SOS	Identity	Tanh
6	MLP 16-2-2	97.1428571	100	100	BFGS 5	SOS	Identity	Tanh
7	MLP 16-2-2	94.2857143	100	100	BFGS 6	SOS	Logistic	Identity
8	MLP 16-2-2	94.2857143	100	100	BFGS 4	SOS	Tanh	Identity

Table 5 (*continued overleaf*): Statistical overview of gene biomarkers identified as differentially expressed between chemotherapy resistant and sensitive Hodgkin's lymphoma patients for Group 16. The top 50 gene biomarkers as measured by their adjusted p-values to produce a FDR <5% are listed

5

Probe ID	*Adj P-Value*	*P-Value*	*t*	*B*	*logFC*	*Gene Symbol*
202877_s_at	0.000133	2.43E-09	11.6518204	10.766889	1.78435714	CD93
230025_at	0.000167	6.10E-09	10.9400388	10.044983	1.41239683	GJD3
205991_s_at	0.000747	4.10E-08	9.5723192	8.490335	1.75162063	PRRX1
210510_s_at	0.001086	7.94E-08	9.1284516	7.933817	1.2726	NRP1
226632_at	0.001243	1.18E-07	8.8671362	7.593381	1.05169206	CYGB
205582_s_at	0.001243	1.36E-07	8.7763016	7.472765	1.91094762	GGT5
213290_at	0.001363	2.10E-07	8.5032838	7.103014	2.06811111	COL6A2
208767_s_at	0.001363	2.11E-07	8.4975419	7.09512	1.66799048	LAPTM4B
209094_at	0.001363	2.24E-07	8.4604733	7.044041	1.60410476	DDAH1
222451_s_at	0.001467	2.68E-07	8.348692	6.888772	1.16314286	ZDHHC9
224861_at	0.001592	3.20E-07	8.2387431	6.73422	1.35432063	GNAQ
212298_at	0.001888	4.14E-07	8.0811009	6.509432	2.3672	NRP1
207277_at	0.00211	5.46E-07	7.9146444	6.267946	3.03822222	CD209
212463_at	0.00211	5.59E-07	7.9003253	6.246973	1.44157143	CD59
208703_s_at	0.00211	5.79E-07	7.8789024	6.215535	1.47861905	APLP2
225262_at	0.002128	6.44E-07	7.8154248	6.121965	1.80221905	FOSL2
217890_s_at	0.002128	7.36E-07	7.7361413	6.004214	1.59586984	PARVA
1558214_s_at	0.002128	7.64E-07	7.7134578	5.970343	1.13446349	CTNNA1
218486_at	0.002128	7.75E-07	7.7049998	5.957693	1.40943492	KLF11
202436_s_at	0.002128	7.97E-07	7.6889253	5.933621	1.78844286	CYP1B1
212091_s_at	0.002128	8.25E-07	7.6684963	5.902969	2.16407937	COL6A1
219872_at	0.002128	8.85E-07	7.6271413	5.840719	1.17368254	FAM198B
211852_s_at	0.002128	9.30E-07	7.5980129	5.796711	1.27689841	ATRN
201551_s_at	0.002128	9.34E-07	7.5951136	5.792324	1.61768413	LAMP1
202368_s_at	0.002358	1.08E-06	7.5112786	5.664878	1.17144603	TRAM2
224895_at	0.002492	1.19E-06	7.4561617	5.580482	1.62590635	YAP1
38918_at	0.002807	1.46E-06	7.3358616	5.394598	0.61377619	SOX13
232053_x_at	0.002807	1.46E-06	7.3356322	5.394242	1.16409206	RHBDD2
212067_s_at	0.002807	1.49E-06	7.3245573	5.377013	2.11216349	C1R
222446_s_at	0.003058	1.68E-06	7.2559825	5.269895	1.41917143	BACE2
37005_at	0.003308	1.92E-06	7.178293	5.14763	1.66252063	NBL1
209297_at	0.003308	2.00E-06	7.1562623	5.112782	1.33423333	ITSN1
223253_at	0.003308	2.04E-06	7.145398	5.095569	1.86142381	EPDR1
220240_s_at	0.003308	2.06E-06	7.1400526	5.087092	0.74083968	TMCO3
204163_at	0.003443	2.24E-06	7.0926896	5.011787	2.15344921	EMILIN1
236297_at	0.003443	2.27E-06	7.0851316	4.999737	1.24897619	
1554679_a_at	0.003739	2.53E-06	7.0232131	4.900668	1.48330159	LAPTM4B
201559_s_at	0.003934	2.82E-06	6.9622711	4.802559	1.53854286	CLIC4
235072_s_at	0.003934	2.84E-06	6.958498	4.796465	1.24865397	
215073_s_at	0.003934	2.88E-06	6.9511579	4.784604	1.91315556	NR2F2
1555326_a_at	0.004066	3.05E-06	6.9189606	4.73247	1.19431587	ADAM9

Probe ID	*Adj P-Value*	*P-Value*	*t*	*B*	*logFC*	*Gene Symbol*
202435_s_at	0.004163	3.23E-06	6.8875259	4.68141	1.69770476	CYP1B1
235438_at	0.004163	3.27E-06	6.8793187	4.668053	1.33092698	
219065_s_at	0.004556	3.67E-06	-6.8166331	4.565671	-0.70693016	MEMO1
209228_x_at	0.004638	3.87E-06	6.7873037	4.517551	0.80019683	TUSC3
218880_at	0.004638	4.07E-06	6.7592444	4.471385	1.53982381	FOSL2
201042_at	0.004638	4.22E-06	6.739528	4.438869	2.97900794	TGM2
201874_at	0.004638	4.30E-06	6.7288651	4.421258	1.14039206	MPZL1
201621_at	0.004638	4.37E-06	6.7194203	4.405643	1.36420317	NBL1

Table 6: Percentage (%) accuracy for training, testing and validation performance for Group 16 outlier samples using the top 4 gene biomarkers with FDR <5% as predictors (refer to Table 5). Training samples 30% (n=5); Test samples 20% (n=3); Validation samples 50% (n=8). Models were developed from resistant and sensitive samples presented to the ANN in randomised sample order. The top 8 models are shown above from Run1 using variable sample and constant network seeding values. The data for Models 1-8 is presented indicating 100% classifying accuracy for training, testing and validation sample sets. Models 1-100 models had 100% correct prediction for all samples in training, testing and validation datasets.

Index	*Net. name*	*Training perf.*	*Test perf.*	*Validation per*	*Training algorithm*	*Error function*	*Hidden activation*	*Output activation*
1	MLP 4-2-2	100.0000	100.0000	100.0000	BFGS 0	SOS	Exponential	Logistic
2	MLP 4-2-2	100.0000	100.0000	100.0000	BFGS 0	Entropy	Exponential	Softmax
3	MLP 4-2-2	100.0000	100.0000	100.0000	BFGS 0	SOS	Identity	Exponential
4	MLP 4-2-2	100.0000	100.0000	100.0000	BFGS 4	SOS	Exponential	Identity
5	MLP 4-2-2	100.0000	100.0000	100.0000	BFGS 0	SOS	Logistic	Tanh
6	MLP 4-2-2	100.0000	100.0000	100.0000	BFGS 4	SOS	Exponential	Logistic
7	MLP 4-3-2	100.0000	100.0000	100.0000	BFGS 4	Entropy	Exponential	Softmax
8	MLP 4-2-2	100.0000	100.0000	100.0000	BFGS 5	SOS	Logistic	Logistic

Conclusions

Rationalising treatment options for patients with HL using molecular based prognosticators has the potential to translate into significantly improved outcomes for these patients. Microarray profiling is a fundamental "omics" technology being intensively exploited to identify expression patterns associated with pathologies of clinical interest and their clinical management e.g. disease progression; recurrence; response to therapeutic intervention. It is in relation to the last example that prognostication could strongly impact the treatment of HL patients by directing the most appropriate therapy towards individuals whom are most likely to benefit. Such molecular tests could also be applied in triaging patients that have a high probability of being refractory to a given regimen enabling alternate treatments to be recommended. The basis of prognostic test development will remain in the identification of biomarkers whose expression pattern is specific to the clinical indication under investigation and robust enough to enable the development of classifiers that can be independently validated. Such a co-ordinated strategy will enable test parameters including limitations and caveats) to be appropriately determined and strengthen the prognosticators clinical utility for predicting chemo-response.

