Effective treatment of psoriasis with etanercept is linked to suppression of IL-17 signaling, not immediate response TNF genes

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Background: TNF inhibitors have revolutionized the treatment of psoriasis vulgaris as well as psoriatic and rheumatoid arthritis and Crohn disease. Despite our understanding that these agents block TNF, their complex mechanism of action in disease resolution is still unclear.

Objective: To analyze globally the genomic effects of TNF inhibition in patients with psoriasis, and to compare genomic profiles of patients who responded or did not respond to treatment.

Methods: In a clinical trial using etanercept TNF inhibitor to treat psoriasis vulgaris (n = 15), Affymetrix gene arrays were used to analyze gene profiles in lesional skin at multiple time points during drug treatment (baseline and weeks 1, 2, 4, and 12) compared with nonlesional skin. Patients were stratified as responders (n = 11) or nonresponders (n = 4) on the basis of histologic disease resolution. Cluster analysis was used to define gene sets that were modulated with similar magnitude and velocity over time.

Results: In responders, 4 clusters of downregulated genes and 3 clusters of upregulated genes were identified. Genes downmodulated most rapidly reflected direct inhibition of myeloid lineage immune genes. Upregulated genes included the stable dendritic cell population genes CD1c and CD207 (langerin). Comparison of responders and nonresponders revealed rapid downmodulation of innate IL-1β and IL-8 sepsis cascade cytokines in both groups, but only responders downregulated IL-17 pathway genes to baseline levels.

Conclusion: Although both responders and nonresponders to etanercept inactivated sepsis cascade cytokines, response to etanercept is dependent on inactivation of myeloid dendritic cell genes and inactivation of the T_H17 immune response. (J Allergy Clin Immunol 2009;124:1022-30.)

Key words: *TNF, psoriasis, etanercept, gene, T_H17, T_H1*

TNF was initially identified in 1976 as the soluble, LPS-dependent serum factor that killed murine fibrosarcoma cells but not normal fibroblasts.[1] Later, TNF was characterized as a macrophage-derived product that rapidly induced expression of IL-1, IL-6, and IL-8, leading to recruitment of innate inflammatory leukocytes within hours of an infectious insult.[2,3] This cytokine sequence, which can be termed the sepsis cascade model,[4] has largely dominated thinking about the function of TNF in chronic inflammatory diseases. The initial rationale for testing TNF antagonists in rheumatoid arthritis was based on demonstrated increases in all sepsis cascade cytokines in synovial fluid of affected joints, as well as abundant neutrophils producing collagen-destroying matrix metalloproteases.[5] Indeed, genomic analysis of peripheral blood during anti-TNF treatment for rheumatoid arthritis showed a downmodulation of several of these acute response genes during response (chemokine C-C motif ligand 4 [CCL4], IL-8, IL-1β).[6]

Extension of these findings led to clinical trials of TNF antagonists in inflammatory bowel disease and psoriasis with subsequent therapeutic success and Food and Drug Administration approval.[7,8] There has been a strong temptation to link the pathogenesis of human inflammatory diseases, and especially those successfully treated with TNF antagonists such as psoriasis and rheumatoid arthritis, to direct effects of sepsis cascade cytokines on innate immunity. However, despite the success of TNF-blocking agents, psoriasis vulgaris has some elements of pathogenesis that are not well explained by sepsis cascade cytokines and neutrophil activation. First, there is a strong T-cell component in psoriasis, including reports of T-cell clonality,[9-11] and there is considerable clinical benefit provided by putative T-cell–targeted therapeutics.[12,13] Second, psoriasis has been induced in several transplanted skin models without apparent involvement of neutrophils in converted grafts.[14] Third, recent success in treating psoriasis with antibodies to the p40 cytokine subunit shared between IL-12 and IL-23 implies a central role for adaptive immunity, specifically T_H1 and/or T_H17 T cells, in the pathogenesis of this disease.[15-19] We sought to understand how TNF is linked to pathogenic actions of T cells in psoriasis.

In the current study, we used Affymetrix arrays (Affymetrix, Inc, Santa Clara, Calif) to study gene expression in psoriasis lesions at several time points during treatment with etanercept. Responding and nonresponding patents show equivalent suppression

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Abbreviations used
DC: Dendritic cell
GSEA: Gene Set Enrichment Analysis
HBEGF: Heparin-binding epidermal growth factor-like growth factor
PLAUR: Plasminogen activator of urokinase receptor

of innate sepsis cytokines (IL-1β, IL-8), but only responding patients demonstrate strong modulation of downstream genes linked to IL-17 signaling. Hence, mechanisms for response success and failure appear to be distinct in psoriasis versus rheumatoid arthritis. These studies define a new way to judge the extent of overall disease reversal on the basis of the degree to which broad disease-related gene sets are suppressed by a specific treatment, and may enable the design of even more effective and simple antipsoriatic therapeutics.

METHODS

Materials, methods, and statistical analysis are described in greater detail in this article's Methods section of the Online Repository at www.jacionline.org.

Patient studies and classification

Twenty adult patients with moderate to severe psoriasis were treated with etanercept 50 mg subcutaneously twice weekly for 12 weeks (clinical trial no. NCT00116181). The clinical and histologic response of patients in this trial was previously published.[20] The gene array was performed on 15 sequential patients.

Immunohistochemistry and immunofluorescence

Frozen skin sections were stained for in a standard manner (see Methods, Immunohistochemistry and Immunofluorescence, in the Online Repository). A 1-tailed Student *t* test was used to compare baseline and week 2 cell counts.

Tissue gene expression by microarray

RNA was extracted from skin biopsies using the RNeasy Mini Kit (Qiagen, Valencia, Calif). For each Affymetrix gene chip, 2 μg total RNA was reverse-transcribed, amplified, and labeled.[21] Tissue microarray data have been deposited in NCBI's Gene Expression Omnibus and are accessible through GEO Series accession number GSE11903 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE11903).

Statistical analysis

The analysis was conducted using R software (http://www.R-project.org) with bioconductor packages (http://www.bioconductor.org). Briefly, expression measures were obtained by using GC Robust Multi-array Average (GCRMA), and probe sets with a SD >0.15 and expression greater than 4 in at least 5 samples were kept for further analysis (see Methods, Statistical Analysis, in the Online Repository). Statistical methods used in the analyses of data are summarized in this article's Table E1 in the Online Repository at www.jacionline.org.

Differential expression criteria

A mixed-effect linear model was used to model gene expression to account for the time-course design of the clinical trial. To define etanercept-modulated genes, a moderated F statistic was used to determine whether any of the expression values across time differed from lesional baseline at any time point. An F test was used to determine genes for which the time profile was different between responders and nonresponders. The *P* values of both tests were adjusted for multiple hypotheses by using the Benjamini-Hochberg method.

Consensus clustering

To find distinct profiles among etanercept-modulated genes as well as between responders and nonresponders, we performed hierarchical average linkage clustering with distance measure equal to 1−Pearson correlation coefficient. The optimal number of discovered clusters was assessed by using the Consensus Clustering algorithm available in GenePattern software (http://www.broadinstitute.org/cancer/software/genepattern/).

RT-PCR

RT-PCR was conducted for IL-1β and IL-8 as previously described.[20]

Response profile of cytokine keratinocyte pathways

We recently defined sets of keratinocyte genes induced by specific cytokines, termed IL-17, and IFN-γ keratinocyte pathways, and developed TNF pathways for this analysis.[22] The microarray data are available at: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE12109. A linear model was used to define the response profile of these pathways during etanercept treatment . The Gene Set Enrichment Analysis (GSEA) approach[23] was used to compare the response profile of the keratinocyte pathways in responders and nonresponders (see this article's Fig E1 in the Online Repository at www.jacionline.org). GSEA is a method to mine correlations of any gene set (eg, keratinocyte pathways) with a specific phenotype (eg, response) rather than a single-gene approach.

RESULTS

Patient population

RNA was extracted for gene array from skin collected at each biopsy time point (nonlesional baseline, lesional baseline, and weeks 1, 2, 4, and 12). Quantifiers of disease resolution included epidermal thickness (a linear measurement in millimeters), Ki67 (a marker of cell proliferation), and K16 gene expression (indicating aberrant keratinocyte differentiation). Patients were stratified as responders (n = 11) or nonresponders (n = 4) on the basis of whether they achieved histologic disease resolution by week 12 of etanercept treatment (decreased epidermal thickening, normalization of Ki67 and K16).[20]

Disease genes were temporally modulated by etanercept in a reverse cascade

Genes with expression values that changed during etanercept treatment (fold change >2 for any time point; false discovery rate <0.05) were selected as etanercept-modulated genes. We identified 978 probe sets that were downregulated during the 12 weeks of treatment with etanercept and 999 probe sets that were upregulated (see this article's Tables E2 and E3, respectively, in the Online Repository at www.jacionline.org). We used consensus clustering to identify 4 clusters that were downregulated (see this article's Fig E2, *A*, in the Online Repository at www.jacionline.org) and 3 clusters that were upregulated (Fig E2, *B*), with distinct kinetics. This gave a cascade of genes that were modulated by etanercept, and because this was reversed as inflammation was quenched, we termed this modulation by etanercept a reverse cascade.

Genes downmodulated by etanercept

Genes downmodulated by etanercept clustered into 4 groups (Fig 1). Gene expression at each time point was normalized to nonlesional baseline expression, and average expression of genes

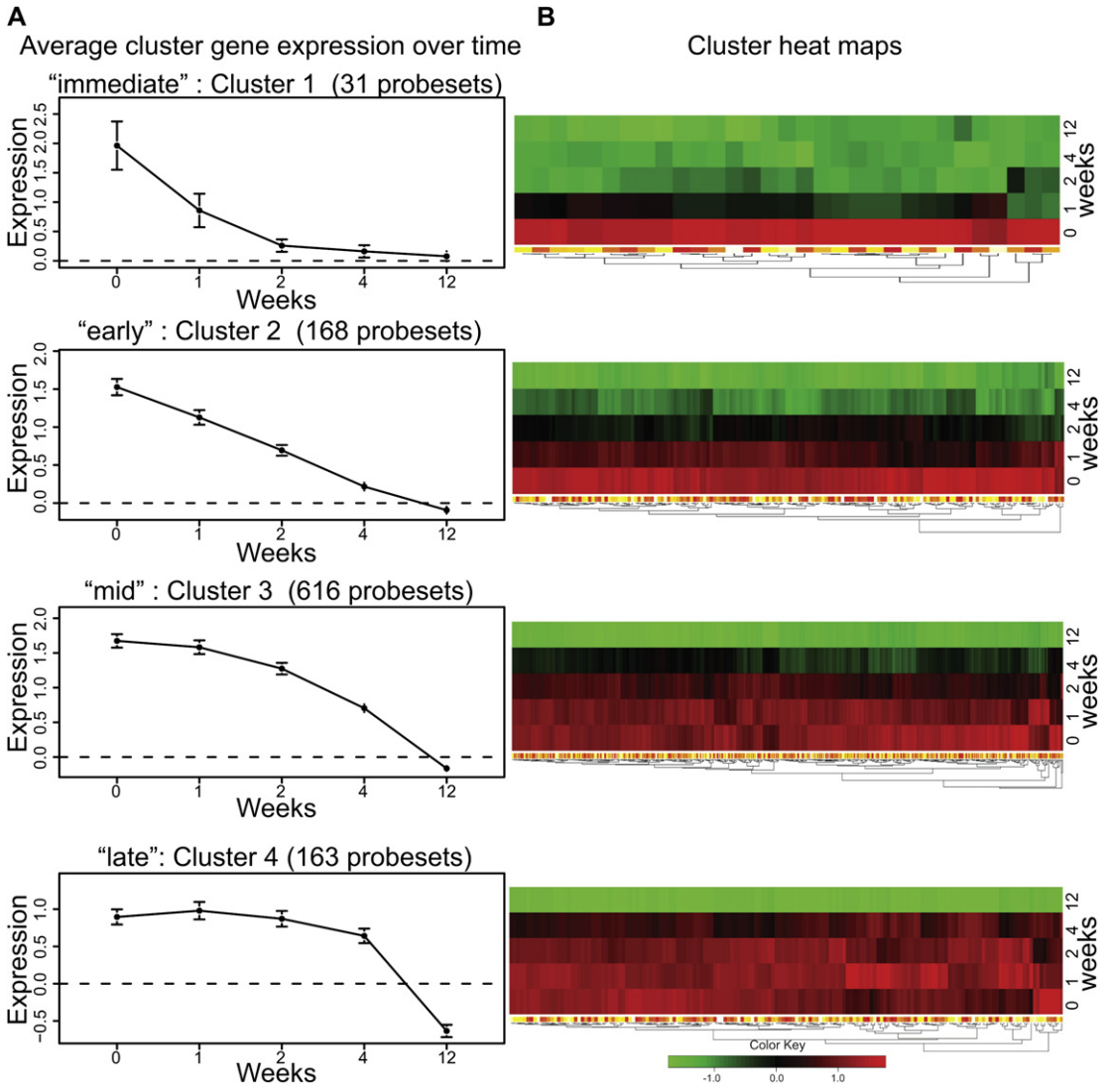


FIG 1. Consensus clustering–grouped genes downregulated by etanercept into 4 clusters. **A,** Consensus clustering of genes downmodulated in patients who responded to etanercept treatment (n = 11) identified 4 gene clusters that were downmodulated at different time points during the course of etanercept treatment: immediate, early, mid, and late clusters. Gene expression in lesional skin at weeks 0, 1, 2, 4, and 12 was normalized to nonlesional gene expression and is shown as average cluster gene expression ± SEMs. **B,** Heat map of each downmodulated gene cluster.

within each cluster was plotted over time (Fig 1, *A*) with corresponding heat maps (Fig 1, *B*). The set of genes that were maximally suppressed by 1 week of treatment (Fig 1, *cluster 1*) are likely to be genes that are directly modulated by TNF. However, with more time, many additional downregulated genes were identified, and these expanded to progressively larger sets of regulated genes over time (Fig 1, *clusters 2-4*).

