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Microarray Analysis of Lymphatic Tissue Reveals Stage-Specific, Gene Expression Signatures in HIV-1 Infection¹

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Abstract

Untreated HIV-1 infection progresses through acute and asymptomatic stages to AIDS. Although each of the three stages has well-known clinical, virologic, and immunologic characteristics, much less is known of the molecular mechanisms underlying each stage. In this study, we report lymphatic tissue microarray analyses, revealing for the first time stage-specific patterns of gene expression during HIV-1 infection. We show that although there is a common set of key genes with altered expression throughout all stages, each stage has a unique gene expression signature. The acute stage is most notably characterized by increased expression of hundreds of genes involved in immune activation, innate immune defenses (e.g., *RIG-1*, *MDA-5*, *TLR7* and *TLR8*, *PKR*, *APOBEC3B*, *3F*, *3G*), adaptive immunity, and in the proapoptotic Fas-Fas ligand pathway. Yet, quite strikingly, the expression of nearly all acute stage genes return to baseline levels in the asymptomatic stage, accompanying partial control of infection. This transition from acute to asymptomatic stage is tied to increased expression of a diverse array of immunosuppressive genes (e.g., *CLEC12B*, *ILT4*, *galectin-3*, *CD160*, *BCMA*, *FGL2*, *LAG3*, *GPNMB*). In the AIDS stage, decreased expression of numerous genes involved in T cell signaling identifies genes contributing to T cell dysfunction. These common and stage-specific gene expression signatures identify potential molecular mechanisms underlying the host response and the slow, natural course of HIV-1 infection.

Untreated HIV-1 infection typically progresses from acute through a clinically asymptomatic stage to full-blown AIDS over the course of 5–10 years. In the acute stage (defined as individuals infected within 4 mo of documented sero-conversion to HIV), the rapid and profound damage to the host's immune system is manifest primarily as massive

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depletion of CD4⁺ T cells, especially in the gut (1, 2). Yet, despite this initial damage, most untreated patients enter a long period of clinical latency, the asymptomatic stage (defined as individuals infected for at least 4 mo with a CD4⁺ T cell count >200 cells/ μ l), in which the pace of immune damage slows. Eventually, however, with continued CD4⁺ T cell depletion and destruction of lymphatic tissue (LT)⁴ architecture, most infected patients progress to AIDS (defined as infected individuals with a CD4⁺ T cell count <200 cells/ μ l) (3).

Each stage has well-described clinical, virologic, and immunological characteristics, but the molecular mechanisms underlying these stage-specific features remain poorly understood. Thus, elucidating the molecular basis responsible for these key virologic and immunologic characteristics of the three stages of infection should improve our understanding of HIV-1 pathogenesis, particularly those genes and pathways that are important in determining the level of virus replication, the degree of immune activation, and the extent/pace of CD4⁺ T cell loss, as well as potentially identify new therapeutic targets.

Microarrays have been used for some time in the study of HIV-1 infection, including monitoring gene expression in cell lines, PBMCs, and PBMC subsets (4, 5). Although these previous studies are informative, they likely do not best represent the gene expression occurring in lymphoid tissue in vivo. To that end, we used Affymetrix Human Genome U133 Plus 2.0 Arrays to examine gene expression in LTs of HIV-1-positive subjects in each clinical stage compared with uninfected subjects (Table I), focusing on LTs because transcriptional profiles at this major site of virus production and pathology (6) should depict host-pathogen interactions directly relevant to pathogenesis. We show that there are stage-specific signatures of genes and pathways in LTs that highlight both a dramatically extensive early host response in acute infection and rapid resolution of that response during the asymptomatic stage, and we identify genes involved in T cell dysfunction in AIDS.

Materials and Methods

Lymph node biopsies, RNA extractions, synthesis of biotin-labeled cRNA probes, and microarray hybridization followed previously published procedures (7).

Lymph node biopsy specimens

Inguinal lymph node biopsies from 22 untreated HIV-1-infected subjects at different clinical stages and 5 uninfected subjects were obtained for this University of Minnesota Institutional Review Board-approved microarray study. Each lymph node biopsy was placed into a Falcon tube and snap frozen by dropping it into liquid nitrogen.

RNA extraction, synthesis of biotin-labeled cRNA probes, and microarray hybridization

Frozen lymph nodes were homogenized with a power homogenizer (Heat Systems Ultrasonic) in TRIzol (catalog no. 15596-018; Invitrogen) without thawing. Total RNA was isolated according to the manufacturer's protocol and further purified with a RNeasy Mini Kit (catalog no. 74104; Qiagen). Double-stranded cDNA and biotin-labeled cRNA probes were synthesized from 5 μ g of total RNA with a MessageAmp II aRNA kit (catalog no. AM1757; Ambion). The cRNA probes were column purified and fragmented with a fragmentation kit (catalog no. 8740; Ambion).

Fifteen micrograms of fragmented cRNA was hybridized to an Affymetrix Human Genome U133 Plus 2.0. After hybridization, chips were washed, stained with streptavidin-PE, and scanned with GeneChip Operating Software at the Biomedical Genomics Center at the

⁴Abbreviations used in this paper: LT, lymphatic tissue; DC, dendritic cell; BID, BH3-interacting domain death agonist.

University of Minnesota. The experiments from each RNA sample were duplicated in the preparation of each cRNA probe and microarray hybridization.

Microarray data analysis

Cel. files were uploaded into the Expressionist program (Genedata; Pro version 4.5) and the expression level for each of the 47,000 transcripts in the arrays were analyzed by using the robust multi-array analysis algorithm. The expression levels from duplicated chips of the same individual's RNA were correlated and averaged. The expression data from all individuals were exported as Excel files for statistical analysis.

Tests for differences between the stages were conducted using the two-sample *t* test, assuming the variance of the measurements are the same in the two groups. Fold differences in the level of gene expression between any two stages were estimated with the ratio of the means in the two stages. All computations were conducted using the software S-plus version 3.4 from MathSoft.

After statistical analysis, data were sorted based on these transcript cutoffs: $p < 0.05$ and fold change > 1.7 . Significantly changed genes and transcripts were uploaded into the NetAffix Analysis Center (<http://www.affymetrix.com/analysis/index.affx>) to query gene ontology information and into Ingenuity Pathways Analysis (Ingenuity Systems, www.ingenuity.com) for gene annotation and pathway analysis.

The data discussed in this publication have been deposited in the National Center for Biotechnology Information's Gene Expression Omnibus (40) and are accessible through GEO Series accession no. GSE16363 (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16363>).

Real-time RT-PCR and immunohistochemical staining

Significantly altered genes (*STAT1*, *RANTES*, *IFN- γ*) in the microarray analysis were confirmed both by LightCycler real-time PCR and by immunohistochemical staining as published previously (7).

Results

We found that HIV-1-infected subjects (22 individuals) were clearly distinguishable from uninfected subjects (5 individuals) and that each disease stage had a distinct gene expression signature. As is evident in Fig. 1, the stages differed compared with uninfected subjects in both the number of genes with altered expression as well as the direction of change in gene expression.

Altogether, from the array's nearly 47,000 transcripts, we found 766 altered genes. Only ~6% (46 genes) of the altered genes were common to all stages (region C1 in Fig. 1), with another ~21% (161 genes) common to two stages (C2, C3, and C4) and ~73% (559 genes) unique to one stage (S1, S2, and S3). Strikingly, ~70% of the 766 genes {536} were altered in the acute stage (S1, C1, C2, and C3), with ~67% (358 genes) of those unique to this stage (S1) and ~81% (289 genes) of those unique genes had increased expression. In sharp contrast, the asymptomatic stage (S2) had few (18 genes) uniquely altered genes. The AIDS stage (S3) had 183 uniquely altered genes, with ~84% (153 genes) decreased in expression.

Based on gene ontology/annotations from the NetAffix Analysis Center, Ingenuity Pathways Analysis, and extensive examination of published literature, we classified ~80% of all altered genes (621 genes) into functional categories shown in Fig. 2 and supplemental Table I.⁵

Common

Common to all stages (region C1) were 46 genes (Fig. 2A), one-half (23 genes) of which have known functions in immune defenses. *STAT1* expression was highly increased, as were defense genes regulated by STAT1 such as *IFN- γ* and a number of IFN-related antiviral genes like 2', 5'-oligoadenylate synthetase 1 (*OAS1*), *ISG15*, *IFI27*, and the guanylate-binding proteins (GBP1, 5). Genes involved in immune activation and cell proliferation accounted for ~25% (12 genes) of common genes, including cell cycle-related genes such as *cyclin B1*. Expression of most of these genes increased. Also, expression increased for genes encoding the important anti-HIV-1 chemokines RANTES and MIP-1 β and their cognate receptor CCR5, as well as eight genes encoding proteins associated with NK cell and CD8⁺ T cell-mediated cytotoxicity, such as CD8, granzymes, and cytotoxic and regulatory T cell molecule.

Acute stage

The acute stage had by far the most (358 genes) uniquely altered genes (region S1), with ~81% (289 genes) increased in expression. Fig. 2B shows the functional categories of 291 unique acute stage genes; the rest appear in supplemental Table I.

Immune activation accounted for ~40% (144 genes) of unique acute stage genes. Notable are: 1) proinflammatory mediators (e.g., *IL-32* and *IL-1R* antagonist); 2) signal transduction molecules (e.g., the T cell-related gene *calmodulin 3*); 3) transcriptional regulators (e.g., *T-box 21* and the thymus hormone *thymopoietin*); 4) activators of cell proliferation (e.g., *Ki-67* and *proliferating cell nuclear Ag*); 5) mediators of cell cycle progression (e.g., *nucleophosmin/B23* and cell division-cycle-associated proteins); and 6) moderators of pathologic processes associated with immune activation (e.g., metallothioneins and thioredoxins to counter free radical damage).

Countering the predominance of increased expression of immune activation genes was an apparent paradoxical increase in genes whose function is clearly immunosuppressive. This may reflect a mechanism to balance the necessary activation of host defenses while avoiding the immunopathologic effects of immune activation but also may be detrimental in dampening the immune response in the face of continuing viral replication. Genes with increased expression in the acute stage linked to immunosuppression included the *C-type lectin domain family 12, member B (CLEC12B)*, *glycoprotein (transmembrane) nmb (GPNMB)*, and *galectin-3*, all inhibitors of macrophage activation and inflammatory processes, *CD160*, and *LAG3*, both negative regulators of T cell activation, *ILT4*, a receptor involved in the tolerization of dendritic cells (DCs), and *IDO*, an enzyme with far-reaching immunosuppressive effects regulating the immune system. The single immunoregulatory gene decreased in expression was *RANKL*, implicated in the maintenance and survival of DCs and peripheral CD4⁺CD25⁺ regulatory T cells.

Immune defenses accounted for ~7% (25 genes) of unique acute stage genes, representative of a broad, innate immune response in which the IFN system is the most prominent component of the host's response to HIV-1, e.g., increased expression of genes encoding *OAS2* and 3, myxovirus resistance 2, polynucleotide phosphorylase, IFN-induced transmembrane protein 1 (9–27), and numerous others. Additional genes of innate immunity included increased expression of three complement and FcR genes as well as a number of antiviral molecules and pattern recognition receptors—genes coding for TLRs 7 and 8 and the C-type lectin receptors Dectin-1 and mannose receptor, the cytoplasmic RNA helicase proteins RIG-I and MDA-5, dsRNA-dependent protein kinase (PKR), and the APOBECs, including not only the known suppressors of HIV-1 replication, APOBEC3G and -3F, but also -3B. In addition, expression of four genes coding for cytotoxic effectors such as

granzymes and killer-specific secretory protein of 37 kDa increased, consistent with innate and adaptive defenses by NK cells and CTL.

Apoptosis accounted for ~4% (14 genes) of unique acute stage genes. Quite selectively, among numerous canonical apoptotic pathways, only the Fas-Fas ligand-mediated cell death pathway was activated (Fig. 3). Proapoptotic genes increased in this pathway included *Fas ligand*, *caspases 3* and *4*, *BH3-interacting domain death agonist (BID)*, and *truncated BID*, highlighting the importance of the Fas-Fas ligand pathway in LT during acute stage infection.

Finally, tissue repair/remodeling and metabolism accounted for, respectively, ~9% (33 genes) and ~24% (87 genes) of unique acute stage genes. Notable are *chitinase 3 like-2*, *decorin*, and *dermatopontin*, genes that could be plausibly involved in collagen formation/deposition, an important pathologic process observed in HIV-1 infection (8). Also, ~90% (78 genes) of metabolism genes were increased in expression, suggesting accelerated cell growth and turnover.

Asymptomatic stage

In contrast to the acute stage, the asymptomatic stage (region S2) had relatively few altered genes (18 genes; Fig. 2C), reflecting a return to baseline levels of nearly all acute stage genes and a major shift in host response to the virus. We return in the *Discussion* to the mechanisms and significance of this striking change.

AIDS stage

Unlike the predominance of increased expression in the acute stage, genes unique to the AIDS stage (region S3) were largely decreased, ~84% of 183 (Fig. 2D). These included genes involved in immune activation, apoptosis, and tissue repair/remodeling. Interestingly, a substantial number of decreased genes were involved in the CD28 T cell costimulatory pathway, key molecules such as CD28, Txk (Tec family of nonreceptor tyrosine kinases), the lymphocyte-specific serine/threonine kinase death-associated protein-related apoptotic kinase 2 (DRAK2/STK17b), and the Ca²⁺-binding protein calmodulin, suggesting, in addition to significant T cell loss, T cell stimulation may be compromised during AIDS.

The small number of AIDS stage genes increased in expression included the antiviral chemokine *MIP-1 α* , the innate antimicrobial molecule *S100A9*, the DCI and monocyte-derived macrophage differentiation marker *decysin*, and the cell surface *proteoglycan syndecan-1*.

Discussion

The major finding of this study is that there are stage-specific transcriptional signatures in LTs during HIV-1 infection. These signatures identify constellations of gene expression relevant to understanding the molecular mechanisms involved in the pathogenesis of each stage.

In the acute stage of infection, the large number of altered genes, most of them increased in expression (~81%), provides a signature consistent with the dramatic pace and magnitude of events in this stage seen clinically, virologically, and immunologically. Although the explosive replication of virus to peak levels in the first month of infection is known to elicit immune activation and host defenses that partially control infection, the transcriptional signatures now provide a comprehensive picture of the genes in LTs involved in immune activation, partial control of infection, and moderation of the pathologic consequences of immune activation.

Another general feature of this acute stage transcriptional signature is that it is a mirror image (opposite) of the transcriptional signature of infected individuals' treated with highly active anti-retroviral therapy. In response to treatment and the control of viral replication, genes related to immune activation and innate/adaptive defenses decreased, in contrast to the increased expression in untreated acute infection shown here (i.e., immune defense genes such as *IFN- γ* , *OAS*, *MX2*, *IDO*, *RIG-1*, granzymes and immune activation genes such as *STAT1*, *FGL2*). This result supports a model proposed by Li et al. (7), namely, that suppression of viral replication via treatment would relieve the stimulus driving gene expression regulating immune activation and defenses that were partially controlling infection, thus leading to decreased expression of these genes. The acute stage signature now confirms that prediction.

Not surprisingly, the host rapidly responds to HIV-1 infection by increasing expression of a large number of genes related to innate and adaptive defenses during the acute stage, such as IFN-related genes and those associated with NK cell- and CD8⁺ T cell-mediated cytotoxicity (Fig. 2B). However, what was surprising was the breadth and distinctive nature of this response and its restriction to acute stage infection. For example, *APOBEC3B*, *-3F*, and *-3G* were only increased during this stage. The potent anti-HIV-1 properties via cytidine deamination-dependent (9) and -independent mechanisms (10) of APOBEC3F and -3G have been well documented, but APOBEC3B, previously considered an intrinsic cellular defense against endogenous retrotransposons (11), has only recently been shown to have anti-HIV-1 activity in vitro (12, 13). The transcriptional signatures now document in vivo deployment of three of the APOBEC proteins as a first line of defense against HIV-1.

A number of key pathogen recognition receptors also were increased in expression only during acute stage infection, e.g., *RIG-I*, *MDA-5*, *PKR*, and *TLRs 7* and *8*. These proteins work in concert to detect and inhibit invading pathogens by recognizing various forms of viral RNA, transducing a downstream signal that activates accessory proteins such as NF- κ B and IFN regulatory factor 3, leading to the production of proinflammatory cytokines and type I IFN (14, 15). In addition to the production of type I IFNs, engagement of TLR7, which is highly expressed in plasmacytoid DCs (16), can enhance HIV-1-specific T cell responses (17) while TLR8 signaling can inhibit HIV-1 replication in susceptible target cells (18). The restricted up-regulation of *TLRs 7* and *8* in acute stage infection is consistent with their importance in early detection of viral infection and the concept of robust expression of sentinel-like molecules to create an antiviral state in the initial stages of HIV-1 infection.

Not surprisingly as well, the largest number of altered genes during acute infection were related to immune activation, encompassing categories from cell cycle to proinflammatory mediators to genes involved in the proliferation of cells. However, what the acute stage signature surprisingly reveals is the distinctive nature of genes in LTs involved in immune activation and their restriction to this stage. For example, among all of the potential proinflammatory cytokines, we only observed increased expression of the gene encoding cytokine IL-32.

IL-32 is an inflammatory cytokine induced by T_H1-type cytokines in various cell types (19, 20) and has only recently received increased attention as an important component in autoimmune and inflammatory diseases through induction of other proinflammatory cytokines such as TNF- α (19–21), IL-1 β (20, 21), IL-8 (19), and MIP-2 (19, 21). Additionally, one report (22) has implicated IL-32 in activation-induced cell death in T cells. This is the first study showing IL-32 expression in LTs in HIV-1 infection. IL-32 likely contributes to the exacerbation of inflammation during HIV-1 infection and may have an important, albeit heretofore unappreciated role in T cell death.

Interestingly, a number of pattern recognition receptors recognizing microbial products were also up-regulated during acute infection. Recent evidence has implicated microbial translocation from the gastrointestinal tract during HIV-1 infection as a factor driving systemic immune activation (23). The up-regulation of genes such as *dectin-1* and *galectin-3* may be key switches utilized by the host to recognize and alert the immune system to deal with an increase in foreign microbial products. Dectin-1 plays a key role in recognizing β -glucan-containing microorganisms and, once engaged, leads to the production of IL-23, a key cytokine involved in the generation of anti-bacterial Th17 cells (24). Galectin-3 has recently been shown to be a negative regulator of LPS-induced inflammation (25). The up-regulation of these genes during acute infection suggests that the host may be responding to an increased presence of bacteria, a compensatory mechanism to curtail aberrant immune activation.

Among several apoptotic pathways, the acute stage signature strongly points to a principal role for Fas-Fas ligand-mediated apoptosis in LTs of HIV-1-infected subjects during this stage. Key apoptosis-related genes map strictly to the Fas-Fas ligand pathway, including downstream effectors such as *BID*, *truncated BID*, and *caspase 3*, all increased in expression (Fig. 3).

In the asymptomatic stage, the rapid return to levels of gene expression indistinguishable from uninfected HIV-1 uninfected subjects and the paucity of altered genes unique to this stage, 18 genes vs 358 unique acute stage genes, is remarkable, given evidence of ongoing viral replication and lymphoid tissue damage during this stage despite its relative clinical quiescence (6, 26). This transition begins in the acute stage with increased expression of numerous immunosuppressive genes such as CLEC12B, ILT4, galectin-3, CD160, BCMA, FGL2, LAG3, GPNMB, and *IDO* at a time of immune activation, consistent with a role in moderating the immunopathological consequences of sustained immune activation and thereby contributing to slow disease progression characteristic of HIV-1, SIV, and other lentiviral infections. However, these moderating effects may come at a price, in dampening the immune response to infection and, in the long term, contributing to a dysfunctional and increasingly “exhausted” immune system (27).

The defining feature of the AIDS stage signature was decreased expression of most (~84%) of the 183 unique genes. Although decreased expression could be due to loss of cells expressing these genes, decreased expression in a particular cell type, or both, the net effect is the same dysfunctional host defenses due to decreased expression of various genes, such as: 1) *CD244/2B4*, a cell surface molecule expressed on NK and memory CD8⁺ T cells that determines the level of activation or inhibition based on the degree of receptor expression and extent of its ligation (28); 2) *CCR7*, the principal chemokine receptor responsible for migration of naive and memory T cells and DCs into lymph nodes (29); and 3) a number of genes involved in T cell activation/costimulation, most prominently the costimulatory signal-transmitting receptor *CD28* (30) and other molecules associated with this pathway such as the *T cell-specific tyrosine kinase Txk* (31), *DRAK2/STK17b*, a serine/threonine kinase expressed specifically in B and T cells that modulates the threshold required for activation/costimulation (32), and *Ca²⁺/calmodulin-dependent protein kinase IV*, a key kinase likely involved in signal transduction events downstream of Txk (33).

Some of the changes in gene expression during AIDS may also contribute to CD4⁺ T cell depletion and limit reconstitution through the microenvironment-impairing deposition of collagen (8), such as increased expression of the gene encoding a cell surface proteoglycan, syndecan-1, which colocalizes with fibrosis-promoting-TGF- β in fibrotic and inflamed areas of cirrhotic human liver (34).

We interpret the small number of genes with altered expression common to all stages as evidence that there is a key set of genes required by the host to partially contain the virus. Many of the altered genes that are common to all stages of infection are related to immune activation and immune defenses, most prominently, *CD38*, a known marker for immune activation and poor prognosis when highly expressed in HIV-1 infection (35, 36), and genes encoding products associated with NK cells, IFNs, CD8⁺ T cell-mediated cytotoxicity, and antiviral chemokines. Altered expression of these genes highlights the importance of innate immunity and the IFN system throughout HIV-1 infection.

Our microarray study revealed very little overlap (<5%) with recent small interfering RNA-knockdown screens (37–39) designed to identify important host factors required for HIV-1 infection. This is likely due to differences between in vitro systems utilizing laboratory-adapted strains of virus and cell lines vs biopsied lymph nodes from HIV-1-infected individuals. Moreover, microarray assays measure change at the mRNA level and would thus not detect posttranscriptional changes in gene expression.

This microarray study is a descriptive approach to glean key insights into systems biology. The genes we identified in stage-specific, transcriptional signatures are a good starting point for further investigations of their roles in HIV-1 pathogenesis using in situ technologies to identify the types of cells in which gene expression has been altered and immunohistochemistry to identify potential changes in protein expression. In addition, it will be fruitful to examine the relationships between gene expression and infected cells, CD4⁺ T cell depletion, and collagen deposition, one pathological consequence of infection. Ultimately, these studies may be used not only to better understand viral pathogenesis during the various stages of HIV-1 disease but also to identify adjunctive approaches to improving treatment and immune reconstitution.

Acknowledgments

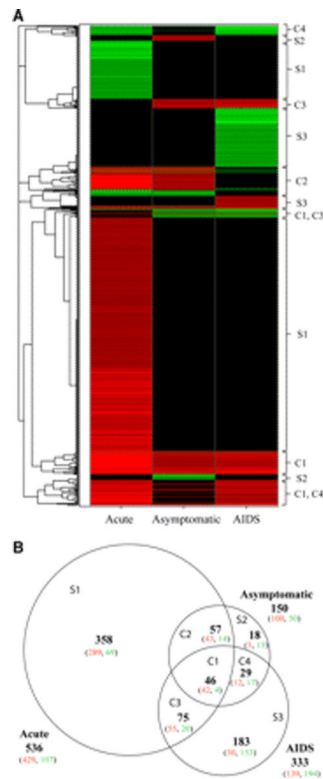
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**FIGURE 1.**

Classification of altered genes in LT from HIV-1-infected patients into disease stages and representative hierarchical clustering reveals stage-specific gene signatures. Genes with altered expression (> 1.7 times the level at uninfected baseline, $p < 0.05$) at the three stages of HIV-1 infection were characterized as the following: unique to the acute stage (S1), asymptomatic stage (S2), or AIDS stage (S3); C1, common to all stages; C2, common to acute and asymptomatic stages; C3, common to asymptomatic and AIDS stages; and C4, common to acute and AIDS stages. *A*, Hierarchical cluster analysis of altered genes from HIV-1-infected subjects (stage indicated at the bottom). Green, red, and black areas indicate, respectively, decreased, increased, and no significant change in expression compared with uninfected controls. *B*, Venn diagram depicting the number of genes with altered expression. The size of each region is proportional to the number of altered genes. Green and red numbers indicate, respectively, decreased and increased expression.