This study utilised DNA microarray expression series GSE17920 obtained from the NCBI Gene Expression Omnibus archive. This dataset was normalised (to account for both intra, inter and batch to batch variation) and was used to explore the development of chemotherapy response binary classifiers. 16 genes (FDR ≤ 5%) were identified as being differentially expressed between the chemo-sensitive (n=92) and chemo-resistant (n=38) HL patients. Multi-layer perceptron ANN architectures were implemented and predictive performance of the individual models was assessed using both test and validation datasets (comprising 70% of total samples). Over 600,000 models were constructed and one classifier in particular assigned 100%, 92% and 91% of training, testing and validation samples to their correct classes (chemo-sensitive/chemo-resistance) respectively and produced an AUC of 0.926 for the ROC plot.

From this initial analysis outliers were identified that performed poorly with respect to prediction and so attention was directed towards the isolation of these samples from the main cohort such that two groups were formed: Group 16 (outliers) and Group 114 (non-outliers). Re-analysis by GEOquery and LIMMA for differentially expressed genes

(between chemo-sensitive and chemo-resistant patients) led to the identification of 1138 and 5344 probe sets for Group 16 and Group 114 respectively (FDR ≤ 5%). Interestingly only one out of the original 16 genes that were identified as being significantly different for all 130 samples remained significant for Group 16 compared to Group 114 where all 16 genes maintained significance (FDR ≤ 5%). While computational systematic effects cannot entirely be ruled out, it is plausible that the outliers may indeed represent a distinct biological population based upon gene expression profiles. For the outliers 22% of the first 50 genes explored have been previously associated with clinical outcome and/or chemotherapy treatment and thus may lend support to the contention that the poor predictive capability initially witnessed for this group could be attributed to an alternate expression pattern. It is unclear whether this difference in expression pattern between the two patient classes, is attributed to alternate effects e.g. sample storage, preparation and/or processing. Retraining of each group in isolation elicited models with 100% classification accuracy for all samples present within the training, testing and validation cohorts.

In summary therefore ANN provide an extremely useful in-silico modelling tool with strong predictive accuracy for classifying chemo-sensitive and chemo-resistant HL patient expression profiles taken from pre-treatment core biopsies. Random combinations of training, testing and validation datasets and predictive modelling have assisted the identification of outliers which might suggest the presence of biological variance in expression pattern compared to pattern exhibited from all 130 samples. When the outliers are removed from the remaining samples, both groups have increased number of differentially expressed genes (FDR ≤ 5%). There is the suggestion therefore that outliers may not only have a negative impact upon the predictive performance of ANN based classifiers but that they may also impact the significance of genes that are initially presented for further interrogation by tools such as LIMMA. This would consequently have a downstream impact as to which biomarkers are given due consideration for biological validation studies.

Methods

Gene Expression Omnibus microarray series GSE17920

GSE17920 data series contained DNA microarray expression data obtained from 130 pre-treatment core biopsies from classic Hodgkin's Lymphoma patients in which 38 patients were clinically resistant and 92 patients were noted to be sensitive to their chemotherapy treatment. DNA microarray analysis was conducted using Affymetrix GeneChip Human Genome U133 Plus 2.0 array. In brief the data were normalized and summaried using the rma function in the Affymetrix package. Batch-normalization was carried out using ComBat.

GEO2R and gene selection

GEO2R is a web based interface allowing users to call GEOquery in order to parse microarray expression data into structures suitable for statistical interrogation by LIMMA. Both software packages (written in R) are available from the Bioconductor project (http://www.bioconductor.org/). Benjamini and Hochberg multiple testing correction analysis was applied to raw p-values (q-values) and genes were selected for ANN model development that had a q-value (false discovery rate) of ≤ 0.05.

ANN model development

All modelling was carried out using Statistica Data Mining software (Statsoft Corporation USA). Supervised learning algorithms were developed using a MLP back propagation ANN and automated search parameters. A classification algorithm was selected and the categorical output was chemotherapeutic response.

Automated ANN modelling was established to both construct and test architecture robustness of the resultant ANN using random cohorts of samples selected by number seeds. Sample sizes for training, testing and validation were set at 30%, 10% and 60% for Group 130 and Group 114. For Group 16 training, testing and validation samples were set at 30%, 20% and 50% respectively. Architectures were built upon the Broyden-Fletcher-Goldfarb-Shanno (BFGS) optimisation algorithm. Activation functions which were used to propagate the input values into a classification result were chosen at

random from a number of transformative formulae for both the hidden and output nodes. These included: a) logistic; b) Tanh; c) Softmax; d) Identity; e) exponential. Sum of squares and entropy were used to measure classification error between actual and network prediction. Error values were back propagated allowing alteration of the weighted links between input/hidden and hidden/output layers. Model development had the flexibility to use either two or three hidden nodes allowing parsimonious algorithms with sufficient power to be produced.

Seeding values were altered to enable different combinations of training, testing and validation while keeping network seed constant. Variable network seeding values were used to examine the effect of varying network weights while keeping training, testing and validation sample sets constant.

20,000 models were run per analysis and the top 100 models with the highest predictive accuracy for training, testing and validation datasets were retained for statistical analysis. 10 runs were conducted for each parameter analysed. Two main variable settings were explored: a) variable sample seed with constant network seed weighting; b) variable network weighting with constant sample seed to ensure the same samples comprised the training, testing and validation datasets. This methodology was repeated for both the "randomised" and "non-randomised" sample order used for presentation to the ANN for model development. This study explored the development of over 1 million computational models.

Predictive accuracy as exemplified by heatmap signatures were produced using Microsoft Excel. Confidence intervals were calculated using a two-tailed t-distribution at the $\alpha \leq 0.05$ level.

EXAMPLE B

Exemplary neural network coding developed using Group 130 (full dataset) and the sixteen gene biomarkers listed in Table 1 (see Example A)

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Exemplary neural network coding developed using Group 16 outliers and the top four gene biomarkers listed in Table 6 (see Example A)

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CLAIMS

1. An *in vitro* method for determining the responsiveness of an individual with Hodgkin's lymphoma to chemotherapeutic drug treatment, the method comprising the steps of:

   a) providing a protein or mRNA sample an individual to be tested;

   b) determining the presence and/or amount in the sample of at least two proteins selected from the group identified in Table A, and/or of mRNA encoding the same

   wherein one or more of the at least two proteins selected from the group defined in Table A is not identified in Table B

   and wherein the presence and/or amount in the sample of the proteins selected from the group defined in Table A, or of the mRNA encoding the same, is indicative of the responsiveness of the individual with Hodgkin's lymphoma to chemotherapeutic drug treatment.

2. A method according to Claim 1 wherein the sample in step (a) is a lymph node tumour biopsy sample.

3. A method according to Claim 1 or 2 wherein step (b) comprises measuring the presence and/or amount in the sample of zinc finger protein 644 (ZNF644) and/or heat shock 70kDa protein 5 (HSPA5), and/or mRNA encoding the same.

4. A method according to any one of the preceding claims wherein step (b) comprises measuring the presence and/or amount in the sample of at least three proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen or more proteins selected from the group identified in Table A, and/or mRNA encoding the same.

5. A method according to Claim 4 wherein step (b) comprises measuring the presence and/or amount in the sample of at least 20 proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least 30, 40, 50, 100, 200, 500, 1000, or more proteins selected from the group identified in Table A, and/or mRNA encoding the same.

6. A method according to any one of the preceding claims wherein the proteins, and/or mRNA encoding the same, measured in step (b) are selected from one of the following groups defined in Table A:

(a) Biomarker nos. 1 to 10;
(b) Biomarker nos. 1 to 20;
(c) Biomarker nos. 1 to 30;
(d) Biomarker nos. 1 to 40;
(e) Biomarker nos. 1 to 50;
(f) Biomarker nos. 1 to 100;
(g) Biomarker nos. 1 to 200;
(h) Biomarker nos. 1 to 500;
(i) Biomarker nos. 1 to 1000;
(j) Biomarker nos. 1 to 2000;
(k) Biomarker nos. 1 to 3000; or
(l) Biomarker nos. 1 to 4000.

7. A method according to any one of the preceding claims wherein none of the at least two proteins selected from the group defined in Table A are identified in Table B.