Cluster 1 genes (31 probe sets) were downmodulated most rapidly and defined as immediately downmodulated genes, cluster 2 with 168 probe sets was early, cluster 3 with 616 probe sets was mid, and cluster 4 with 163 probe sets was late. All downregulated genes are listed by cluster in Table E2. Rapidly downmodulated cluster 1 genes included those involved in leukocyte chemotaxis: IL-8, CCL4 (macrophage inflammatory protein 1β), CCL3 (macrophage inflammatory protein 1α), formyl peptide receptor 1 (FPR1), and plasminogen activator of urokinase receptor (PLAUR). This cluster also contained several genes involved in antiapoptosis, such as BCL2A1; cell cycle genes AURKA, NCAPG, CDC6, and SPC25; and keratinocyte genes DSC2, SPRR3 and heparin-binding epidermal growth factor-like growth factor (HBEGF). There were also several genes involved in lipid metabolism, such as LIPG, LDLR, LRP8, and APOBEC3A (expansion of these genes is available in Table E2). Two cytokines included in this cluster were IL-1β and IL-19. IL-1β is an acute-phase cytokine produced by many cell types, particularly monocytes. The regulation of IL-1β by TNF is well appreciated, and hence rapid downmodulation of IL-1β by TNF inhibition is to be expected. IL-19 is a recently discovered cytokine belonging to the IL-10 family of cytokines and is produced by monocytes as well as epithelial and endothelial cells during inflammation.[24] Although some of these genes are known TNF early response genes, many of them have not

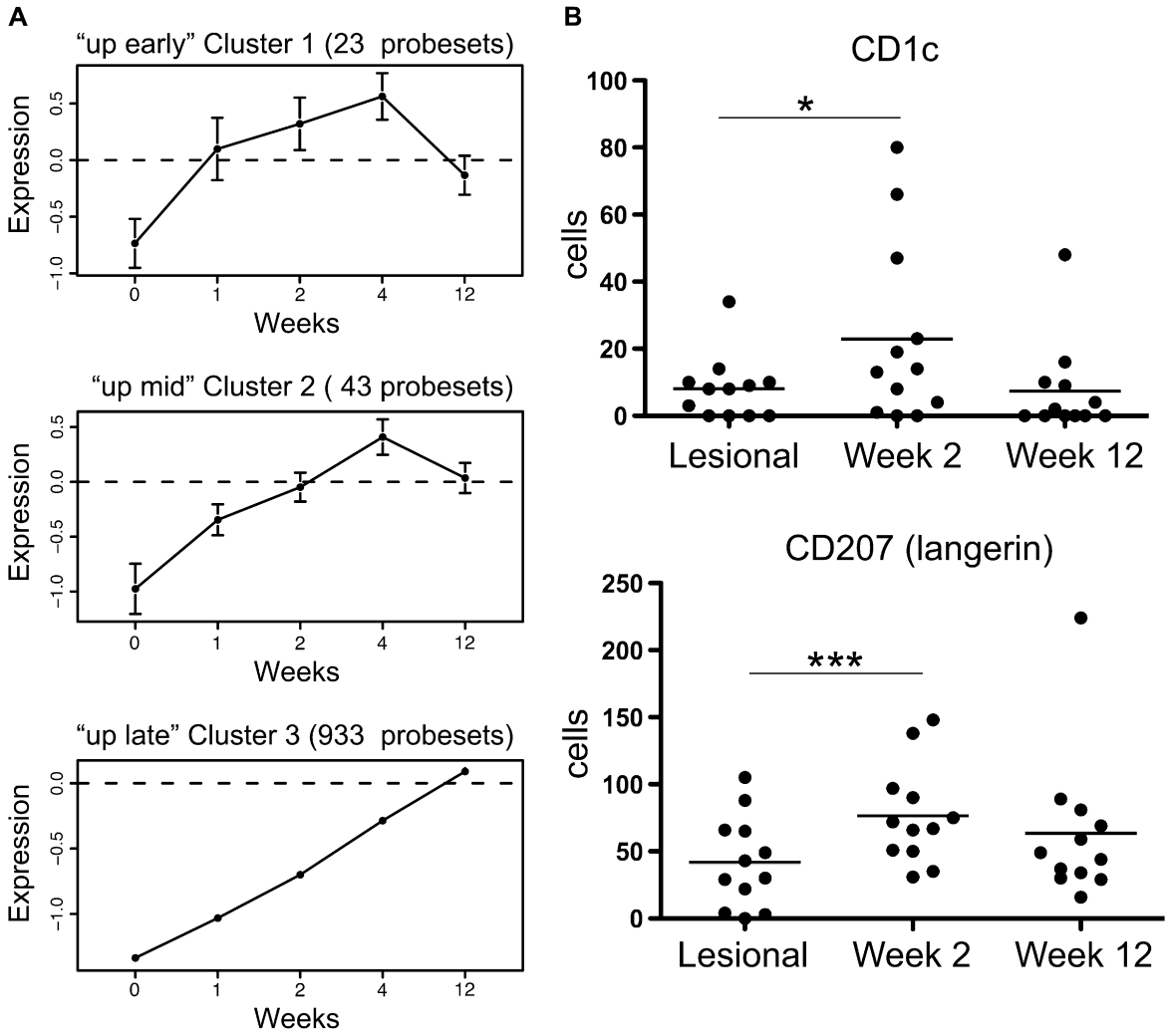


FIG 2. Consensus clustering–grouped genes upregulated by etanercept into 3 clusters. **A,** Consensus clustering of genes upregulated in patients who responded to etanercept treatment (n = 11) identified 3 clusters: up early, up mid, and up late. **B,** Cell counts for CD1c and CD207 (langerin) for psoriasis lesional skin, weeks 2 and 12. Mean cell counts indicated. $*P < .05$; $***P < .001$.

been previously identified as TNF early response genes in human skin.

Genes most rapidly downmodulated by etanercept were enriched with myeloid specific genes

To determine which leukocyte lineages were most rapidly inhibited by etanercept treatment, we used the expression values of myeloid cells ($CD33^+$ and $CD14^+$), T cells ($CD4^+$ and $CD8^+$), and skin from the Novartis normal tissue compendium.[25] This article's Fig E3, *A,* in the Online Repository at www.jacionline.org shows the expression of immediately downregulated genes (cluster 1) in this data set. Myeloid cells, not T cells, expressed genes that were rapidly downmodulated with etanercept. T-cell–specific genes were modulated later, in cluster 2 (see this article's Fig E4 in the Online Repository at www.jacionline.org), suggesting that TNF inhibition directly modulates myeloid-lineage gene products, which subsequently affect T cells.

There were 2 particularly interesting myeloid-specific genes contained within the rapidly downmodulated cluster 1 that we confirmed by using double-label immunofluorescence: HBEGF (Fig E3, *B*) and PLAUR (Fig E3, *C*). There was a large increase in HBEGF within myeloid $CD11c^+$ dermal dendritic cells (DCs; coexpression giving a yellow color) in lesional compared with nonlesional skin. At week 2 of etanercept treatment, HBEGF and CD11c expression were decreased, and by week 12, expression of both markers normalized to nonlesional levels. PLAUR, another downmodulated immediate cluster 1 myeloid-specific gene, was also rapidly decreased at the protein level by week 2 of etanercept treatment. PLAUR is a key molecule in the regulation of cell-surface plasminogen activation and may be involved in inflammation.[26]

Resident DC genes were upregulated during etanercept treatment

Etanercept upregulated 999 probe sets (816 genes) in responding patients, and these were clustered into 3 groups. The 3 clusters are shown in Fig 2, *A* (up early, up mid, and up late), and genes in each cluster are listed in Table E3. Inspection of genes contained

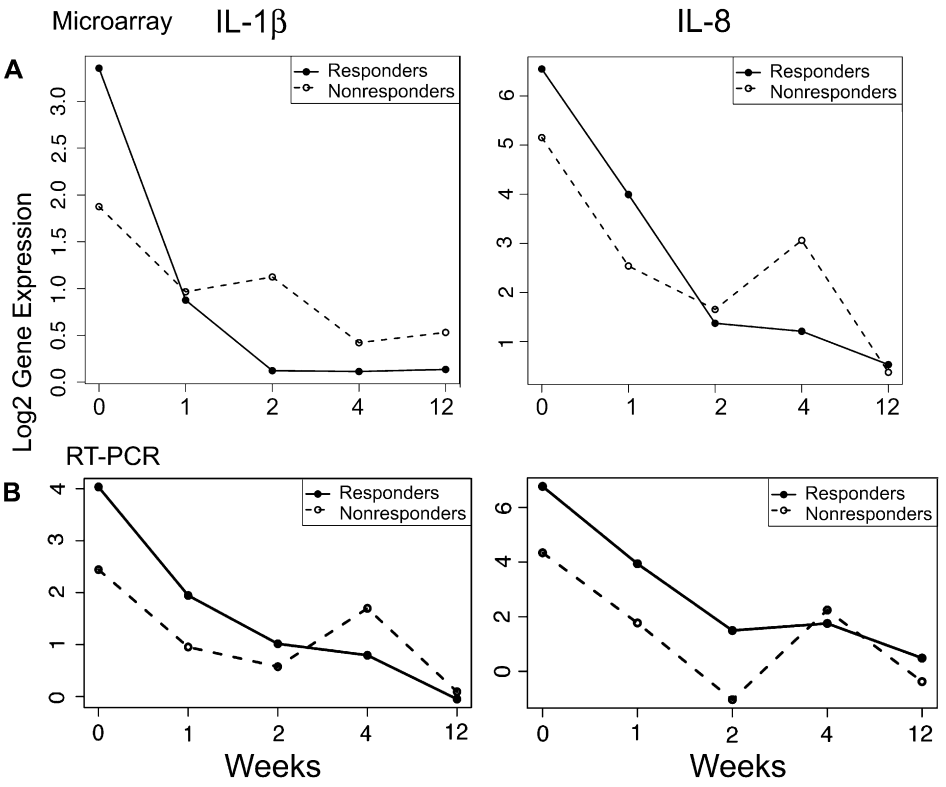


FIG 3. Mean gene expression profile for sepsis cascade genes IL-1β and IL-8. **A,** Downmodulation of gene expression for IL-1β and IL-8 in both responders (n = 11; *filled line*) and nonresponders (n = 4; *dashed line*; microarray data). **B,** Mean log2 expression normalized to human acidic ribosomal protein (HARP) for IL-1β and IL-8 in responders *(filled line)* and nonresponders *(dashed line)* during etanercept treatment (RT-PCR data). At week 12, there was significant reduction of IL-1β in responders ($P < .0001$) and nonresponders ($P = .020$). Similarly, at week 12, there was significant reduction of IL-8 in responders ($P < .0001$) and nonresponders ($P = .004$).

within the most rapidly upregulated clusters 1 and 2 revealed several DC genes: myeloid DC genes CD1c and CD1e were contained within cluster 1, and Langerhans cell genes CD207 (langerin) and CD1a were both in cluster 2. In normal human skin, there are 2 resident DC populations: dermal DCs that coexpress the myeloid lineage marker CD11c and CD1c, and epidermal Langerhans cells (langerin and $CD1a^+$).[27] Therefore, the genomic upregulation of CD1c and CD207 could represent a normalization of these stable resident DC populations with treatment. We confirmed this on a cellular level by performing cell counts on sections from biopsies collected at lesional baseline and week 2 of etanercept treatment (Fig 2, *B*). $CD1c^+$ resident myeloid DCs were increased by approximately 3-fold (mean 7 cells at baseline and 23 cells at week 2; $P = .03$), and $CD207^+$ cells were increased approximately 2-fold (mean 39 and 72 cells, respectively; $P = .001$). However, week 12 counts of CD1c and $CD207^+$ cells (mean 8 and 64 cells, respectively) were not significantly different from baseline lesional skin. In contrast, there was a large influx of inflammatory $CD11c^+$ cells that do not coexpress CD1c in psoriasis lesions (we have termed them inflammatory myeloid DCs),[28] and these cells were decreased rapidly with etanercept treatment by week 2.[20] Therefore, although etanercept decreases inflammatory myeloid DCs after 2 weeks of treatment, stable resident myeloid DCs and Langerhans cells were temporarily increased.