FIGURE 2. In human LT of HIV-1-infected subjects, the general functional categories of genes with altered expression (1.7 times the level at baseline, $p < 0.05$). *A*, Common to all stages (C1); *B*, unique to the acute stage (S1); *C*, unique to the asymptomatic stage (S2); and *D*, unique to the AIDS stage (S3). Green and red letters indicate, respectively, decreased and increased expression. The size of each sector in a pie diagram is proportional to the number of genes in its category (in parentheses). All genes and their names derived from abbreviations can be found in supplemental Table I.

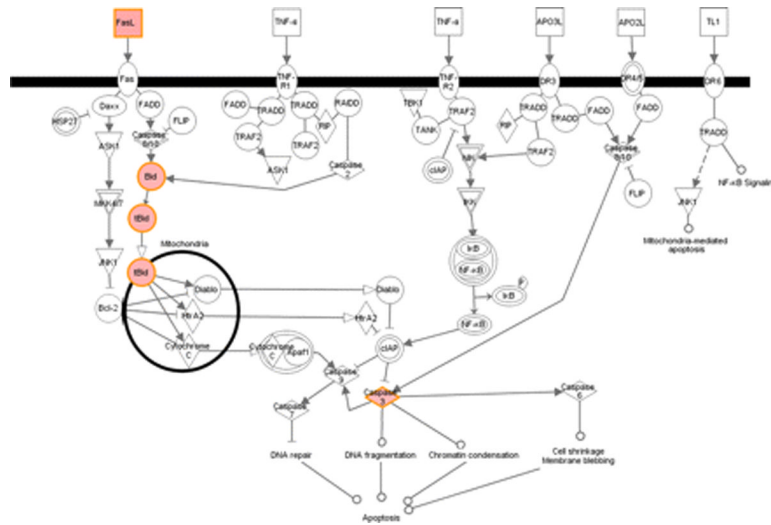


FIGURE 3. Illustration of altered genes in the acute stage related to canonical apoptotic signaling pathways reveals activation of the Fas-Fas ligand pathway. Ingenuity Pathways Analysis software was used to identify altered genes related to canonical apoptotic pathways; red indicates genes significantly increased in expression and black indicates no significant change in gene expression.

Table I

Clinical characteristics of study subjects

Patient	Disease Stage	Gender	Age (years)	Race	Blood CD4 ⁺ T Cell Count (cells/ μ l)	Plasma HIV-1 RNA Level (copies/ml)
1476	Uninfected	Female	28	Hispanic	704	Undetectable
1472	Uninfected	Female	52	Caucasian	837	Undetectable
1442	Uninfected	Female	45	Caucasian	485	Undetectable
1452	Uninfected	Male	40	Hispanic	742	Undetectable
1467	Uninfected	Male	26	Caucasian	326	Undetectable
1324	Acute	Male	41	Caucasian	494	14,696
1430	Acute	Male	26	Caucasian	683	3,610
1458	Acute	Male	51	Caucasian	400	439,000
1329	Acute	Male	59	Caucasian	370	484,694
1389	Acute	Male	32	Caucasian	824	32,173
1449	Acute	Male	30	Caucasian	333	>100,000
1435	Acute	Male	42	Caucasian	410	>100,000
1391	Acute	Male	37	African American	414	24,718
1455	Acute	Male	23	African American	209	19,400
1463	Asympt ^a	Male	23	African American	259	27,200
1335	Asympt	Male	32	Caucasian	400	15,284
1431	Asympt	Male	34	Caucasian	333	71,200
1464	Asympt	Male	34	Caucasian	202	122,000
1456	Asympt	Male	49	Caucasian	478	174,000
1408	Asympt	Male	39	Caucasian	685	20,014
1436	Asympt	Male	63	Caucasian	248	46,400
1407	Asympt	Male	35	Caucasian	372	31,922
1459	Asympt	Male	36	Caucasian	286	>100,000
1438	AIDS	Male	49	Caucasian	147	4,960
1406	AIDS	Male	45	African American	188	10,684
1462	AIDS	Male	43	Caucasian	81	35,000
1327	AIDS	Female	40	African American	112	12,046

Note. Undetectable, assay limit of detection (50 copies/ml).

^aAsympt, Asymptomatic stage.

Significantly Altered Genes and Their Functional Categories at Each Stage of HIV-1 Infection

Gene Name	Gene Title	Acute FC	Acute P-Value	Asymt FC	Asymt P-Value	AIDS FC	AIDS P-Value	Affymetrix ID	Functional Category	Functional Sub-category
APOL3	apolipoprotein L 3	1.7	0.000550359	1.3	0.01894438	1.6	0.065761871	221087_s_at	Apoptosis	Inducer of Apoptosis
BID	BH3 interacting domain death agonist	1.9	3.64935E-05	1.3	0.010049428	1.5	0.005251678	211725_s_at	Apoptosis	Inducer of Apoptosis
CASP3	caspace 3, apoptosis-related cysteine peptidase	1.7	2.65052E-05	1.3	0.005318547	1.4	0.026186587	202763_at	Apoptosis	Inducer of Apoptosis
CASP4	caspace 4, apoptosis-related cysteine peptidase	1.7	7.76881E-05	1.3	0.009469784	1.3	0.092836188	209310_s_at	Apoptosis	Inducer of Apoptosis
MTCH2	mitochondrial carrier homolog 2 (C. elegans)	1.7	0.000961464	1.2	0.025602811	1.4	0.107933252	217772_s_at	Apoptosis	Inducer of Apoptosis
PP1F	peptidylprolyl isomerase F (cyclophilin F)	1.8	0.001216762	1.3	0.033233958	1.4	0.025995993	201489_at	Apoptosis	Inducer of Apoptosis
PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform	1.7	0.004009797	1.2	0.124002807	1.3	0.224744066	213305_s_at	Apoptosis	Inducer of Apoptosis
BCL2A1	BCL2-related protein A1	1.9	0.000548014	1.4	0.021596602	1.7	0.119287129	205681_at	Apoptosis	Inhibitor of Apoptosis
BIRC5 (SURVIVIN)	baculoviral IAP repeat-containing 5 (survivin)	1.9	0.000213927	1.3	0.065288151	1.4	0.200883104	210334_x_at	Apoptosis	Inhibitor of Apoptosis
BIRC5 (SURVIVIN)	baculoviral IAP repeat-containing 5 (survivin)	1.9	0.000108161	1.3	0.065870924	1.3	0.088140021	1555826_at	Apoptosis	Inhibitor of Apoptosis
BIRC5 (SURVIVIN)	baculoviral IAP repeat-containing 5 (survivin)	3.0	0.000525642	1.7	0.030957476	2.1	0.060889243	202095_s_at	Apoptosis	Inhibitor of Apoptosis
COP1	caspace-1 dominant-negative inhibitor pseudo-ICE	1.8	0.000121756	1.2	0.041477831	1.4	0.208602385	1552703_s_at	Apoptosis	Inhibitor of Apoptosis
COP1	caspace-1 dominant-negative inhibitor pseudo-ICE	2.1	9.35204E-05	1.3	0.009599198	1.7	0.12071017	1552701_a_at	Apoptosis	Inhibitor of Apoptosis
HSPE1(HSP10)	heat shock 10kDa protein 1 (chaperonin 10)	1.7	1.56915E-05	1.2	0.056062891	1.1	0.341244062	205133_s_at	Apoptosis	Inhibitor of Apoptosis
PLAC8	placenta-specific 8	2.0	4.12178E-05	1.2	0.049715392	1.4	0.06913446	219014_at	Apoptosis	Inhibitor of Apoptosis
SORBS1	sorbin and SH3 domain containing 1	-2.7	0.017020019	-1.6	0.06618026	-1.2	0.473628232	218087_s_at	Apoptosis	Inhibitor of Apoptosis
SORBS1	sorbin and SH3 domain containing 1	-1.8	0.046918803	-1.6	0.060873125	-1.2	0.523432542	222513_s_at	Apoptosis	Inhibitor of Apoptosis
SORBS2	sorbin and SH3 domain containing 2	-1.8	0.040291647	-1.4	0.14404208	-1.1	0.52711676	225728_at	Apoptosis	Inhibitor of Apoptosis
SORBS2	sorbin and SH3 domain containing 2	-2.4	0.035293141	-1.5	0.130583284	-1.0	0.48300689	227826_s_at	Apoptosis	Inhibitor of Apoptosis
SORBS2	sorbin and SH3 domain containing 2	-2.7	0.010869871	-1.7	0.068133464	1.1	0.497785713	238751_at	Apoptosis	Inhibitor of Apoptosis
SORBS2	sorbin and SH3 domain containing 2	-3.0	0.01201063	-1.4	0.116867632	1.1	0.469537147	227827_at	Apoptosis	Inhibitor of Apoptosis
AICDA	activation-induced cytidine deaminase	3.0	0.010337545	1.9	0.0779427	2.2	0.322775708	219841_at	B Cell Proliferation/Differentiation	
AICDA	activation-induced cytidine deaminase	3.2	0.015767557	1.8	0.118734799	2.0	0.427486194	224499_s_at	B Cell Proliferation/Differentiation	
SLAMF8 (BLAME)	SLAM family member 8	1.8	0.000526199	1.3	0.021201858	1.8	0.058876099	219386_s_at	B Cell Proliferation/Differentiation	
TNFSF13B (BAFF)	tumor necrosis factor (ligand) superfamily, member 13b	1.7	0.001688875	1.2	0.094624757	1.6	0.107999986	223502_s_at	B Cell Proliferation/Differentiation	
HELLS	CDNA FLJ34225 fis, clone FCCBF3023372	1.7	0.00461868	1.1	0.509448106	1.1	0.735656331	242890_at	Immune Activation	Activation/Proliferation
HELLS	helicase, lymphoid-specific	1.8	0.000302412	1.3	0.072333551	1.2	0.519026452	220085_at	Immune Activation	Activation/Proliferation
HELLS	CDNA FLJ11381 fis, clone HEMBA1000501	1.7	0.003700421	1.2	0.180187343	1.2	0.611009594	227350_at	Immune Activation	Activation/Proliferation
HELLS	helicase, lymphoid-specific	1.8	0.002001521	1.2	0.338624895	1.3	0.308345928	223556_at	Immune Activation	Activation/Proliferation
BOLA2	bolA homolog 2 (E. coli) /// bolA homolog 2B (E. coli)	1.7	6.36317E-05	1.3	0.004446001	1.5	0.130628565	209836_x_at	Immune Activation	Activation/Proliferation
LYAR	Ly1 antibody reactive homolog	1.8	4.23834E-05	1.3	0.006340311	1.3	0.011556465	223413_s_at	Immune Activation	Activation/Proliferation
LYAR	Ly1 antibody reactive homolog	1.8	0.000183058	1.4	0.002665172	1.6	0.001830034	223414_s_at	Immune Activation	Activation/Proliferation
MKI67 (KI-67)	antigen identified by monoclonal antibody Ki-67	2.0	0.001131895	1.3	0.092429114	1.4	0.047756773	212021_s_at	Immune Activation	Activation/Proliferation
MKI67 (KI-67)	antigen identified by monoclonal antibody Ki-67	2.3	0.000996184	1.5	0.047696137	1.7	0.039490105	212022_s_at	Immune Activation	Activation/Proliferation
MKI67 (KI-67)	antigen identified by monoclonal antibody Ki-67	2.4	0.000115884	1.5	0.02240406	1.8	0.12082065	212023_s_at	Immune Activation	Activation/Proliferation
MOBK1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	1.8	0.000653855	1.3	0.054425523	1.5	0.073315961	201298_s_at	Immune Activation	Activation/Proliferation
PCNA	PCNA	2.1	0.001188115	1.4	0.02848839	1.6	0.120907557	201202_at	Immune Activation	Activation/Proliferation
SHCBP1	SHC SH2-domain binding protein 1	3.0	0.003953264	1.9	0.056139477	2.0	0.163194369	219493_at	Immune Activation	Activation/Proliferation
SLC30A7(ZNT-7)	Solute carrier family 30 (zinc transporter), member 7	1.9	0.003299475	1.2	0.585789686	1.3	0.685591956	240277_at	Immune Activation	Activation/Proliferation
TPX2 (p100)	TPX2, microtubule-associated, homolog (Xenopus laevis)	1.9	0.000980903	1.3	0.126383215	1.4	0.09713899	210052_s_at	Immune Activation	Activation/Proliferation
TTK	TTK protein kinase	2.4	0.001542137	1.5	0.077252255	1.7	0.07417002	204922_at	Immune Activation	Activation/Proliferation
TXN	Thioredoxin	1.8	0.000115901	1.2	0.157073641	1.5	0.038286078	208864_s_at	Immune Activation	Antioxidants, Hypoxia, Protectants
TXN	Thioredoxin	1.9	0.001786451	1.1	0.457318926	1.8	0.058131799	216609_at	Immune Activation	Antioxidants, Hypoxia, Protectants
CLEC7A	C-type lectin domain family 7, member A	2.1	0.003708088	1.2	0.391283402	1.6	0.094812827	1555756_a_at	Immune Activation	Antigen Presentation and Immune Response
CLEC7A	C-type lectin domain family 7, member A	1.8	0.005036452	1.2	0.124427128	1.7	0.137972307	221698_s_at	Immune Activation	Antigen Presentation and Immune Response
ANLN	anillin, actin binding protein	1.9	0.007727829	1.3	0.268341088	1.2	0.49495395	1552619_a_at	Immune Activation	Cell Cycle
ANLN	anillin, actin binding protein	2.9	0.002937209	1.6	0.077043344	1.8	0.120685872	222608_s_at	Immune Activation	Cell Cycle
AURKB	aurora kinase B	2.5	0.000471081	1.7	0.013051652	1.9	0.163007427	209464_at	Immune Activation	Cell Cycle
BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	3.0	0.00106706	1.7	0.059903617	1.7	0.071855928	209642_at	Immune Activation	Cell Cycle
BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta	2.6	0.003469168	1.7	0.06421069	1.7	0.195449264	203755_at	Immune Activation	Cell Cycle
CASC5	cancer susceptibility candidate 5	2.4	0.002738093	1.5	0.079584318	1.7	0.052506629	228323_at	Immune Activation	Cell Cycle
CDC25A	cell division cycle 25 homolog A (S. pombe)	1.7	0.00264218	1.0	0.899834357	1.0	0.860428747	1555772_a_at	Immune Activation	Cell Cycle
CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)	1.7	8.85628E-05	1.3	0.010546176	1.4	0.110302233	204126_s_at	Immune Activation	Cell Cycle
CDC6	cell division cycle 6 homolog (S. cerevisiae)	1.9	0.00450101	1.2	0.346639026	1.4	0.420965085	203967_at	Immune Activation	Cell Cycle
CDCA2	cell division cycle associated 2	2.8	0.000635166	1.6	0.03434925	1.8	0.10843015	226661_at	Immune Activation	Cell Cycle
CDCA3	cell division cycle associated 3	1.8	0.001781799	1.4	0.027146823	1.5	0.170251554	221436_s_at	Immune Activation	Cell Cycle
CDCA3	cell division cycle associated 3	1.9	0.001102085	1.4	0.040429377	1.5	0.202454866	223307_at	Immune Activation	Cell Cycle
CDCA8	cell division cycle associated 8	1.7	0.001304877	1.2	0.240909798	1.3	0.109375063	221520_s_at	Immune Activation	Cell Cycle
CENPE	centromere protein E, 312kDa	2.4	0.000822871	1.5	0.056849459	1.6	0.064392115	205046_at	Immune Activation	Cell Cycle
CENPF	centromere protein F, 350/400ka (mitosin)	1.9	0.002078971	1.2	0.422482408	1.4	0.269009104	209172_s_at	Immune Activation	Cell Cycle
CENPF	centromere protein F, 350/400ka (mitosin)	2.1	0.001549894	1.5	0.054367187	1.5	0.075590434	207828_s_at	Immune Activation	Cell Cycle
CENPH	centromere protein H	1.9	0.002367692	1.2	0.142712988	1.2	0.426785693	231772_x_at	Immune Activation	Cell Cycle
CENPK	centromere protein K	1.9	0.000528958	1.3	0.078929845	1.0	0.967111713	222848_at	Immune Activation	Cell Cycle
CENPL	centromere protein L	1.8	0.000191962	1.2	0.077113507	1.2	0.299025754	232065_x_at	Immune Activation	Cell Cycle
CENPM	centromere protein M	2.0	0.00092628	1.5	0.032789198	1.5	0.159080071	218741_at	Immune Activation	Cell Cycle

CENPN	centromere protein N	2.1	0.000717707	1.3	0.079168534	1.4	0.108624395	21955_s_at	Immune Activation	Cell Cycle
CENPN	CDNA clone IMAGE:6043059	2.0	0.000278653	1.3	0.047745093	1.5	0.192627131	228559_at	Immune Activation	Cell Cycle
CEP55	centrosomal protein 55kDa	2.8	0.001383213	1.6	0.085239024	1.7	0.176848914	218542_at	Immune Activation	Cell Cycle
CHEK1	CHK1 checkpoint homolog (S. pombe)	2.6	0.000759023	1.4	0.149723532	1.4	0.211950211	205394_at	Immune Activation	Cell Cycle
CHEK1	CHK1 checkpoint homolog (S. pombe)	2.8	0.00088345	1.6	0.041952503	1.7	0.201133877	205393_s_at	Immune Activation	Cell Cycle
CKS1B	CDC28 protein kinase regulatory subunit 1B	2.0	1.199066E-05	1.3	0.009364884	1.4	0.058511097	201897_s_at	Immune Activation	Cell Cycle
DBF4	DBF4 homolog (S. cerevisiae)	1.8	0.008375107	1.2	0.078846513	1.2	0.272929175	204244_s_at	Immune Activation	Cell Cycle
DLEU2	deleted in lymphocytic leukemia, 2	1.7	0.001044355	1.3	0.077039013	1.3	0.080187011	216870_x_at	Immune Activation	Cell Cycle
DLEU2	deleted in lymphocytic leukemia, 2 /// deleted in lymphocytic leukemia, 2	1.8	0.00180862	1.3	0.094757345	1.3	0.22828096	215629_s_at	Immune Activation	Cell Cycle
DTL	denticleless homolog (Drosophila)	2.4	0.000798066	1.3	0.343096038	1.4	0.218366529	222680_s_at	Immune Activation	Cell Cycle
DTL	denticleless homolog (Drosophila)	2.7	0.000261094	1.5	0.040282974	1.7	0.031669977	218585_s_at	Immune Activation	Cell Cycle
ECT2	epithelial cell transforming sequence 2 oncogene	2.4	0.001777532	1.5	0.059105477	1.7	0.088172292	219787_s_at	Immune Activation	Cell Cycle
ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	1.8	0.002027721	1.1	0.648098429	1.2	0.39576211	235178_x_at	Immune Activation	Cell Cycle
ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	1.9	0.001146352	1.4	0.058945206	1.5	0.130947286	38158_at	Immune Activation	Cell Cycle
FBXO5	F-box protein 5	1.8	0.011468551	1.2	0.16329637	1.2	0.391328588	234863_x_at	Immune Activation	Cell Cycle
FBXO5	F-box protein 5	2.0	0.002568717	1.3	0.138082684	1.3	0.405968821	218875_s_at	Immune Activation	Cell Cycle
KIF14	kinesin family member 14	2.8	0.000341813	1.6	0.045609135	1.5	0.061607439	206364_at	Immune Activation	Cell Cycle
KIF14	kinesin family member 14	2.8	0.000460186	1.6	0.05342481	1.6	0.055314984	236641_at	Immune Activation	Cell Cycle
KIF15	kinesin family member 15	2.3	0.000139089	1.4	0.086711651	1.5	0.160528793	219306_at	Immune Activation	Cell Cycle
KIF18A	kinesin family member 18A	2.1	0.002137875	1.3	0.142752801	1.6	0.308275244	221258_s_at	Immune Activation	Cell Cycle
KIF20A	kinesin family member 20A	2.5	0.001652047	1.6	0.064530815	1.7	0.127429121	218755_at	Immune Activation	Cell Cycle
KIF22	similar to Kinesin-like protein KIF22	1.7	0.00564487	1.4	0.015428855	1.4	0.049958841	216969_s_at	Immune Activation	Cell Cycle
KIF23	kinesin family member 23	3.1	0.000419637	1.7	0.027444465	1.7	0.076573685	204709_s_at	Immune Activation	Cell Cycle
KIF2C	kinesin family member 2C	1.8	0.00214775	1.3	0.07965598	1.3	0.320505067	211519_s_at	Immune Activation	Cell Cycle
KIF2C	kinesin family member 2C	2.0	0.000242558	1.4	0.052975129	1.4	0.101962708	209408_at	Immune Activation	Cell Cycle
KIFC1	kinesin family member C1	1.7	0.000216018	1.3	0.033558038	1.3	0.109117652	209680_s_at	Immune Activation	Cell Cycle
MELK	maternal embryonic leucine zipper kinase	2.6	0.000830536	1.6	0.040199831	1.6	0.070506421	204825_at	Immune Activation	Cell Cycle
NCAPH	non-SMC condensin I complex, subunit H	1.9	0.001339539	1.3	0.093289793	1.4	0.105959174	212949_at	Immune Activation	Cell Cycle
NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	1.7	0.000113617	1.2	0.039114775	1.2	0.306239443	221923_s_at	Immune Activation	Cell Cycle
NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. pombe)	3.1	0.001570634	1.8	0.050284693	1.8	0.186731248	223381_at	Immune Activation	Cell Cycle
PLK4	polo-like kinase 4 (Drosophila)	1.8	8.08669E-05	1.2	0.068132246	1.3	0.059944175	204887_s_at	Immune Activation	Cell Cycle
PLK4	polo-like kinase 4 (Drosophila)	2.0	0.001774923	1.3	0.116584144	1.5	0.161373536	204886_at	Immune Activation	Cell Cycle
PRC1	protein regulator of cytokinesis 1	1.8	0.003207034	1.4	0.104629872	1.5	0.231801857	218009_s_at	Immune Activation	Cell Cycle
RAN	RAN, member RAS oncogene family	1.8	0.000163286	1.2	0.07599545	1.2	0.289323598	200750_s_at	Immune Activation	Cell Cycle
RBBP8	retinoblastoma binding protein 8	1.9	0.000187621	1.4	0.009627116	1.5	0.04949702	203344_s_at	Immune Activation	Cell Cycle
SGOL2	shugoshin-like 2 (S. pombe)	2.1	0.000822119	1.4	0.049264111	1.4	0.237649419	230165_at	Immune Activation	Cell Cycle
SGOL2	shugoshin-like 2 (S. pombe)	2.1	0.002340506	1.6	0.040242658	1.5	0.053694913	235425_at	Immune Activation	Cell Cycle
SKA1	chromosome 18 open reading frame 24	1.8	0.001229687	1.2	0.310056122	1.3	0.221550916	217640_x_at	Immune Activation	Cell Cycle
SMC2	structural maintenance of chromosomes 2	1.8	0.010378535	1.2	0.182995274	1.2	0.346869232	204240_s_at	Immune Activation	Cell Cycle
SMC4	structural maintenance of chromosomes 4	1.7	0.040695598	1.2	0.39641729	1.2	0.335143581	201663_s_at	Immune Activation	Cell Cycle
SPAG5	sperm associated antigen 5	2.1	0.000240455	1.4	0.032855478	1.4	0.194654105	203145_at	Immune Activation	Cell Cycle
SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. pombe)	1.8	7.90137E-06	1.3	0.006103529	1.4	0.222582495	235572_at	Immune Activation	Cell Cycle
STIL	SCL/TAL1 interrupting locus	2.2	0.000115978	1.4	0.050365086	1.5	0.091157316	205339_at	Immune Activation	Cell Cycle
TIPIN	TIMELESS interacting protein	2.3	0.000480289	1.4	0.050601851	1.5	0.169693488	219258_at	Immune Activation	Cell Cycle
ZWINT	ZW10 interactor	2.6	0.000695622	1.7	0.029754697	1.7	0.073070604	204026_s_at	Immune Activation	Cell Cycle
CLEC12A /// CLEC12	C-type lectin domain family 12, member A /// C-type lectin domain family 12, member A	1.8	0.001388351	1.3	0.031126887	1.7	0.062043969	1552398_a_at	Immune Activation	Moderators of Activation/Inflammation
FGL2	fibrinogen-like 2	1.7	0.013501245	1.2	0.064470911	1.9	0.212981055	204834_at	Immune Activation	Moderators of Activation/Inflammation
GPNMB	glycoprotein (transmembrane) nmb	1.9	0.026125217	1.4	0.082027847	2.3	0.077425957	1554018_at	Immune Activation	Moderators of Activation/Inflammation
IL1RN	interleukin 1 receptor antagonist	1.9	0.003342967	1.1	0.371543971	1.4	0.086402845	212657_s_at	Immune Activation	Moderators of Activation/Inflammation
IL-32	interleukin 32	1.8	0.008303062	1.3	0.134163491	1.2	0.227383505	203828_s_at	Immune Activation	Moderators of Activation/Inflammation
LILRB2	leukocyte Ig-like receptor, subfamily B (with TM and ITIM domain)	2.5	0.00151238	1.5	0.000785871	2.1	0.143650356	210146_x_at	Immune Activation	Moderators of Activation/Inflammation
MICB	MHC class I polypeptide-related sequence B	1.8	0.000104623	1.1	0.212035684	1.4	0.073162025	206247_at	Immune Activation	Moderators of Activation/Inflammation
MT1H	metallothionein 1H	1.7	0.00033614	1.2	0.177331074	1.4	0.188105731	206461_x_at	Immune Activation	Moderators of Activation/Inflammation
MT1P2	metallothionein 1 pseudogene 2	1.8	0.000516649	1.2	0.118084165	1.5	0.103048006	211456_x_at	Immune Activation	Moderators of Activation/Inflammation
MT1X	metallothionein 1X	1.8	0.000523957	1.2	0.098847718	1.6	0.155887135	208581_x_at	Immune Activation	Moderators of Activation/Inflammation
PP1L5	peptidylprolyl isomerase (cyclophilin)-like 5	1.8	0.000845421	1.2	0.136641929	1.3	0.16073503	235113_at	Immune Activation	Moderators of Activation/Inflammation
SAMD9	sterile alpha motif domain containing 9	2.0	0.008514111	1.3	0.01936761	1.6	0.024495056	219691_at	Immune Activation	Moderators of Activation/Inflammation
SAMD9	sterile alpha motif domain containing 9	2.0	6.19501E-05	1.3	0.010793236	1.6	0.087654905	228531_at	Immune Activation	Moderators of Activation/Inflammation
TRAF4FA1	TRAF4 associated factor 1, chromosome 15 open reading frame 1	1.9	0.000391932	1.2	0.099277336	1.4	0.10210494	225300_at	Immune Activation	Moderators of Activation/Inflammation
TXNL5	thioredoxin-like 5	1.8	6.02751E-05	1.4	0.003844142	1.4	0.007369903	224511_s_at	Immune Activation	Moderators of Activation/Inflammation
MRC1	mannose receptor, C type 1 /// mannose receptor, C type 1-like 1	-1.8	0.002286048	-1.4	0.019945726	-1.8	0.158945068	204438_at	Immune Activation	Moderators of Activation/Inflammation
MSRB3	methionine sulfoxide reductase B3	-1.8	0.004592169	-1.4	0.027697419	-1.2	0.422589928	225782_at	Immune Activation	Moderators of Activation/Inflammation
NRP1	neuropilin 1	-1.9	0.003294991	-1.5	0.024006976	-1.7	0.169822183	212298_at	Immune Activation	Moderators of Activation/Inflammation
TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	-1.7	0.017057444	-1.4	0.067491996	-1.6	0.100902758	210643_at	Immune Activation	Moderators of Activation/Inflammation
IGF2	insulin-like growth factor 2 (somatomedin A)	-2.1	0.04623018	-1.4	0.214187193	-1.4	0.417775429	202409_at	Immune Activation	Activation/Proliferation
ARHGAP6	Rho GTPase activating protein 6	-1.7	0.00743932	-1.4	0.046205372	-1.3	0.31335211	206167_s_at	Immune Activation	Signal Transduction
FZD7	frizzled homolog 7 (Drosophila)	-1.8	0.002066957	-1.4	0.015933928	-1.5	0.171779913	203706_s_at	Immune Activation	Signal Transduction
IGFBP5	insulin-like growth factor binding protein 5	-1.8	0.007251053	-1.2	0.153009008	-1.3	0.324867968	211958_at	Immune Activation	Signal Transduction
IGFBP5	insulin-like growth factor binding protein 5	-2.4	0.001371126	-1.3	0.078049632	-1.2	0.414188591	203424_s_at	Immune Activation	Signal Transduction