8. A method according to any one of the preceding claims wherein step (b) comprises measuring the presence and/or amount in the sample of at least one protein, and/or mRNA encoding the same, selected from the group consisting of:

(a) Zinc finger protein 644 (ZNF644) ;
(b) Colipase, pancreatic (CLPS) ;
(c) EST tu05b03.x1;
(d) relaxin 1 (RLN1);

(e) phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D);
(f) EMI domain containing 2 (EMID2);
(g) heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa; HSPA5));
(h) spermatogenesis associated 12 (SPATA12);
(i) kinectin 1 (kinesin receptor; KTN1);
(j) pentraxin 3, long (PTX3);
(k) erythropoietin receptor (EPOR);
(l) DC-STAMP domain containing 2 (DCST2);
(m) golgi to ER traffic protein 4 homolog (*S. cerevisiae*; GET4);
(n) mitogen-activated protein kinase 14 (MAPK14); and
(o) chromosome 1 open reading frame 163 (C1orf163).

9. A method according to Claim 8 wherein step (b) comprises measuring the presence and/or amount in the sample of all of the following proteins, and/or mRNA encoding the same:

(a) Zinc finger protein 644 (ZNF644) ;
(b) Colipase, pancreatic (CLPS) ;
(c) EST tu05b03.x1;
(d) relaxin 1 (RLN1);
(e) phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D);
(f) EMI domain containing 2 (EMID2);
(g) heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa; HSPA5));
(h) spermatogenesis associated 12 (SPATA12);
(i) kinectin 1 (kinesin receptor; KTN1);
(j) pentraxin 3, long (PTX3);
(k) erythropoietin receptor (EPOR);
(l) DC-STAMP domain containing 2 (DCST2);
(m) golgi to ER traffic protein 4 homolog (*S. cerevisiae*; GET4);
(n) mitogen-activated protein kinase 14 (MAPK14); and
(o) chromosome 1 open reading frame 163 (C1orf163).

10. A method according to any one of the preceding claims wherein step (b) comprises measuring the presence and/or amount in the sample of mRNA encoding the proteins selected from the group identified in Table A.

11. A method according to Claim 10 wherein measuring the presence and/or amount in the sample of the mRNA is performed using binding agents capable of binding to the said mRNA.

12. A method according to Claim 11 wherein the binding agents are oligonucleotides.

13. A method according to any one of the preceding claims wherein step (b) comprises measuring the presence and/or amount in the sample of the proteins selected from the group identified in Table A.

14. A method according to Claim 13 wherein measuring the presence and/or amount in the sample of the proteins is performed using binding agents capable of binding to said proteins.

15. A method according to Claim 14 wherein the binding agents comprise or consist of an antibody or an antigen-binding fragment thereof.

16. A method according to Claim 15 wherein the antibody or antigen-binding fragment is selected from the group consisting of intact antibodies, Fv fragments (*e.g.* single chain Fv and disulphide-bonded Fv), Fab-like fragments *(e.g.* Fab fragments, Fab' fragments and $F(ab)_2$ fragments), single variable domains (*e.g.* V_H and V_L domains) and domain antibodies (dAbs, including single and dual formats [*i.e.* dAb-linker-dAb]).

17. A method according to Claim 16 wherein the antibody or antigen-binding fragment is a single chain Fv (scFv).

18. A method according to Claim 14 wherein the binding agent comprises or consists of an antibody-like binding agent, for example an affibody or aptamer.

19. A method according to any one of the preceding claims wherein the proteins in the sample are labelled with a detectable moiety prior to performing step (b).

20. A method according to Claim 19 wherein the detectable moiety is selected from the group consisting of: a fluorescent moiety; a luminescent moiety; a chemiluminescent moiety; a radioactive moiety; an enzymatic moiety.

21. A method according to any one of the preceding claims wherein measuring the presence and/or amount of the proteins, or mRNA encoding the same, in the sample is performed using a gene expression profiling array.

22. A method according to Claim 21 wherein the array is a surface-based array.

23. A method according to Claim 21 wherein the array is a bead-based array.

24. A method according to any one of Claims 21 to 23 wherein the array is selected from the group consisting of: macroarray; microarray; nanoarray.

25. A method according to any one of the preceding claims further comprising step (c) of comparing the presence and/or amount of the proteins, or mRNA encoding the same, with one or more reference values for said proteins or mRNA.

26. A method according to Claim 25 wherein the reference values correspond to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals selected from the group consisting of healthy individuals, individuals diagnosed with Hodgkin's lymphoma who are responsive to chemotherapeutic drug treatment and individuals diagnosed with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment.

27. A method according to Claim 25 or 26 wherein the amount of the proteins, or mRNA encoding the same, obtained in step (b) and the reference values for said proteins or mRNA are normalised prior to being compared.

28. A method according to any one of Claims 25 to 27 wherein step (c) comprises the use of a predictive model.

29. A method according to any one of Claims 25 to 28 wherein step (c) comprises use of a computer-implemented adaptive learning algorithm.

30. A method according to Claim 29 wherein the adaptive learning algorithm is an artificial neural network.

31. A method according to Claim 30 wherein the artificial neural network is a multilayer perceptron.

32. A method according to any one of Claims 28 to 31 wherein the predictive model has an accuracy of at least 90% for classification.

33. A method according to Claim 32 wherein the predictive model has an accuracy of at least 95% for classification.

34. A method according to Claim 33 wherein the predictive model has an accuracy of at least 99% for classification.

35. A method according to any one of Claims 26 to 34 wherein:

(a) an elevation in the amount of one or more of the following proteins (or mRNA encoding the same) relative to reference values corresponding to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment

HSPA5, PTX3, C1orf163, KTN1, MAPK14 and/or EPOR

and/or

(b) a decrease in the amount of one or more of the following proteins (or mRNA encoding the same) relative to reference values corresponding to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment

ZNF644, EMID2, RLN1, SPATA12, CLPS, EST tu05b03.x1, PDE6D, GET 4 and/or DCST2

is indicative of the individual with Hodgkin's lymphoma being responsive to chemotherapeutic drug treatment.

36. A method according to any one of Claims 26 to 34 wherein:

(a) an elevation in the amount of one or more of the following proteins (or mRNA encoding the same) relative to reference values corresponding to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals with Hodgkin's lymphoma who are responsive to chemotherapeutic drug treatment

ZNF644, EMID2, RLN1, SPATA12, CLPS, EST tu05b03.x1, PDE6D, GET 4 and/or DCST2

and/or

(b) a decrease in the amount of one or more of the following proteins (or mRNA encoding the same) relative to reference values corresponding to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals with Hodgkin's lymphoma who are responsive to chemotherapeutic drug treatment

HSPA5, PTX3, C1orf163, KTN1, MAPK14 and/or EPOR

is indicative of the individual with Hodgkin's lymphoma being resistant to chemotherapeutic drug treatment.

37. A method according to any one of Claims 26 to 36 wherein step (c) comprises identifying the individual as exhibiting atypical gene expression.

38. A method according to Claim 37 further comprising step (d) of determining the presence and/or amount in the sample of at least two proteins selected from the group identified in Table D, and/or of mRNA encoding the same.

39. A method according to Claim 38 wherein step (d) comprises measuring the presence and/or amount in the sample of at least three proteins selected from the group identified in Table D, and/or mRNA encoding the same, for example at least four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen or more proteins selected from the group identified in Table D, and/or mRNA encoding the same.

40. A method according to Claim 39 wherein step (d) comprises measuring the presence and/or amount in the sample of at least 20 proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least 30, 40, 50, 100, 200, 500, 1000, or more proteins selected from the group identified in Table D, and/or mRNA encoding the same.

41. A method according to any one of Claims 38 to 40 wherein the proteins, and/or mRNA encoding the same, measured in step (d) are selected from one of the following groups defined in Table D:

(a) Biomarker nos. 1 to 10;
(b) Biomarker nos. 1 to 20;
(c) Biomarker nos. 1 to 30;
(d) Biomarker nos. 1 to 40;
(e) Biomarker nos. 1 to 50;
(f) Biomarker nos. 1 to 100;
(g) Biomarker nos. 1 to 200;
(h) Biomarker nos. 1 to 500; or
(i) Biomarker nos. 1 to 1000.

42. A method according to any one of Claims 38 to 41 wherein step (d) comprises measuring the presence and/or amount in the sample of at least one protein, and/or mRNA encoding the same, selected from the group consisting of

(a) CD93 molecule (CD93);
(b) Gap junction protein, delta 3, 31.9 kDa (GJD3);
(c) Paired related homeobox 1 (PRRX1);
(d) Neuropilin 1 (NRP1);
(e) Cytoglobin (CYGB);
(f) Gamma-glutamyl transferase 5 (GGT5);
(g) Collagen, type VI, alpha 2 (COL6A2);
(h) Lysosomal protein transmembrane 4 beta (LAPTM4B);
(i) Dimethylarginine dimethylaminohydrolase 1 (DDAH1); and
(j) Zinc finger, DHHC-type containing 9 (ZDHHC9).