Cluster 3 was the largest group of upregulated genes containing 933 probe sets. The genes in this group include cutaneous structural proteins such as laminin (α4 and β4), collagen type V and VI, heparin sulfate proteoglycan 2, fibronectin, and keratins such as 15, 18, and 19. Upregulation of these genes during effective treatment suggests normalization of regenerative hyperplasia.

Both responders and nonresponders rapidly downmodulated TNF early response genes IL-1β and IL-8

It is possible that some patients do not respond to etanercept treatment because complete TNF blockade is not achieved. We tested this hypothesis by determining the genomic behavior of TNF immediate response genes IL-1β and IL-8 in both responders and nonresponders (Fig 3). We determined that IL-1β and IL-8 are rapidly downmodulated with etanercept treatment, irrespective of the patient's ultimate phenotypic response, suggesting that nonresponse cannot be explained by inadequate dosing. PCR analysis of IL-1β and IL-8 confirms that these cytokines are similarly downregulated in responders and nonresponders (Fig 3, *B*). We have previously published RT-PCR data for these 2 cytokines for responders (n = 11).[20] For the nonresponders (n = 4), there was also a significant reduction in these 2 cytokines by week 12. There was no significant difference in the time profiles of either of these cytokines between the responders and nonresponders (IL-1β: F-statistic 1.57, $P = .177$; IL-8: F-statistic 1.47, $P = .209$).

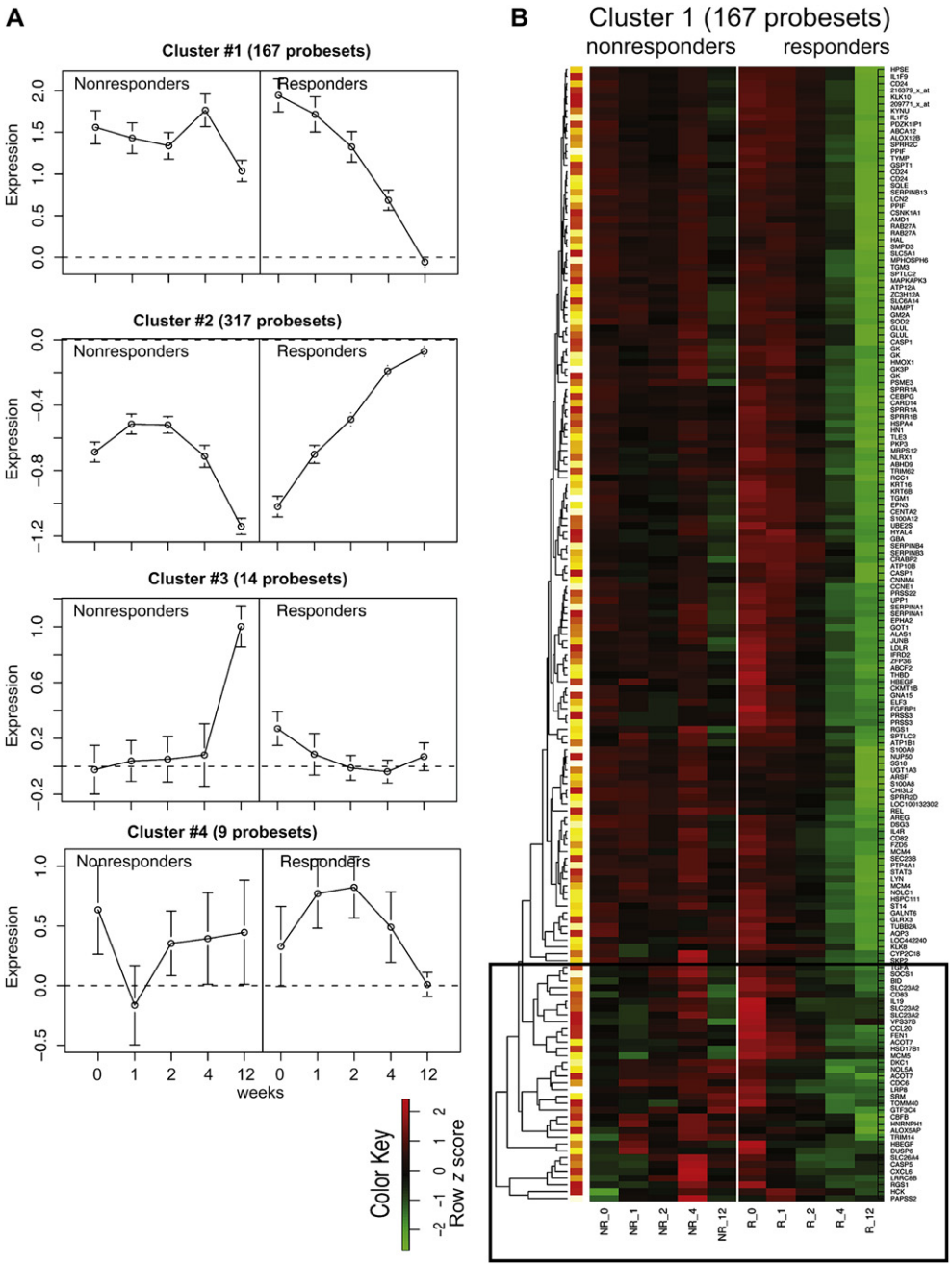


FIG 4. Consensus clustering–grouped genes that were different in responders and nonresponders. **A,** Consensus clustering of genes that were different in responders and nonresponders grouped genes into 4 clusters. **B,** Heat map of cluster 1. There was a group of genes that were downregulated at baseline in nonresponders but not responders *(black box)*.

Differences between responders and nonresponders

To determine the key genomic differences over time between responders and nonresponders, we performed consensus clustering on probe sets for which the time profile differed for responders versus nonresponders (fold change >2, false discovery rate <0.2 using the moderated F-statistic). A 7-cluster structure was identified, with 4 clusters containing more than 6 probe sets (see this article's Fig E5 in the Online Repository at www.jacionline.org; Fig 4, *A*). These genes are listed in this article's Table E4 in the Online Repository at www.jacionline.org.

Cluster 1 contained genes that were strongly downmodulated over time in responders but not in nonresponders. Inspection of the cluster 1 heat-map revealed an interesting pattern (Fig 4, *B*). In nonresponders, a group of probe sets *(black box)* was downregulated at week 0 compared with nonlesional skin *(green)*, but upregulated compared with nonlesional skin *(red)* in responders. Patients who responded to etanercept downregulated these genes during treatment, whereas those who did not respond had increased expression of these genes by week 4. Most notably, this group contains CCL20, a T-cell and DC chemoattractant involved in the trafficking of $CCR6^+$ T_H17 T cells into inflamed psoriatic

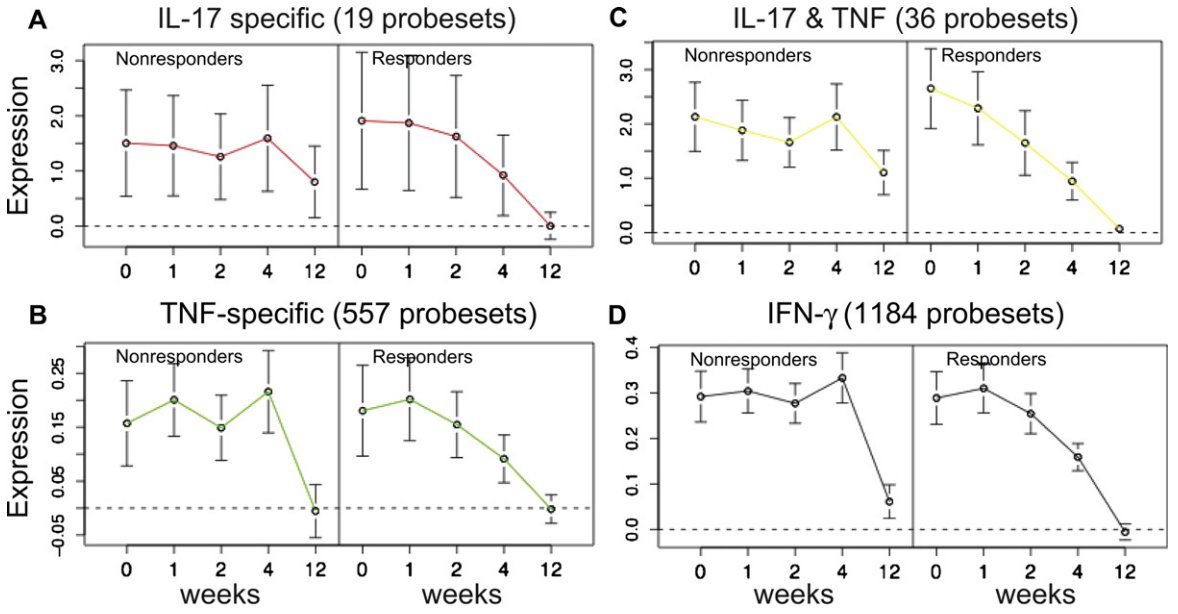


FIG 5. Profiles of cytokine pathways in etanercept gene sets in responders and nonresponders using GSEA. Keratinocyte cytokine pathways were created by culturing primary human keratinocytes with IL-17, TNF, or IFN-γ and defining cytokine pathway gene sets (IL-17, TNF-specific, IL-17 and TNF, and IFN-γ).[22] **A-D,** Genes modulated by etanercept over time were analyzed by GSEA. Average normalized expression (±95% CI) was plotted over time. Responders showed significant downmodulation of IL-17 pathway genes compared with nonresponders.

lesions.[29] High expression of these black box genes in lesional skin may be predictive of response to etanercept. Also contained in cluster 1 was signal transducer and activator of transcription 3 (STAT3), a transcription factor that induces T_H17 polarization. Thus, key IL-17 pathway genes were strongly downmodulated in responders but not in nonresponders.

Cluster 2 contained genes that were upregulated in responders, and after a slight increase in the first week, these genes were downregulated in nonresponders. Included in this list are many cell cycle proteins and keratinocyte genes, likely representing the normalization of keratinocyte proliferation and differentiation in responders but not in nonresponders.

IL-17 pathway genes are strongly downmodulated in etanercept responders but not in nonresponders

To evaluate further the difference between responders and nonresponders in keratinocyte pathways, we performed GSEA to determine how genes contained within each cytokine pathway were modulated over time in responders and nonresponders (Fig 5, Fig E7, and Fig E8). GSEA demonstrated that the IL-17, TNF, IL-17 plus TNF (genes regulated both by TNF and IL-17), and IFN-γ pathways were significantly different in responders and nonresponders (see this article's Table E5 and E6 in the Online Repository at www.jacionline.org). IL-17 pathway genes were highly expressed in both responders and nonresponders but returned to baseline nonlesional levels by week 12 only in the responders (Fig 5, *A*). The TNF pathway genes were reduced to baseline in both responders and nonresponders (Fig 5, *B*). This supports our interpretation that there is adequate dosing of etanercept. The combination of TNF and IL-17 had a pattern closer to IL-17, again suggesting that resolution of disease is associated with reduction in IL-17 genes (Fig 5, *C*). In fact, the IL-17 plus TNF pathway genes exhibit the most different profile in responders and nonresponders. IFN-γ pathway genes were downregulated in both responders and nonresponders but with different kinetics (responders were more gradual), and nonresponders did not reach baseline nonlesional levels completely (Fig 5, *D*). In summary, IL-17–regulated genes were expressed at higher levels than TNF and IFN-γ genes in psoriatic lesional skin, and IL-17 genes were only downmodulated in responders.

DISCUSSION

The original impetus for testing anti-TNF drugs in rheumatoid arthritis was born from established elevation of TNF regulated sepsis cascade cytokines IL-1β and IL-8 in inflamed synovial fluid. The same principle was applied to patients with psoriatic arthritis. Interestingly, however, it was soon noted that the kinetics of disease resolution differed between the joint and the skin component of psoriatic arthritis. In most patients, joint disease improved within 2 weeks, whereas the skin inflammation did not maximally resolve for greater than 12 weeks.[30] This in itself presented the possibility that the arthritic and skin disease components had a different mechanism of action, with TNF as a common upstream cytokine.

In rheumatoid arthritis, suppression of the sepsis cascade does indeed govern response to etanercept TNF inhibition: responders downregulate IL-1β and IL-8 in PBMCs by 72 hours, and nonresponders do not downregulate these cytokines.[6] Our current study, however, suggests that a more complex model is operating in psoriasis skin lesions. Both responders and nonresponders rapidly downregulate IL-1β and IL-8, indicating that downregulation of sepsis cascade cytokines is not sufficient for psoriasis lesion resolution. Therefore, the rapid response of arthritis to TNF inhibition may be explained by disease directly regulated by TNF and TNF

early response genes. Psoriasis, however, requires a more complex model of disease that is only indirectly modulated by TNF.

Recent studies in genetics have shown that alleles of genes encoding p19 and p40 subunits of IL-23, and IL-23R confer risk for development of psoriasis.[31] This pathway controls the development of T_H17 T cells, which may contribute IL-17 and IL-22 to an inflammatory skin environment. The importance of this pathway is also supported by therapeutic response of psoriasis to mAbs that inhibit IL-12 and IL-23, producing major improvement in 70% to 80% of cases.[32] Because TNF inhibitors can also confer nearly equivalent therapeutic benefit, there may be some overlap in inflammatory circuits regulated by TNF and p40 cytokines. One possible intersection between TNF and T_H17 T cells has been suggested from our previous study of the effect of etanercept effect on synthesis of IL-23, IL-17, and IL-22, namely that TNF may serve as a DC activator for IL-23 production, which then promotes activation of T_H17 T cells.