ITSN1	intersectin 1 (SH3 domain protein)	-2.0	0.000933817	-1.4	0.017306753	-1.9	0.083478707	209298_s_at	Immune Activation	Signal Transduction
MYH11	myosin, heavy chain 11, smooth muscle	-2.0	0.013141658	-1.3	0.111847518	1.1	0.638267556	201497_x_at	Immune Activation	Signal Transduction
MYH11	myosin, heavy chain 11, smooth muscle	-2.9	0.0022113975	-1.4	0.108960556	1.3	0.712483255	201496_x_at	Immune Activation	Signal Transduction
MYL9	myosin, light chain 9, regulatory	-2.2	0.006075	-1.3	0.160819844	1.1	0.645552642	201058_s_at	Immune Activation	Signal Transduction
MYLK	myosin, light chain kinase	-2.0	0.000766568	-1.5	0.010571489	-1.3	0.363395494	224823_at	Immune Activation	Signal Transduction
MYLK	myosin, light chain kinase	-1.9	0.001376253	-1.3	0.072862974	1.0	0.61224786	202555_s_at	Immune Activation	Signal Transduction
NTRK2	neurotrophic tyrosine kinase, receptor, type 2	-2.0	0.02451929	-1.4	0.161427939	-1.5	0.312465927	221796_at	Immune Activation	Signal Transduction
PHLDB2	pleckstrin homology-like domain, family B, member 2	-1.8	0.00318008	-1.3	0.066707007	-1.4	0.290879876	225688_s_at	Immune Activation	Signal Transduction
PLN	phospholamban	-2.6	0.018302119	-1.4	0.135017478	-1.1	0.514256102	204940_at	Immune Activation	Signal Transduction
PLN	phospholamban	-2.1	0.025903816	-1.5	0.073296798	-1.0	0.562451638	204938_s_at	Immune Activation	Signal Transduction
PLN	Phospholamban	-2.6	0.024540725	-1.4	0.125584797	1.2	0.557677715	228202_at	Immune Activation	Signal Transduction
PLN	phospholamban	-2.7	0.017983914	-1.2	0.220913231	1.3	0.654662721	204939_s_at	Immune Activation	Signal Transduction
RERG	RAS-like, estrogen-regulated, growth inhibitor	-1.8	0.016271447	-1.4	0.070974648	-1.3	0.35186544	227758_at	Immune Activation	Signal Transduction
SDPR	serum deprivation response (phosphatidylserine binding protein)	-1.9	0.003268886	-1.5	0.011339312	-1.6	0.214113618	222717_at	Immune Activation	Signal Transduction
ATAD2	ATPase family, AAA domain containing 2	1.8	0.006227574	1.2	0.218490975	1.4	0.27607797	218782_s_at	Immune Activation	Signal Transduction
ATAD2	ATPase family, AAA domain containing 2	2.1	0.006194501	1.2	0.214154929	1.4	0.166015846	222740_at	Immune Activation	Signal Transduction
CHAC2	ChaC, cation transport regulator homolog 2 (E. coli)	2.2	0.000367875	1.6	0.003388301	1.7	0.218336198	235117_at	Immune Activation	Signal Transduction
EFHD2	EF-hand domain family, member D2, SWI/PROSIN 1	1.7	0.000778791	1.3	0.018925261	1.6	0.000726448	222483_at	Immune Activation	Signal Transduction
GPR171	G protein-coupled receptor 171	1.9	0.000139326	1.2	0.049212217	1.5	0.343811894	207651_at	Immune Activation	Signal Transduction
KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	2.1	0.004425004	1.3	0.151060893	1.4	0.180620898	211762_s_at	Immune Activation	Signal Transduction
LY6E	lymphocyte antigen 6 complex, locus E	2.3	0.001796368	1.5	0.006015597	2.1	0.109022516	202145_at	Immune Activation	Signal Transduction
MASTL	microtubule associated serine/threonine kinase-like	1.8	0.007832651	1.2	0.190248699	1.3	0.095591521	228468_at	Immune Activation	Signal Transduction
OIP5	Opa interacting protein 5	1.2	0.00206563	1.2	0.115944124	1.3	0.127672166	213599_at	Immune Activation	Signal Transduction
PTTG3	pituitary tumor-transforming 3	1.8	0.000449067	1.3	0.062240169	1.5	0.212927209	208511_at	Immune Activation	Signal Transduction
RAB27A	RAB27A, member RAS oncogene family	2.1	0.000271047	1.4	0.041326452	1.5	0.007623403	210951_x_at	Immune Activation	Signal Transduction
RAB27A	RAB27A, member RAS oncogene family	2.1	0.000140003	1.4	0.01620736	1.5	0.003263652	209514_s_at	Immune Activation	Signal Transduction
RACGAP1	Rac GTPase activating protein 1	2.6	0.000434778	1.6	0.027007928	1.7	0.083843537	222077_s_at	Immune Activation	Signal Transduction
SAMD3	SMAD family member 3	1.8	0.017021268	1.3	0.128078121	-1.0	0.963349957	1566608_at	Immune Activation	Signal Transduction
SAMD3	SMAD family member 3	2.3	0.000519084	1.3	0.09433239	1.2	0.523290138	236782_at	Immune Activation	Signal Transduction
SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative)	2.2	0.000146816	1.6	0.007329983	1.6	0.004600474	211210_x_at	Immune Activation	Signal Transduction
SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative)	2.3	0.000120241	1.6	0.002654622	1.7	0.001745418	211209_x_at	Immune Activation	Signal Transduction
SH2D1A	SH2D1A (includes EG:4068)	2.3	0.000136148	1.6	0.007339892	1.7	0.003612624	211211_x_at	Immune Activation	Signal Transduction
STMN1	stathmin 1/oncoprotein 18	1.8	0.000821298	1.2	0.146795655	1.3	0.445912722	200783_s_at	Immune Activation	Signal Transduction
STMN1	stathmin 1/oncoprotein 18	1.9	0.000498989	1.3	0.028780629	1.4	0.149561533	200853_at	Immune Activation	Signal Transduction
TESC	tescalcin	1.8	0.001191289	1.3	0.016192595	1.6	0.067505147	218872_at	Immune Activation	Signal Transduction
VRK1	vaccinia related kinase 1	1.7	0.000815168	1.3	0.013313247	1.3	0.121456862	203856_at	Immune Activation	Signal Transduction
WDHD1	WD repeat and HMG-box DNA binding protein 1	1.9	0.005706382	1.2	0.457782304	1.3	0.297775721	216228_s_at	Immune Activation	Signal Transduction
NR2F2	nuclear receptor subfamily 2, group F, member 2	-1.9	0.00029549	-1.4	0.010488854	-1.5	0.227553614	215073_s_at	Immune Activation	Transcriptional Regulator
RUNX1T1	runx-related transcription factor 1; translocated to, 1 (cyclin D-	-1.7	0.003989596	-1.4	0.046499925	-1.2	0.416636828	205528_s_at	Immune Activation	Transcriptional Regulator
VGLL3	vestigial like 3 (Drosophila)	-1.8	0.010209539	-1.5	0.033584546	-1.7	0.170947439	227399_at	Immune Activation	Transcriptional Regulator
EZH2	enhancer of zeste homolog 2 (Drosophila)	-2.3	0.002550625	-1.5	0.069567568	1.8	0.103358_s_at	203358_s_at	Immune Activation	Transcriptional Regulator
SOX5	MRNA; cDNA DKFZp564P016 (from clone DKFZp564P016)	1.9	0.040073014	1.5	0.070299491	1.8	0.097748917	215768_at	Immune Activation	Transcriptional Regulator
BRCA1	breast cancer 1, early onset	2.0	0.001008344	1.4	0.041966461	1.6	0.1949238	204531_s_at	Immune Activation	Transcriptional Regulator
C6ORF173	chromosome 6 open reading frame 173	2.2	0.001097182	1.5	0.037255985	1.5	0.062905762	226936_at	Immune Activation	Transcriptional Regulator
CDC47	cell division cycle associated 7	2.5	0.01019214	1.7	0.072949009	1.8	0.134042852	224428_s_at	Immune Activation	Transcriptional Regulator
DEPDC1	DEP domain containing 1	2.0	0.007057691	1.3	0.277005945	1.3	0.385930308	232278_s_at	Immune Activation	Transcriptional Regulator
DEPDC1	DEP domain containing 1	2.2	0.004097295	1.4	0.133407496	1.5	0.359457554	222958_s_at	Immune Activation	Transcriptional Regulator
DEPDC1B	DEP domain containing 1B	2.9	0.001832749	1.6	0.090065409	1.7	0.145938624	226980_at	Immune Activation	Transcriptional Regulator
E2F7	E2F transcription factor 7	1.8	0.007115844	1.1	0.550195895	1.2	0.407504318	228033_at	Immune Activation	Transcriptional Regulator
E2F8	E2F transcription factor 8	1.7	0.005091791	1.6	0.089825151	1.7	0.251875188	219990_at	Immune Activation	Transcriptional Regulator
H2AFV	H2A histone family, member V	1.8	0.000109623	1.3	0.085319869	1.3	0.282297894	202487_s_at	Immune Activation	Transcriptional Regulator
H2AFX	H2A histone family, member X	2.2	0.000236499	1.5	0.016205788	1.8	0.153491672	205436_s_at	Immune Activation	Transcriptional Regulator
HMGA1	high mobility group AT-hook 1	1.9	0.000292953	1.4	0.034494806	1.5	0.263741025	206074_s_at	Immune Activation	Transcriptional Regulator
HMGB2	high-mobility group box 2	1.8	0.009504517	1.4	0.077013931	1.4	0.075068843	208808_s_at	Immune Activation	Transcriptional Regulator
MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	1.8	0.000987504	1.3	0.043019637	1.5	0.251936198	201710_at	Immune Activation	Transcriptional Regulator
MYCBP	c-myc binding protein	1.7	0.001705754	1.2	0.188728961	1.2	0.371483177	203360_s_at	Immune Activation	Transcriptional Regulator
PHF19	PHD finger protein 19	2.0	0.000394482	1.3	0.044517451	1.4	0.15418309	227212_s_at	Immune Activation	Transcriptional Regulator
PHF19	PHD finger protein 19	2.1	0.000139865	1.4	0.013622917	1.4	0.017136262	227211_at	Immune Activation	Transcriptional Regulator
PRIC285	peroxisomal proliferator-activated receptor A interacting comp	1.7	0.002986961	1.2	0.012029808	1.6	0.013666441	228230_at	Immune Activation	Transcriptional Regulator
RNF213	ring finger protein 213	1.8	0.015316959	1.3	0.292046196	1.3	0.218984139	230000_at	Immune Activation	Transcriptional Regulator
SLURP	chromosome 14 open reading frame 156	1.8	2.15586E-05	1.5	0.004001899	1.5	0.000769133	221434_s_at	Immune Activation	Transcriptional Regulator
SUB1 (PC4)	SUB1 homolog (S. cerevisiae)	1.9	3.58703E-07	1.4	0.000546386	1.5	0.00671478	214512_s_at	Immune Activation	Transcriptional Regulator
TBX21	T-box 21	2.4	7.55518E-05	1.4	0.016408251	1.7	0.005034808	220684_at	Immune Activation	Transcriptional Regulator
TFDP1	transcription factor Dp-1	2.0	0.00114127	1.4	0.018059715	1.6	0.184279062	242939_at	Immune Activation	Transcriptional Regulator
THOC4	THO complex 4	1.9	0.03973363	1.2	0.19074427	1.2	0.342771114	226319_s_at	Immune Activation	Transcriptional Regulator
THOC4	THO complex 4	1.9	0.009361284	1.4	0.028179942	1.4	0.106234314	226320_at	Immune Activation	Transcriptional Regulator
TMPO	thymopoietin	1.7	0.004013858	1.2	0.260619217	1.2	0.286803242	203432_at	Immune Activation	Transcriptional Regulator
TRIP13	thyroid hormone receptor interactor 13	1.8	0.000558289	1.2	0.121953757	1.2	0.212809225	204033_at	Immune Activation	Transcriptional Regulator
UHRF1	ubiquitin-like, containing PHD and RING finger domains, 1	2.8	0.001224701	1.5	0.096772533	1.6	0.198611393	225655_at	Immune Activation	Transcriptional Regulator

ZNF367	zinc finger protein 367	1.9	0.002125658	1.2	0.139168671	1.3	0.335774031	229551_x_at	Immune Activation	Transcriptional Regulator
APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-1	2.3	0.011860416	1.4	0.158653087	1.3	0.295555405	206632_s_at	Immune Defenses	Antiviral Chemokines & Proteins
APOBEC3F	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-2	1.9	0.032601884	1.3	0.130181447	1.4	0.034705934	214995_s_at	Immune Defenses	Antiviral Chemokines & Proteins
APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-3	1.8	0.000132207	1.4	0.008780739	1.5	0.007499183	204205_at	Immune Defenses	Antiviral Chemokines & Proteins
DDX58 (RIG-I)	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	1.8	0.005986407	1.2	0.116253914	1.7	0.132055749	218943_s_at	Immune Defenses	Antiviral Chemokines & Proteins
EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	1.9	0.000311093	1.3	0.045818353	1.6	0.118315856	204211_x_at	Immune Defenses	Antiviral Chemokines & Proteins
IFIH1 (MDA-5)	interferon induced with helicase C domain 1	2.0	0.000526031	1.3	0.004823123	1.9	0.053317663	219209_at	Immune Defenses	Antiviral Chemokines & Proteins
TLR7	toll-like receptor 7	1.8	0.000517479	1.2	0.102458357	1.7	0.023488104	220146_at	Immune Defenses	Antiviral Chemokines & Proteins
TLR8	toll-like receptor 8	2.0	0.003602204	1.4	0.035278357	2.1	0.068132036	229560_at	Immune Defenses	Antiviral Chemokines & Proteins
C1QB	complement component 1, q subcomponent, B chain	2.1	0.007926095	1.6	0.010325912	2.5	0.154463766	202953_at	Immune Defenses	C' and FcR's
C1QBP	complement component 1, q subcomponent binding protein	1.7	0.00182001	1.1	0.212570415	1.2	0.402016355	214214_s_at	Immune Defenses	C' and FcR's
FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide chain	1.8	0.010001794	1.4	0.021891262	1.8	0.061695099	1554899_s_at	Immune Defenses	C' and FcR's
HERC5	hect domain and RLD 5	2.4	0.001374681	1.5	0.029399134	2.2	0.073273004	219863_at	Immune Defenses	Interferon-related
IFITM1	interferon induced transmembrane protein 1 (9-27)	1.8	0.001041428	1.2	0.016652619	1.5	0.045550277	214022_s_at	Immune Defenses	Interferon-related
IFITM1	interferon induced transmembrane protein 1 (9-27)	1.9	0.001786875	1.3	0.003847517	1.7	0.112292726	201601_x_at	Immune Defenses	Interferon-related
INDO	indoleamine-pyrrole 2,3 dioxygenase	1.4	0.002115483	1.1	0.306832003	1.7	0.088651006	210029_at	Immune Defenses	Interferon-related
IRF7	interferon regulatory factor 7	2.0	0.000286318	1.3	0.016895341	1.8	0.055079527	208436_s_at	Immune Defenses	Interferon-related
MX2	myxovirus (influenza virus) resistance 2 (mouse)	2.0	0.005239176	1.3	0.039893151	1.8	0.067518985	204994_at	Immune Defenses	Interferon-related
NMI	N-myc (and STAT) interactor	1.9	0.000134133	1.3	0.000395284	1.6	0.019010706	203964_at	Immune Defenses	Interferon-related
OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	2.4	0.002106728	1.3	0.063844545	1.8	0.107958757	204972_at	Immune Defenses	Interferon-related
OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	1.8	0.002272358	1.3	0.077015129	2.2	0.12318049	228607_at	Immune Defenses	Interferon-related
OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	2.5	0.002562049	1.3	0.064837032	2.2	0.149494141	218400_at	Immune Defenses	Interferon-related
PNP1	polynucleotide nucleotidyltransferase 1	1.1	0.001731208	1.1	0.157792452	1.1	0.026800559	225291_at	Immune Defenses	Interferon-related
USP18	ubiquitin specific peptidase 18 /// similar to ubiquitin specific peptidase 18	1.7	0.000380014	1.6	0.008400859	2.1	0.173908939	219211_at	Immune Defenses	Interferon-related
CLEC2B	C-type lectin domain family 2, member B	1.8	0.000247936	1.4	0.015569746	1.6	0.075026011	209732_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
FGFBP2 (KSP37)	fibroblast growth factor binding protein 2	3.5	0.000157711	1.5	0.007020131	1.5	0.339694528	223836_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
GZMB	granzyme B	2.8	0.004799765	1.2	0.40225845	1.3	0.101316996	210164_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
GZMM	granzyme M	1.8	0.003154041	1.4	0.019226829	1.4	0.1779215	207460_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
GMD5	GDP-mannose 4,6-dehydratase	1.8	0.019640694	1.5	0.032559587	1.8	0.289841088	204875_s_at	Metabolism	Glucose
ABC8	ATP-binding cassette, sub-family A (ABC1), member 8	-2.2	0.032548897	-1.5	0.158474735	-1.5	0.340549531	204719_at	Metabolism	ATP/Drug Transporter
CHGN	chondroitin beta1,4 N-acetylgalactosaminyltransferase	-1.8	0.004937816	-1.4	0.056658615	-1.6	0.125871286	219049_at	Metabolism	Glucose
GLTD2	glycosyltransferase 8 domain containing 2	-1.8	0.007551786	-1.4	0.058270868	-1.8	0.165488876	227070_at	Metabolism	Glucose
SLC26A7	solute carrier family 26, member 7	-1.8	0.001113927	-1.4	0.01327231	-1.5	0.232898711	239006_at	Metabolism	Metals/Ions
PTRF	polymerase I and transcript release factor	-1.7	0.001987368	-1.4	0.01904538	-1.4	0.232457841	208790_s_at	Metabolism	Nucleic Acids
RNASE1	ribonuclease, RNase A family, 1 (pancreatic)	-1.9	0.012807958	-1.4	0.046704716	-2.0	0.088140929	201785_at	Metabolism	Nucleic Acids
CYBRD1	cytochrome b reductase 1	-1.7	0.007536461	-1.4	0.035437499	-1.4	0.248711223	222453_at	Metabolism	Proteins
PRSS23	protease, serine, 23	-1.7	0.022981705	-1.3	0.108718225	-1.5	0.22969293	239262_at	Metabolism	Proteins
PCYOX1	prenylcysteine oxidase 1	-1.8	0.000903641	-1.3	0.027686778	-1.4	0.091336203	203803_at	Metabolism	Proteins
ETNK1	Ethanolamine kinase 1	1.7	0.004709214	1.0	0.635867858	1.0	0.812515374	231576_at	Metabolism	Lipids
PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase IIb)	1.7	0.013702795	1.2	0.150934448	1.7	0.095458859	206214_at	Metabolism	Lipids
SLC31A1	solute carrier family 31 (copper transporters), member 1	1.8	0.001580836	1.4	0.015508346	1.6	0.00286247	203971_at	Metabolism	Metals/Ions
ADA	adenosine deaminase	2.0	0.002749142	1.4	0.052820169	1.7	0.00480724	216705_s_at	Metabolism	Nucleic Acids
ADA	adenosine deaminase	2.0	0.000112489	1.3	0.019685667	1.7	0.010480375	204639_at	Metabolism	Nucleic Acids
C12orf48	chromosome 12 open reading frame 48	1.9	0.002035547	1.2	0.151829063	1.4	0.295350016	220060_s_at	Metabolism	Nucleic Acids
C12orf48	chromosome 12 open reading frame 48	1.9	0.002447535	1.3	0.143774402	1.5	0.228740941	227928_at	Metabolism	Nucleic Acids
CDT1	Chromatin licensing and DNA replication factor 1	1.8	5.04479E-05	1.1	0.771237944	1.4	0.177331886	228868_x_at	Metabolism	Nucleic Acids
FEN1	flap structure-specific endonuclease 1	2.0	0.001564404	1.3	0.123099842	1.2	0.259572323	204768_s_at	Metabolism	Nucleic Acids
FEN1	flap structure-specific endonuclease 1	2.2	0.000522852	1.5	0.024387465	1.5	0.090128149	204767_s_at	Metabolism	Nucleic Acids
GINS1	GINS complex subunit 1 (Psf1 homolog)	2.2	0.000174479	1.4	0.044803022	1.5	0.20105855	206102_at	Metabolism	Nucleic Acids
GINS2	GINS complex subunit 2 (Psf2 homolog)	2.1	0.000524219	1.4	0.081087013	1.6	0.136664586	221521_s_at	Metabolism	Nucleic Acids
GINS4	GINS complex subunit 4 (Sid5 homolog)	1.8	0.006137641	1.4	0.065363601	1.3	0.481470316	211767_at	Metabolism	Nucleic Acids
HNRPU	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment site A)	1.8	0.019167184	1.3	0.408752517	1.1	0.843257216	236244_at	Metabolism	Nucleic Acids
KIAA1794	Fanconi anemia, complementation group I	2.4	9.4271E-05	1.4	0.029695905	1.7	0.070705982	213007_at	Metabolism	Nucleic Acids
MCM10	minichromosome maintenance complex component 10	2.3	6.61055E-05	1.3	0.140910692	1.4	0.13147913	220651_s_at	Metabolism	Nucleic Acids
MCM10	minichromosome maintenance complex component 10	2.0	0.000343268	1.3	0.11508409	1.4	0.240203466	222962_s_at	Metabolism	Nucleic Acids
MCM2	minichromosome maintenance complex component 2	1.9	0.000262212	1.2	0.079540676	1.3	0.22893669	202107_s_at	Metabolism	Nucleic Acids
MCM4	minichromosome maintenance complex component 4	2.2	0.005952588	1.4	0.117603163	1.3	0.293297971	212141_at	Metabolism	Nucleic Acids
MCM4	minichromosome maintenance complex component 4	2.4	0.000514065	1.6	0.019504037	1.5	0.17701717	222036_s_at	Metabolism	Nucleic Acids
MCM4	minichromosome maintenance complex component 4	2.0	0.001653083	1.2	0.232196539	1.5	0.334123705	222037_at	Metabolism	Nucleic Acids
MCM6	minichromosome maintenance complex component 6	2.0	0.000303155	1.3	0.031322216	1.4	0.246355213	201930_at	Metabolism	Nucleic Acids
MTHFD2	methylene tetrahydrofolate dehydrogenase (NADP+ dependent)	1.9	0.001979578	1.3	0.102349874	1.5	0.042671739	201761_at	Metabolism	Nucleic Acids
NT5C3	5'-nucleotidase, cytosolic III	2.0	0.000259162	1.2	0.055912024	1.6	0.116784519	223298_s_at	Metabolism	Nucleic Acids
NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	1.7	3.87509E-05	1.3	0.004172957	1.3	0.041299577	204766_s_at	Metabolism	Nucleic Acids
NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	1.9	0.000190038	1.3	0.044518008	1.4	0.079079583	202697_at	Metabolism	Nucleic Acids
PAICS	phosphoribosylaminoimidazole carboxylase	1.7	0.001193374	1.2	0.17807551	1.2	0.468722708	201013_s_at	Metabolism	Nucleic Acids
PAICS	phosphoribosylaminoimidazole carboxylase	1.9	0.006916994	1.2	0.217882755	1.2	0.545736301	201014_s_at	Metabolism	Nucleic Acids
POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	2.0	0.000331038	1.2	0.16224508	1.3	0.320054468	205909_at	Metabolism	Nucleic Acids
RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	2.5	0.000619311	1.4	0.07395247	1.5	0.140144389	205024_s_at	Metabolism	Nucleic Acids
RFC3	replication factor C (activator 1) 3, 38kDa	1.8	0.0250107	1.2	0.586066563	1.3	0.560085554	204128_s_at	Metabolism	Nucleic Acids