43. A method according to Claim 42 wherein step (d) comprises measuring the presence and/or amount in the sample of all of the following proteins, and/or mRNA encoding the same:

(a) CD93 molecule (CD93);
(b) Gap junction protein, delta 3, 31.9 kDa (GJD3);
(c) Paired related homeobox 1 (PRRX1); and
(d) Neuropilin 1 (NRP1).

44. A method according to any one of Claims 38 to 43 further comprising step (e) of comparing the presence and/or amount of the proteins, or mRNA encoding the same, with one or more reference values for said proteins or mRNA.

45. A method according to Claim 44 wherein the reference values correspond to the presence and/or amount of said proteins or mRNA in lymph node tissue from one or more individuals selected from a group consisting of healthy individuals, individuals diagnosed with Hodgkin's lymphoma who are responsive to chemotherapeutic drug treatment and individuals diagnosed with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment.

46. A method according to Claim 44 or 45 wherein the amount of the proteins, or mRNA encoding the same, obtained in step (e) and the reference values for said proteins or mRNA are normalised prior to being compared.

47. A method according to any one of the preceding claims further comprising the step of determining the medication history of the individual.

48. A method according to Claim 47 wherein determining the medication history of the individual comprises determining whether the patient has taken any HIV drug therapies prior to providing the sample.

49. A method for treating an individual with Hodgkin's lymphoma comprising:

(a) identifying an individual with Hodgkin's lymphoma who is responsive to chemotherapeutic drug treatment using a method according to any one of Claims 1 to 48; and

(b) administering a chemotherapeutic drug to the individual identified in step (a).

50. A method for treating an individual with Hodgkin's lymphoma comprising:

(a) identifying an individual with Hodgkin's lymphoma who is resistant to chemotherapeutic drug treatment using a method according to any one of Claims 1 to 48; and

(b) administering a therapeutic agent other than a chemotherapeutic drug to the individual identified in step (a).

51. A method according to Claim 50 wherein the therapeutic agent other than a chemotherapeutic drug is radiation therapy.

52. A method for treating an individual with Hodgkin's lymphoma comprising:

(a) determining the responsiveness of an individual with Hodgkin's lymphoma to chemotherapeutic drug treatment using a method according to any one of Claims 1 to 48;

(b) selecting an effective therapeutic agent for administration to the individual based on the responsiveness of the patient to chemotherapeutic drug treatment; and

(c) administering said effective therapeutic agent identified in step (b) to the individual.

53. An array for use in a method according any one of Claims 1 to 48, the array comprising binding agents for two or more of the proteins identified in Table A and/or D, or mRNA encoding the same.

54. An array according to Claim 53 wherein the array comprises binding agents for fewer then 1000 different proteins identified in Table A and/or D, or mRNA coding the same, for example fewer than 500, 400, 300, 200, 100, 50, 25, or 20 different proteins, or mRNA coding the same.

55. An array according to Claim 53 or 54 wherein the array comprises binding agents for all of the proteins identified in Table C, or mRNA encoding the same.

56. An array according to Claim 55 wherein the array comprises binding agents for all of the proteins identified in Table A, or mRNA encoding the same.

57. An array according to any one of Claims 53 to 56 wherein the array comprises binding agents for all of the proteins identified in Table D, or mRNA encoding the same.

58. An array according to any one of Claims 53 to 57 wherein the array comprises binding agents for all of the proteins identified in Tables A and D.

59. An array according to any one of Claims 53 to 57 wherein the array comprises binding agents for mRNA encoding all of the proteins in Tables A and D.

60. An array according to any one of Claims 53 to 59 wherein the binding agents are immobilised.

61. An array according to any one of Claims 53 to 60 wherein the array is a surface-based array or bead-based array.

62. An array according to any one of Claims 53 to 61 wherein the array is suitable for use with high-throughput screening methods of gene profiling.

63. A kit for performing a method according to any one of Claims 1 to 48 comprising:

(a) an array according to any one of Claims 53 to 62; and

(b) instructions for performing a method according to any one of Claims 1 to 48.

64. A kit according to Claim 63 further comprising one or more reagents for use in a method according to any one of Claims 1 to 48.

65. A kit according to Claim 63 or 64 further comprising a positive control sample and/or a negative control sample.

66. A computer-implemented method for classifying a sample from an individual with Hodgkin's lymphoma, comprising:

(a) providing a dataset associated with the sample, wherein said dataset comprises quantitative data for at least two proteins, and/or mRNA encoding the same, selected from the group defined in Table A;

(b) inputting said dataset into an analytical process on a computer that compares said dataset against one or more reference datasets; and

(c) classifying said sample according to the output of said analytical process

wherein one or more of the at least two proteins selected from the group defined in Table A is not identified in Table B.

and wherein in step (c) the sample is classified as from an individual with Hodgkin's lymphoma who is responsive to chemotherapeutic drug treatment or

from an individual with Hodgkin's lymphoma who is resistant to chemotherapeutic drug treatment.

67. A computer-implemented method according to Claim 66 wherein the dataset in step (a) comprises quantitative data for zinc finger protein 644 (ZNF644) and/or heat shock 70kDa protein 5 (HSPA5), and/or mRNA encoding the same.

68. A computer-implemented method according to Claim 66 or 67 wherein the dataset in step (a) comprises quantitative data for at least three proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen or more proteins selected from the group identified in Table A, and/or mRNA encoding the same.

69. A computer-implemented method according to Claim 68 wherein the dataset in step (a) comprises quantitative data for at least 20 proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least 30, 40, 50, 100, 200, 500, 1000, or more proteins selected from the group identified in Table A, and/or mRNA encoding the same.

70. A computer-implemented method according to any one of Claims 66 to 69 wherein the proteins, and/or mRNA encoding the same, for which quantitative data are provided in step (a) are selected from one of the following groups defined in Table A:

(a) Biomarker nos. 1 to 10;
(b) Biomarker nos. 1 to 20;
(c) Biomarker nos. 1 to 30;
(d) Biomarker nos. 1 to 40;
(e) Biomarker nos. 1 to 50;
(f) Biomarker nos. 1 to 100;
(g) Biomarker nos. 1 to 200;
(h) Biomarker nos. 1 to 500;
(i) Biomarker nos. 1 to 1000;
(j) Biomarker nos. 1 to 2000;

(k) Biomarker nos. 1 to 3000; or

(l) Biomarker nos. 1 to 4000.

71. A computer-implemented method according to any one of Claims 66 to 70 wherein none of the at least two proteins selected from the group identified in Table A are identified in Table B.

72. A computer-implemented method according to Claim 66 or 71 wherein the dataset in step (a) comprises quantitative data for at least one protein, and/or mRNA encoding the same, selected from the group consisting of:

(a) Zinc finger protein 644 (ZNF644) ;
(b) Colipase, pancreatic (CLPS) ;
(c) EST tu05b03.x1;
(d) relaxin 1 (RLN1);
(e) phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D);
(f) EMI domain containing 2 (EMID2);
(g) heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa; HSPA5));
(h) spermatogenesis associated 12 (SPATA12);
(i) kinectin 1 (kinesin receptor; KTN1);
(j) pentraxin 3, long (PTX3);
(k) erythropoietin receptor (EPOR);
(l) DC-STAMP domain containing 2 (DCST2);
(m) golgi to ER traffic protein 4 homolog (*S. cerevisiae*; GET4);
(n) mitogen-activated protein kinase 14 (MAPK14); and
(o) chromosome 1 open reading frame 163 (C1orf163).

73. A computer-implemented method according to Claim 66 or 72 wherein the dataset in step (a) comprises quantitative data for all of the following proteins, and/or mRNA encoding the same:

(a) Zinc finger protein 644 (ZNF644) ;
(b) Colipase, pancreatic (CLPS) ;
(c) EST tu05b03.x1;

(d) relaxin 1 (RLN1);
(e) phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D);
(f) EMI domain containing 2 (EMID2);
(g) heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa; HSPA5));
(h) spermatogenesis associated 12 (SPATA12);
(i) kinectin 1 (kinesin receptor; KTN1);
(j) pentraxin 3, long (PTX3);
(k) erythropoietin receptor (EPOR);
(l) DC-STAMP domain containing 2 (DCST2);
(m) golgi to ER traffic protein 4 homolog (*S. cerevisiae*; GET4);
(n) mitogen-activated protein kinase 14 (MAPK14); and
(o) chromosome 1 open reading frame 163 (C1orf163).