The current study further expands the analysis of the effect of etanercept on inflammatory pathways. Broad sets of genes distinctly regulated by TNF, IL-17, and IFN-γ can be measured during a many week period of disease improvement induced by etanercept. Because the set of inflammatory genes regulated by etanercept increases over time, our results suggest additional indirect effects of TNF on more complex cellular or molecular circuits. For example, TNF has been shown to be a costimulus for T-cell activation as well as a critical molecule for DC development and maturation.[33]

We considered 2 hypotheses for the actions of TNF in psoriasis, and therefore the effects of etanercept on gene expression. Under the first model, TNF would act as a direct activator of nuclear factor-κB (classic TNF transcription factor), and therefore, genes primarily regulated by this transcription factor would normalize as the activation stimulus (TNF) was attenuated by etanercept. Under the second hypothesis, we considered that TNF has additional, broader, downstream or indirect actions—for example, as an activator of DCs and as a T-cell costimulus. In this hypothesis, etanercept might regulate many different transcription factor pathways over time, and TNF inhibition might produce different kinetics for normalization of genes driven by diverse transcription factors in multiple cell types, and the involution response might be considered a reverse cascade over time. Hence, an effect of TNF blockade may be progressive collapse of cellular elements needed to sustain skin inflammation, a domino effect.

The earliest effects of TNF blockade in responders, as we show in this article, are the downregulation of myeloid lineage cells and the rapid upmodulation of stable DC lineage genes CD1c and CD207 (langerin). This suggests that both resident CD1c and Langerhans cells either may not play an active role in TNF-mediated inflammation or may be protective. Previous work by our group has shown rapid downregulation of $CD11c^+$ inflammatory DC cell counts and their inflammatory products inducible nitric oxide synthase (iNOS) and IL-23 (p19 and p40 subunit) by RT-PCR.[20] Later downmodulation of IL-17 pathway genes, but not TNF or IFN-γ pathway genes, is predictive of response to etanercept, thus solidifying the importance of IL-17 in TNF-dependent psoriatic inflammation.

This article's Fig E6, *A*, in the Online Repository at www.jacionline.org outlines how TNF-dependent DC activation might be primarily blocked by etanercept in responding patients. Patients with psoriasis who do not respond to TNF inhibition must have TNF-independent inflammatory pathways leading to the psoriatic phenotype (Fig 6, *B*). Three pathway models could explain why nonresponders do not downregulate the IL-17 pathway. In nonresponders, DCs may be activated independently of TNF by cytokines (for example, IFN) or direct T-cell–induced DC maturation (for example, CD40 ligand), or nonresponders may have DC-independent activation of T_H17 cells by cytokines other than IL-23, such as IL-6, TGF-β, and IL-15.[34,35] Clearly, further studies will be required to determine how the IL-17 pathway is sustained in nonresponders.

In conclusion, our study characterizes a sequence of gene expression changes in inflamed skin lesions as these resolve with etanercept treatment. Genes that are regulated immediately after starting etanercept are candidates for direct TNF gene targets and expand the roster of potential TNF-regulated genes in skin inflammation. The progressively larger set of genes that are altered over time suggests that many cellular activation circuits, and especially those linked to DCs and adaptive immunity, are affected by blocking TNF in a therapeutic context. The resolution of psoriasis by etanercept thus appears to be linked more to modulation of adaptive immune circuits than innate immune circuits, although both pathways are modulated by this TNF antagonist.

Key messages

- **Cluster analysis on psoriasis skin lesions over time during treatment with the TNF-inhibiting drug etanercept demonstrated a domino effect model of disease involution.**
- **Many downmodulated TNF early response genes were myeloid lineage genes, whereas upregulated genes include resident DC genes.**
- **In psoriasis, both etanercept responders and nonresponders rapidly downmodulated sepsis cascade cytokines IL-1β and IL-8. This contrasts with patients with rheumatoid arthritis, in whom only responders downregulated IL-1β and IL-8.**
- **In psoriasis, only responders downregulated IL-17 pathway cytokines to baseline values after 12 weeks, suggesting that ultimate T_H17 suppression is necessary for response to TNF-inhibiting drugs.**

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METHODS

The clinical trial was conducted according to the principles expressed in the Declaration of Helsinki. The clinical protocol was approved by the Rockefeller University Institutional Review Board, and informed consent was obtained from all patients.

Immunohistochemistry and immunofluorescence

Immunohistochemistry. Frozen skin sections were fixed with acetone and blocked in 10% normal horse serum (Vector Laboratories, Burlingame, Calif) for 30 minutes. Primary antibodies blood dendritic cell antigen (BDCA-1)/CD1c (clone AD5-8E7, 1:100; Miltenyi, Bergisch Gladbach, Germany) and langerin (clone DCGM4, 1:100; Immunotech/Coulter, Marseille, France) were incubated overnight. Biotin-labeled horse antimouse secondary antibody (Vector Laboratories) was used to detect the primary antibody. The staining signal was amplified with avidin-biotin complex (Vector Laboratories) and developed using chromogen 3-amino-9-ethylcarbazole (Sigma-Aldrich, St Louis, Mo). The number of positive cells per mm was counted manually by using computer-assisted image analysis (NIH Image 6.1; http://rsb.info.nih.gov/nih-image). Some of the CD1c cell counts have been published before but are analyzed differently here and reported to confirm gene expression with protein staining.[E1]

Immunofluorescence. Primary antibody CD11c (clone B-ly6, dilution 1:100; BD Pharmingen, San Jose, Calif) was incubated overnight at 4°C, followed by the secondary antibody goat-antimouse Alexa 488 (Invitrogen/Molecular Probes, Eugene, Ore). Heparin-binding epidermal growth factor-like growth factor (HBEGF) (406316, 1:10; R&D Systems, Minneapolis, Minn) was stained overnight at 4°C and amplified with goat antimouse IgG_1 conjugated to Alexa 568 (Invitrogen/Molecular Probes). PLAUR (clone 2F11, 1:50; GeneTex, San Antonio, Tex) was also stained overnight at 4°C and amplified with goat antimouse IgG_1 conjugated to Alexa 568 ($n = 3$ for each pair). Images were acquired by using appropriate filters of a Zeiss Axioplan 2 microscope with Plan Apochromat 20 × 0.7 numerical aperture lens (Carl Zeiss Microimaging Inc, Thornwood, NY) and a Hamamatsu orca ER-cooled charge-coupled device camera (Hamamatsu, Bridgewater, NJ), controlled by METAVUE software (MDS Analytical Technologies, Downington, Pa). Dermal collagen fibers gave green autofluorescence (Fig E3). A white line denoted the dermo-epidermal junction.

Statistical analysis

Methods used for statistical analysis of microarray data are summarized in Table E1.

Quality control, preprocessing, and filtering. GeneChip .CEL files were scrutinized for spatial artifacts by using the *Harshlight* package.[E2] Classic microarray quality control report was obtained by using the affy*QCReport* package from Bioconductor. Intensity values (.CEL files) were preprocessed to obtain expression values by using the GC Robust Multi-array Average (GCRMA) algorithm. Expression values were filtered to eliminate probe sets with low variation or intensity. Probe sets with an SD greater than 0.15 and expression values greater than 4 in at least 5 samples were kept for further analysis. Affymetrix control probes were also eliminated. A total of 12,864 probe sets passed these filters.

Differential expression criteria. A mixed-effect linear model was used to model gene expression to account for the time-course design of the clinical trial. A model was considered with time, a between-factor group (responders/nonresponders), interaction time × group, and patient as random effect.

Model fitting and hypothesis testing were conducted using the *limma* package from Bioconductor (www.bioconductor.org).[E3] Limma uses an empirical Bayes method to moderate the SEs of the estimated comparisons. The empirical Bayes approach is equivalent to shrinkage of the estimated sample variances toward a pooled estimate, resulting in far more stable inference and improved power when the number of arrays is small. The moderated t statistic is shown to follow a t distribution with augmented degrees of freedom. The moderated t inferential approach extends to accommodate tests of composite null hypotheses through the use of moderated F statistics.

From the proposed model, the time profile for each gene (for responders and nonresponders) can be derived and defined as the gene response profile. All hypotheses tested were derived from this model. For each hypothesis, the *P* value of the corresponding statistic (moderated F or moderated t) was adjusted for multiple hypothesis testing, controlling the false discovery rate (FDR) by using the Benjamini-Hochberg procedure. In addition, to determine whether individual comparisons were significant, FDR adjustments were made across time.

To determine disease-related genes, a moderated *t* test was used between nonlesional and lesional measures. To identify genes that varied across time for responders (defined as etanercept-modulated genes), a moderated F test was used to determine whether any of the expression values across time (weeks 1, 2, 4, and 12) differed from the lesional baseline. To determine genes with different time profiles among responders versus nonresponders (interaction term time × group), we used an E test to identify significant interaction terms.

Consensus clustering. To find distinct profiles among etanercept-modulated genes, as well as between responders and nonresponders, we performed hierarchical average linkage clustering with distance measure equal to 1−Pearson correlation coefficient. The optimal number of discovered clusters (K) was assessed by using the consensus clustering (CC) algorithm available in GenePattern software (http://www.broadinstitute.org/cancer/software/genepattern/).[E4]

Given a set of items to be clustered (items can be either genes or chips/experiments), CC represents the consensus across multiple runs of a clustering algorithm and assessment of the stability of the discovered K clusters. To this end, perturbations of the original data are simulated by resampling techniques. The clustering algorithm of choice is applied to each of the perturbed data sets, and the agreement, or consensus, among the multiple runs is assessed and summarized in a consensus matrix. Each matrix entry is indexed by an item pair, and it measures the proportion of times the pair's items are clustered together across the resampling iterations (ideally, always, or never). A distinct consensus matrix is generated for each of the number of clusters considered (eg, if Kmax = 5, consensus matrices corresponding to K = 2, 3, 4, and 5 clusters will be generated). Visual inspection of the consensus matrices and of the corresponding summary statistics can be used to determine the best number of clusters.

The optimal number of clustering is selected by using the consensus matrix and the statistics associated with the cumulative distribution function (CDF) of the consensus matrix. As K increases, the area under the CDF markedly increases as long as K is less than or equal to K true. The ideal partition will have a clear consensus matrix, and any further increase in the number of clusters does not lead to an increase in the area under the CDF.

Cluster analysis of etanercept-modulated genes. The heat map for the etanercept-modulated genes (2004 genes) clearly shows 2 large clusters. The existence of 2 major clusters was confirmed by CC using only 10 simulations. Because of the computational burden of the CC with such a large number of genes, we applied CC to both clusters separately to assess the stability of the clustering structure inside each of them using a larger number of simulations (1000).

The CC statistics for the Down set had a peak at K = 3, but the proportion of increase in Delta area was still high for K = 4, and the latter (K = 4) presented a clear pattern of the CC matrix. For the Up set, there were 2 peaks for 3 and 5 clusters, but the consensus matrix for K = 3 showed a clear matrix pattern. We chose K = 4 for the Down list and K = 3 for cluster analysis of the Up list. Fig E2 demonstrates the consensus matrices and statistics for CC of downmodulated and upmodulated genes.

The relative velocity of gene downmodulation is visualized in each cluster graph by the dotted red line, marking the time taken to achieve 1/2 maximal gene expression ($t_{1/2}$). Immediate genes achieved $t_{1/2}$ between weeks 0 and 1 of etanercept treatment, early $t_{1/2}$ fell between weeks 1 and 2, mid was between weeks 2 and 4, and late was between weeks 4 and 12.

Consensus clustering of genes with a different profile between responders and nonresponders. When applying CC to the set of genes that significantly change between responder versus nonresponder data, the area under the CDF function suggested that the number of clusters was 6 or 7. By inspection of the consensus matrix, a 7-cluster structure clearly emerged, as shown in Fig E5.

GSEA. As illustrated in Fig E1, this was our approach to define the response profile of the cytokines pathways during etanercept treatment. The first step was to generate cytokine pathways. The second step was to generate the etanercept response profile for each gene by using a mixed-effect model with time (discrete) and a random effect for each patient.

We needed a method to evaluate the response profile of the cytokines pathways during etanercept treatment. One straightforward approach is to determine whether each of the early, middle, and late gene lists is enriched for any of the cytokines pathways by using overlap statistics such as the cumulative hypergeometric distribution. This approach has been broadly criticized in favor of approaches that capture coordinated changes in expression in functional sets like GSEA.[E5] GSEA-like approaches in our experimental setting considered all of the gene profiles in the experiment, not only those that were significant, and assessed the significance of each pathway profile by a permutation approach that preserved gene-gene correlations, providing a more accurate null model.