RFC3	replication factor C (activator 1) 3, 38kDa	1.9	0.003088142	1.4	0.027682669	1.6	0.239646636	204127_at	Metabolism	Nucleic Acids
RPA3	replication protein A3, 14kDa	2.0	8.0189E-07	1.4	0.002038017	1.5	0.062346993	209507_at	Metabolism	Nucleic Acids
RRM1	ribonucleotide reductase M1 polypeptide	1.9	0.000116653	1.3	0.05228578	1.3	0.227571654	201477_s_at	Metabolism	Nucleic Acids
SNRPD1	SNRPD1	1.9	0.000188815	1.4	0.021680644	1.4	0.136741481	202690_s_at	Metabolism	Nucleic Acids
SNRPG	small nuclear ribonucleoprotein polypeptide G	1.9	0.000255053	1.3	0.018552615	1.4	0.013623815	205644_s_at	Metabolism	Nucleic Acids
SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	1.7	0.016667505	1.2	0.19083478	1.3	0.27512337	1555427_s_at	Metabolism	Nucleic Acids
SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	1.8	0.006347211	1.2	0.112630407	1.3	0.095399555	209025_s_at	Metabolism	Nucleic Acids
TK1	thymidine kinase 1, soluble	1.8	0.002322908	1.4	0.029815303	1.5	0.133625287	202338_at	Metabolism	Nucleic Acids
TK1	thymidine kinase 1, soluble	2.3	0.001545505	1.5	0.03391885	1.7	0.171421619	1554408_a_at	Metabolism	Nucleic Acids
XRCC4	X-ray repair complementing defective repair in Chinese hamst	1.8	0.001756401	1.3	0.016537835	1.3	0.103705157	205072_s_at	Metabolism	Nucleic Acids
XRCC4	X-ray repair complementing defective repair in Chinese hamst	1.7	0.000499832	1.2	0.023847461	1.4	0.168105443	210813_s_at	Metabolism	Nucleic Acids
C16ORF33	chromosome 16 open reading frame 33	1.8	0.000205108	1.3	0.028903534	1.4	0.19325269	218493_at	Metabolism	Nucleic Acids & Proteins
DHFR	dihydrofolate reductase	1.8	0.000489746	1.2	0.100685323	1.2	0.584320815	202534_x_at	Metabolism	Nucleic Acids & Proteins
DHFR	dihydrofolate reductase	1.8	0.001077005	1.4	0.013135947	1.2	0.399911955	202532_s_at	Metabolism	Nucleic Acids & Proteins
DHFR	dihydrofolate reductase	1.9	6.56135E-05	1.3	0.005349417	1.3	0.233867665	48808_at	Metabolism	Nucleic Acids & Proteins
DHFR	dihydrofolate reductase /// similar to Dihydrofolate reductase	2.0	0.000959175	1.4	0.059519281	1.5	0.36991046	202533_s_at	Metabolism	Nucleic Acids & Proteins
IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	2.0	0.045072226	1.7	0.110007546	1.7	0.370566778	203820_s_at	Metabolism	Nucleic Acids & Proteins
PSAT1	phosphoserine aminotransferase 1	2.2	0.000163101	1.6	0.011012265	1.6	0.09391363	223062_s_at	Metabolism	Nucleic Acids & Proteins
UBE2S	ubiquitin-conjugating enzyme E2S	2.6	0.001924233	1.6	0.042007067	1.8	0.176499006	202779_s_at	Metabolism	Nucleic Acids & Proteins
ACP1	acid phosphatase 1, soluble	1.9	0.000286215	1.5	0.000818364	1.5	0.004252127	201629_s_at	Metabolism	Proteins
ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, sub	1.8	2.13269E-06	1.3	0.002474241	1.3	0.038238805	207508_at	Metabolism	Proteins
CACYBP	calycylin binding protein	1.7	0.00470024	1.1	0.162405095	1.2	0.251087167	210691_s_at	Metabolism	Proteins
COX5A	cytochrome c oxidase subunit Va	1.9	5.14204E-05	1.3	0.014837459	1.5	0.005995857	203663_s_at	Metabolism	Proteins
EIF1AY	Eukaryotic translation initiation factor 1A, Y-linked	2.0	0.044635695	1.7	0.074254426	1.3	0.514624365	244482_at	Metabolism	Proteins
EIF1AY	eukaryotic translation initiation factor 1A, Y-linked	2.3	0.034529978	1.8	0.079337189	1.4	0.469041322	204410_at	Metabolism	Proteins
EIF1AY	eukaryotic translation initiation factor 1A, Y-linked	2.9	0.042914494	2.2	0.065846393	1.6	0.463601646	204409_s_at	Metabolism	Proteins
EIF4E2	eukaryotic translation initiation factor 4E family member 2	1.7	4.55884E-05	1.2	0.034930245	1.3	0.021495733	213571_s_at	Metabolism	Proteins
EIF5A	Eukaryotic translation initiation factor 5A	2.0	0.004021218	1.4	0.064114822	1.4	0.297011563	213757_at	Metabolism	Proteins
FBXO31	F-box protein 31	1.7	0.000130817	1.4	0.003674079	1.4	0.008669278	219785_s_at	Metabolism	Proteins
FBXO6	F-box protein 6	1.9	0.005732467	1.3	0.090730112	1.7	0.036417463	231769_at	Metabolism	Proteins
GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)	1.9	0.000657051	1.3	0.126308784	1.6	0.01490576	204224_s_at	Metabolism	Proteins
GGH	gamma-glutamyl hydrolase (conjugase, fitylpolyyammagglutar	1.7	0.000870687	1.4	0.015020179	1.5	0.130788847	203560_at	Metabolism	Proteins
GLRX	glutaredoxin (thioltransferase)	1.8	1.83758E-05	1.4	0.001830757	1.5	0.005139055	209276_s_at	Metabolism	Proteins
HERC6	hect domain and RLD 6	2.4	0.00339154	1.3	0.191779942	2.1	0.171778809	219352_at	Metabolism	Proteins
IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	1.9	0.000951406	1.5	0.014341774	1.7	0.007004203	210046_s_at	Metabolism	Proteins
IMP1L	IMP1 inner mitochondrial membrane peptidase-like (S. cerevis	1.7	0.000677536	1.3	0.023219513	1.2	0.279011164	230556_at	Metabolism	Proteins
MRPL13	mitochondrial ribosomal protein L13	1.8	7.66379E-05	1.2	0.041154376	1.3	0.036058114	218049_s_at	Metabolism	Proteins
MRPL15	mitochondrial ribosomal protein L15	1.7	0.000905296	1.2	0.027182405	1.3	0.061970936	218027_at	Metabolism	Proteins
MRPL19	mitochondrial ribosomal protein L19	1.8	0.002274063	1.2	0.030062378	1.3	0.105582645	203465_at	Metabolism	Proteins
MRPL44	mitochondrial ribosomal protein L44	1.8	0.011191139	1.2	0.259828543	1.4	0.007806987	222555_s_at	Metabolism	Proteins
MRPS18C	mitochondrial ribosomal protein S18C	1.7	1.76848E-05	1.2	0.089638533	1.3	0.002724384	228019_s_at	Metabolism	Proteins
NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	1.8	1.07321E-05	1.3	0.000811813	1.4	0.004284576	202941_at	Metabolism	Proteins
NUP37	nucleoporin 37kDa	1.7	0.004152298	1.2	0.082996516	1.3	0.11719337	218622_at	Metabolism	Proteins
PGAP1	GPI deacylase	1.9	0.014128568	1.1	0.486686934	1.1	0.472465444	220576_at	Metabolism	Proteins
PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2	1.8	5.78254E-06	1.3	0.013631325	1.4	0.003188405	201317_s_at	Metabolism	Proteins
PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4	1.7	9.12488E-06	1.2	0.01270353	1.3	0.007165624	203396_at	Metabolism	Proteins
PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5	1.8	2.07375E-05	1.3	0.011955218	1.5	0.006857164	201274_at	Metabolism	Proteins
PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6	1.7	1.56466E-05	1.3	0.005064337	1.4	0.008637005	208805_at	Metabolism	Proteins
PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	1.9	6.191E-06	1.3	0.005738529	1.4	0.046161944	202659_at	Metabolism	Proteins
PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	1.8	0.000202181	1.3	0.01436007	1.5	0.001917108	200039_s_at	Metabolism	Proteins
PSMB8	proteasome subunit, beta type, 8	1.9	4.46759E-06	1.3	0.008897827	1.5	0.00060658	209040_s_at	Metabolism	Proteins
PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 b	2.0	9.18265E-06	1.4	0.003694353	1.7	0.005074594	201762_s_at	Metabolism	Proteins
RPL22L1	ribosomal protein L22-like 1	1.8	9.24473E-08	1.3	0.003220863	1.4	0.095149499	225541_at	Metabolism	Proteins
SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (lp)	1.7	0.000568162	1.2	0.037773869	1.4	0.006076131	202675_at	Metabolism	Proteins
TRIM59	tripartite motif-containing 59	2.0	0.000199101	1.3	0.055581629	1.3	0.321979139	227801_at	Metabolism	Proteins
UBE2C	ubiquitin-conjugating enzyme E2C	2.7	0.000358504	1.7	0.021099501	1.7	0.062302296	202954_at	Metabolism	Proteins
UBE2L3	ubiquitin-conjugating enzyme E2L 3	1.8	7.37798E-06	1.2	0.013313152	1.3	0.015083856	200682_s_at	Metabolism	Proteins
UBE2T	ubiquitin-conjugating enzyme E2T (putative)	2.3	3.7918E-05	1.4	0.022771548	1.5	0.144578824	223229_at	Metabolism	Proteins
UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	1.7	0.009669577	1.6	0.023153725	1.7	0.362101828	201387_s_at	Metabolism	Proteins
UCHL5	ubiquitin carboxyl-terminal hydrolase L5	1.7	0.007491842	1.2	0.126440927	1.3	0.198023761	220083_x_at	Metabolism	Proteins
DHRS9	dehydrogenase/reductase (SDR family) member 9	2.0	0.000828753	1.5	0.021501136	1.6	0.106037747	219799_s_at	Metabolism	Retinoic Acid Biosynthesis
DHRS9	dehydrogenase/reductase (SDR family) member 9	2.4	0.001469612	1.7	0.018457735	2.0	0.092040988	224009_x_at	Metabolism	Retinoic Acid Biosynthesis
DHRS9	dehydrogenase/reductase (SDR family) member 9	2.2	0.000717542	1.5	0.014099802	1.8	0.130728979	223952_x_at	Metabolism	Retinoic Acid Biosynthesis
EDIL3 (DEL1)	EGF-like repeats and discoidin like domains 3	-2.1	0.038823826	-1.5	0.115678654	1.1	0.730536033	225275_at	Tissue Repair/Remodeling	Blood Vessel Related
ACTA2	ACTA2	-2.1	0.003658704	-1.4	0.066868996	-1.1	0.564846288	200974_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
ACTG2	actin, gamma 2, smooth muscle, enteric	-1.7	0.027859245	-1.3	0.11928582	1.1	0.716279865	202274_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
CALD1	caldesmon 1	-1.8	0.015311695	-1.6	0.001455532	-1.4	0.248388349	201617_x_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
DCN	decorin	-2.0	0.012453209	-1.4	0.085934866	-1.6	0.223485114	209335_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
DCN	decorin	-1.9	0.007889226	-1.4	0.085262727	-1.6	0.23590617	211896_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues

DCN	decorin	-1.7	0.007262062	-1.3	0.061624119	-1.5	0.198158072	201893_x_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
DPT	dermatopontin	-1.7	0.046057596	-1.3	0.238280113	-1.5	0.24438039	207977_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
DPT	dermatopontin	-1.7	0.044319458	-1.3	0.202467999	-1.4	0.317472076	213071_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
EDNRA	endothelin receptor type A	-1.7	0.00213553	-1.7	0.001869818	-1.4	0.27935434	204463_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
FBLN1	fibulin 1	-2.0	0.026176162	-1.6	0.076462087	-1.3	0.399938745	202995_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
HMCN1	hemicentin 1	-1.8	0.007076569	-1.4	0.035958216	-1.7	0.135218958	235944_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
PDZRN3	PDZ domain containing RING finger 3	-1.9	0.004761922	-1.4	0.041560581	-1.4	0.274911535	212915_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
SYNPO2	synaptopodin 2	-1.8	0.001996214	-1.3	0.024320703	-1.2	0.375417117	227662_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TAGLN	transgelin	-1.8	0.010633903	-1.4	0.060653141	-1.0	0.599507778	1555724_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TAGLN	transgelin	-1.9	0.011316259	-1.4	0.085043877	1.0	0.669065011	205547_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TIMP3	TIMP metalloproteinase inhibitor 3 (Sorsby fundus dystrophy, p	-1.7	0.002206116	-1.3	0.051486271	-1.5	0.231855382	201147_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TIMP3	TIMP metalloproteinase inhibitor 3 (Sorsby fundus dystrophy, p	-1.8	0.003235711	-1.2	0.139986221	-1.4	0.275683341	201150_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TMEM47	transmembrane protein 47	-1.8	0.005982484	-1.4	0.030629691	-1.2	0.4568404	209656_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TMEM47	transmembrane protein 47	-1.8	0.000134367	-1.6	0.000541507	-1.1	0.467564421	209655_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TNS1	Tensin 1	-1.8	0.024360615	-1.4	0.139852075	-1.3	0.372581484	221748_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TPM1	tropomyosin 1 (alpha)	-2.0	0.002007399	-1.3	0.054232369	-1.2	0.450890873	210986_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TPM1	tropomyosin 1 (alpha)	-1.9	0.001818857	-1.4	0.031509933	-1.1	0.488824326	210987_x_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TPM1	tropomyosin 1 (alpha)	-1.8	0.003493297	-1.2	0.100632246	-1.0	0.562371465	206116_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TPM2	tropomyosin 2 (beta)	-1.7	0.037776304	-1.2	0.194956067	-1.1	0.65555797	204083_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
ARPC5L	actin related protein 2/3 complex, subunit 5-like	1.7	2.95604E-05	1.4	0.00015492	1.5	0.034905289	223101_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
CAPG	capping protein (actin filament), gelsolin-like	1.7	0.000929725	1.3	0.033703843	1.6	0.039586016	201850_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
CH3L2 (YKL-39)	chitinase 3-like 2	2.2	0.001151658	1.4	0.05183183	1.7	0.082493192	213060_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
CKAP2L	cytoskeleton associated protein 2-like	1.7	0.00368686	1.2	0.270544184	1.2	0.057492823	229610_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	1.8	0.010059221	1.3	0.035190084	2.1	0.065557513	200923_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
LMNB1	lamin B1	2.0	0.01128812	1.3	0.397631207	1.3	0.516814023	203276_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
TMM10	translocase of inner mitochondrial membrane 10 homolog (ye	1.7	0.003624152	1.1	0.394083924	1.1	0.333777137	1555764_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
VNN2	vanin 2	1.7	0.014218803	1.4	0.028236888	1.8	0.141426002	205922_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
ANP32E	Acidic (leucine-rich) nuclear phosphoprotein 32 family, membe	2.0	0.000151729	1.2	0.847514237	1.3	0.525278614	229128_s_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, membe	2.1	0.000969345	1.2	0.209860752	1.4	0.382297422	208103_s_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
SNAP29	synaptosomal-associated protein, 29kDa	1.7	1.43342E-05	1.2	0.122513423	1.2	0.01196146	218327_s_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
HN1	hematological and neurological expressed 1	2.2	0.000208333	1.4	0.027250856	1.6	0.07544163	217755_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
VAMP5	vesicle-associated membrane protein 5 (myobrevin)	1.7	0.000796108	1.3	0.000677444	1.7	0.008960036	204929_s_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
CNTN1	Contactin 1	-1.8	0.005204179	-1.6	0.010876391	-1.9	0.062159196	227202_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
NEGR1	neuronal growth regulator 1	-1.7	0.014728207	-1.5	0.027282036	-1.8	0.157650694	229461_x_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
PCDH7	protocadherin 7	-2.0	0.000748214	-1.6	0.002772524	-1.9	0.085467792	228640_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
HSD17B4	sushi, nidogen and EGF-like domains 1	-2.2	0.001399475	-1.5	0.006731162	-1.2	0.215073487	235743_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
CXCL2	chemokine (C-X-C motif) ligand 2	-2.0	0.033844659	-1.8	0.05636059	-1.5	0.318183749	209774_x_at	Trafficking	Chemokine Receptors and Ligands
STAB1	stabilin 1	-1.7	0.001027351	-1.4	0.011351042	-1.5	0.086948179	204150_at	Trafficking	Chemokine Receptors and Ligands
STAB2	stabilin 2	-1.8	0.005169481	-1.3	0.076871826	-1.9	0.054991985	220114_s_at	Trafficking	Chemokine Receptors and Ligands
AOC3 (VAP-1)	amine oxidase, copper containing 3 (vascular adhesion protei	-1.8	0.017961783	-1.3	0.11759469	-1.2	0.423484687	204894_s_at	Trafficking	Vascular Adhesion
CX3CR1	chemokine (C-X3-C motif) receptor 1	2.0	0.016784408	1.1	0.162407467	1.1	0.95863927	205898_at	Trafficking	Chemokine Receptors and Ligands
HMMR (CD168)	hyaluronan-mediated motility receptor (RHAMM)	2.9	0.001991891	1.7	0.068889696	1.9	0.090714614	207165_at	Trafficking	Vascular Adhesion
HMMR (CD168)	hyaluronan-mediated motility receptor (RHAMM)	2.4	0.002011658	1.5	0.086671844	1.7	0.122495575	209709_s_at	Trafficking	Vascular Adhesion
---	Transcribed locus	1.7	0.001249365	1.2	0.211579245	1.2	0.350535064	235609_at	Unknown Transcript	
---	CDNA clone IMAGE:4842353	1.7	0.006541564	1.2	0.257177257	1.2	0.712208963	235609_at	Unknown Transcript	
---	Homo sapiens, clone IMAGE:4723617, mRNA	1.8	0.003028215	1.4	0.010889583	1.4	0.277006617	1559916_a_at	Unknown Transcript	
---	Transcribed locus	1.7	0.006761378	1.2	0.363601129	1.5	0.613505893	239680_at	Unknown Transcript	
---	Transcribed locus	1.7	0.002854049	1.5	0.01275619	1.6	0.070283871	229490_s_at	Unknown Transcript	
---	Transcribed locus	1.9	0.001741237	1.4	0.072596025	1.8	0.084102221	238725_at	Unknown Transcript	
---	similar to olfactory receptor 472	1.9	0.000108136	1.4	0.008723744	2.0	0.089927375	235229_at	Unknown Transcript	
---	Transcribed locus	-1.9	0.000329048	-1.6	0.001465541	-1.6	0.095032158	236179_at	Unknown Transcript	
---	CDNA clone IMAGE:5273964	-2.0	0.001939401	-1.3	0.073022821	-1.5	0.165120029	236335_at	Unknown Transcript	
---	CDNA FLJ38472 fis, clone FBRA2022148	-1.8	0.005271321	-1.3	0.100896761	-1.5	0.158169458	239672_at	Unknown Transcript	
---	Transcribed locus	-1.7	0.006966225	-1.4	0.049344845	-1.4	0.186180767	226806_s_at	Unknown Transcript	
---	Transcribed locus	-1.7	0.009655009	-1.1	0.319466297	-1.3	0.343080984	229580_at	Unknown Transcript	
CForf41	chromosome 7 open reading frame 41	-1.8	0.007710584	-1.5	0.034283592	-1.7	0.014849994	226018_at	Gene Unknown Function	
EFHA2	EF-hand domain family, member A2	-1.7	0.002340919	-1.6	0.006859864	-1.7	0.102583102	238458_at	Gene Unknown Function	
FAM13C1	family with sequence similarity 13, member C1	-1.9	0.003099058	-1.4	0.014703754	-1.3	0.30476801	1554547_at	Gene Unknown Function	
FLJ22655	hypothetical protein FLJ22655	-3.1	0.043378509	-1.4	0.238171968	-1.5	0.321034012	220276_at	Gene Unknown Function	
LOC387763	hypothetical LOC387763	-2.1	0.008453667	-1.4	0.073048035	1.3	0.929451093	227099_s_at	Gene Unknown Function	
LOC399959	hypothetical gene supported by BX6476708	-2.0	0.002384232	-1.4	0.056005297	-1.4	0.22040601	225381_at	Gene Unknown Function	
LOC728264	Hypothetical protein LOC728264	-1.9	0.033723203	-1.4	0.1335015	1.3	0.97703832	1558828_s_at	Gene Unknown Function	
MAMDC2	MAM domain containing 2	-2.5	0.018025546	-1.3	0.182361962	-1.1	0.547079104	228885_at	Gene Unknown Function	
APOL	Apolipoprotein O-like	1.8	0.018326456	1.2	0.258660141	1.2	0.211163658	244187_at	Gene Unknown Function	
C11orf48	chromosome 11 open reading frame 48	1.8	2.41634E-06	1.4	0.000182872	1.4	0.033875873	221637_s_at	Gene Unknown Function	
C16ORF75	chromosome 16 open reading frame 75	1.8	0.002943574	1.4	0.084240496	2.0	0.18227362	226456_at	Gene Unknown Function	
C1orf31	chromosome 1 open reading frame 31	1.7	2.18585E-05	1.2	0.004045411	1.3	0.002821244	225638_at	Gene Unknown Function	
C1orf41	chromosome 1 open reading frame 41	1.8	2.746E-05	1.3	0.004081566	1.4	0.043076039	215691_x_at	Gene Unknown Function	
C1orf41	chromosome 1 open reading frame 41	2.0	2.627E-05	1.4	0.006121125	1.5	0.039950254	203960_s_at	Gene Unknown Function	