74. A computer-implemented method according to any one of Claims 66 to 73 wherein the dataset in step (a) comprises quantitative data for at least two proteins selected from the group identified in Table D, and/or of mRNA encoding the same.

75. A computer-implemented method according to Claim 74 wherein the dataset in step (a) comprises quantitative data for at least three proteins selected from the group identified in Table D, and/or mRNA encoding the same, for example at least four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen or more proteins selected from the group identified in Table D, and/or mRNA encoding the same.

76. A computer-implemented method according to Claim 75 wherein the dataset in step (a) comprises quantitative data for at least 20 proteins selected from the group identified in Table A, and/or mRNA encoding the same, for example at least 30, 40, 50, 100, 200, 500, 1000, or more proteins selected from the group identified in Table D, and/or mRNA encoding the same.

77. The computer-implemented according to any one of Claims 74 to 76 wherein the proteins, and/or mRNA encoding the same, for which quantitative data are provided in step (a) are selected from one of the following groups defined in Table D:

(a) Biomarker nos. 1 to 10;
(b) Biomarker nos. 1 to 20;
(c) Biomarker nos. 1 to 30;
(d) Biomarker nos. 1 to 40;
(e) Biomarker nos. 1 to 50;
(f) Biomarker nos. 1 to 100;
(g) Biomarker nos. 1 to 200;
(h) Biomarker nos. 1 to 500; or
(i) Biomarker nos. 1 to 1000.

78. A computer-implemented method according to Claim 74 or 77 wherein the dataset in step (a) comprises quantitative data for at least one protein, and/or mRNA encoding the same, selected from the group consisting of:

(a) CD93 molecule (CD93);
(b) Gap junction protein, delta 3, 31.9 kDa (GJD3);
(c) Paired related homeobox 1 (PRRX1);
(d) Neuropilin 1 (NRP1);
(e) Cytoglobin (CYGB);
(f) Gamma-glutamyl transferase 5 (GGT5);
(g) Collagen, type VI, alpha 2 (COL6A2);
(h) Lysosomal protein transmembrane 4 beta (LAPTM4B);
(i) Dimethylarginine dimethylaminohydrolase 1 (DDAH1); and
(j) Zinc finger, DHHC-type containing 9 (ZDHHC9).

79. A computer-implemented method according to Claim 78 wherein the dataset in step (a) comprises quantitative data for all of the following proteins, and/or mRNA encoding the same:

(a) CD93 molecule (CD93);
(b) Gap junction protein, delta 3, 31.9 kDa (GJD3);
(c) Paired related homeobox 1 (PRRX1); and
(d) Neuropilin 1 (NRP1).

80. A computer-implemented method according to any one of Claims 66 to 79 wherein the dataset in step (a) and the reference datasets are normalised.

81. A computer-implemented method according to any one of Claims 66 to 80 wherein said analytical process in step (b) comprises use of a predictive model which comprises the one or more reference datasets.

82. A computer-implemented method according to Claim 81 wherein said one or more reference datasets comprise quantitative data obtained from one or more individuals selected from a group consisting of healthy individuals, individuals diagnosed with Hodgkin's lymphoma who are responsive to chemotherapeutic drug treatment and individuals diagnosed with Hodgkin's lymphoma who are resistant to chemotherapeutic drug treatment.

83. A computer-implemented method according to any one of Claims 66 to 82 wherein said analytical process in step (b) comprises use of an adaptive learning algorithm.

84. A computer-implemented method according to Claim 83 wherein the adaptive learning algorithm is an artificial neural network.

85. A computer-implemented method according to Claim 84 wherein the artificial neural network is a multilayer perceptron.

86. A computer-implemented method according to any one of Claims 66 to 85 wherein the predictive model has an accuracy of at least 90% for classification.

87. A computer-implemented method according to Claim 86 wherein the predictive model has an accuracy of at least 95% for classification.

88. A computer-implemented method according to Claim 87 wherein the predictive model has an accuracy of at least 99% for classification.

89. A computer system for performing a computer-implemented method according to any one of Claims 66 to 88, wherein the system comprises a digital computer and

computer readable program means for enabling the computer to perform said computer-implemented method.

90. A computer system according to Claim 89 further comprising a computer-readable storage medium comprising reference datasets.

91. A computer-readable storage medium comprising computer readable program means for enabling the computer to perform a computer-implemented method according to any one of Claims 66 to 88.

92. A computer-readable storage medium according to Claim 91 further comprising reference datasets.

93. An *in vitro* method for determining the responsiveness of an individual with Hodgkin's lymphoma to chemotherapeutic drug treatment substantially as herein described with reference to the Examples.

94. A method for treating an individual with Hodgkin's lymphoma substantially as herein described with reference to the Examples.

95. An array substantially as herein described with reference to the Examples.

96. A kit substantially as herein described with reference to the Examples.

97. A computer-implemented method for classifying a sample from an individual with Hodgkin's lymphoma substantially as herein described with reference to the Examples.

98. A computer system substantially as herein described with reference to the Examples.

99. A computer-readable storage medium substantially as herein described with reference to the Examples.

FIGURE 1

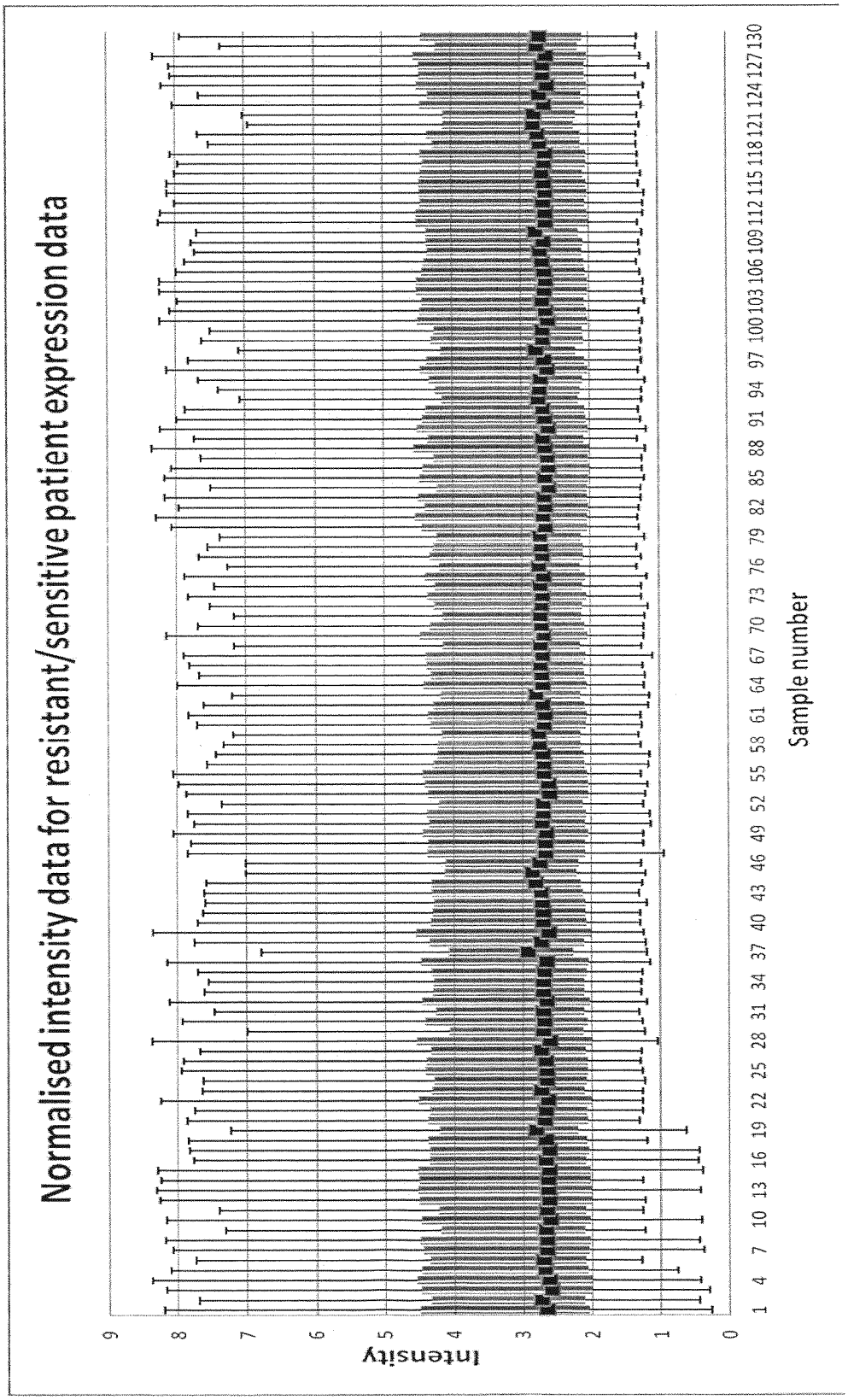

Normalised intensity data for resistant/sensitive patient expression data
Intensity
0
1
2
3
4
5
6
7
8
9
Sample number
1 4 7 10 13 16 19 22 25 28 31 34 37 40 43 46 49 52 55 58 61 64 67 70 73 76 79 82 85 88 91 94 97 100 103 106 109 112 115 118 121 124 127 130