Gene set enrichment analysis uses a general framework in which any collection of gene sets (eg, Kyoto Encyclopedia of Genes and Genomes [KEGG] or Biocarta Pathways) can be mined for correlations with a specific phenotype, which is defined by the biological question being posed (ie, disease/healthy in the 2-group scenario). For each gene set in a given collection, enrichment for a phenotype is assessed by the following:

1. Ranking the available probesets with respect to the phenotype (ie, fold-change between 2 groups).
2. Determining the position of each member of the gene set in the ranked list.
3. Using the Kolmogorov-Smirnov statistic to measure the proximity of the gene set to the top of the list, called enrichment score (ES; higher score indicates that genes in the gene set rank highly in the ranked phenotype list); this can be normalized for the number of genes in the gene set (normalized ES).
4. Calculating the *P* value of the observed ES by using the1000 permutation test.

In the simple case of differences between paired samples (ie, week 12−baseline), the phenotype is defined by the ranked list of fold changes. To address our specific and more complex design, this needed to be modified. The phenotype of interest in this experiment is how individual genes on a chip change over time with therapy and return to baseline nonlesional levels. We generated a slope value for every gene in the microarray chip as they change over time with etanercept treatment.

For every gene, the time profile was modeled with a linear model with time as a factor and random intercept for each patient. The coefficient of time (or time slope) was used as a surrogate marker of response of each gene. Genes were ranked by the time slope so that genes rapidly downregulated with time were at the end of the list. To determine whether any gene sets had coordinate profiles greater than expected by chance alone, the enrichment score was calculated, and the associated *P* value was estimated via simulation. A negative score indicates that genes in the pathway have higher proximity with the lower end of the list, where the slope is more negative, which indicates strong downregulation with time.

As Table E6 shows, the 4 pathways queried were enriched for genes that were downregulated over time with etanercept treatment. All enrichment scores had highly significant *P* values, and FDR <.003. Table E6 shows that genes belonging to IL-17 and TNF pathways were most highly enriched for genes (ie, had the highest ES) that were strongly downregulated over time with etanercept treatment.

Another method confirming this finding was the leading edge subset (LES) for each pathway (Fig E7; see reference[E5] for more details). The LES of a gene set is the subset of members that contribute most to the ES. For a negative ES, it is the set of members that appear subsequent to the peak score. Genes that are in the LES for the IL-17 pathway are precisely those that intercept with TNF.

GSEA of genes that were different in responders versus nonresponders. The methodology explained in the previous section can be easily extended to test whether the profile of those pathways significantly differs between responders and nonresponders. For every gene, the time profile was modeled with a linear model with time and response as factors and random intercept for each patient. Genes were ranked by the difference between the time slope for responders and nonresponders so that genes rapidly downregulated with time in responders and not in nonresponders are at the end of the list. To determine whether any gene sets had differences in responder versus nonresponder profiles greater than expected by chance alone, the enrichment score was calculated, and the associated *P* value was estimated via simulation.

As Table E5 shows, the 4 pathways queried were enriched for genes that were more strongly downregulated in etanercept-responder patients than nonresponders. All enrichment scores had highly significant *P* values and null FDR. Table E5 shows that genes belonging to IL-17 and TNF pathways are most highly enriched for genes (ie, have the highest ES), indicating that the differences in downregulation after etanercept treatment between responders and nonresponders are higher in TNF and IL-17 genes than in the IL-17–specific and TNF-specific genes (Fig E8).

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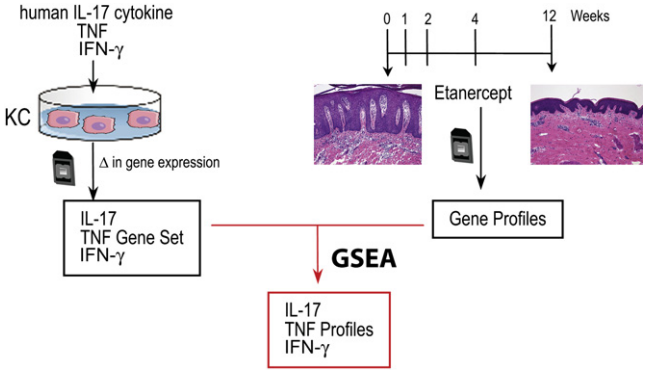


FIG E1. Schemata for overlay of *in vitro* keratinocyte (KC) pathway data with etanercept clinical trial data from biopsy specimens.

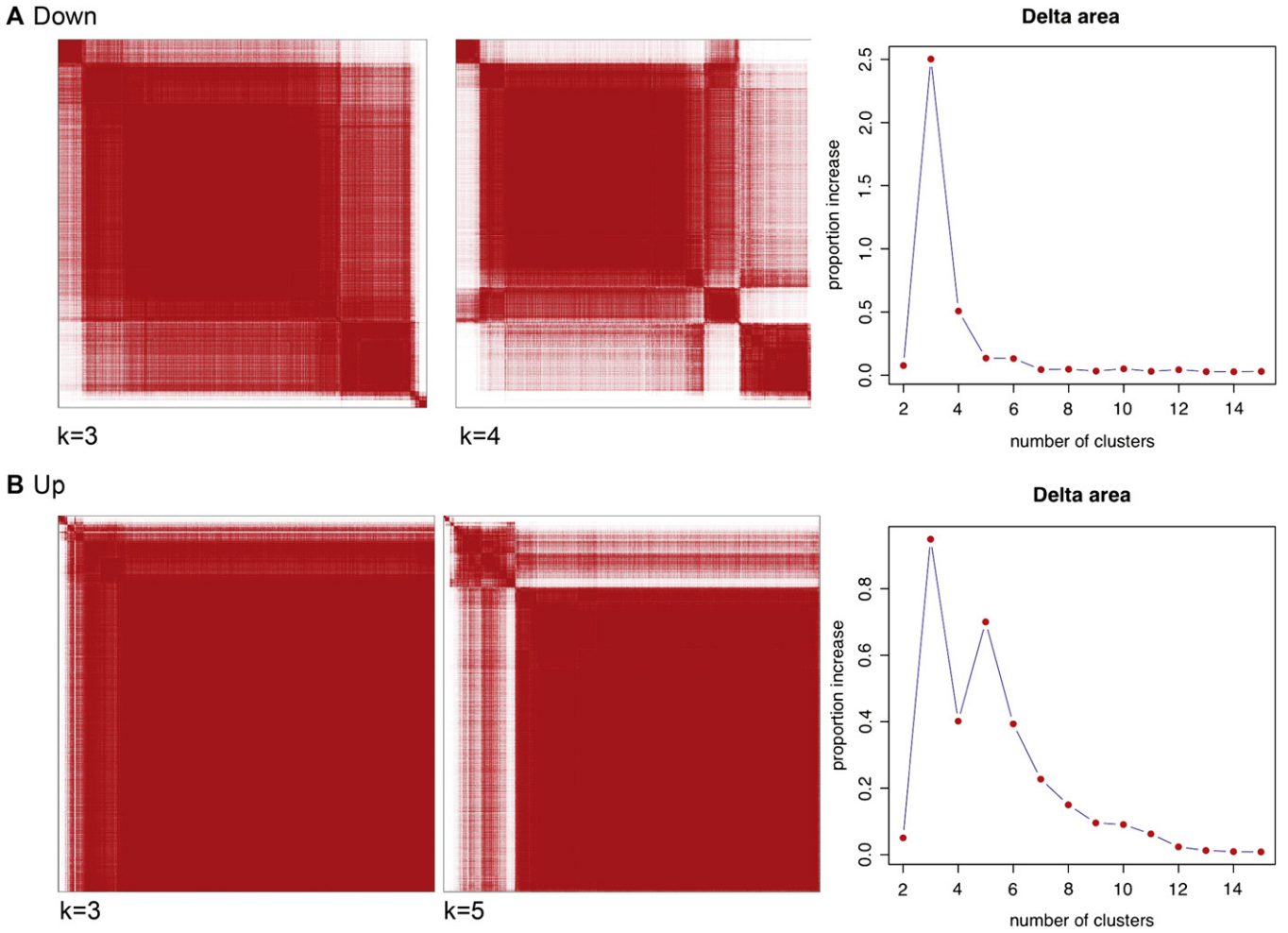


FIG E2. Consensus matrices and statistics for CC for downregulated and upregulated genes in responders.

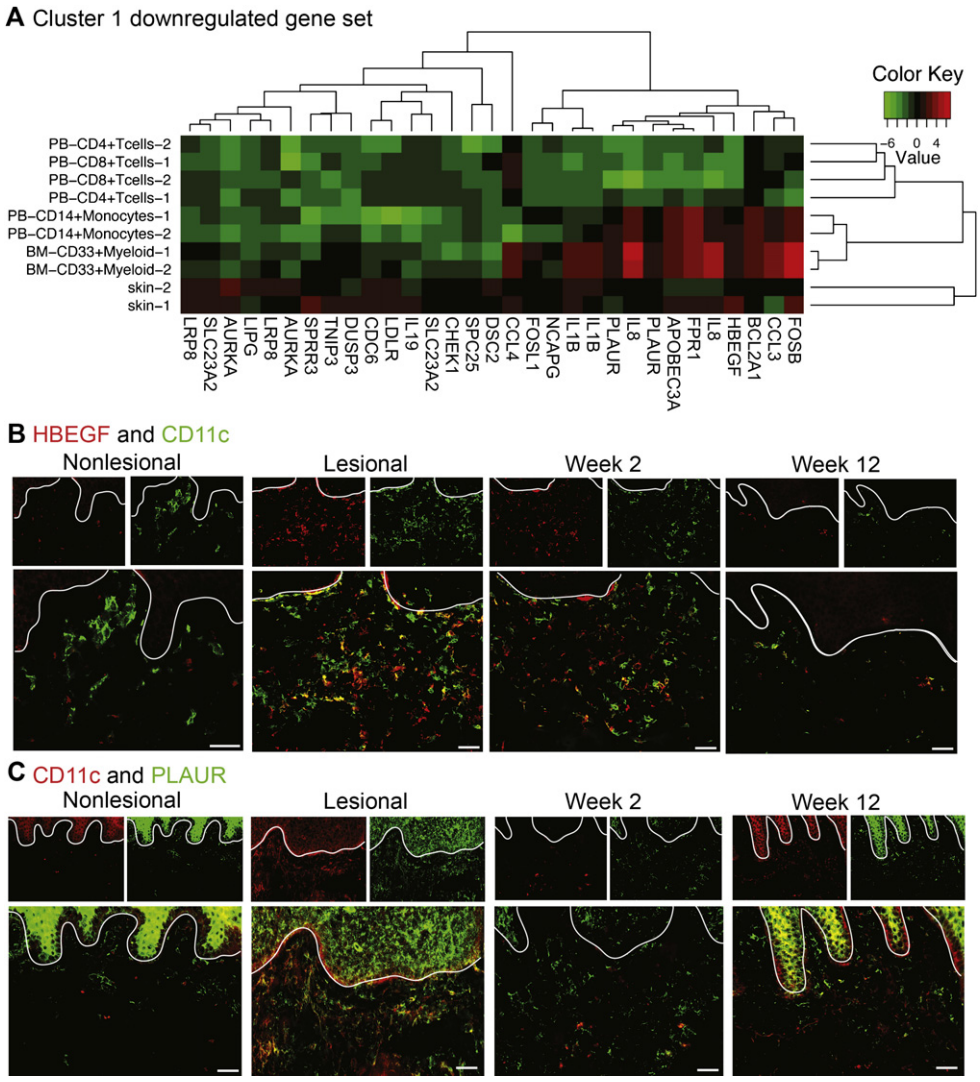


FIG E3. Immediate downregulated genes in responders only (cluster 1, Fig 1) contained many myeloid activation genes. **A,** Published myeloid cell (Novartis normal tissue compendium) genes are highly represented in the immediate cluster. **B and C,** Two-color immunofluorescence of myeloid DCs (CD11c) and HBEGF and PLAUR. Both are expressed in $CD11c^{+}$ dermal cells (*yellow* cells in lesional skin) and decreased with treatment.