C3orf14	chromosome 3 open reading frame 14	1.8	0.001248178	1.3	0.049348266	1.4	0.102916662	219288_at	Gene Unknown Function	
C6orf125	chromosome 6 open reading frame 125	1.8	3.05806E-05	1.3	0.001369406	1.5	0.004116856	224448_s_at	Gene Unknown Function	
C6orf129	chromosome 6 open reading frame 129	1.7	4.8218E-05	1.3	0.032694914	1.3	0.093110922	225723_at	Gene Unknown Function	
C6orf190	chromosome 6 open reading frame 190	1.7	0.005567054	1.3	0.100501704	1.4	0.141410342	1558972_s_at	Gene Unknown Function	
C6orf51	chromosome 6 open reading frame 51	1.9	5.13733E-06	1.3	0.005489086	1.5	0.02525411	225083_at	Gene Unknown Function	
CS0DF027YP13	Full-length cDNA clone CS0DF027YP13 of Fetal brain of Homo sapiens	1.7	0.00266766	1.1	0.447791391	1.3	0.137883514	213979_s_at	Gene Unknown Function	
CS0DK002YF13	Full-length cDNA clone CS0DK002YF13 of HeLa cells	1.7	0.002943475	1.2	0.190871813	1.5	0.260858907	213294_at	Gene Unknown Function	
DCC1	defective in sister chromatid cohesion homolog 1 (S. cerevisiae)	1.9	0.000534216	1.4	0.021380057	1.4	0.088037758	219000_s_at	Gene Unknown Function	
DKFZp762E1312	hypothetical protein DKFZp762E1312	1.9	0.000309443	1.4	0.016559766	1.5	0.042887591	218726_at	Gene Unknown Function	
FAM26F	family with sequence similarity 26, member F	1.8	0.012161989	1.3	0.050941829	1.6	0.189100514	229391_s_at	Gene Unknown Function	
FAM26F	family with sequence similarity 26, member F	1.7	0.012102998	1.2	0.482595923	1.9	0.160024766	229543_at	Gene Unknown Function	
FAM54A	family with sequence similarity 54, member A	2.4	0.000238157	1.4	0.045088475	1.6	0.136878349	228069_at	Gene Unknown Function	
FAM83D	family with sequence similarity 83, member D	2.0	4.94011E-05	1.3	0.075425076	1.4	0.145389775	225687_at	Gene Unknown Function	
FLJ20035	hypothetical protein FLJ20035	2.2	0.000811852	1.4	0.011788099	1.8	0.112392896	218986_s_at	Gene Unknown Function	
FLJ31033	hypothetical protein FLJ31033	1.8	0.003688082	1.2	0.260705268	1.5	0.183241152	228152_s_at	Gene Unknown Function	
FLJ34964	CDNA FLJ34964 fis, clone NTONG2004095	1.8	0.000427518	1.3	0.058708528	1.3	0.077729019	1558750_a_at	Gene Unknown Function	
FLJ42418	FLJ42418 protein	1.9	0.007941289	1.5	0.061345386	2.8	0.176616415	231455_at	Gene Unknown Function	
HSPC111	hypothetical protein HSPC111	1.7	0.001669786	1.2	0.108376712	1.2	0.355405669	203023_at	Gene Unknown Function	
KIAA1267	---	1.8	0.010325265	1.7	0.009320119	-1.0	0.773531492	238774_at	Gene Unknown Function	
KIAA1524	KIAA1524	1.8	0.000946147	1.3	0.107477928	1.3	0.131684666	231855_at	Gene Unknown Function	
LOC146909	hypothetical protein LOC146909	2.6	0.00207664	1.6	0.07970955	1.6	0.089940467	222039_at	Gene Unknown Function	
OCC-1	overexpressed in colon carcinoma-1	1.9	0.001442979	1.3	0.04036199	1.5	0.015793446	225105_at	Gene Unknown Function	
TMEM167	transmembrane protein 167	1.7	0.000129386	1.3	0.026368727	1.3	0.037233423	226276_at	Gene Unknown Function	
FCRL5	Fc receptor-like 5	1.4	0.099665801	1.9	0.017440187	1.5	0.388871857	224405_at	B Cell Proliferation/Differentiation	
TNFRSF17	tumor necrosis factor receptor superfamily, member 17	1.4	0.015343101	2.0	0.000978252	1.9	0.089578505	206641_at	B Cell Proliferation/Differentiation	
STYK1	serine/threonine/tyrosine kinase 1	1.6	0.003456996	2.0	8.7862E-05	2.7	0.050106268	220030_at	Immune Activation	Signal Transduction
GREB1	GREB1 protein	-1.4	0.04436858	-1.7	0.003684624	-1.6	0.029124569	205862_at	Immune Activation	Activation/Proliferation
LAMP3	lysosomal-associated membrane protein 3	-1.1	0.66408003	-1.9	0.038309519	-1.7	0.110623168	205569_at	Immune Activation	Moderators of Activation/Inflammation
MSRB3	methionine sulfoxide reductase B3	-1.6	0.010949063	-1.7	0.002089442	-1.5	0.185864716	225790_at	Immune Activation	Moderators of Activation/Inflammation
EGR1	early growth response 1	-1.9	0.088379318	-2.3	0.029749683	-1.1	0.708652911	201693_s_at	Immune Activation	Signal Transduction
ERRF1	ERBB receptor feedback inhibitor 1, Transcribed locus	-1.6	0.016594991	-1.8	0.004982907	-1.4	0.233669259	235419_at	Immune Activation	Signal Transduction
FHL1	four and a half LIM domains 1	-1.5	0.083790247	-1.2	0.022591757	-1.2	0.405710231	214505_s_at	Immune Activation	Transcriptional Regulator
TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor 9B	-1.3	0.104409049	-1.8	0.000762331	-1.9	0.05029534	221618_s_at	Immune Activation	Transcriptional Regulator
SRGN	serglycin	-1.4	0.243699406	-1.8	0.047257613	-1.0	0.850962829	1554676_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
PKD4	pyruvate dehydrogenase kinase, isozyme 4	-1.5	0.013435532	-1.9	0.000777106	-1.8	0.0872244	205960_at	Metabolism	Glucose
PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	-1.6	0.000575088	-1.8	4.95879E-05	-1.9	0.05384576	203736_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
ROR1 (includes EG-4)	Full-length cDNA clone CS0DD009YB17 of Neuroblastoma	-1.9	0.063741592	-2.1	0.027884346	-2.1	0.082497889	232060_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
CXCL2	chemokine (C-X-C motif) ligand 2	-1.7	0.063665897	-1.8	0.043581101	-1.6	0.142004733	1569203_at	Trafficking	Chemokine Receptors and Ligands
KIAA1102	hypothetical protein	-1.7	0.007493712	-1.7	0.004285956	-1.9	0.058990286	212328_at	Gene Unknown Function	
LOC730259	hypothetical protein LOC730259	-1.6	0.115077432	-2.2	0.014194555	-1.7	0.127269089	239624_at	Gene Unknown Function	
XIST	X (inactive)-specific transcript (non-protein coding)	-38.7	0.069175113	-49.7	0.049939862	-2.0	0.405432329	224588_at	Immune Activation	Transcriptional Regulator
CNKSR2	connector enhancer of kinase suppressor of Ras 2	-1.1	0.15797351	-1.4	0.002455001	-1.8	0.002216198	229116_at	Apoptosis	Inducer of Apoptosis
GAS2	growth arrest-specific 2	-1.3	0.076322531	-1.4	0.021638262	-1.7	0.00662611	205848_at	Apoptosis	Inducer of Apoptosis
STK17B	serine/threonine kinase 17b	-1.3	0.149664339	-1.7	0.001557085	-1.9	0.033660079	243797_at	Apoptosis	Inducer of Apoptosis
TNFRSF25	tumor necrosis factor receptor superfamily, member 25	-1.4	0.029275955	-1.5	0.017597398	-2.4	0.002501073	219423_x_at	Apoptosis	Inducer of Apoptosis
TNFRSF25	tumor necrosis factor receptor superfamily, member 25	-1.3	0.071969861	-1.3	0.039957201	-1.7	0.003606227	211282_x_at	Apoptosis	Inducer of Apoptosis
TNFRSF25	tumor necrosis factor receptor superfamily, member 25	-1.3	0.057927176	-1.4	0.027456547	-2.1	0.004301705	210847_x_at	Apoptosis	Inducer of Apoptosis
FAIM3	Fas apoptotic inhibitory molecule 3	-1.3	0.431452576	-1.4	0.160324339	-1.8	0.041638239	221601_s_at	Apoptosis	Inhibitor of Apoptosis
TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy receptor	-1.3	0.024638166	-1.4	0.003951392	-1.8	0.002774962	227345_at	Apoptosis	Inhibitor of Apoptosis
NLRP1	NLR family, pyrin domain containing 1	-1.3	0.030122592	-1.4	0.004032468	-1.8	0.001187013	211824_x_at	Apoptosis	Inducer of Apoptosis
NUCB2	nucleobindin 2	1.7	0.000116546	1.5	0.001187863	1.8	0.025204469	203675_at	Apoptosis	Inducer of Apoptosis
APOL1	apolipoprotein L, 1	1.7	0.000816073	1.3	0.003819129	1.8	0.007191119	209546_s_at	Apoptosis	Inducer of Apoptosis
PARP14	poly (ADP-ribose) polymerase family, member 14	1.6	0.000173628	1.2	0.059723698	1.7	0.033118855	224701_at	Apoptosis	Inhibitor of Apoptosis
IGHV4-31	immunoglobulin heavy locus III immunoglobulin heavy constant region 4	1.2	0.277313823	1.6	0.037785429	1.9	0.007236897	211639_x_at	B Cell Proliferation/Differentiation	
IGHV4-31	immunoglobulin heavy locus III immunoglobulin heavy constant region 4	1.0	0.890756272	1.6	0.031037053	1.9	0.025268577	217236_x_at	B Cell Proliferation/Differentiation	
IGHM	immunoglobulin heavy constant mu	1.2	0.496746481	2.2	0.083413051	2.7	0.009104238	211634_x_at	B Cell Proliferation/Differentiation	
IGHM	immunoglobulin heavy constant mu	1.1	0.787681051	1.9	0.063169272	2.1	0.010569558	216491_x_at	B Cell Proliferation/Differentiation	
IGHM	immunoglobulin heavy constant mu	1.4	0.111410059	1.6	0.090186704	2.0	0.028793726	209374_s_at	B Cell Proliferation/Differentiation	
IGK @ /// IGKC /// IGKB	immunoglobulin kappa locus III immunoglobulin kappa constant region 1	-1.0	0.778011705	1.4	0.121646029	1.7	0.029083155	211644_x_at	B Cell Proliferation/Differentiation	
IGK @ /// IGKC /// LOC	immunoglobulin kappa locus III immunoglobulin kappa constant region 1	1.1	0.785284457	1.5	0.025887956	1.7	0.014329442	217157_x_at	B Cell Proliferation/Differentiation	
IGKC	immunoglobulin kappa constant III immunoglobulin kappa variable region 1	1.1	0.694539178	1.5	0.042282198	1.8	0.014898695	216207_x_at	B Cell Proliferation/Differentiation	
IGKC	immunoglobulin kappa constant	1.1	0.483486475	1.7	0.033791835	1.8	0.026283661	211645_x_at	B Cell Proliferation/Differentiation	
IGKV	immunoglobulin kappa light chain (IGKV gene), cell line JMV-2	1.2	0.341438619	1.6	0.05877291	2.0	0.011291156	216401_x_at	B Cell Proliferation/Differentiation	
ATOX1	ATOX1 antioxidant protein 1 homolog (yeast)	1.7	0.000227592	1.3	0.044480903	1.7	0.000655416	203454_s_at	Immune Activation	Antioxidants, Hypoxia, Protectants
ADAMDEC1	ADAM-like, decysin 1	1.6	0.032012899	1.3	0.172750371	2.1	0.007195977	206134_at	Immune Activation	Antigen Presentation and Immune Response
CLEC4E (MINCLE)	C-type lectin domain family 4, member E	1.7	0.000719308	1.3	0.029440536	1.7	0.028154788	222934_s_at	Immune Activation	Moderators of Activation/Inflammation
EMR2	egf-like module containing, mucin-like, hormone receptor-like 2	1.7	0.065793204	1.2	0.126356285	1.7	0.035577359	207610_s_at	Immune Activation	Moderators of Activation/Inflammation
GM2A	GM2 ganglioside activator	1.6	8.21615E-06	1.3	0.005203427	1.7	0.039459124	35820_at	Immune Activation	Moderators of Activation/Inflammation
PLRA	paired immunoglobulin-like type 2 receptor alpha	1.6	0.015978755	1.3	0.006505273	1.7	0.034156394	222218_s_at	Immune Activation	Moderators of Activation/Inflammation

CD1C	CD1c molecule	-1.4	0.037609416	-1.4	0.027211185	-1.9	0.006999696	205987_at	Immune Activation	Moderators of Activation/Inflammation
LILRB5	leukocyte immunoglobulin-like receptor, subfamily B (with TM	-1.5	0.009237361	-1.2	0.14022235	-2.0	7.87701E-05	206856_at	Immune Activation	Moderators of Activation/Inflammation
PYROXD1	pyridine nucleotide-disulphide oxidoreductase domain 1	-1.0	0.875130645	-1.3	0.027365997	-1.7	0.011027893	231173_at	Immune Activation	Moderators of Activation/Inflammation
CD28	CD28 molecule	1.0	0.87796452	-1.4	0.00833792	-2.0	0.003307401	206545_at	Immune Activation	Activation/Proliferation
CD44	CD44 molecule (Indian blood group)	-1.2	0.087705998	-1.3	0.012816654	-1.7	0.000411536	217523_at	Immune Activation	Activation/Proliferation
CD47	CD47 molecule	-1.0	0.689292025	-1.4	0.09891811	-1.8	0.019849811	227259_at	Immune Activation	Activation/Proliferation
TIMD4	T-cell immunoglobulin and mucin domain containing 4	-1.5	0.027974665	-1.4	0.010599611	-2.3	0.006457526	1552280_at	Immune Activation	Activation/Proliferation
AXIN2	axin 2 (conductin, axil)	-1.7	0.002328893	-1.7	0.001868765	-2.1	0.000442313	222696_at	Immune Activation	Signal Transduction
CALM	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (p	-1.3	0.114356341	-1.6	0.010385614	-1.7	0.005435033	213688_at	Immune Activation	Signal Transduction
CHRM3	cholinergic receptor, muscarinic 3	-1.0	0.563331992	-1.2	0.027787112	-1.9	2.51549E-06	239479_x_at	Immune Activation	Signal Transduction
CHRM3	cholinergic receptor, muscarinic 3	-1.2	0.119563834	-1.5	0.002993311	-4.5	0.000604504	1557733_a_at	Immune Activation	Signal Transduction
CHRM3	cholinergic receptor, muscarinic 3	1.1	0.931104225	-1.1	0.33501384	-1.7	8.75825E-05	241038_at	Immune Activation	Signal Transduction
DGKA	diacylglycerol kinase, alpha 80kDa	-1.1	0.322912295	-1.3	0.023910064	-1.9	0.002318356	203385_at	Immune Activation	Signal Transduction
DGKA	diacylglycerol kinase, alpha 80kDa	-1.5	0.036025388	-1.6	0.000106221	-2.5	0.004847815	211272_s_at	Immune Activation	Signal Transduction
F2RL1	coagulation factor II (thrombin) receptor-like 1	-1.2	0.151418693	-1.5	0.002281862	-2.0	0.001337595	213506_at	Immune Activation	Signal Transduction
GPRASP1	G protein-coupled receptor associated sorting protein 1	-1.5	0.004494652	-1.6	0.000909174	-1.8	0.008228193	204793_at	Immune Activation	Signal Transduction
LDLRAP1	low density lipoprotein receptor adaptor protein 1	-1.0	0.529303358	-1.4	0.011639275	-1.8	0.003751611	57082_at	Immune Activation	Signal Transduction
LOC440345 /// LOC6	hypothetical protein LOC440345 /// PI-3-kinase-related kinase	-1.2	0.16554655	-1.4	0.022841968	-1.7	0.029362598	231989_s_at	Immune Activation	Signal Transduction
LRN3	leucine rich repeat neuronal 3	-1.3	0.050730473	-1.5	0.001243831	-2.3	0.016956192	209840_s_at	Immune Activation	Signal Transduction
MAL	mal, T-cell differentiation protein	-1.0	0.497629114	-1.4	0.00613411	-2.1	7.91972E-05	204777_s_at	Immune Activation	Signal Transduction
MEGF6	multiple EGF-like-domains 6	-1.5	0.00452746	-1.4	0.016093554	-1.9	0.02313079	226869_at	Immune Activation	Signal Transduction
MTMR1	myotubularin related protein 1	-1.2	0.175564152	-1.5	0.002450501	-1.8	0.000549761	214975_s_at	Immune Activation	Signal Transduction
PKIA	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-1.3	0.032735555	-1.4	0.003601807	-1.9	3.97087E-06	226864_at	Immune Activation	Signal Transduction
PKIA	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-1.0	0.487912502	-1.3	0.007309165	-1.7	3.18615E-05	204612_at	Immune Activation	Signal Transduction
PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-1.3	0.026342687	-1.5	0.00155379	-2.1	0.001088643	1563217_at	Immune Activation	Signal Transduction
PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	-1.1	0.405676022	-1.5	0.004333198	-1.7	0.001460199	235744_at	Immune Activation	Signal Transduction
PRKCA	protein kinase C, alpha	-1.2	0.055048013	-1.4	0.001726072	-1.9	0.000389761	213093_at	Immune Activation	Signal Transduction
RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	-1.1	0.318881412	-1.4	0.0112985	-1.9	0.00401662	208206_s_at	Immune Activation	Signal Transduction
RP6-213H19.1	serine/threonine protein kinase MST4	-1.1	0.390434287	-1.5	0.010064843	-2.0	0.014518044	224407_s_at	Immune Activation	Signal Transduction
SH3YL1	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	-1.2	0.075264036	-1.4	0.005060454	-1.9	3.59833E-06	204019_s_at	Immune Activation	Signal Transduction
TBC1D4	TBC1 domain family, member 4	-1.2	0.119832459	-1.4	0.012714999	-1.8	0.001689426	203387_s_at	Immune Activation	Signal Transduction
TIAM1	T-cell lymphoma invasion and metastasis 1	-1.2	0.147846125	-1.5	0.00722674	-1.9	0.001778665	213135_at	Immune Activation	Signal Transduction
TRAF3IP3	TRAF3 interacting protein 3	-1.2	0.059403807	-1.3	0.003831196	-1.8	0.001563737	215275_at	Immune Activation	Signal Transduction
TRAF3IP3	TRAF3 interacting protein 3	-1.4	0.024834436	-1.4	0.000721624	-2.4	0.001604076	240265_at	Immune Activation	Signal Transduction
TXK	TXK tyrosine kinase	-1.1	0.356674095	-1.6	0.001119339	-2.6	0.001595584	206828_at	Immune Activation	Signal Transduction
F2R	coagulation factor II (thrombin) receptor	1.5	0.053784358	1.4	0.092093942	1.8	0.02156685	203989_x_at	Immune Activation	Signal Transduction
PRKD2	protein kinase D2	1.6	0.096248099	1.8	0.074167227	2.0	0.039554871	241669_x_at	Immune Activation	Signal Transduction
PTGER3	prostaglandin E receptor 3 (subtype EP3)	1.9	0.053011647	1.7	0.085958214	1.9	0.045916079	211909_x_at	Immune Activation	Signal Transduction
ANKRD55	ankyrin repeat domain 55	-1.1	0.311910966	-1.5	0.003613372	-2.1	0.00010963	220112_at	Immune Activation	Transcriptional Regulator
BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	1.0	0.810176245	-1.2	0.066119158	-1.8	0.042303977	233302_at	Immune Activation	Transcriptional Regulator
DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	-1.2	0.1636150521	-1.2	0.069096161	-1.7	0.038286467	202971_s_at	Immune Activation	Transcriptional Regulator
FOXP1	Transcribed locus	-1.2	0.077704476	-1.4	0.002786868	-2.0	2.71938E-05	244845_at	Immune Activation	Transcriptional Regulator
ING5 /// LOC727773	inhibitor of growth family, member 5 /// similar to p28 ING5	-1.2	0.116001432	-1.4	0.001419496	-1.7	9.6333E-05	228287_at	Immune Activation	Transcriptional Regulator
METTL8	methyltransferase like 8	-1.5	0.028642929	-1.6	0.011209712	-1.7	0.007262318	232533_at	Immune Activation	Transcriptional Regulator
METTL8	methyltransferase like 8	-1.4	0.185419005	-1.5	0.068433046	-1.9	0.040555803	1554667_s_at	Immune Activation	Transcriptional Regulator
NCOA2	nuclear receptor coactivator 2	-1.3	0.123181719	-1.6	0.011392948	-1.9	0.009299402	205732_s_at	Immune Activation	Transcriptional Regulator
RAB8B	RAB8B, member RAS oncogene family	-1.2	0.25506003	-1.6	0.004377099	-1.8	0.022639412	222846_at	Immune Activation	Transcriptional Regulator
RUNX2	run-related transcription factor 2	-1.1	0.450655288	-1.4	0.001990865	-1.7	0.000351788	232231_at	Immune Activation	Transcriptional Regulator
TCF7	transcription factor 7 (T-cell specific, HMG-box)	-1.1	0.230043663	-1.3	0.012199779	-1.7	0.000871757	205254_x_at	Immune Activation	Transcriptional Regulator
TSC22D3	TSC22 domain family, member 3	-1.2	0.241067741	-1.7	0.00867253	-1.7	0.021556011	208763_s_at	Immune Activation	Transcriptional Regulator
ZNF542	Zinc finger protein 542	-1.3	0.062432929	-1.2	0.079199736	-1.8	0.048870952	229187_at	Immune Activation	Transcriptional Regulator
ZNF655	zinc finger protein 655	-1.3	0.141355961	-1.4	0.042867707	-1.7	0.006168221	1554726_at	Immune Activation	Transcriptional Regulator
ELL2	elongation factor, RNA polymerase II, 2	1.4	0.071193978	1.6	0.050008702	2.0	0.011620813	226099_at	Immune Activation	Transcriptional Regulator
BHLHB8	basic helix-loop-helix domain containing, class B, 8	1.1	0.628716783	1.7	0.057173196	1.8	0.042433204	235965_at	Immune Activation	Transcriptional Regulator
TFCF	transcription factor EC	1.7	0.008411828	1.2	0.197857276	2.1	0.008614823	206715_at	Immune Activation	Transcriptional Regulator
CCL3 (MIP-1-a)	similar to chemokine (C-C motif) ligand 3-like 3	1.5	0.039588452	1.2	0.187152301	2.2	0.021345883	205114_s_at	Immune Defenses	Antiviral Chemokines & Proteins
S100A9	S100 calcium binding protein A9	1.8	0.057015983	1.5	0.149018666	1.8	0.045955357	203535_at	Immune Defenses	Antiviral Chemokines & Proteins
CD244 (2B4 or SLAM	CD244 molecule, natural killer cell receptor 2B4	1.5	0.011413717	1.5	0.01167896	1.7	0.047632206	220307_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
IRF5	interferon regulatory factor 5	-1.2	0.326054399	-1.6	0.032590564	-1.9	0.048630202	239412_at	Immune Defenses	Interferon-related
PDE3B	Phosphodiesterase 3B, cGMP-inhibited	1.2	0.346941876	-1.4	0.075246831	-1.9	0.043753738	222317_at	Metabolism	Lipids
SERN1C5	CDNA: FLJ22642 fis, clone HSI06970	-1.0	0.528149922	-1.4	0.009846212	-1.8	0.000267464	212812_at	Metabolism	Lipids
AK7	adenylate kinase 7	-1.5	0.008142226	-1.3	0.045145818	-1.8	0.000779113	1553734_at	Metabolism	Nucleic Acids
3ORNF95	Nicotinamide riboside kinase 1, chromosome 9 open reading f	-1.5	0.032698518	-1.6	0.013329432	-1.9	0.003459733	1562761_at	Metabolism	Nucleic Acids
CLK9	CDC-like kinase 4	-1.4	0.039579114	-1.6	0.004137194	-2.2	0.000419558	1568836_at	Metabolism	Nucleic Acids
HNRP1	heterogeneous nuclear ribonucleoprotein H1 (H)	-1.4	0.103977578	-1.4	0.061272334	-2.2	0.026253331	213472_at	Metabolism	Nucleic Acids
SFR55	splicing factor, arginine/serine-rich 5	-1.4	0.032113199	-1.6	0.000590725	-1.8	0.000778947	210077_s_at	Metabolism	Nucleic Acids
SFR56	splicing factor, arginine/serine-rich 6	1.1	0.532029172	-1.4	0.544088281	-2.6	0.037700487	206108_s_at	Metabolism	Nucleic Acids
OXNAD1	oxidoreductase NAD-binding domain containing 1	1.1	0.71924414	-1.3	0.039839991	-1.7	6.18575E-05	227686_at	Metabolism	Nucleic Acids, Proteins, Lipids and Glucose
MBNL1	muscleblind-like (Drosophila)	-1.2	0.234271345	-1.6	0.00845633	-1.7	0.02945133	201151_s_at	Metabolism	Nucleic Acids