FIGURE 2

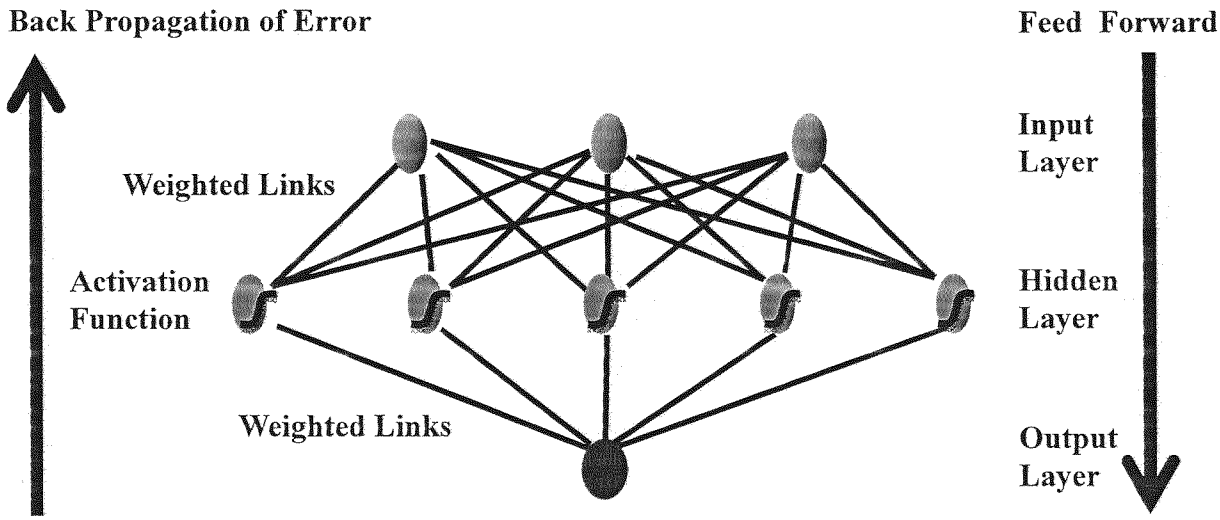

Back Propagation of Error
Feed Forward
Weighted Links
Activation Function
Weighted Links
Input Layer
Hidden Layer
Output Layer

FIGURE 3

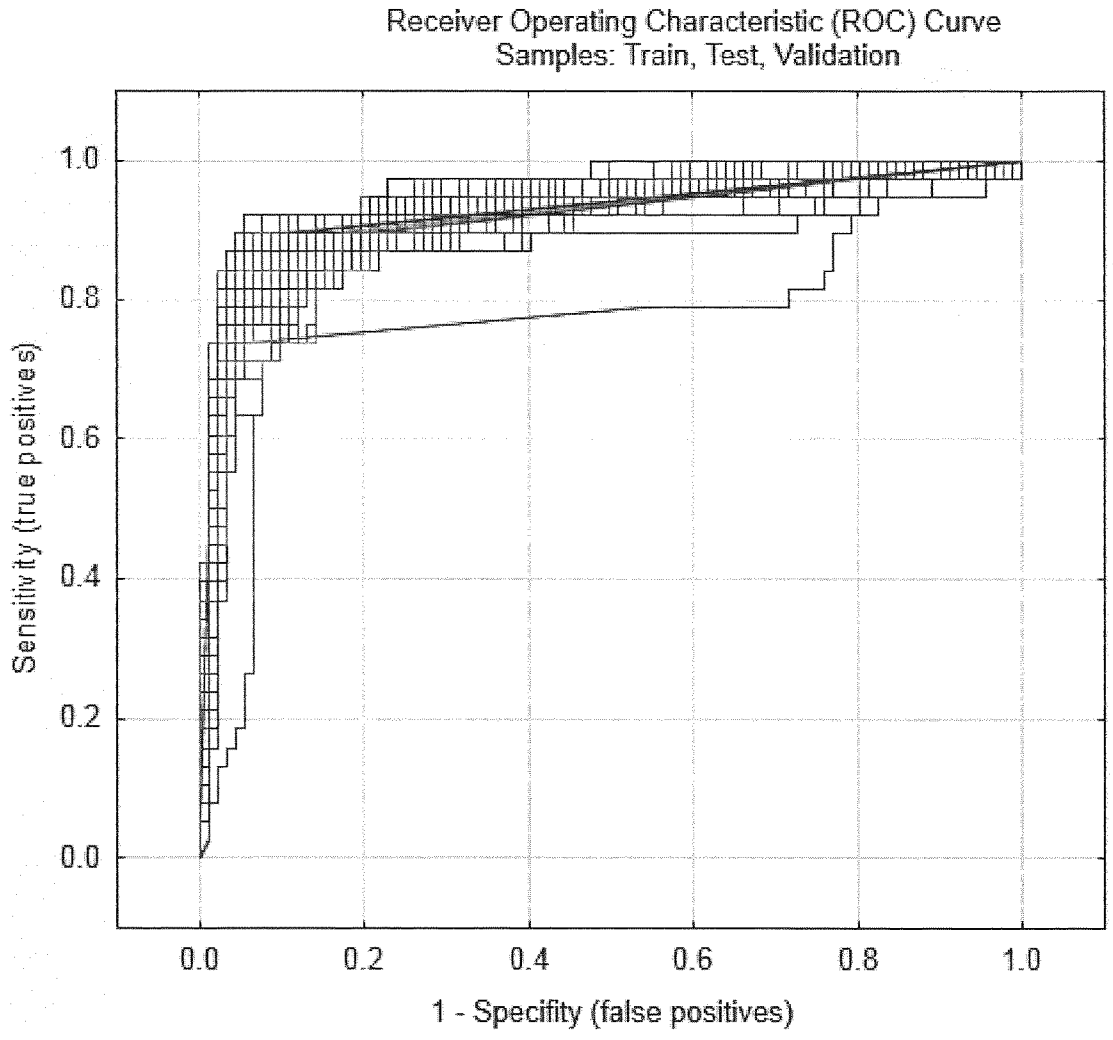
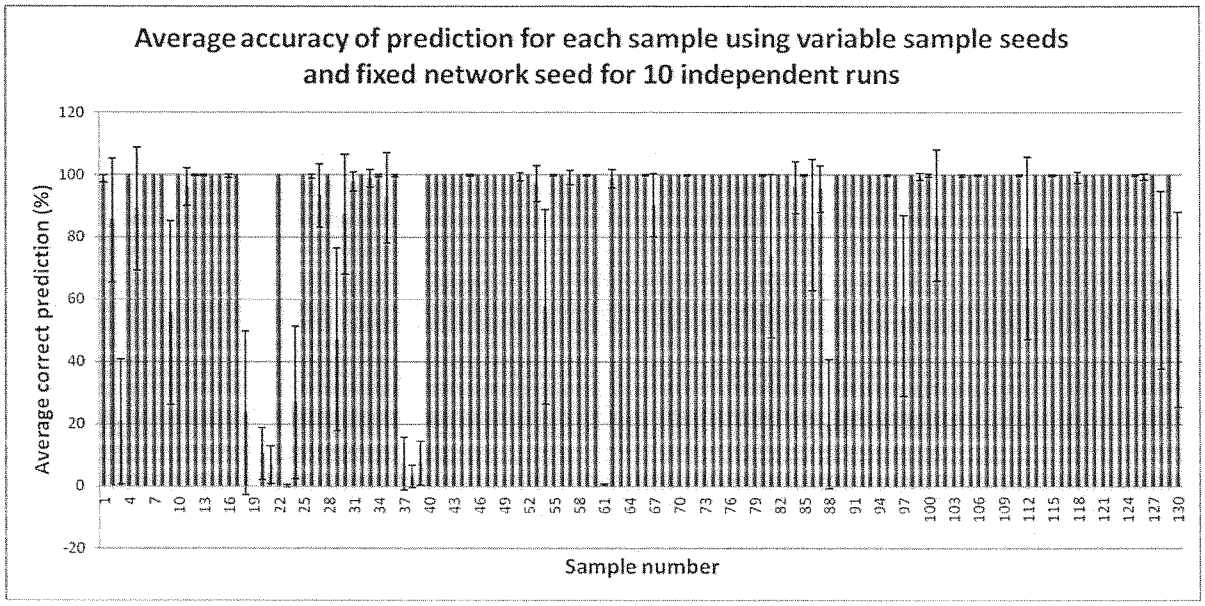