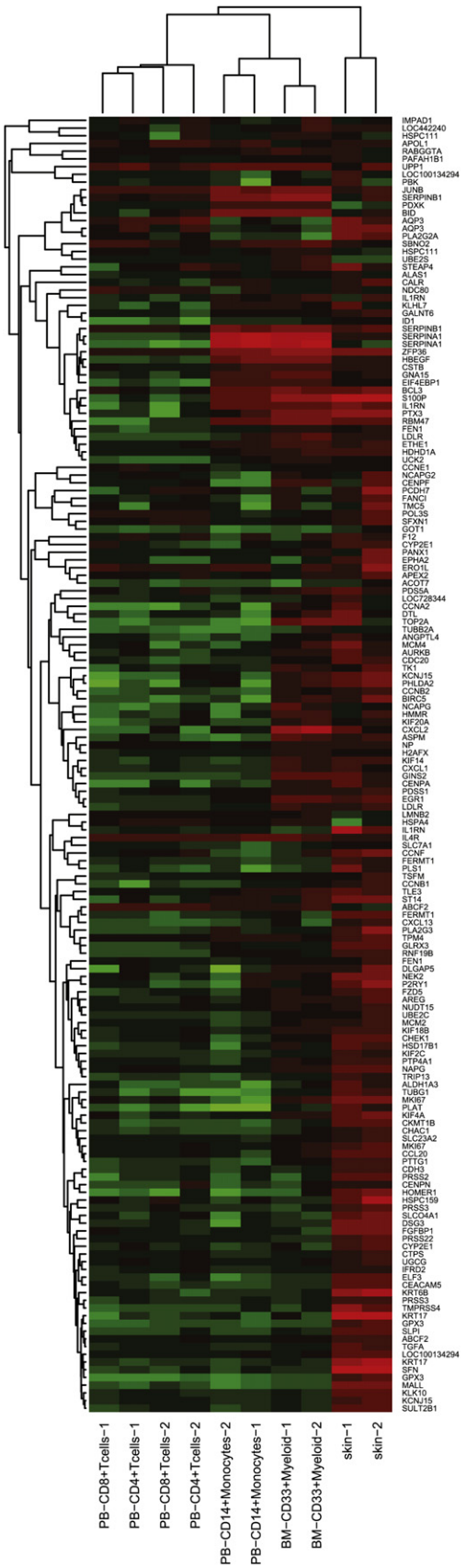


FIG E4. Early downregulated genes in responders only (cluster 2, Fig 1) contained many myeloid activation genes. Published myeloid cell genes (Novartis normal tissue compendium) are highly represented in the immediate cluster.

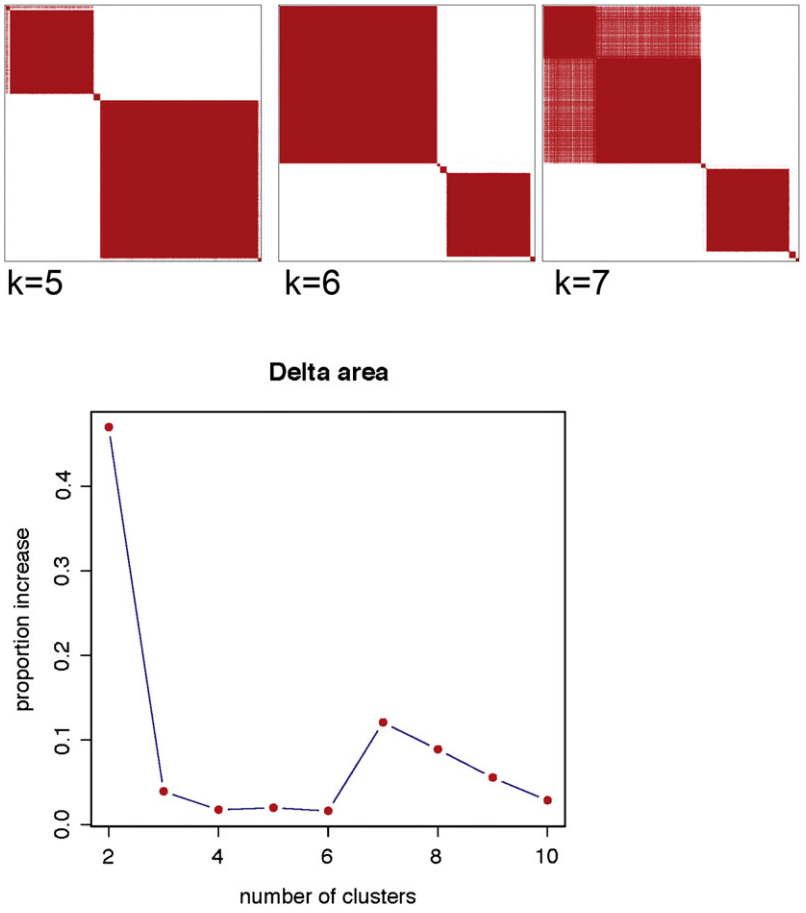


FIG E5. Consensus matrices and statistics for CC for genes differentially regulated in responders versus nonresponders.

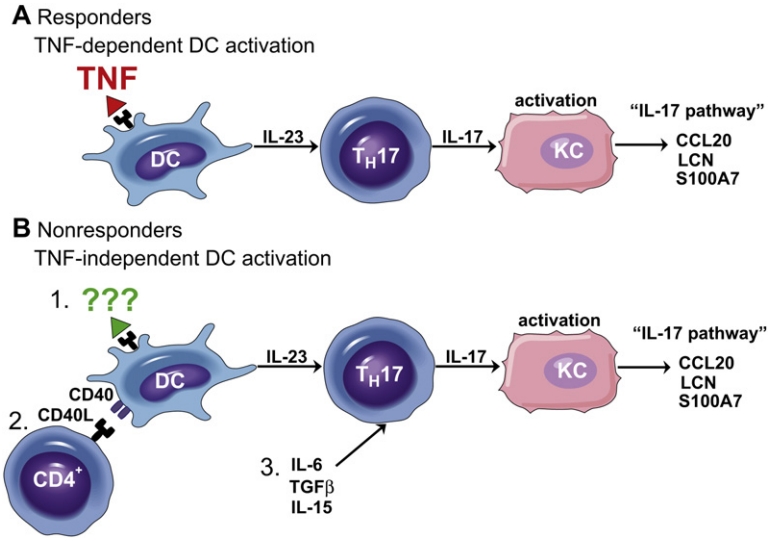
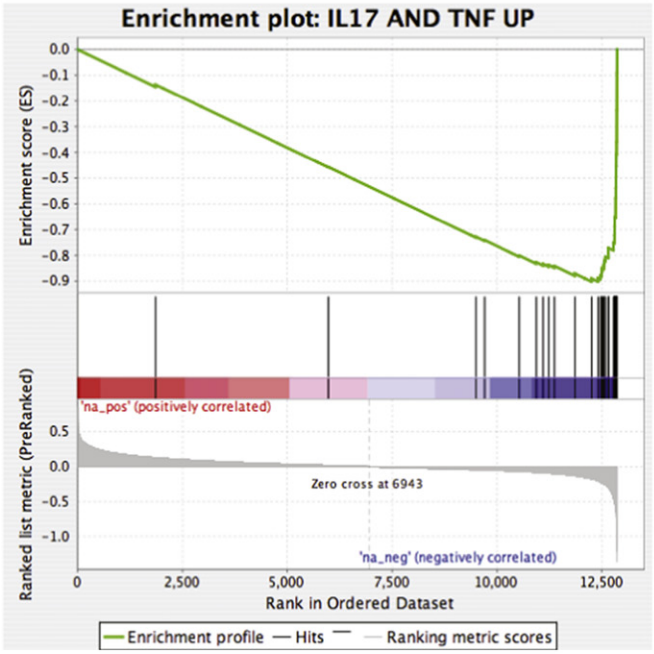
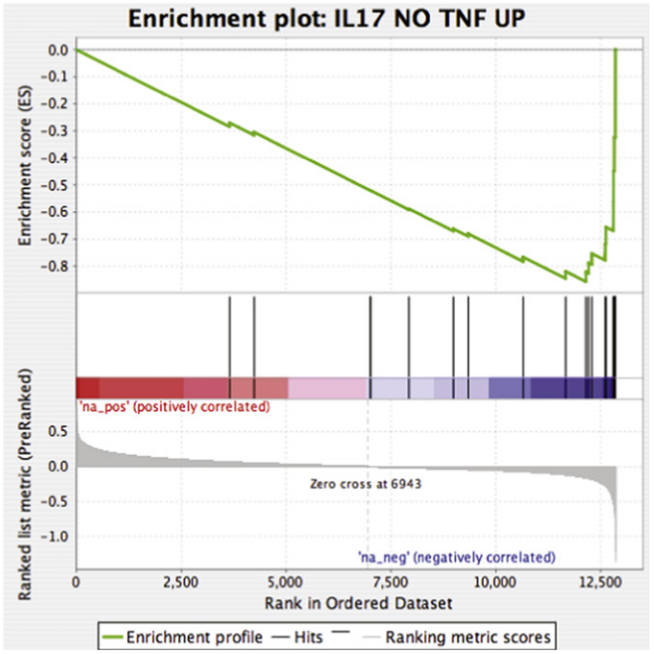


FIG E6. Proposed model of TNF effects in psoriasis pathogenesis and inhibition with etanercept in responders. **A,** TNF has both direct and downstream or indirect effects in psoriasis pathogenesis. In responders, it is likely that both direct and indirect genes are modulated, as demonstrated by the domino effect of genomic resolution. **B,** In nonresponders, there must be TNF-independent pathways to drive T_H17 pathway activation. For example, other cytokines may activate DCs *(1)*, CD40 ligand $(CD40L)^+$ T cells may activate DCs *(2)*, or there may be T_H17 activation by additional cytokines such as IL-6, TGF-β, or IL-15 *(3)*. *KC,* Keratinocyte; *CCL20,* chemokine C-C motif ligand 20; *LCN,* lipocallin.

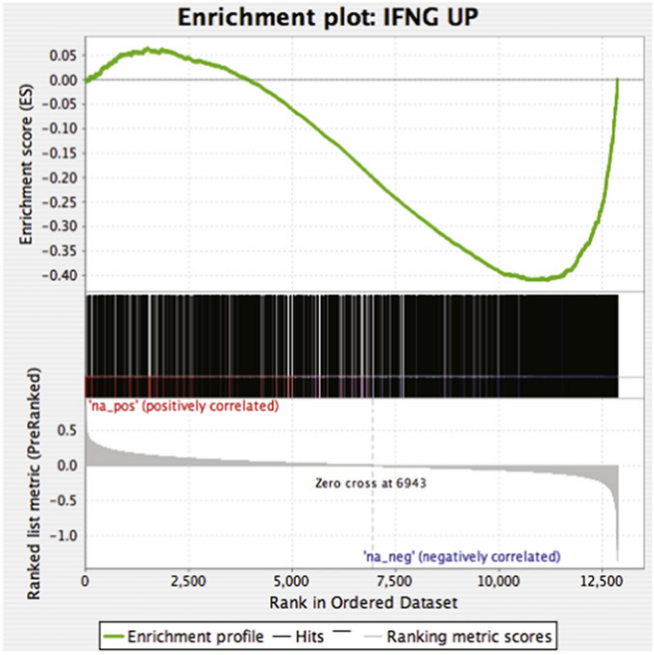
IL-17 and TNF



IL-17–specific



IFN-γ



TNF specific

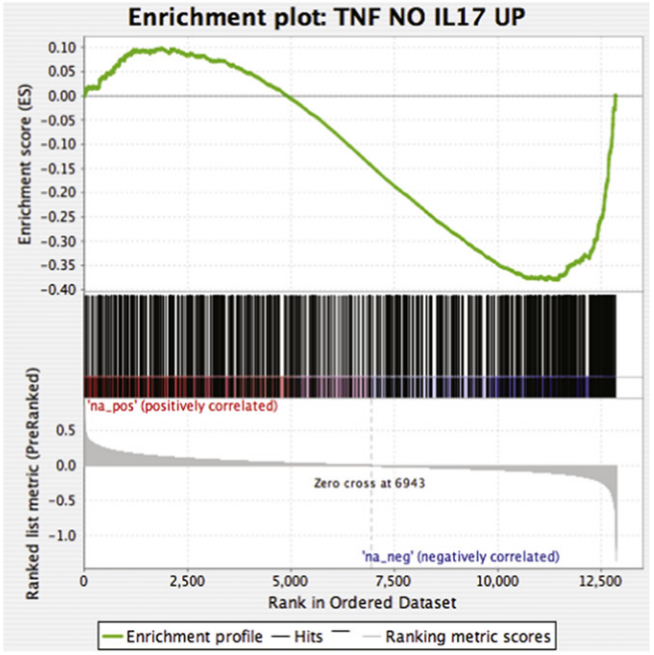
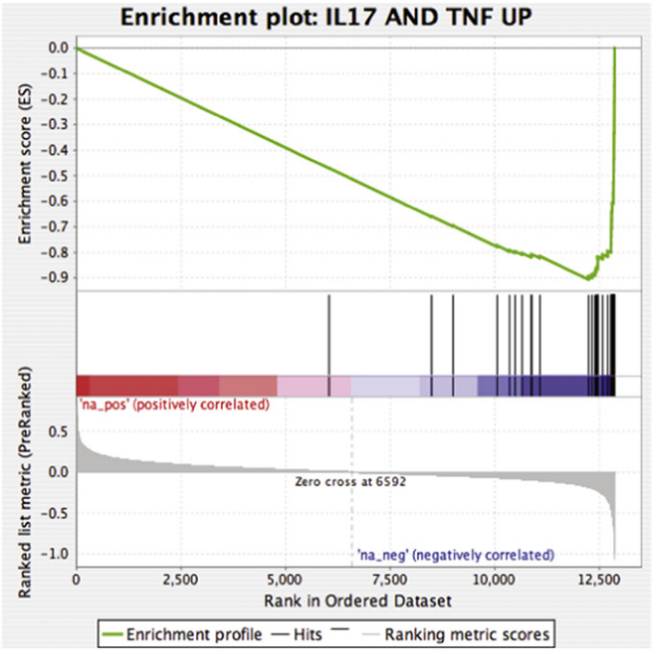
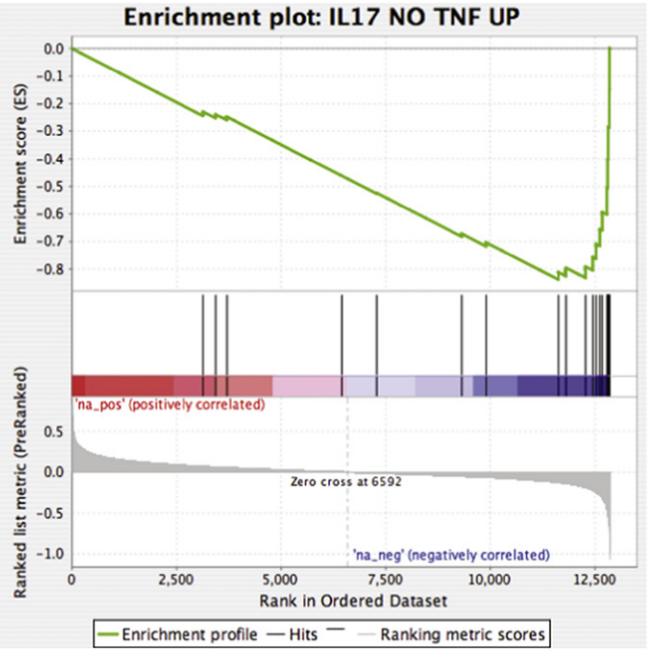


FIG E7. GSEA enrichment plots for responders.