ARTS-1	type 1 tumor necrosis factor receptor shedding aminopeptidase	-1.2	0.960080779	1.2	0.947587874	-2.2	0.0145835	214012_at	Metabolism	Proteins
GOLGA8A	golgi autoantigen, golgin subfamily a, 8A /// golgi autoantigen,	-1.4	0.028902866	-1.6	0.00400308	-1.9	0.001543523	210424_s_at	Metabolism	Proteins
GOLGA8A	golgi autoantigen, golgin subfamily a, 8A /// golgi autoantigen,	-1.4	0.016054459	-1.6	0.002135591	-1.9	0.007505727	210425_x_at	Metabolism	Proteins
GOLGA8A	golgi autoantigen, golgin subfamily a, 8A /// golgi autoantigen,	-1.3	0.018047629	-1.5	0.003951645	-1.8	0.017496532	208798_x_at	Metabolism	Proteins
MAT2A	methionine adenosyltransferase II, alpha	-1.2	0.173406426	-1.4	0.009469255	-1.7	0.015453282	200769_s_at	Metabolism	Proteins
MGEA5	Meningioma expressed antigen 5 (hyaluronidase)	-1.3	0.103605351	-1.5	0.023513763	-1.9	0.002970961	235868_at	Metabolism	Proteins
USP53	ubiquitin specific peptidase 53	-1.5	0.011724527	-1.5	0.003854453	-1.7	0.042606101	231817_at	Metabolism	Proteins
PLA2G2D	phospholipase A2, group IID	1.6	0.028689254	1.4	0.130849274	2.0	0.022599715	220423_at	Metabolism	Lipids
APOC1	apolipoprotein C-1	1.6	0.004016322	1.3	0.005689406	1.8	0.029079273	204416_x_at	Metabolism	Lipids
MKLN1	muskelin 1, intracellular mediator containing kelch motifs	-1.3	0.084373948	-1.6	0.004605615	-2.0	0.000601421	244171_at	Tissue Repair/Remodeling	Blood Vessel Related
NAP5	Nck-associated protein 5	-1.4	0.011654833	-1.6	0.000477985	-1.7	0.005718583	239650_at	Tissue Repair/Remodeling	Blood Vessel Related
SDC1	syndecan 1	-1.1	0.307556881	1.6	0.063102801	1.7	0.016210956	201287_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
SDC1	syndecan 1	1.0	0.889041221	1.6	0.024220864	1.8	0.048334043	201286_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
ADAM12	ADAM metalloproteinase domain 12	-1.2	0.14299191	-1.6	4.09036E-05	-1.8	0.000781441	202952_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
AQP3	aquaporin 3 (Gill blood group)	-1.0	0.704242309	-1.3	0.012168714	-1.7	0.007576683	39248_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
CXADR	coxsackie virus and adenovirus receptor	1.4	0.029999176	-1.4	0.001978663	-1.8	0.035264975	203917_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	-1.2	0.20525704	-1.6	0.001100504	-2.2	0.011863133	227361_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
RDX	radixin	-1.4	0.026366271	-1.5	0.009127879	-1.7	0.012678569	204969_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan	-1.2	0.150286372	-1.4	0.003688722	-2.0	0.012941664	202524_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
XLKD1	extracellular link domain containing 1	-1.5	0.038294096	-1.2	0.103471865	-2.6	0.00768578	220037_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
XLKD1	extracellular link domain containing 1	-1.3	0.078927657	-1.1	0.203231617	-2.0	0.017479656	219059_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
EPHA1	EPH receptor A1	-1.1	0.312515992	-1.3	0.021486732	-1.8	0.000497671	205977_s_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
NLGN4X	neuroligin 4, X-linked	-1.3	0.046406255	-1.4	0.00525773	-1.8	0.012324671	221933_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
NOG	Noggin	-1.1	0.552205705	-1.4	0.017161128	-2.6	0.002923242	231798_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
RELN	reelin	-1.2	0.121251884	-1.2	0.066977119	-1.7	0.004154137	205923_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
SCNA9	sodium channel, voltage-gated, type IX, alpha subunit	-1.4	0.002944398	-1.5	0.001894974	-2.1	0.028194475	206950_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
SDK2	sidekick homolog 2 (chicken)	-1.8	0.064542343	-1.7	0.070111516	-2.2	0.020046039	242064_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
SORL1	sortilin-related receptor, (LDLR class) A repeats-containing	-1.1	0.470714989	-1.2	0.028264179	-1.7	0.007352391	203509_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
SORL1	sortilin-related receptor, (LDLR class) A repeats-containing	-1.1	0.327845149	-1.3	0.008550525	-1.8	0.01005181	212560_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
TTC3	tetratricopeptide repeat domain 3	-1.5	0.012246049	-1.7	0.000320542	-2.1	4.08734E-05	1569472_s_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
NTN2L	Netrin 2-like (chicken)	1.3	0.323581916	2.5	0.05662872	2.9	0.012743326	211640_x_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
NTN2L	Netrin 2-like (chicken)	1.1	0.53751721	1.6	0.357010176	1.8	0.001365802	211635_x_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
CCR7	chemokine (C-C motif) receptor 7	-1.0	0.907421757	-1.5	0.113322523	-2.0	0.017766989	206337_at	Trafficking	Chemokine Receptors and Ligands
RYK	RYK receptor-like tyrosine kinase	-1.4	0.055052586	-1.4	0.029903468	-1.7	0.014181479	232205_at	Gene Unknown Function	
ALS2CR13	amyotrophic lateral sclerosis 2 (juvenile) chromosome region,	-1.2	0.14355216	-1.5	0.000529499	-1.8	8.85237E-06	226431_at	Gene Unknown Function	
C20orf197	chromosome 20 open reading frame 197	-1.1	0.210089832	-1.4	0.011502276	-1.8	0.000280236	1553311_at	Gene Unknown Function	
C4orf12	chromosome 4 open reading frame 12	-1.5	0.011019983	-1.6	0.007637676	-1.8	0.032920766	230801_at	Gene Unknown Function	
C6orf105	chromosome 6 open reading frame 105	-1.6	0.451129307	-1.9	0.186574652	-2.6	0.048310868	229070_at	Gene Unknown Function	
CCDC100	coiled-coil domain containing 100	-1.3	0.093417823	-1.7	0.000813192	-1.9	0.022454149	1554606_at	Gene Unknown Function	
Clone pp6489	Clone pp6489 unknown mRNA	1.0	0.533071551	-1.2	0.129273549	-1.8	0.027859957	1562250_at	Gene Unknown Function	
DKFZp667F083	MRNA; cDNA DKFZp667F083 (from clone DKFZp667F083)	1.2	0.766764577	-1.2	0.08997111	-1.7	0.000516481	1566040_at	Gene Unknown Function	
DKFZp667K1619	MRNA; cDNA DKFZp667K1619 (from clone DKFZp667K1619)	-1.3	0.049594781	-1.4	0.006671951	-1.8	0.000660101	1558569_at	Gene Unknown Function	
FAM101B	family with sequence similarity 101, member B	-1.2	0.116137907	-1.6	0.002625147	-2.2	0.000249521	226905_at	Gene Unknown Function	
FAM101B	family with sequence similarity 101, member B	-1.2	0.140177515	-1.5	0.005732931	-2.0	0.001811892	226876_at	Gene Unknown Function	
FAM118A	family with sequence similarity 118, member A	-1.2	0.443489754	-1.4	0.154178204	-1.8	0.037162061	226475_at	Gene Unknown Function	
FAM134B	family with sequence similarity 134, member B	-1.2	0.070207493	-1.4	0.000685069	-2.1	0.001260344	218532_s_at	Gene Unknown Function	
FAM82B	Family with sequence similarity 82, member B	-1.2	0.052929818	-1.2	0.082069768	-1.7	0.000156985	229843_at	Gene Unknown Function	
FLJ38048	CDNA FLJ38048 fis, clone CTONG2014264 /// CDNA FLJ390	-1.4	0.044294129	-1.6	0.001024077	-1.8	0.021389766	234975_at	Gene Unknown Function	
FLJ38379	hypothetical protein FLJ38379	1.1	0.049924285	-1.5	0.015060959	-1.9	0.043493547	1556473_at	Gene Unknown Function	
FLJ42259	CDNA FLJ42259 fis, clone TKIND2011289	-1.4	0.500632917	-1.4	0.001903618	-2.3	0.000277483	241365_at	Gene Unknown Function	
FLJ44826	CDNA FLJ44826 fis, clone BRACE3046762	-1.4	0.003316163	-1.4	0.001467499	-1.8	0.000532423	240246_at	Gene Unknown Function	
KIAA1199	KIAA1199	-1.7	0.01361038	-1.2	0.143879955	-2.0	0.020619187	212942_s_at	Gene Unknown Function	
LIX1L	Lix1 homolog (mouse)-like	-1.5	0.016295053	-1.6	0.001161084	-1.9	0.001813138	235036_at	Gene Unknown Function	
LOC129293	hypothetical protein LOC129293	1.0	0.88243306	-1.3	0.006511182	-1.8	2.75513E-05	227867_at	Gene Unknown Function	
LOC283788	FSHD region gene 1 /// similar to FRG1 protein (FSHD region	-1.6	0.00951339	-1.6	0.002072333	-2.2	0.000230325	235535_x_at	Gene Unknown Function	
LOC283788	hypothetical protein LOC283788	-1.5	0.026117693	-1.4	0.018186633	-2.5	0.005640267	229007_at	Gene Unknown Function	
LOC338620	hypothetical protein LOC338620	-1.4	0.026551063	-1.5	0.006682976	-1.9	0.000881707	230930_at	Gene Unknown Function	
LOC400713	Zinc finger-like	-1.1	0.463780799	-1.4	0.034195223	-2.1	0.009063728	232315_at	Gene Unknown Function	
LOC439949	hypothetical gene supported by AY007155	-1.1	0.566465928	-1.2	0.046655066	-1.9	6.01223E-06	232001_at	Gene Unknown Function	
LOC440993	Hypothetical gene supported by AK128346	-1.3	0.105297773	-1.2	0.186943039	-2.0	0.028063697	1558220_at	Gene Unknown Function	
LOC647979	hypothetical protein LOC647979	-1.7	0.018790885	-1.6	0.002370209	-2.0	0.02557728	1558028_x_at	Gene Unknown Function	
LOC730391	hypothetical protein LOC728555 /// hypothetical protein LOC7	-1.2	0.14579799	-1.5	0.013730401	-1.8	0.002657381	242491_at	Gene Unknown Function	
LRRCS5	Leucine rich repeat containing 55	-1.7	0.023258864	-1.4	0.088551979	-1.9	0.037278442	232856_at	Gene Unknown Function	
NY-REN-7	hypothetical protein LOC202134 /// NY-REN-7 antigen /// hypo	-1.3	0.032729131	-1.7	0.00092572	-2.8	2.7594E-05	214945_at	Gene Unknown Function	
PNMAL1	PNMA-like 1	-1.2	0.097358809	-1.2	0.113408141	-1.7	0.000866897	218824_at	Gene Unknown Function	
TMEM71	transmembrane protein 71	-1.1	0.859501682	-1.3	0.02193001	-1.7	0.000249104	238429_at	Gene Unknown Function	
YH97G12	Full length insert cDNA YH97G12	-1.1	0.302698799	-1.4	0.001541735	-1.9	0.000263922	1556932_at	Gene Unknown Function	
ZD79H10	Full length insert cDNA clone ZD79H10	-1.2	0.081754556	-1.5	0.000847879	-2.6	0.001460753	226272_at	Gene Unknown Function	
LOC339562	similar to hCG1742442	1.1	0.754495588	1.5	0.060369448	1.8	0.018902042	217480_x_at	Gene Unknown Function	

LOC652128	Similar to Ig heavy chain V-II region ARH-77 precursor	1.1	0.74323598	1.8	0.071485707	2.1	0.011787771	211637_x_at	Gene Unknown Function	
LOC96610	hypothetical gene LOC96610	1.5	0.162051947	2.0	0.052713984	2.5	0.013362516	224342_x_at	Gene Unknown Function	
---	Clone 24629 mRNA sequence	-1.2	0.385255361	-1.6	0.017882178	-2.4	0.001321226	215262_at	Unknown Transcript	
---	Transcribed locus	-1.3	0.01695979	-1.6	0.000404379	-2.3	3.14213E-06	236220_at	Unknown Transcript	
---	Transcribed locus	1.0	0.824678898	-1.4	0.003039019	-1.7	1.10981E-05	236016_at	Unknown Transcript	
---	Transcribed locus	-1.2	0.100902375	-1.4	0.000535044	-1.8	4.03107E-05	238744_at	Unknown Transcript	
---	Transcribed locus	-1.3	0.04064088	-1.3	0.022586672	-1.8	6.33798E-05	229687_s_at	Unknown Transcript	
---	---	-1.3	0.020516014	-1.6	0.000301289	-2.0	6.36443E-05	226777_at	Unknown Transcript	
---	Transcribed locus	-1.2	0.093004469	-1.2	0.085730013	-1.8	0.00014957	244535_at	Unknown Transcript	
---	Transcribed locus	1.1	0.535396777	-1.3	0.021970094	-1.9	0.0002554	229029_at	Unknown Transcript	
---	Transcribed locus	-1.1	0.362131156	-1.4	0.021777083	-1.9	0.000403187	1561166_a_at	Unknown Transcript	
---	Transcribed locus	-1.5	0.012851148	-1.2	0.150647571	-1.8	0.000443403	241885_at	Unknown Transcript	
---	Transcribed locus	-1.3	0.012699659	-1.1	0.325594777	-1.7	0.000613804	1569482_at	Unknown Transcript	
---	Transcribed locus	-1.2	0.07870688	-1.4	0.016843468	-1.7	0.001071541	1561195_at	Unknown Transcript	
---	Transcribed locus	-1.4	0.042745107	-1.6	0.002832966	-1.9	0.001451029	232752_at	Unknown Transcript	
---	Transcribed locus	-1.3	0.045186152	-1.3	0.045186152	-1.7	0.001514676	241299_at	Unknown Transcript	
---	Transcribed locus	-1.2	0.119175691	-1.5	0.000211732	-1.8	0.001689053	1556097_at	Unknown Transcript	
---	Transcribed locus	-1.4	0.041973303	-1.4	0.033238524	-1.8	0.002418922	243512_x_at	Unknown Transcript	
---	Transcribed locus	-1.5	0.034700727	-1.6	0.01283832	-2.0	0.002482799	1558409_at	Unknown Transcript	
---	Transcribed locus	-1.6	0.004559125	-1.5	0.003509179	-2.5	0.002595333	229199_at	Unknown Transcript	
---	Transcribed locus	-1.2	0.131635435	-1.3	0.007224421	-1.7	0.002816216	244414_at	Unknown Transcript	
---	Transcribed locus	-1.3	0.077810244	-1.5	0.009880806	-1.7	0.00485881	238420_at	Unknown Transcript	
---	Transcribed locus	-1.2	0.223215474	-1.3	0.084247105	-1.7	0.006271028	241774_at	Unknown Transcript	
---	Transcribed locus	-1.2	0.142077759	-1.3	0.02850352	-1.9	0.007326059	241893_at	Unknown Transcript	
---	Transcribed locus	-1.4	0.056158781	-1.4	0.016391989	-2.3	0.007752896	239317_at	Unknown Transcript	
---	Transcribed locus	-1.3	0.01515129	-1.6	0.000306487	-1.8	0.00965471	213790_at	Unknown Transcript	
---	Transcribed locus	-1.6	0.042012884	-1.5	0.054086336	-1.9	0.011441905	232286_at	Unknown Transcript	
---	Transcribed locus	-1.2	0.477028813	-1.4	0.055732319	-1.9	0.018416681	242057_at	Unknown Transcript	
---	Transcribed locus	-1.1	0.458225584	-1.2	0.077296843	-1.8	0.018639334	229994_at	Unknown Transcript	
---	Transcribed locus	-1.2	0.270557685	-1.6	0.003896219	-1.7	0.021770248	1562053_at	Unknown Transcript	
---	---	-1.3	0.210265465	-1.4	0.135356801	-2.1	0.025531537	1554636_at	Unknown Transcript	
---	Transcribed locus	-1.4	0.019997624	-1.3	0.025576117	-1.7	0.031038435	236383_at	Unknown Transcript	
---	Transcribed locus	-1.6	0.093800167	-1.5	0.121213053	-1.9	0.038628714	232614_at	Unknown Transcript	
CCDC42	Coiled-coil domain containing 42	1.0	0.754534659	-1.3	0.010615048	-2.0	0.00088759	224533_s_at	Gene Unknown Function	
---	Anti-thyroglobulin light chain variable region	1.4	0.197450238	1.9	0.057921598	2.4	0.021297526	217179_x_at	Unknown Transcript	
APOL6	apolipoprotein L, 6	1.8	1.30672E-05	1.5	0.000167157	1.8	0.018325459	1557116_at	Apoptosis	Inducer of Apoptosis
APOL6	apolipoprotein L, 6	2.2	0.006651803	1.7	0.037956914	1.9	0.123280516	241869_at	Apoptosis	Inducer of Apoptosis
HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase	-1.9	0.024343959	-1.9	0.013052659	-3.4	0.00085761	232397_at	Apoptosis	Inducer of Apoptosis
ASPM	asp (abnormal spindle) homolog, microcephaly associated (D	1.8	0.003991724	1.4	0.069895194	1.6	0.147493958	232238_at	Immune Activation	Cell Cycle
ASPM	asp (abnormal spindle) homolog, microcephaly associated (D	2.0	0.00033612	1.4	0.000335264	1.6	0.0722513	239002_at	Immune Activation	Cell Cycle
ASPM	asp (abnormal spindle) homolog, microcephaly associated (D	3.3	0.000851905	1.9	0.032023432	2.0	0.048168671	219918_s_at	Immune Activation	Cell Cycle
AURKA	aurora kinase A	1.9	0.000823814	1.3	0.073864404	1.5	0.131982827	204092_s_at	Immune Activation	Cell Cycle
AURKA	aurora kinase A	3.0	0.000530286	1.7	0.029702287	1.9	0.073611536	208079_s_at	Immune Activation	Cell Cycle
CCNB1	cyclin B1	2.7	0.001284342	1.5	0.12909659	1.6	0.340803099	228729_at	Immune Activation	Cell Cycle
CCNB1	cyclin B1	1.0	0.863615265	1.7	0.090863967	1.7	0.039589618	214768_x_at	Immune Activation	Cell Cycle
CCNB1	cyclin B1	3.5	0.00036944	1.9	0.019511377	2.1	0.116556034	214710_s_at	Immune Activation	Cell Cycle
DLG7	discs, large homolog 7 (Drosophila)	3.4	0.000536239	1.7	0.045514825	2.1	0.044637838	203764_at	Immune Activation	Cell Cycle
NCAPG	non-SMC condensin I complex, subunit G, NCAPG (includes E	3.2	0.001653874	1.9	0.052188424	1.9	0.064323946	218663_at	Immune Activation	Cell Cycle
NCAPG	non-SMC condensin I complex, subunit G, NCAPG (includes E	3.5	0.000508862	2.2	0.010543789	2.5	0.021938316	218662_s_at	Immune Activation	Cell Cycle
NDC80	NDC80 homolog, kinetochore complex component (S. cerevis	3.7	0.000312632	2.0	0.014913178	2.1	0.019376849	204162_at	Immune Activation	Cell Cycle
SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, ant	3.1	0.000574539	2.0	0.002483201	3.9	0.002201015	202833_at	Immune Activation	Moderators of Activation/Inflammation
SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, ant	2.7	4.48534E-05	1.8	0.000311652	3.2	0.0103303	211429_s_at	Immune Activation	Moderators of Activation/Inflammation
CST7	cystatin F (leukocystatin)	2.7	0.000163781	2.0	0.001927405	2.5	0.004035909	210140_at	Immune Activation	Moderators of Activation/Inflammation
CD1E	CD1e molecule	-2.3	0.045608163	-2.6	0.023235527	-2.8	0.039128137	215784_at	Immune Activation	Moderators of Activation/Inflammation
CD38	CD38 molecule	2.5	0.000426156	2.1	0.001581968	2.6	0.000456485	205692_s_at	Immune Activation	Signal Transduction
CD38	CD38 molecule	2.2	0.00388894	1.8	0.020061768	2.3	0.014765514	236191_at	Immune Activation	Signal Transduction
ANKRD22	ankyrin repeat domain 22	4.7	0.000400225	2.2	0.004540471	4.1	0.003581677	238439_at	Immune Activation	Transcriptional Regulator
EOMES	eomesodermin homolog (Xenopus laevis)	2.2	0.005704379	2.1	0.010592665	2.3	0.007241058	231776_at	Immune Activation	Transcriptional Regulator
FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	2.5	0.002284692	1.8	0.001232829	2.9	0.005232015	216950_s_at	Immune Defenses	C' and FcR's
FCGR1A	Fc fragment of IgG, high affinity Ib, receptor (CD64)	3.1	0.00133303	1.9	0.004023618	3.6	0.011120701	214511_x_at	Immune Defenses	C' and FcR's
FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	3.1	0.01119202	2.3	0.024860709	2.6	0.002960795	204006_s_at	Immune Defenses	C' and FcR's
FCGR3B	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	2.3	0.008271611	1.8	0.040841682	2.2	0.008434282	204007_at	Immune Defenses	C' and FcR's
FCER1A (FcεR1)	Fc fragment of IgE, high affinity I, receptor for; alpha polypept	-2.8	0.010727143	-2.3	0.013797634	-4.1	0.004614923	211734_s_at	Immune Defenses	C' and FcR's
GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	3.1	5.81944E-05	1.9	0.004438037	2.9	0.004713979	231577_s_at	Immune Defenses	Interferon-related
GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	3.4	5.49217E-05	1.9	0.006089423	3.0	0.005131655	202269_x_at	Immune Defenses	Interferon-related
GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	2.7	0.000929042	1.7	0.030521827	2.4	0.011360278	202270_at	Immune Defenses	Interferon-related
GBP5	Guanylate binding protein 5	3.0	5.6225E-05	2.0	0.001625023	3.1	0.012903584	229625_at	Immune Defenses	Interferon-related
GBP5	Guanylate binding protein 5	2.7	0.000129432	1.9	0.00165952	3.1	0.02013162	238581_at	Immune Defenses	Interferon-related
IFI27	interferon, alpha-inducible protein 27	3.7	0.000487051	1.9	0.006804119	3.9	0.046757563	202411_at	Immune Defenses	Interferon-related