Receiver Operating Characteristic (ROC) Curve
Samples: Train, Test, Validation
Sensitivity (true positives)
1 - Specifity (false positives)
0.0
0.2
0.4
0.6
0.8
1.0

FIGURE 4

(A)


Average accuracy of prediction for each sample using variable sample seeds and fixed network seed for 10 independent runs
Average correct prediction (%)
120
100
80
60
40
20
0
-20
1 4 7 10 13 16 19 22 25 28 31 34 37 40 43 46 49 52 55 58 61 64 67 70 73 76 79 82 85 88 91 94 97 100 103 106 109 112 115 118 121 124 127 130
Sample number

(B)

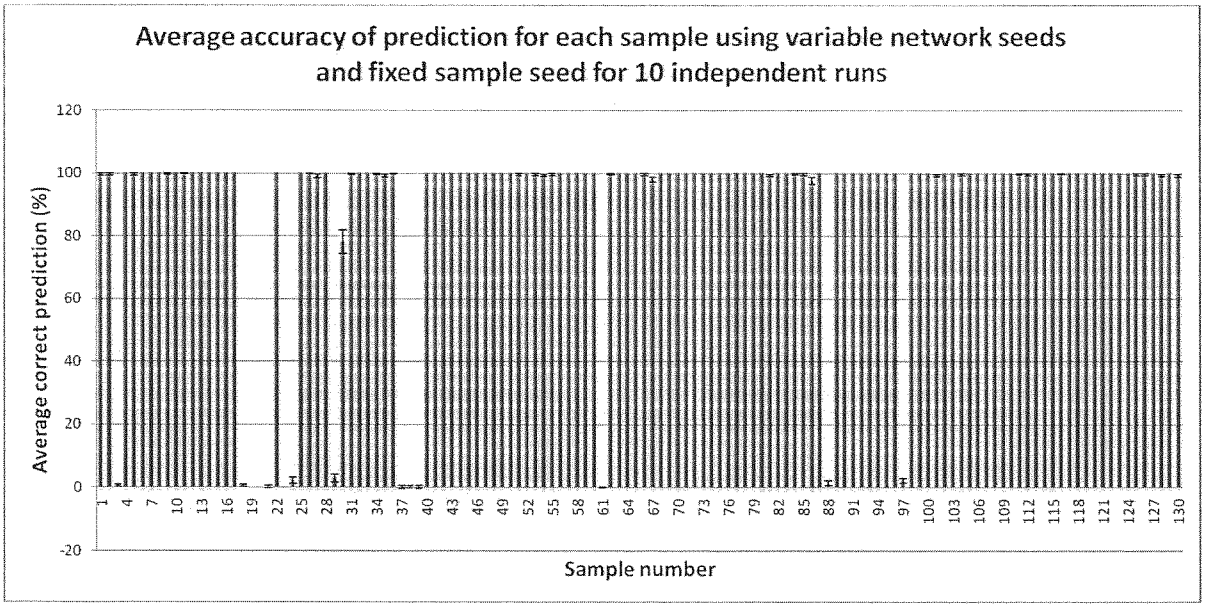

Average accuracy of prediction for each sample using variable network seeds and fixed sample seed for 10 independent runs
Average correct prediction (%)
120
100
80
60
40
20
0
-20
1 4 7 10 13 16 19 22 25 28 31 34 37 40 43 46 49 52 55 58 61 64 67 70 73 76 79 82 85 88 91 94 97 100 103 106 109 112 115 118 121 124 127 130
Sample number

FIGURE 5

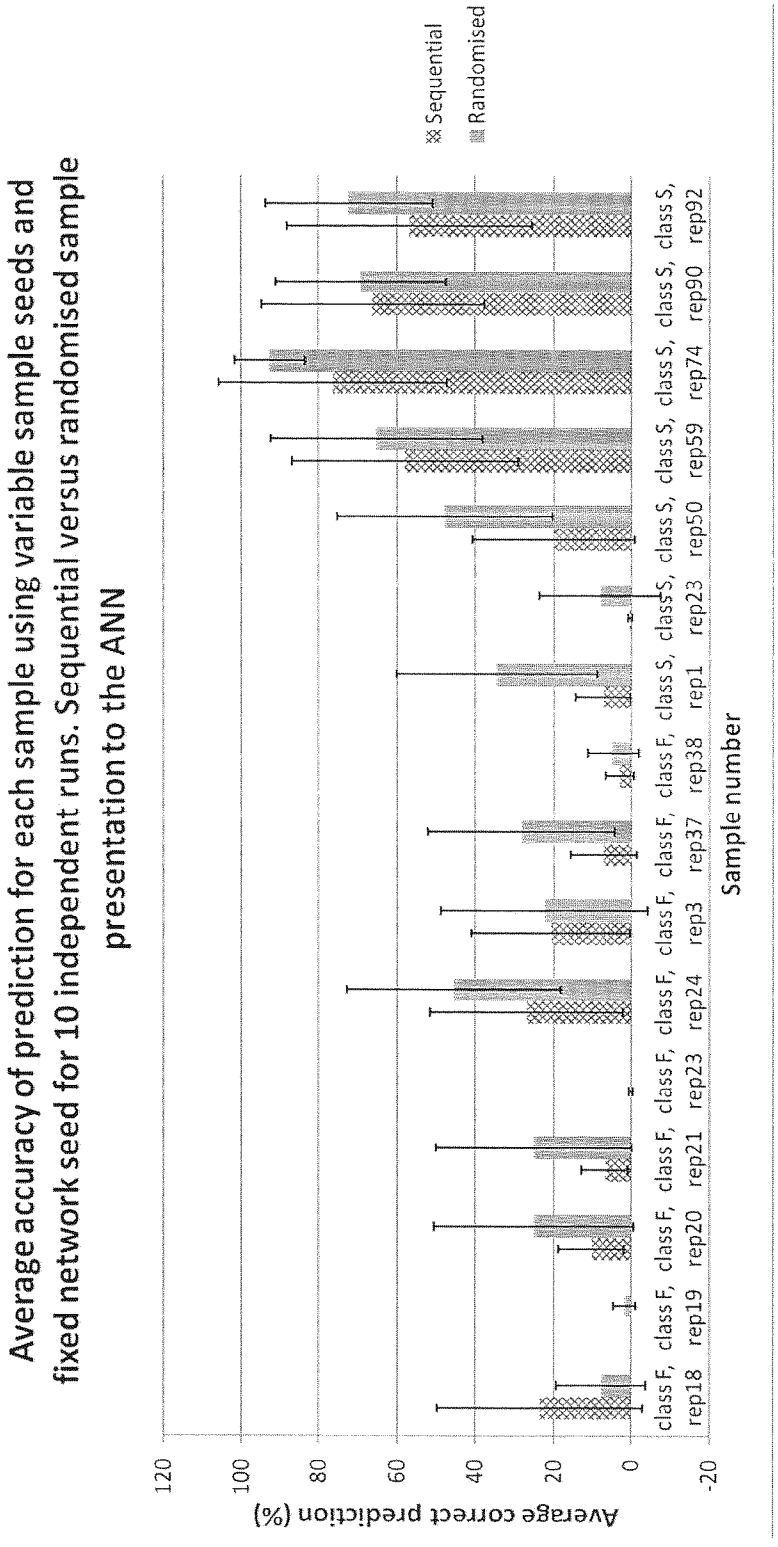

Average accuracy of prediction for each sample using variable sample seeds and fixed network seed for 10 independent runs. Sequential versus randomised sample presentation to the ANN
Sequential
Randomised
Average correct prediction (%)
120
100
80
60
40
20
0
-20
Sample number
class F, rep18
class F, rep19
class F, rep20
class F, rep21
class F, rep23
class F, rep24
class F, rep3
class F, rep37
class F, rep38
class S, rep1
class S, rep23
class S, rep50
class S, rep59
class S, rep74
class S, rep90
class S, rep92