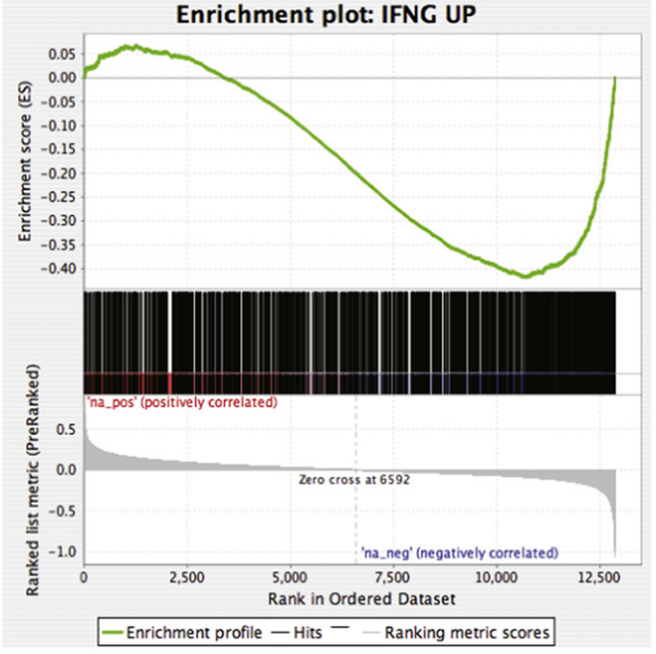
IL-17 and TNF



IL-17–specific



IFN-γ



TNF specific

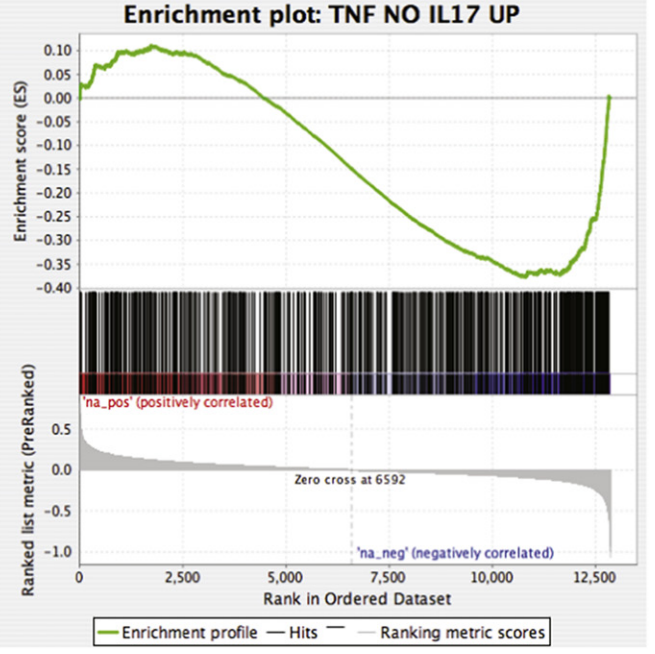


FIG E8. GSEA enrichment plots for responder versus nonresponder data.

TABLE E1. Statistical methods used for analysis

Result	Method	Section of Online Repository
Etanercept-modulated genes	Mixed-effect linear model, moderated F statistic.	Quality control, preprocessing, and filtering Differential expression criteria
• Genes downregulated and upregulated by etanercept in responders • Genes differentially regulated by etanercept in responders and nonresponders	Hierarchical average linkage clustering with distance measure equal to 1 Pearson correlation coefficient. Optimal number of discovered clusters was assessed using CC algorithm available in GenePattern software.	Consensus clustering Cluster analysis of etanercept-modulated genes Cluster clustering of genes with a different profile between responders and nonresponders
Time-response profile of cytokine keratinocyte pathways	Define IL-17, TNF, and IFN-γ keratinocyte pathways, respectively. A linear model was used to define the response profile of these pathways during etanercept treatment. GSEA was used to query which pathways were downregulated with etanercept in responders.	GSEA analysis
Comparing time-response profile responders and nonresponders	GSEA analysis to compare response profiles of the keratinocyte pathways in responders and nonresponders.	GSEA analysis of genes that were different in responders versus nonresponders

TABLE E2. Genes down-modulated by etanercept in responders

R_1vs0	Log2 Fold change between Wk1 vs Wk0 in Responders
R_2vs0	Log2 Fold change between Wk2 vs Wk0 in Responders
R_4vs0	Log2 Fold change between Wk4 vs Wk0 in Responders
R_12vs0	Log2 Fold change between Wk12 vs Wk0 in Responders
R_NL	Mean expression value estimate (Log2) for Responders in NL skin
R_0	Mean expression value estimate (Log2) for Responders in LS skin
R_1	Mean expression value estimate (Log2) for Responders in LS at Wk 1
R_2	Mean expression value estimate (Log2) for Responders in LS at Wk 2
R_4	Mean expression value estimate (Log2) for Responders in LS at Wk 4
R_12	Mean expression value estimate (Log2) for Responders in LS at Wk 12
Cluster	Final cluster membership

Probe	Symbol	Description	GenBank	Gene	UniGene	Gene Ontology	Pathway	R_1vs0	R_2vs0	R_4vs0	R_12vs0	R_NL	R_0	R_1	R_2	R_4	R_12	Cluster
210873 _x_at	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	U03891	200315	Hs.348983	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0003674: molecular_function, GO:0008270: zinc ion binding, GO:0016787: hydrolase activity, GO:0016814: hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines, GO:0046872: metal ion binding	00791: Atrazine degradation	−1.4534	−1.1034	−1.8232	−1.817	3.09	5.01	3.56	3.91	3.19	3.19	1
203968 _s_at	CDC6	cell division cycle 6 homolog (S. cerevisiae)	NM_001254	990	Hs.405958	GO:0000076: DNA replication checkpoint, GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0006260: DNA replication, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007089: traversing start control point of mitotic cell cycle, GO:0008156: negative regulation of DNA replication, GO:0008285: negative regulation of cell proliferation, GO:0051301: cell division, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005819: spindle, GO:0000166: nucleotide binding, GO:0003682: chromatin binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0017111: nucleoside-triphosphatase activity	04110: Cell cycle	−0.8607	−1.1129	−1.2552	−1.3977	2.89	4.18	3.32	3.07	2.93	2.78	1
205282_at	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	NM_004631	7804	Hs.576154	GO:0006508: proteolysis, GO:0006629: lipid metabolic process, GO:0006897: endocytosis, GO:0006897: endocytosis, GO:0007165: signal transduction, GO:0019221: cytokine and chemokine mediated signaling pathway, GO:0005886: plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004888: transmembrane receptor activity, GO:0005509: calcium ion binding, GO:0008034: lipoprotein binding, GO:0030227: apolipoprotein E receptor activity, GO:0030227: apolipoprotein E receptor activity, GO:0030227: apolipoprotein E receptor activity		−0.7972	−1.0046	−1.1951	−1.2973	3.84	5.09	4.29	4.09	3.9	3.79	1

(*Continued*)

TABLE E2. (*Continued*)

209237_s_at	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	AF164142	9962	Hs.516866	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006810: transport, GO:0006811: ion transport, GO:0006814: sodium ion transport, GO:0015851: nucleobase transport, GO:0015993: molecular hydrogen transport, GO:0019852: L-ascorbic acid metabolic process, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005215: transporter activity, GO:0008523: sodium-dependent multivitamin transmembrane transporter activity, GO:0015205: nucleobase transmembrane transporter activity, GO:0015293: symporter activity, GO:0031402: sodium ion binding		−1.2688	−1.7025	−1.9247	−2.0137	1.87	3.88	2.61	2.17	1.95	1.86	1
218990_s_at	SPRR3	small proline-rich protein 3	NM_005416	6707	Hs.139322	GO:0008544: epidermis development, GO:0030216: keratinocyte differentiation, GO:0031424: keratinization, GO:0042060: wound healing, GO:0001533: cornified envelope, GO:0005737: cytoplasm, GO:0005198: structural molecule activity, GO:0005515: protein binding		−1.1473	−1.711	−1.9917	−1.9702	2.58	4.68	3.54	2.97	2.69	2.71	1
205393_s_at	CHEK1	CHK1 checkpoint homolog (S. pombe)	NM_001274	1111	Hs.24529	GO:0000077: DNA damage checkpoint, GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0000086: G2/M transition of mitotic cell cycle, GO:0006281: DNA repair, GO:0006468: protein amino acid phosphorylation, GO:0007049: cell cycle, GO:0007131: meiotic recombination, GO:0007276: gamete generation, GO:0008285: negative regulation of cell proliferation, GO:0000794: condensed nuclear chromosome, GO:0005634: nucleus, GO:0005657: replication fork, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04110: Cell cycle, 04115: p53 signaling pathway	−0.522	−0.7397	−1.0081	−0.8704	4.14	5.12	4.6	4.39	4.12	4.25	1
209891_at	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	AF225416	57405	Hs.421956	GO:0007049: cell cycle, GO:0007067: mitosis, GO:0051301: cell division, GO:0000775: chromosome, pericentric region, GO:0005515: protein binding		−0.6074	−0.8868	−1.0115	−0.9044	3.35	4.32	3.72	3.44	3.31	3.42	1

(*Continued*)

TABLE E2. (*Continued*)

39402_at	IL1B	interleukin 1, beta	M15330	3553	Hs.126256	GO:0000074: regulation of progression through cell cycle, GO:0001660: fever, GO:0006915: apoptosis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0008283: cell proliferation, GO:0008285: negative regulation of cell proliferation, GO:0030593: neutrophil chemotaxis, GO:0045080: positive regulation of chemokine biosynthetic process, GO:0045410: positive regulation of interleukin-6 biosynthetic process, GO:0050900: leukocyte migration, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0004871: signal transducer activity, GO:0005149: interleukin-1 receptor binding, GO:0005515: protein binding	04010: MAPK signaling pathway, 04060: Cytokine-cytokine receptor interaction, 04210: Apoptosis, 04620: Toll-like receptor signaling pathway, 04640: Hematopoietic cell lineage, 04940: Type I diabetes mellitus, 05010: Alzheimer's disease	−2.4777	−3.2312	−3.2402	−3.2179	2.69	6.05	3.57	2.81	2.81	2.83	1
204420_at	FOSL1	FOS-like antigen 1	BG251266	8061	Hs.283565	GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006935: chemotaxis, GO:0006968: cellular defense response, GO:0008284: positive regulation of cell proliferation, GO:0009615: response to virus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity	04310: Wnt signaling pathway	−1.5432	−1.8161	−1.8959	−1.8833	1.99	3.88	2.34	2.06	1.98	2	1
205067_at	IL1B	interleukin 1, beta	NM_000576	3553	Hs.126256	GO:0000074: regulation of progression through cell cycle, GO:0001660: fever, GO:0006915: apoptosis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0008283: cell proliferation, GO:0008285: negative regulation of cell proliferation, GO:0030593: neutrophil chemotaxis, GO:0045080: positive regulation of chemokine biosynthetic process, GO:0045410: positive regulation of interleukin-6 biosynthetic process, GO:0050900: leukocyte migration, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0004871: signal transducer activity, GO:0005149: interleukin-1 receptor binding, GO:0005515: protein binding	04010: MAPK signaling pathway, 04060: Cytokine-cytokine receptor interaction, 04210: Apoptosis, 04620: Toll-like receptor signaling pathway, 04640: Hematopoietic cell lineage, 04940: Type I diabetes mellitus, 05010: Alzheimer's disease	−1.6791	−2.0352	−2.0085	−2.0947	2.59	4.64	2.96	2.6	2.63	2.54	1
211924_s_at	PLAUR	plasminogen activator, urokinase receptor	AY029180	5329	Hs.466871	GO:0006928: cell motility, GO:0006935: chemotaxis, GO:0007166: cell surface receptor linked signal transduction, GO:0007596: blood coagulation, GO:0030162: regulation of proteolysis, GO:0005886: plasma membrane, GO:0009986: cell surface, GO:0016021: integral to membrane, GO:0019898: extrinsic to membrane, GO:0019899: enzyme binding, GO:0030377: U-plasminogen activator receptor activity, GO:0048503: GPI anchor binding	04610: Complement and coagulation cascades	−0.7574	−1.3167	−1.3842	−1.0972	4.68	6.28	5.52	4.96	4.9	5.18	1