IFI44L	interferon-induced protein 44-like	5.4	0.000214671	2.6	0.011321229	4.8	0.031533563	204439_at	Immune Defenses	Interferon-related
IFI6	interferon, alpha-inducible protein 6	4.5	0.000373112	2.2	0.022024426	3.7	0.040486962	204415_at	Immune Defenses	Interferon-related
IFIT3	interferon-induced protein with tetratricopeptide repeats 3	4.8	0.000209052	2.1	0.006852408	4.0	0.020601561	229450_at	Immune Defenses	Interferon-related
IFIT3	interferon-induced protein with tetratricopeptide repeats 3	3.3	0.001949212	1.6	0.027155877	2.7	0.024562277	204747_at	Immune Defenses	Interferon-related
IFNG	interferon, gamma	2.8	0.000454832	2.4	0.00223319	3.3	0.002142122	210354_at	Immune Defenses	Interferon-related
ISG15	ISG15 ubiquitin-like modifier	4.5	0.000162656	2.2	0.004497822	3.7	0.041948517	205483_s_at	Immune Defenses	Interferon-related
OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	2.9	0.000146167	1.8	0.002295715	2.2	0.006814506	202869_at	Immune Defenses	Interferon-related
OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	3.4	0.000161429	2.1	0.006516529	2.7	0.007154137	205552_s_at	Immune Defenses	Interferon-related
CD8A	CD8a molecule	2.8	0.001375761	2.2	0.006177823	2.6	0.002248745	205758_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
CD8B	CD8b molecule	2.1	0.001355917	1.6	0.027077884	1.6	0.010562123	207979_s_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
CD8B	CD8b molecule	2.5	0.000567018	1.9	0.00459597	2.2	0.011635942	215332_s_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
CRTAM	cytotoxic and regulatory T cell molecule	2.1	0.013769179	1.9	0.02538487	2.4	0.010496522	206914_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
GZMA	granzyme A	3.9	8.33696E-05	2.3	0.002485356	2.8	0.001922654	205488_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
GZMH	granzyme H	4.3	0.000717049	3.0	0.003587085	3.5	0.001468881	210321_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
GZMK	granzyme K (granzyme 3; tryptase II)	2.6	0.000663059	1.7	0.011532035	1.8	0.009710333	206666_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
NKG7	natural killer cell group 7 sequence	3.7	0.001594651	2.8	0.005401111	3.8	0.001778457	213915_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
SLAMF7	SLAM family member 7	1.9	0.006032687	1.9	0.019457467	2.4	0.00078356	219159_s_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
SLAMF7	SLAM family member 7	2.3	0.000411381	2.1	0.001712535	2.9	0.002160729	222838_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
SLAMF7	SLAM family member 7	1.6	0.004927776	1.5	0.042473761	1.8	0.001756416	234306_s_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
STAT1	signal transducer and activator of transcription 1, 91kDa	2.3	0.020786693	1.4	0.329386093	1.6	0.040622029	M97935_5_at	Immune Defenses	Transcriptional Regulator
STAT1	signal transducer and activator of transcription 1, 91kDa	3.7	2.73445E-05	2.2	0.001580107	3.3	0.002770893	209969_s_at	Immune Defenses	Transcriptional Regulator
STAT1	signal transducer and activator of transcription 1, 91kDa	2.0	0.000785053	1.5	0.018962211	2.0	0.004343813	200887_s_at	Immune Defenses	Transcriptional Regulator
STAT1	CDNA FLJ12169 fis, clone MAMMA1000643	2.5	0.000156504	1.6	0.010443265	2.0	0.008405899	232375_at	Immune Defenses	Transcriptional Regulator
STAT1	signal transducer and activator of transcription 1, 91kDa	2.2	0.000215334	1.6	0.007069784	2.2	0.009734741	M97935_3_at	Immune Defenses	Transcriptional Regulator
STAT1	signal transducer and activator of transcription 1, 91kDa	2.2	0.013378442	1.5	0.080717061	2.0	0.012529439	M97935_MB_at	Immune Defenses	Transcriptional Regulator
STAT1	signal transducer and activator of transcription 1, 91kDa	2.3	0.007134903	1.5	0.095849849	1.9	0.012734014	M97935_MA_at	Immune Defenses	Transcriptional Regulator
LEPR	leptin receptor	-1.5	0.000641491	-1.7	1.35784E-05	-1.8	0.017264846	211354_s_at	Metabolism	Lipids
LEPR	leptin receptor	-1.6	0.000545846	-1.7	7.65803E-05	-1.8	0.022473964	211356_x_at	Metabolism	Lipids
LEPR	leptin receptor	-1.6	0.000355067	-1.7	2.20909E-05	-1.8	0.028733959	211355_x_at	Metabolism	Lipids
LEPR	leptin receptor	-2.0	0.002481397	-1.6	0.006476656	-1.6	0.19888602	209894_at	Metabolism	Lipids
SPC3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	1.9	0.000316904	1.8	0.001217029	2.3	0.009989175	222753_s_at	Metabolism	Proteins
CCL4 (MIP-1-b)	chemokine (C-C motif) ligand 4	2.3	0.003893113	1.7	0.026482826	2.9	0.004456191	204103_at	Trafficking	Chemokine Receptors and Ligands
CCL5 (RANTES)	chemokine (C-C motif) ligand 5	3.3	0.001543671	2.7	0.003982504	3.2	0.001655284	204655_at	Trafficking	Chemokine Receptors and Ligands
CCL5 (RANTES)	chemokine (C-C motif) ligand 5	3.3	0.002570903	2.8	0.005468219	3.4	0.001995087	1555759_a_at	Trafficking	Chemokine Receptors and Ligands
CCL5 (RANTES)	chemokine (C-C motif) ligand 5	3.6	0.002860812	2.7	0.008722004	3.4	0.003715683	1405_i_at	Trafficking	Chemokine Receptors and Ligands
CCR5	chemokine (C-C motif) receptor 5	2.7	0.000115301	1.9	0.002905687	2.3	0.002927792	206991_s_at	Trafficking	Chemokine Receptors and Ligands
CXCL11 (IP-9)	chemokine (C-X-C motif) ligand 11	5.5	0.000122597	2.5	0.007254826	7.4	0.012785343	210163_at	Trafficking	Chemokine Receptors and Ligands
CXCL11 (IP-9)	chemokine (C-X-C motif) ligand 11	5.3	0.000771978	2.6	0.00866919	6.5	0.018258993	211122_s_at	Trafficking	Chemokine Receptors and Ligands
CXCL9 (MIG)	chemokine (C-X-C motif) ligand 9	4.5	0.00055733	2.4	0.018193593	4.7	0.004401721	203915_at	Trafficking	Chemokine Receptors and Ligands
LOC129607	hypothetical protein LOC129607	4.0	0.000295559	1.9	0.024071864	3.3	0.039951728	226702_at	Gene Unknown Function	
MGC4677	hypothetical protein MGC4677	2.5	0.000221315	1.7	0.00393654	2.2	0.002048042	225799_at	Gene Unknown Function	
MGC61571	hypothetical protein MGC61571	2.0	0.001742787	2.0	0.001532359	2.1	0.021660605	228283_at	Gene Unknown Function	
---	Transcribed locus	1.7	0.048540475	2.3	0.01012002	1.9	0.020731689	234884_x_at	Unknown Transcript	
IGL@	Immunoglobulin lambda locus	1.9	0.02888778	2.2	0.000813033	1.8	0.067097746	234366_x_at	B Cell Proliferation/Differentiation	
IGL@	Immunoglobulin lambda light chain /// Immunoglobulin lambda	2.4	0.023413537	2.6	0.081053597	1.2	0.142710998	233969_at	B Cell Proliferation/Differentiation	
IGL@	immunoglobulin lambda locus /// carboxypeptidase, vitellogenin	1.0	0.847544963	1.5	0.231155272	1.8	0.03639552	216430_x_at	B Cell Proliferation/Differentiation	
IGL@	immunoglobulin lambda locus /// carboxypeptidase, vitellogenin	1.1	0.713707711	1.5	0.229641229	1.8	0.042437624	217258_x_at	B Cell Proliferation/Differentiation	
IGL@	Immunoglobulin lambda locus	1.3	0.243471698	2.2	0.017300121	2.1	0.045677309	216853_x_at	B Cell Proliferation/Differentiation	
IGL@	immunoglobulin lambda locus /// carboxypeptidase, vitellogenin	1.4	0.144154965	2.5	0.002255832	2.3	0.046714747	216365_x_at	B Cell Proliferation/Differentiation	
PTTG1	pituitary tumor-transforming 1	2.5	0.000365408	1.7	0.009709437	2.0	0.07113482	203554_x_at	Apoptosis	Inhibitor of Apoptosis
IGHV1-69	immunoglobulin heavy variable 1-69	1.4	0.201127666	2.0	0.083964548	2.4	0.014257433	216541_x_at	B Cell Proliferation/Differentiation	
IGHV1-69	immunoglobulin heavy variable 1-69	2.9	0.007701144	2.2	0.008598129	3.6	0.01642753	240915_at	B Cell Proliferation/Differentiation	
KIAA0101	KIAA0101	3.3	0.000972646	1.9	0.030200612	2.0	0.065942604	202503_s_at	Immune Activation	Activation/Proliferation
CCNB2 (cyclin B2)	cyclin B2	3.4	0.000700294	1.9	0.025697711	2.2	0.117816525	202705_at	Immune Activation	Cell Cycle
CCNE2 (cyclin E2)	cyclin E2	2.2	0.00381394	1.4	0.161756986	1.5	0.17099561	205034_at	Immune Activation	Cell Cycle
CDC2	Cell division cycle 2, G1 to S and G2 to M	1.8	0.001157432	1.1	0.810453555	1.2	0.248674969	231534_at	Immune Activation	Cell Cycle
CDC2	cell division cycle 2, G1 to S and G2 to M	3.1	0.002603818	1.9	0.04337144	1.9	0.076762418	203213_at	Immune Activation	Cell Cycle
CDC2	cell division cycle 2, G1 to S and G2 to M	3.1	0.001701862	1.7	0.065746414	1.9	0.139214462	210559_s_at	Immune Activation	Cell Cycle
CDC2	cell division cycle 2, G1 to S and G2 to M	2.8	0.001668509	1.6	0.068359099	1.7	0.179360376	203214_x_at	Immune Activation	Cell Cycle
GTSE1	G-2 and S-phase expressed 1	2.0	0.00260968	1.4	0.076781041	1.3	0.145074686	204315_s_at	Immune Activation	Cell Cycle
GTSE1	G-2 and S-phase expressed 1	2.3	0.000945954	1.7	0.017159484	1.9	0.132783084	204318_s_at	Immune Activation	Cell Cycle
GTSE1	G-2 and S-phase expressed 1	2.5	0.000732041	1.7	0.011901511	1.9	0.060877914	215942_s_at	Immune Activation	Cell Cycle
CDC20	cell division cycle 20 homolog (S. cerevisiae)	3.2	0.000615744	1.9	0.019294711	2.2	0.12667513	202870_s_at	Immune Activation	Cell Cycle
CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual spe	3.2	0.000937023	2.0	0.017637032	2.3	0.064721249	209714_s_at	Immune Activation	Cell Cycle
CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual spe	2.7	0.001623261	1.7	0.052264124	1.9	0.15755156	1555758_a_at	Immune Activation	Cell Cycle
CENPA	centromere protein A	3.1	0.000835449	1.8	0.030428965	2.0	0.093975462	204962_s_at	Immune Activation	Cell Cycle
CKS2	CDC28 protein kinase regulatory subunit 2	3.0	0.000401561	1.9	0.011404648	2.1	0.068190178	204170_s_at	Immune Activation	Cell Cycle
KIF11	kinesin family member 11	2.9	0.001240307	1.8	0.043882994	2.0	0.109174897	204444_at	Immune Activation	Cell Cycle
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	2.3	0.000441529	1.4	0.039423032	1.4	0.140713285	1554768_a_at	Immune Activation	Cell Cycle

MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	3.0	0.000384866	1.7	0.011798051	1.7	0.105400705	203362_s_at	Immune Activation	Cell Cycle
MLF1IP	MLF1 interacting protein	3.0	0.002157203	1.9	0.020101049	1.7	0.093294765	218883_s_at	Immune Activation	Cell Cycle
MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	2.9	0.001575816	1.8	0.039015903	2.0	0.190894358	223700_at	Immune Activation	Cell Cycle
NEK2	NIMA (never in mitosis gene a)-related kinase 2	3.1	0.000804265	1.8	0.038955253	2.0	0.11310395	204641_at	Immune Activation	Cell Cycle
NUSAP1	nucleolar and spindle associated protein 1	2.2	0.004661856	1.5	0.075457211	1.7	0.267998582	219978_s_at	Immune Activation	Cell Cycle
NUSAP1	nucleolar and spindle associated protein 1	3.0	0.001303922	1.8	0.036222966	2.0	0.095501929	218039_at	Immune Activation	Cell Cycle
SPC25	SPC25, NDC80 kinetochore complex component, homolog (S	3.8	0.000294813	1.9	0.03379795	2.0	0.234038133	209891_at	Immune Activation	Cell Cycle
TRGC2	T cell receptor gamma constant 2	2.0	0.007218024	1.7	0.022243026	2.2	0.07046733	216920_s_at	Immune Activation	Moderators of Activation/Inflammation
TRGV9	T cell receptor gamma variable 10	2.0	0.009329744	1.7	0.025248348	2.2	0.068650438	215806_x_at	Immune Activation	Moderators of Activation/Inflammation
TRGV9	T cell receptor gamma variable 9	1.9	0.010507918	1.7	0.031467486	2.2	0.074945099	209813_x_at	Immune Activation	Moderators of Activation/Inflammation
TRGV9	T cell receptor gamma variable 9	1.9	0.010028472	1.7	0.029308654	2.2	0.077921768	211144_x_at	Immune Activation	Moderators of Activation/Inflammation
DUSP1	dual specificity phosphatase 1	-2.0	0.015444388	-2.9	0.001200733	-1.0	0.610813337	201041_s_at	Immune Activation	Moderators of Activation/Inflammation
TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulat	-1.8	0.001844197	-1.8	0.000466584	-2.0	0.068725397	209676_at	Immune Activation	Moderators of Activation/Inflammation
MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	1.7	0.009079066	1.7	0.004171562	1.6	0.011313918	213013_at	Immune Activation	Signal Transduction
PBK	PDZ binding kinase	3.6	0.002542448	2.2	0.029520329	2.6	0.094986676	219148_at	Immune Activation	Signal Transduction
RHOB	ras homolog gene family, member B	-1.8	0.007127256	-1.8	0.003893317	-1.3	0.38539539	212099_at	Immune Activation	Signal Transduction
JUN (AP-1)	Jun oncogene	-2.2	0.02389322	-2.4	0.009171654	-1.4	0.37346799	213281_at	Immune Activation	Transcriptional Regulator
JUN (AP-1)	Jun oncogene	-2.4	0.044663368	-2.7	0.025320028	-1.4	0.45557826	201466_s_at	Immune Activation	Transcriptional Regulator
JUN (AP-1)	Jun oncogene	-1.7	0.07038554	-1.9	0.0256284	-1.3	0.464679507	201464_x_at	Immune Activation	Transcriptional Regulator
ZFP36L2	zinc finger protein 36, C3H type-like 2	-1.7	0.014815652	-1.7	0.001104518	-2.1	0.056460179	201367_s_at	Immune Activation	Transcriptional Regulator
EAF2	Activator	2.0	0.005212779	1.8	0.012085402	1.8	0.067795132	219551_at	Immune Activation	Transcriptional Regulator
FCRL4	Fc receptor-like 4	2.0	0.012960892	1.9	0.039155413	2.3	0.206393428	224403_at	Immune Defenses	C' and FcR's
FCRL4	Fc receptor-like 4	2.0	0.010119294	1.3	0.146143778	1.5	0.245791898	224401_s_at	Immune Defenses	C' and FcR's
FCRL4	Fc receptor-like 4	2.4	0.013690714	1.6	0.070377414	1.9	0.281996887	224402_s_at	Immune Defenses	C' and FcR's
CXCL10 (IP-10)	chemokine (C-X-C motif) ligand 10	3.9	5.86446E-05	2.0	0.004688205	4.0	0.063473309	204533_at	Immune Defenses	Chemokine Receptors and Ligands
RSAD2 (CIG5/VIPER)	radical S-adenosyl methionine domain containing 2	3.4	0.002193479	1.8	0.056321053	2.5	0.092584422	213797_at	Immune Defenses	Interferon-related
RSAD2 (CIG5/VIPER)	radical S-adenosyl methionine domain containing 2	4.2	0.00688873	2.2	0.032887645	3.8	0.054721372	242625_at	Immune Defenses	Interferon-related
IFI44 (p44)	interferon-induced protein 44	3.1	0.000358064	1.9	0.016652817	3.0	0.103079485	214453_s_at	Immune Defenses	Interferon-related
IFI44 (p44)	interferon-induced protein 44	2.1	0.026289815	1.2	0.346101753	1.9	0.278530853	214059_at	Immune Defenses	Interferon-related
IFIT1	interferon-induced protein with tetratricopeptide repeats 1	3.7	0.000896977	1.7	0.03999293	3.3	0.11071717	203153_at	Immune Defenses	Interferon-related
MX1	myxovirus (influenza virus) resistance 1, interferon-inducible p	3.4	0.000166367	1.8	0.011463884	2.8	0.061214792	202086_at	Immune Defenses	Interferon-related
CD160 (BY55)	CD160 molecule	2.2	0.014304315	2.3	0.058878815	2.7	0.058878815	207840_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
KLRD1(CD94)	killer cell lectin-like receptor subfamily D, member 1	2.8	0.000530191	2.0	0.004655261	2.5	0.063214926	210606_x_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
KLRD1(CD94)	killer cell lectin-like receptor subfamily D, member 1	2.2	0.00077188	1.6	0.01562236	1.8	0.077672308	207796_x_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
KLRD1(CD94)	killer cell lectin-like receptor subfamily D, member 1	3.2	0.000274106	2.0	0.005459615	2.4	0.080043178	207795_s_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
KLRK1	killer cell lectin-like receptor subfamily K, member 2	2.3	0.005835738	1.8	0.024822298	1.6	0.119023911	1555691_s_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
KLRK1	killer cell lectin-like receptor subfamily K, member 1	2.3	0.003464442	1.8	0.019024302	1.8	0.074375476	205821_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
UGCG	UDP-glucose ceramide glucosyltransferase	-1.8	0.017183178	-1.8	0.001628723	-1.4	0.17731562	221765_at	Metabolism	Lipids & Glucose
RRM2	ribonucleotide reductase M2 polypeptide	3.8	0.00073495	2.1	0.031415643	2.4	0.050057208	209773_s_at	Metabolism	Nucleic Acids
RRM2	ribonucleotide reductase M2 polypeptide	3.3	0.001535326	1.9	0.035329074	2.1	0.084825281	201890_at	Metabolism	Nucleic Acids
TOP2A	topoisomerase (DNA) II alpha 170kDa	3.2	0.002096794	2.0	0.042170546	1.8	0.064624926	201291_s_at	Metabolism	Nucleic Acids
TOP2A	topoisomerase (DNA) II alpha 170kDa	3.4	0.001082338	1.9	0.03650135	2.0	0.067758976	201292_at	Metabolism	Nucleic Acids
TYMS	thymidylate synthetase	3.0	0.000873955	1.8	0.031454664	1.8	0.080999142	202589_at	Metabolism	Nucleic Acids
TYMS	thymidylate synthetase	2.5	0.003422222	1.4	0.108824453	1.7	0.199285707	1554696_s_at	Metabolism	Nucleic Acids
BCAT1	branched chain aminotransferase 1, cytosolic	1.9	0.000634272	1.3	0.090562843	1.5	0.233908868	214452_at	Metabolism	Proteins
BCAT1	branched chain aminotransferase 1, cytosolic	2.0	0.001906172	1.3	0.112580221	1.7	0.159016738	225285_at	Metabolism	Proteins
BCAT1	branched chain aminotransferase 1, cytosolic	1.8	0.009232048	1.3	0.138341917	1.7	0.115364806	226517_at	Metabolism	Proteins
CD36	CD36 molecule (thrombospondin receptor)	-2.1	0.044404038	-2.0	0.030534722	-1.7	0.306935873	209555_s_at	Tissue Repair/Remodeling	Blood Vessel Related
THBS1	thrombospondin 1	-2.0	0.002356956	-2.0	0.000788629	-1.4	0.285975206	201109_s_at	Tissue Repair/Remodeling	Blood Vessel Related
THBS1	thrombospondin 2	-2.3	0.000962026	-2.0	0.001376261	-1.2	0.401980867	201110_s_at	Tissue Repair/Remodeling	Blood Vessel Related
CTGF	connective tissue growth factor	-2.0	0.006505924	-1.9	0.004292309	1.4	0.948780439	209101_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
MGP	matrix Gla protein	-1.8	0.010048563	-2.0	0.00335951	-1.8	0.09298709	238481_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
VIM	vimentin	-1.7	0.014386964	-1.8	0.005747411	-1.4	0.232588978	1555938_x_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
CHI3L1 (YKL-40)/HC-	chitinase 3-like 1 (cartilage glycoprotein-39)	4.6	0.001626862	3.3	0.004069958	7.8	0.057515774	209395_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
CHI3L1 (YKL-40)/HC-	chitinase 3-like 1 (cartilage glycoprotein-39)	2.8	0.002372258	1.9	0.005221844	4.7	0.072602423	209396_s_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
GP6A	glycoprotein 6A	-1.9	0.045180686	-2.0	0.021117691	-2.6	0.096416072	209470_s_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
XCL2 (LYMPHOTAC1)	chemokine (C motif) ligand 2	1.9	0.002674293	1.6	0.003635676	1.8	0.184357313	206366_x_at	Trafficking	Chemokine Receptors and Ligands
XCL2 (LYMPHOTAC1)	chemokine (C motif) ligand 1 /// chemokine (C motif) ligand 2	1.9	0.003284094	1.8	0.003613647	2.0	0.143825964	214567_s_at	Trafficking	Chemokine Receptors and Ligands
CDNA FLJ13266	CDNA FLJ13266 fis, clone OVARC1000960	-1.8	0.005999308	-2.0	0.00016043	-1.8	0.121689347	231979_at	Gene Unknown Function	
FAM72A	similar to family with sequence similarity 72, member A	3.1	0.000744463	1.8	0.037061142	1.9	0.096252284	225834_at	Gene Unknown Function	
LOC644246	hypothetical protein LOC644246	2.2	0.002099366	2.0	0.005620049	1.1	0.644526978	230388_s_at	Gene Unknown Function	
---	Transcribed locus	-2.0	0.001857373	-1.8	0.002831822	-1.7	0.072573965	1558101_at	Unknown Transcript	
---	Homo sapiens, clone IMAGE:4723617, mRNA	2.2	0.030055867	2.0	0.043040752	1.7	0.343821251	1560800_at	Unknown Transcript	
---	Transcribed locus	3.9	0.005566237	4.0	0.000802946	1.7	0.767583782	239591_at	Unknown Transcript	
---	Transcribed locus	2.8	0.000376192	1.7	0.01924623	1.9	0.108316614	228273_at	Unknown Transcript	
ARHGAP24 (p73)	Rho GTPase activating protein 25	-1.7	0.036084186	-1.7	0.079039668	-2.5	0.026615496	1566825_at	Apoptosis	Inducer of Apoptosis
ARHGAP24 (p73)	Rho GTPase activating protein 24	-1.6	0.054658178	-1.4	0.107529077	-1.8	0.027004889	223422_s_at	Apoptosis	Inducer of Apoptosis
EBF3	early B-cell factor 3	-1.9	0.002057917	-1.6	0.001063509	-1.9	0.041598188	227242_s_at	Apoptosis	Inducer of Apoptosis
TNFRSF21	tumor necrosis factor receptor superfamily, member 21	-1.7	0.002546079	-1.7	0.000294749	-2.1	0.046656126	214581_x_at	Apoptosis	Inducer of Apoptosis