FIGURE 6

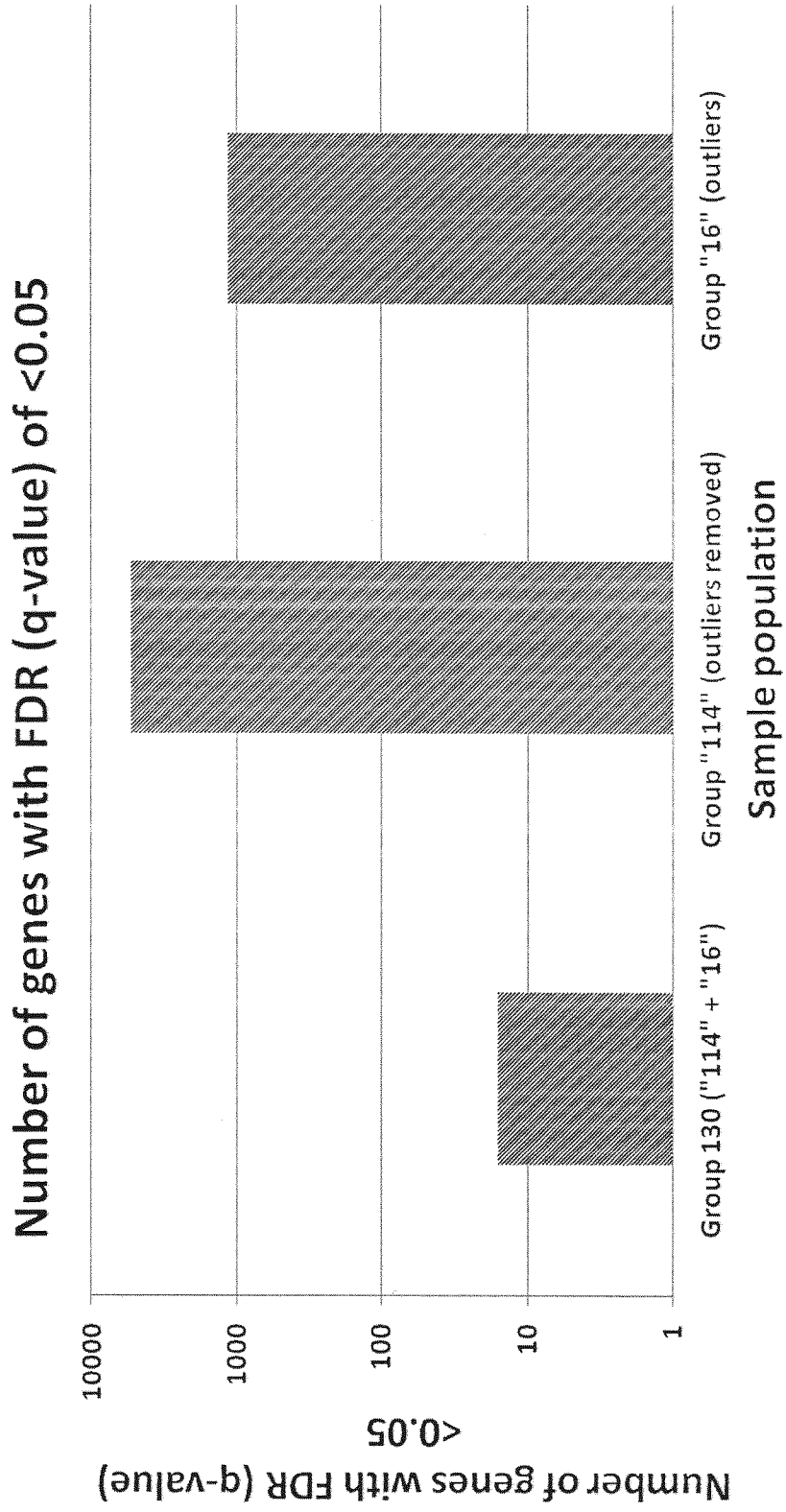
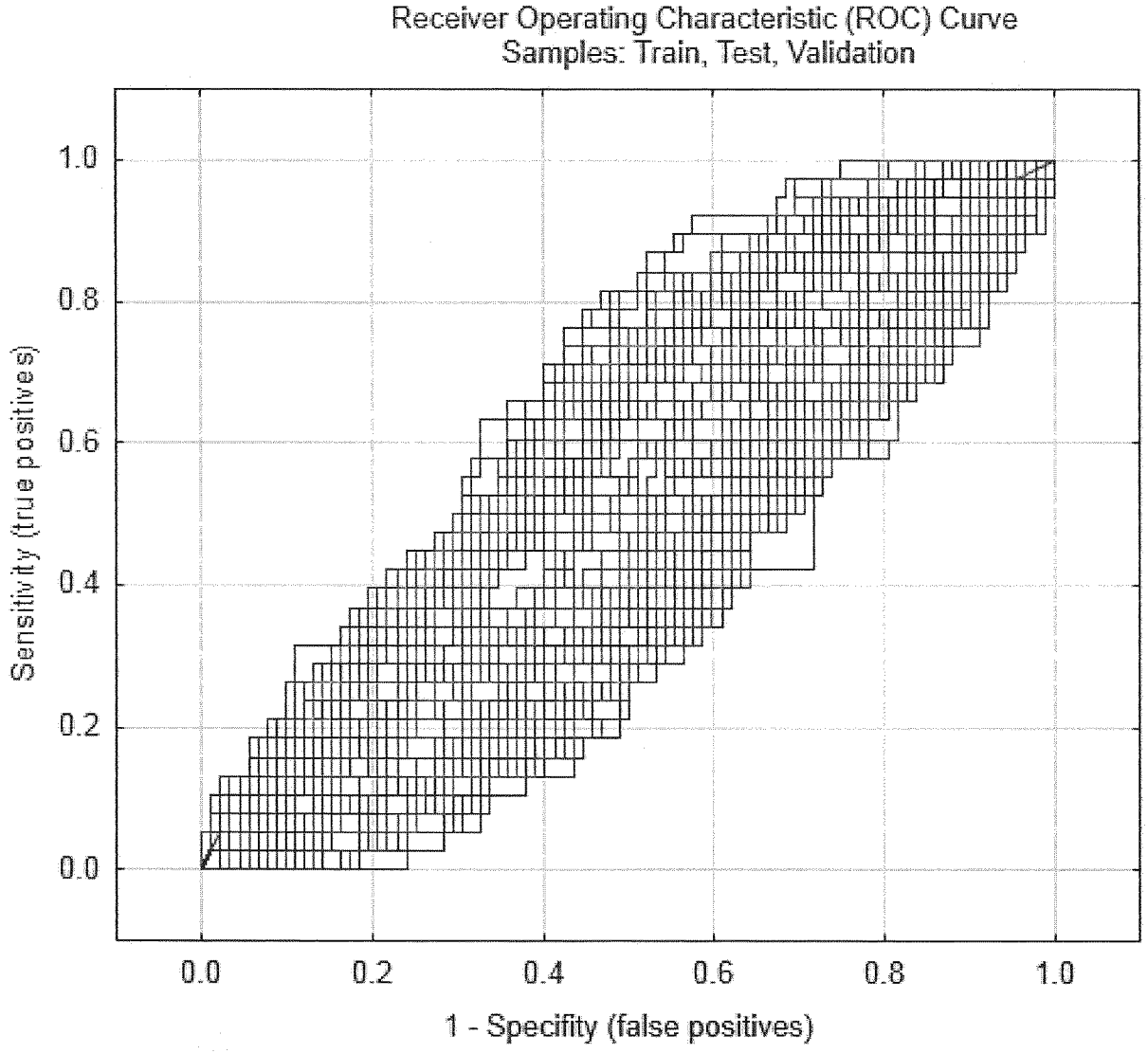

Number of genes with FDR (q-value) of <0.05
10000
1000
100
10
1
Group 130 ("114" + "16")
Group "114" (outliers removed)
Group "16" (outliers)
Sample population
Number of genes with FDR (q-value) <0.05

FIGURE 7


Receiver Operating Characteristic (ROC) Curve
Samples: Train, Test, Validation
Sensitivity (true positives)
1 - Specifity (false positives)
0.0
0.2
0.4
0.6
0.8
1.0