BIRC4BP (XAF1)	XIAP associated factor-1	2.5	0.000148778	1.6	0.004633116	2.4	0.045781004	228617_at	Apoptosis	Inducer of Apoptosis
BIRC4BP (XAF1)	XIAP associated factor-1	2.1	0.008040152	1.6	0.036731518	2.1	0.079205184	242234_at	Apoptosis	Inducer of Apoptosis
BIRC4BP (XAF1)	XIAP associated factor-1	2.2	0.020909296	1.5	0.100621828	2.1	0.083946512	206133_at	Apoptosis	Inducer of Apoptosis
FASLG	Fas ligand (TNF superfamily, member 6)	1.8	0.001899263	1.3	0.096597953	1.6	0.010280366	211333_s_at	Apoptosis	Inducer of Apoptosis
FASLG	Fas ligand (TNF superfamily, member 6)	2.1	0.000204158	1.4	0.035213793	1.7	0.022036289	210865_at	Apoptosis	Inducer of Apoptosis
BST2	bone marrow stromal cell antigen 2	1.9	0.000136265	1.5	0.001672637	2.2	0.016655898	201641_at	B cell Proliferation/Differentiation	
C4ORF7 (FDC-SP)	chromosome 4 open reading frame 7	2.0	0.020725591	1.8	0.053367653	2.3	0.04201403	229152_at	B Cell Proliferation/Differentiation	
CD72	CD72 molecule	1.9	0.002075507	1.5	0.009893648	1.8	0.00908026	215925_s_at	B Cell Proliferation/Differentiation	
CCNA2	cyclin A2	2.2	0.000852056	1.3	0.05970905	1.4	0.027832302	213226_at	Immune Activation	Cell Cycle
CCNA2	cyclin A2	2.7	0.00063157	1.5	0.060341856	1.8	0.045901491	203418_at	Immune Activation	Cell Cycle
FAM33A	family with sequence similarity 33, member A	2.4	0.000469329	1.5	0.04052525	1.7	0.029019373	225686_at	Immune Activation	Cell Cycle
CLEC4G	C-type lectin superfamily 4, member G	-2.4	0.002075087	-1.6	0.015962553	-3.1	0.027294365	1559065_s_at	Immune Activation	Moderators of Activation/Inflammation
IL18	interleukin 18 (interferon-gamma-inducing factor)	1.7	0.012324867	1.3	0.09200378	1.8	0.032801253	206295_at	Immune Activation	Moderators of Activation/Inflammation
LAG3	lymphocyte-activation gene 3	2.2	0.000561077	1.5	0.015449541	2.2	0.001878125	206486_at	Immune Activation	Moderators of Activation/Inflammation
MT2A	metallothionein 2A	2.1	0.000202261	1.3	0.020310134	1.8	0.043265517	212185_x_at	Immune Activation	Moderators of Activation/Inflammation
RARRES3 (Rig-1)	retinoic acid receptor responder (tazarotene induced) 3	2.1	0.000203544	1.6	0.006057043	2.0	0.009691258	204070_at	Immune Activation	Moderators of Activation/Inflammation
S100A8	S100 calcium binding protein A8	2.6	0.021256573	1.7	0.122403067	2.6	0.042874178	202917_s_at	Immune Activation	Moderators of Activation/Inflammation
SAMD9L	Transcribed locus	2.4	9.60368E-05	1.6	0.000815666	2.1	0.01601002	243271_at	Immune Activation	Moderators of Activation/Inflammation
SAMD9L	sterile alpha motif domain containing 9-like	2.3	0.000184324	1.4	0.016929827	2.2	0.026552602	226603_at	Immune Activation	Moderators of Activation/Inflammation
SAMD9L	sterile alpha motif domain containing 9-like	2.2	0.000221907	1.4	0.013647626	1.8	0.040650211	230036_at	Immune Activation	Moderators of Activation/Inflammation
SAMD9L	sterile alpha motif domain containing 9-like	2.2	0.001783053	1.7	0.014456056	2.1	0.040695205	235643_at	Immune Activation	Moderators of Activation/Inflammation
GPR56	G protein-coupled receptor 56	1.8	0.000662624	1.6	0.000803281	1.9	0.006035708	212070_at	Immune Activation	Signal Transduction
JAKMIP1	janus kinase and microtubule interacting protein 1	2.2	0.000512979	1.9	0.010774538	1.9	0.008834076	238600_at	Immune Activation	Signal Transduction
RTP4	RTP4	2.5	0.050691E-05	1.5	0.005544209	1.9	0.037039779	219684_at	Immune Activation	Signal Transduction
SH2D1A	SH2D1A (includes EG:4068)	2.1	0.001356297	1.6	0.012853791	1.8	0.009724539	210116_at	Immune Activation	Signal Transduction
IGFBP3	insulin-like growth factor binding protein 3	-1.8	0.007206954	-1.5	0.001978942	-2.1	0.026221341	212143_s_at	Immune Activation	Signal Transduction
IGFBP3	insulin-like growth factor binding protein 3	-1.8	0.002705826	-1.4	0.003906194	-1.9	0.063291119	210095_s_at	Immune Activation	Signal Transduction
PDE7A	phosphodiesterase 7A	-1.1	0.055783445	-1.3	0.004586849	-1.8	0.00027466	1552343_s_at	Immune Activation	Signal Transduction
PDE7A	phosphodiesterase 7A	-1.3	0.094166916	-1.7	0.000133971	-2.1	0.001920845	224046_s_at	Immune Activation	Signal Transduction
PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha	-1.4	0.095516154	-1.8	0.00330165	-2.2	0.005646034	200604_s_at	Immune Activation	Signal Transduction
ANKRD23	ankyrin repeat domain 23	2.2	0.002653548	1.4	0.017736044	2.0	0.03225575	239196_at	Immune Activation	Transcriptional Regulator
ZNF533	zinc finger protein 533	-1.8	0.002176748	-1.6	0.002938078	-1.9	0.030925634	1555801_s_at	Immune Activation	Transcriptional Regulator
ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix p	-2.8	0.000371556	-1.5	0.033484064	-1.9	0.045639583	209292_at	Immune Activation	Transcriptional Regulator
ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix p	-2.6	0.000315665	-1.7	0.008093983	-1.7	0.08256351	209291_at	Immune Activation	Transcriptional Regulator
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog 1	-1.8	0.06908E-05	-1.4	0.011423249	-1.7	0.002431069	1566324_x_at	Immune Activation	Transcriptional Regulator
APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-1	3.8	2.004091626	3.0	0.098099431	3.0	0.042692032	210873_x_at	Immune Defenses	Antiviral Chemokines & Proteins
FCN1	ficolin (collagen/fibrinogen domain containing) 1	2.8	0.004097167	1.7	0.012926709	2.6	0.021270504	205237_at	Immune Defenses	C' and FcR's
CD209 (DC SIGN)	CD209 molecule	-2.1	0.004901329	-1.4	0.016378306	-2.9	0.003255739	207277_at	Immune Defenses	Immune Response
GBP2	---	1.8	0.000294046	1.4	0.066190734	1.9	0.004929018	242907_at	Immune Defenses	Interferon-related
GBP2	guanylate binding protein 2, interferon-inducible	2.2	3.39943E-05	1.6	0.002806489	2.1	0.016457485	202748_at	Immune Defenses	Interferon-related
GBP4	guanylate binding protein 4	2.1	0.000556203	1.6	0.004584754	2.2	0.001256241	235175_at	Immune Defenses	Interferon-related
IFI30	interferon, gamma-inducible protein 30	1.7	0.70688E-05	1.5	0.001769589	2.2	0.000683784	201422_at	Immune Defenses	Interferon-related
IFI35	interferon-induced protein 35	2.5	0.000123829	1.6	0.000345181	2.1	0.002963717	209417_s_at	Immune Defenses	Interferon-related
IFIT2	interferon-induced protein with tetratricopeptide repeats 2	3.1	0.000399064	1.5	0.070356129	2.4	0.043293192	226757_at	Immune Defenses	Interferon-related
ISG20	interferon stimulated exonuclease gene 20kDa	2.6	1.27647E-05	1.6	0.003660271	2.0	0.006020834	33304_at	Immune Defenses	Interferon-related
ISG20	interferon stimulated exonuclease gene 20kDa	2.8	6.47355E-06	1.6	0.003687473	2.1	0.012268096	204698_at	Immune Defenses	Interferon-related
OASL	2'-5'-oligoadenylate synthetase-like	2.6	3.82101E-05	1.6	0.00413836	2.3	0.038841507	205660_at	Immune Defenses	Interferon-related
OASL	2'-5'-oligoadenylate synthetase-like	2.2	0.001433956	1.4	0.047631276	1.9	0.06408299	210797_s_at	Immune Defenses	Interferon-related
PARP9	poly (ADP-ribose) polymerase family, member 9	3.3	3.6929E-05	1.5	0.006569165	2.0	0.032906441	223220_s_at	Immune Defenses	Interferon-related
PRF1 (Perforin 1)	perforin 1 (pore forming protein)	2.0	9.37093E-05	1.7	0.007021586	2.4	0.003359588	214617_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
PRF1 (Perforin 1)	perforin 1 (pore forming protein)	2.1	0.002098929	1.5	0.013403817	1.8	0.003527613	1553681_a_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
ACOT7	acyl-CoA thioesterase 7	2.0	0.00070511	1.4	0.010039183	1.7	0.001294613	208002_s_at	Metabolism	Lipids
FABP5	fatty acid binding protein 5	2.2	0.000298191	1.4	0.023833303	1.7	0.003304222	202345_s_at	Metabolism	Lipids
SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	2.9	3.69651E-05	1.5	0.0047494	1.8	0.009859408	205768_s_at	Metabolism	Lipids
SLC27A2	---	2.3	0.000124965	1.4	0.003372864	1.5	0.027113245	205769_at	Metabolism	Lipids
SLC31A2	solute carrier family 31 (copper transporters), member 2	2.1	0.000399365	1.4	0.012497644	2.2	0.041265687	204204_at	Metabolism	Metals/Ions
GMNN	geminin, DNA replication inhibitor	2.5	0.000256789	1.6	0.014126774	1.8	0.048881577	218350_s_at	Metabolism	Nucleic Acids
NME1	non-metastatic cells 1, protein (NM23A) expressed in	2.3	7.18924E-05	1.6	0.007045088	1.8	0.046946778	201577_at	Metabolism	Nucleic Acids
ORC6L	origin recognition complex, subunit 6 like (yeast)	1.8	0.002426263	1.3	0.073136744	1.3	0.314957227	219105_x_at	Metabolism	Nucleic Acids
ORC6L	origin recognition complex, subunit 6 like (yeast)	1.5	0.003294302	1.7	0.002088882	1.9	0.025952104	219117_s_at	Metabolism	Nucleic Acids
RAD51AP1	RAD51 associated protein 1	2.6	0.00067711	1.5	0.036353009	1.7	0.026361432	204146_at	Metabolism	Nucleic Acids
LAP3	leucine aminopeptidase 3	1.8	0.002199155	1.3	0.044579288	1.7	0.011876343	217933_s_at	Metabolism	Proteins
PSMB9	proteasome subunit, beta type, 9	2.1	8.15925E-05	1.5	0.007407192	1.8	0.000764999	204279_at	Metabolism	Proteins
SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	2.1	0.000639179	1.5	0.003810698	2.5	0.000229022	205241_at	Metabolism	Proteins
TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	2.0	9.66136E-06	1.4	0.000706855	1.8	0.009480544	202307_s_at	Metabolism	Proteins
UBE2L6	ubiquitin-conjugating enzyme E2L 6	2.2	2.66513E-05	1.5	0.004591423	1.9	0.003355488	201649_at	Metabolism	Proteins
WARS	tryptophanyl-tRNA synthetase	2.1	0.000117348	1.4	0.010508458	2.1	0.006823934	200629_at	Metabolism	Proteins
F13A1	coagulation factor XIII, A1 polypeptide	-2.6	0.000396895	-1.6	0.014568557	-2.2	0.018248825	203305_at	Tissue Repair/Remodeling	Blood Vessel Related
ECGF1	endothelial cell growth factor 1 (platelet-derived)	1.8	0.001293559	1.4	0.013496945	1.9	0.013198227	217497_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues

EPST11	epithelial stromal interaction 1 (breast)	2.3	0.004932811	1.4	0.085862604	1.9	0.02224259	239979_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
EPST11	epithelial stromal interaction 1 (breast)	2.2	0.003059903	1.4	0.072173417	1.8	0.023491155	235276_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
EPST11	epithelial stromal interaction 1 (breast)	2.3	0.000274817	1.3	0.074905943	1.8	0.029155537	227609_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
KCNJ10	potassium inwardly-rectifying channel, subfamily J, member 10	1.8	0.000307343	1.5	0.013592204	1.7	0.011822571	228581_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
C11ORF75 (FN5)	chromosome 11 open reading frame 75	1.9	0.001045151	1.3	0.008735762	2.0	0.015085583	219806_s_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	-1.6	0.016903609	-1.5	0.036523928	-2.0	0.005162412	205229_s_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	-1.9	0.007654423	-1.5	0.032813515	-2.3	0.003336718	1554242_a_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
INADL	InaD-like (Drosophila)	-1.3	0.048999725	-1.5	0.007476057	-2.1	0.000100277	214705_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
INADL	InaD-like (Drosophila)	-1.2	0.021328322	-1.2	0.122812374	-1.8	0.009937327	223681_s_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
SLC44A5	solute carrier family 44, member 5	-1.9	0.000501889	-1.5	0.016612483	-2.3	0.000280374	235763_at	Tissue Repair/Remodeling	Nerve-related Growth Factors, Receptors, & Guidance Molecules
CCL14 /// CCL15	chemokine (C-C motif) ligand 14 /// chemokine (C-C motif) ligand 15	-1.8	0.009115244	-1.5	0.018791925	-2.2	0.011918891	205392_s_at	Trafficking	Chemokine Receptors and Ligands
CCR1	chemokine (C-C motif) receptor 1	2.4	6.3588E-05	1.5	0.001333362	2.0	0.019289958	205098_at	Trafficking	Chemokine Receptors and Ligands
CCR1	chemokine (C-C motif) receptor 1	2.3	3.69372E-05	1.4	0.00876232	2.1	0.043397738	205099_s_at	Trafficking	Chemokine Receptors and Ligands
CXCR6	chemokine (C-X-C motif) receptor 6	1.7	0.000228851	1.4	0.005909627	1.7	0.000369253	211469_s_at	Trafficking	Chemokine Receptors and Ligands
CXCR6	chemokine (C-X-C motif) receptor 6	2.0	0.000168035	1.5	0.003641903	2.0	0.007942693	206974_at	Trafficking	Chemokine Receptors and Ligands
VSIG9		1.7	0.002401378	1.4	0.039541571	1.8	0.005766931	240070_at	Trafficking	Vascular Adhesion
C19orf6	chromosome 19 open reading frame 6	-1.4	0.070717725	-1.3	0.042886215	-1.8	0.035179909	213986_s_at	Gene Unknown Function	
PLEKH2	pleckstrin homology domain containing, family H (with MyTH4)	-1.5	0.000612786	-1.5	0.000620535	-1.8	0.029689218	239568_at	Gene Unknown Function	
PLEKH2	pleckstrin homology domain containing, family H (with MyTH4)	-2.0	0.001184661	-1.5	0.011675411	-1.6	0.192212029	227148_at	Gene Unknown Function	
C15ORF48	chromosome 15 open reading frame 48	2.3	6.67134E-05	1.5	0.00692061	2.6	0.039287738	223484_at	Gene Unknown Function	
LOC440836	similar to MGC52679 protein	1.7	0.002447474	1.5	0.001591607	2.3	0.009574558	238327_at	Gene Unknown Function	
MIAT	myocardial infarction associated transcript (non-protein coding)	1.8	0.002411177	1.6	0.005903051	1.8	0.008296157	227168_at	Gene Unknown Function	
MIAT	myocardial infarction associated transcript (non-protein coding)	1.8	0.00708761	1.7	0.010507006	1.7	0.092727074	228658_at	Gene Unknown Function	
TMEM155	transmembrane protein 155	1.7	0.028172635	1.4	0.117487382	1.7	0.03271668	230137_at	Gene Unknown Function	
---	Transcribed locus	-1.7	0.006578601	-1.5	0.016370379	-1.7	0.00542653	239292_at	Unknown Transcript	
---	Transcribed locus	-1.7	0.010842601	-1.5	0.019032527	-2.0	0.026254495	1555929_s_at	Unknown Transcript	
---	Transcribed locus	1.7	0.027172996	1.6	0.038312779	1.7	0.020841499	231655_x_at	Unknown Transcript	
HIPK3	homeodomain interacting protein kinase 3	-1.5	0.020845745	-1.9	0.000746092	-2.1	0.000338777	210148_at	Apoptosis	Inhibitor of Apoptosis
Mdm4	Mdm4, transformed T3 cell double min	-1.7	0.201615075	-2.1	0.046251933	-3.0	0.01929575	205655_at	Apoptosis	Inhibitor of Apoptosis
IGLJ3	immunoglobulin lambda joining 3	1.2	0.37136157	1.8	0.01229537	2.0	0.036478645	211881_x_at	B cell Proliferation, Differentiation	
IGHG1	Immunoglobulin heavy constant gamma 1 (G1m marker)	1.3	0.351874921	1.8	0.052991328	2.3	0.042736923	211647_x_at	B Cell Proliferation/Differentiation	
IGHG1	Immunoglobulin heavy constant gamma 1 (G1m marker)	1.2	0.519266774	2.1	0.026702703	2.5	0.002672599	211633_x_at	B Cell Proliferation/Differentiation	
IGHG1	Immunoglobulin heavy constant gamma 1 (G1m marker)	1.0	0.94504346	2.2	0.023289029	2.6	0.026770259	211648_at	B Cell Proliferation/Differentiation	
PLEKH1 (RTKN2)	pleckstrin homology domain containing, family K member 1	-1.0	0.281684556	-2.0	0.034795564	-3.2	0.003936026	230469_at	Immune Activation	Activation/Proliferation
HLA-C	Major histocompatibility complex, class I, C	1.2	0.505648519	2.9	0.005526295	2.7	0.009196718	216829_at	Immune Activation	Moderators of Activation/Inflammation
HLA-C	Major histocompatibility complex, class I, C	1.1	0.835071793	1.9	0.020310829	2.2	0.011275523	216576_x_at	Immune Activation	Moderators of Activation/Inflammation
HLA-C	Major histocompatibility complex, class I, C	1.3	0.226301395	2.0	0.026203062	2.4	0.023989967	216517_at	Immune Activation	Moderators of Activation/Inflammation
HLA-C	Major histocompatibility complex, class I, C	1.1	0.696036248	1.9	0.032693669	2.2	0.025983896	211643_x_at	Immune Activation	Moderators of Activation/Inflammation
PRDX4	peroxiredoxin 4	1.3	0.083586	1.7	0.017044206	1.9	0.01626425	201923_at	Immune Activation	Moderators of Activation/Inflammation
IL7R	interleukin 7 receptor	-1.3	0.164008025	-1.9	0.002674929	-2.7	0.001532554	205798_at	Immune Activation	Moderators of Activation/Inflammation
IL7R	interleukin 7 receptor	-1.3	0.126034847	-2.0	0.001547863	-3.1	0.001919249	226218_at	Immune Activation	Moderators of Activation/Inflammation
TFPI2	tissue factor pathway inhibitor 2	1.2	0.813034148	-1.9	0.041401196	-2.5	0.015070451	209277_at	Immune Activation	Moderators of Activation/Inflammation
TFPI2	tissue factor pathway inhibitor 2	1.1	0.662610391	-1.9	0.04846285	-2.4	0.020947647	209278_s_at	Immune Activation	Moderators of Activation/Inflammation
TXNIP	thioredoxin interacting protein	-1.7	0.011821191	-1.8	0.000720434	-1.9	0.016970851	201008_s_at	Immune Activation	Moderators of Activation/Inflammation
TXNIP	thioredoxin interacting protein	-1.6	0.008723517	-1.6	0.0052318	-1.7	0.0400408	201009_s_at	Immune Activation	Moderators of Activation/Inflammation
LEF1	lymphoid enhancer-binding factor 1	-1.3	0.131319001	-1.7	0.001181839	-2.6	8.02655E-05	210948_s_at	Immune Activation	Transcriptional Regulator
LEF1	lymphoid enhancer-binding factor 1	-1.2	0.235355282	-1.5	0.003318299	-3.0	0.000520915	221558_s_at	Immune Activation	Transcriptional Regulator
MAP3K1	mitogen-activated protein kinase kinase kinase 1	-1.4	0.05073905	-1.8	0.001189479	-2.0	0.03702768	214786_at	Immune Activation	Signal Transduction
PHTF2	putative homeodomain transcription factor 2	-1.4	0.055759623	-1.7	0.00161271	-2.0	0.006767856	217097_s_at	Immune Activation	Transcriptional Regulator
ZNF238	Repressor (sequence-specific DNA-binding protein with transcription factor 2)	-1.4	0.052195513	-1.8	0.000382532	-2.0	0.001357996	207164_s_at	Immune Activation	Transcriptional Regulator
XBP1	X-box binding protein 1	1.2	0.262151215	1.8	0.025144845	1.9	0.005130976	200670_at	Immune Activation	Transcriptional Regulator
KLRG1	killer cell lectin-like receptor subfamily G, member 1	1.5	0.041990804	1.7	0.00215141	1.8	0.011490427	210288_at	Immune Defenses	NK cells & CD8+ T Cells/Cytotoxic Effectors
SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	-1.2	0.171482355	-1.8	0.000411277	-1.9	0.000570378	210286_s_at	Metabolism	Metals/Ions
EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	-1.4	0.072697102	-1.8	0.002050129	-2.0	0.03641624	1555996_s_at	Metabolism	Nucleic Acids & Proteins
EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	-1.5	0.151854965	-2.1	0.016121962	-2.4	0.024748531	205321_at	Metabolism	Proteins
FKBP11	FK506 binding protein 11, 19 kDa	1.3	0.049577279	1.7	0.008294802	2.0	0.010648047	219118_at	Metabolism	Proteins
SENP7	SUMO1/sentrin specific peptidase 7	-1.6	0.02552111	-1.9	0.000683038	-2.2	0.033420006	220735_s_at	Metabolism	Proteins
SLC16A10	solute carrier family 16, member 10 (aromatic amino acid transporter)	-1.4	0.001089247	-1.7	0.000132225	-2.2	0.003647174	219915_s_at	Metabolism	Proteins
SPOCK3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 3	-1.6	0.023599094	-1.9	0.000755782	-3.4	0.001168461	235342_at	Tissue Repair/Remodeling	Extracellular Matrix Structural Components, Cells, & Tissues
FAM46C (Muc10)	family with sequence similarity 46, member C (Mucin 10)	1.2	0.185294429	1.7	0.015249115	2.0	0.003835378	226811_at	Trafficking	
DKFZP686A01247	hypothetical protein	-1.5	0.012509117	-1.8	0.001074557	-1.9	0.011682066	212325_at	Gene Unknown Function	
LOC283663	hypothetical protein LOC283663	-1.6	0.030880058	-1.8	0.006233968	-1.8	0.018404801	230245_s_at	Gene Unknown Function	
LOC100130100	similar to hCG26659	1.2	0.547653867	1.7	0.028360915	1.9	0.005919157	217378_x_at	Gene Unknown Function	
MGC29506	hypothetical protein MGC29506	1.5	0.038401387	2.2	0.001528715	2.8	0.030732323	221286_s_at	Gene Unknown Function	
MGC29506	hypothetical protein MGC29506	1.5	0.062182373	2.4	0.003782185	2.9	0.044901562	223565_at	Gene Unknown Function	
SPATS1 /// TMEM151	maturation associated, serine-rich 1 /// transmembrane protein 151	1.6	0.040541249	1.7	0.030888742	1.8	0.019721583	1564066_at	Gene Unknown Function	
SPATS1 /// TMEM151	maturation associated, serine-rich 1 /// transmembrane protein 151	1.6	0.039721361	1.7	0.034483404	1.7	0.02241822	1564067_x_at	Gene Unknown Function	
---	Transcribed locus	1.1	0.820819953	2.1	0.00392497	2.4	0.024842299	234415_x_at	Unknown Transcript	