(*Continued*)

TABLE E2. (*Continued*)

220745_at	IL19	interleukin 19	NM_013371	29949	Hs.661017	GO:0006800: oxygen and reactive oxygen species metabolic process, GO:0006915: apoptosis, GO:0006917: induction of apoptosis, GO:0006955: immune response, GO:0006955: immune response, GO:0007165: signal transduction, GO:0042226: interleukin-6 biosynthetic process, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005125: cytokine activity, GO:0005125: cytokine activity	04060: Cytokine-cytokine receptor interaction, 04630: Jak-STAT signaling pathway	−1.673	−2.181	−2.0872	−2.0795	1.82	4.07	2.4	1.89	1.98	1.99	1
210845 _s_at	PLAUR	plasminogen activator, urokinase receptor	U08839	5329	Hs.466871	GO:0006928: cell motility, GO:0006935: chemotaxis, GO:0007166: cell surface receptor linked signal transduction, GO:0007596: blood coagulation, GO:0030162: regulation of proteolysis, GO:0005886: plasma membrane, GO:0009986: cell surface, GO:0016021: integral to membrane, GO:0019898: extrinsic to membrane, GO:0019899: enzyme binding, GO:0030377: U-plasminogen activator receptor activity, GO:0048503: GPI anchor binding	04610: Complement and coagulation cascades	−1.2179	−1.9208	−1.791	−1.737	3.85	5.94	4.72	4.02	4.15	4.2	1
211572 _s_at	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	AF092511	9962	Hs.516866	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006810: transport, GO:0006811: ion transport, GO:0006814: sodium ion transport, GO:0015851: nucleobase transport, GO:0015993: molecular hydrogen transport, GO:0019852: L-ascorbic acid metabolic process, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005215: transporter activity, GO:0008523: sodium-dependent multivitamin transmembrane transporter activity, GO:0015205: nucleobase transmembrane transporter activity, GO:0015293: symporter activity, GO:0031402: sodium ion binding		−1.081	−1.4796	−1.455	−1.5018	2.32	3.83	2.75	2.35	2.37	2.33	1
205119 _s_at	FPR1	formyl peptide receptor 1	NM_002029	2357	Hs.753	GO:0000187: activation of MAPK activity, GO:0006928: cell motility, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007188: G-protein signaling, coupled to cAMP nucleotide second messenger, GO:0007263: nitric oxide mediated signal transduction, GO:0005768: endosome, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004982: N-formyl peptide receptor activity	04080: Neuroactive ligand-receptor interaction	−0.82	−1.1227	−1.1598	−1.184	2	3.19	2.37	2.06	2.03	2	1

(*Continued*)

TABLE E2. (*Continued*)

208433_s_at	LRP8	low density lipoprotein receptor-related protein 8, apolipoproteine receptor	NM_017522	7804	Hs.576154	GO:0006508: proteolysis, GO:0006629: lipid metabolic process, GO:0006897: endocytosis, GO:0006897: endocytosis, GO:0007165: signal transduction, GO:0019221: cytokine and chemokine mediated signaling pathway, GO:0005886: plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004888: transmembrane receptor activity, GO:0005509: calcium ion binding, GO:0008034: lipoprotein binding, GO:0030227: apolipoprotein E receptor activity, GO:0030227: apolipoprotein E receptor activity, GO:0030227: apolipoprotein E receptor activity		−0.8521	−1.022	−1.0247	−1.0664	3.15	4.2	3.35	3.18	3.18	3.14	1
202768_at	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	NM_006732	2354	Hs.590958	GO:0000074: regulation of progression through cell cycle, GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0007610: behavior, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0008134: transcription factor binding, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity		−1.4209	−1.3178	−1.6324	−1.5866	2.85	3.87	2.45	2.56	2.24	2.29	1
38037_at	HBEGF	heparin-binding EGF-like growth factor	M60278	1839	Hs.799	GO:0007165: signal transduction, GO:0007173: epidermal growth factor receptor signaling pathway, GO:0007517: muscle development, GO:0008016: regulation of heart contraction, GO:0035313: wound healing, spreading of epidermal cells, GO:0048661: positive regulation of smooth muscle cell proliferation, GO:0051549: positive regulation of keratinocyte migration, GO:0005615: extracellular space, GO:0005887: integral to plasma membrane, GO:0009986: cell surface, GO:0016020: membrane, GO:0004872: receptor activity, GO:0005154: epidermal growth factor receptor binding, GO:0008083: growth factor activity, GO:0008201: heparin binding	04012: ErbB signaling pathway, 04912: GnRH signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection	−1.1532	−1.1368	−1.3291	−1.364	3.43	4.81	3.66	3.67	3.48	3.45	1

(*Continued*)

TABLE E2. (*Continued*)

205114_s_at	CCL3	chemokine (C-C motif) ligand 3	NM_002983	6348	Hs.514107	GO:0006874: cellular calcium ion homeostasis, GO:0006887: exocytosis, GO:0006928: cell motility, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007010: cytoskeleton organization and biogenesis, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007267: cell-cell signaling, GO:0045069: regulation of viral genome replication, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0004871: signal transducer activity, GO:0008009: chemokine activity, GO:0042056: chemoattractant activity	04060: Cytokine-cytokine receptor interaction, 04620: Toll-like receptor signaling pathway	−0.5691	−1.859	−2.0428	−1.7881	2.35	4.49	3.92	2.63	2.44	2.7	1
220655_at	TNIP3	TNFAIP3 interacting protein 3	NM_024873	79931	Hs.208206			−0.375	−1.4279	−1.3708	−1.3592	2.81	4.37	4	2.95	3	3.01	1		
219181_at	LIPG	lipase, endothelial	NM_006033	9388	Hs.465102	GO:0016042: lipid catabolic process, GO:0004465: lipoprotein lipase activity, GO:0004806: triacylglycerol lipase activity, GO:0005515: protein binding, GO:0008201: heparin binding, GO:0008970: phospholipase A1 activity, GO:0016787: hydrolase activity	00561: Glycerolipid metabolism	−0.7141	−1.8244	−1.7661	−2.0807	2.1	4.34	3.63	2.52	2.57	2.26	1		
204103_at	CCL4	chemokine (C-C motif) ligand 4	NM_002984	6351	Hs.75703	GO:0006928: cell motility, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007155: cell adhesion, GO:0007163: establishment and/or maintenance of cell polarity, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0009615: response to virus, GO:0019079: viral genome replication, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0004716: receptor signaling protein tyrosine kinase activity, GO:0008009: chemokine activity	04060: Cytokine-cytokine receptor interaction, 04620: Toll-like receptor signaling pathway	−0.603	−1.5446	−1.3996	−1.6233	1.99	3.75	3.15	2.21	2.35	2.13	1		
204750_s_at	DSC2	desmocollin 2	BF196457	1824	Hs.95612	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005911: intercellular junction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding	01430: Cell Communication	−1.3513	−2.4678	−2.5136	−2.6909	3.52	6.17	4.81	3.7	3.65	3.48	1		
205681_at	BCL2A1	BCL2-related protein A1	NM_004049	597	Hs.227817	GO:0006916: anti-apoptosis, GO:0042981: regulation of apoptosis, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005515: protein binding		−1.0881	−2.1273	−2.1201	−2.22	2.99	5.68	4.59	3.55	3.56	3.46	1		

(*Continued*)

TABLE E2. (*Continued*)

211506_s_at	IL8	interleukin 8	AF043337	3576	Hs.624, Hs.449585, Hs.551925, Hs.561078, Hs.654584	GO:0001525: angiogenesis, GO:0006928: cell motility, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007050: cell cycle arrest, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007242: intracellular signaling cascade, GO:0007267: cell-cell signaling, GO:0008285: negative regulation of cell proliferation, GO:0019722: calcium-mediated signaling, GO:0030155: regulation of cell adhesion, GO:0030593: neutrophil chemotaxis, GO:0042119: neutrophil activation, GO:0045091: regulation of retroviral genome replication, GO:0050930: induction of positive chemotaxis, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005153: interleukin-8 receptor binding, GO:0005515: protein binding, GO:0008009: chemokine activity	04060: Cytokine-cytokine receptor interaction, 04620: Toll-like receptor signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection, 05219: Bladder cancer	−2.104	−3.8898	−3.7198	−3.9451	3.09	7.3	5.2	3.41	3.58	3.35	1
208079_s_at	AURKA	aurora kinase A	NM_003158	6790	Hs.250822	GO:0000278: mitotic cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0007051: spindle organization and biogenesis, GO:0007067: mitosis, GO:0031647: regulation of protein stability, GO:0048015: phosphoinositide-mediated signaling, GO:0005634: nucleus, GO:0005819: spindle, GO:0000166: nucleotide binding, GO:0004672: protein kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0031625: ubiquitin protein ligase binding		−0.7088	−1.3607	−1.5197	−1.7398	3.57	5.51	4.8	4.15	3.99	3.77	1
218662_s_at	NCAPG	non-SMC condensin I complex, subunit G	NM_022346	64151	Hs.446201, Hs.567567	GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007076: mitotic chromosome condensation, GO:0051301: cell division, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003674: molecular_function, GO:0005515: protein binding		−0.4878	−0.8652	−0.9659	−1.1117	6.71	7.83	7.34	6.97	6.87	6.72	1

(*Continued*)

TABLE E2. (*Continued*)

202859_x_at	IL8	interleukin 8	NM_000584	3576	Hs.624, Hs.449585, Hs.551925, Hs.561078, Hs.654584	GO:0001525: angiogenesis, GO:0006928: cell motility, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007050: cell cycle arrest, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007242: intracellular signaling cascade, GO:0007267: cell-cell signaling, GO:0008285: negative regulation of cell proliferation, GO:0019722: calcium-mediated signaling, GO:0030155: regulation of cell adhesion, GO:0030593: neutrophil chemotaxis, GO:0042119: neutrophil activation, GO:0045091: regulation of retroviral genome replication, GO:0050930: induction of positive chemotaxis, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005153: interleukin-8 receptor binding, GO:0005515: protein binding, GO:0008009: chemokine activity	04060: Cytokine-cytokine receptor interaction, 04620: Toll-like receptor signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection, 05219: Bladder cancer	−2.5546	−5.1749	−5.3383	−6.0165	3.32	9.87	7.32	4.7	4.54	3.86	1
204092_s_at	AURKA	aurora kinase A	NM_003600	6790	Hs.250822	GO:0000278: mitotic cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0007051: spindle organization and biogenesis, GO:0007067: mitosis, GO:0031647: regulation of protein stability, GO:0048015: phosphoinositide-mediated signaling, GO:0005634: nucleus, GO:0005819: spindle, GO:0000166: nucleotide binding, GO:0004672: protein kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0031625: ubiquitin protein ligase binding		−0.5138	−0.9285	−0.9446	−1.2249	5.01	6.08	5.57	5.16	5.14	4.86	1
201538_s_at	DUSP3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	AL048503	1845	Hs.181046	GO:0006470: protein amino acid dephosphorylation, GO:0006470: protein amino acid dephosphorylation, GO:0004725: protein tyrosine phosphatase activity, GO:0008138: protein tyrosine/serine/threonine phosphatase activity, GO:0016787: hydrolase activity, GO:0016791: phosphoric monoester hydrolase activity	04010: MAPK signaling pathway	−0.6148	−0.797	−1.0356	−1.1572	3.41	4.48	3.86	3.68	3.44	3.32	1

(*Continued*)

TABLE E2. (*Continued*)

217173_s_at	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	S70123	3949	Hs.213289	GO:0006493: protein amino acid O-linked glycosylation, GO:0006629: lipid metabolic process, GO:0006869: lipid transport, GO:0006897: endocytosis, GO:0008202: steroid metabolic process, GO:0008203: cholesterol metabolic process, GO:0030299: cholesterol absorption, GO:0030301: cholesterol transport, GO:0042157: lipoprotein metabolic process, GO:0042632: cholesterol homeostasis, GO:0005768: endosome, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004872: receptor activity, GO:0004888: transmembrane receptor activity, GO:0005041: low-density lipoprotein receptor activity, GO:0005319: lipid transporter activity, GO:0005509: calcium ion binding, GO:0008034: lipoprotein binding		−1.2414	−1.6983	−1.8889	−2.4046	3.74	5.7	4.46	4	3.81	3.3	1
209464_at	AURKB	aurora kinase B	AB011446	9212	Hs.442658	GO:0006468: protein amino acid phosphorylation, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0051301: cell division, GO:0000775: chromosome, pericentric region, GO:0005694: chromosome, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity		−0.5688	−1.0821	−1.4552	−1.4936	3.05	4.56	3.99	3.47	3.1	3.06	2
218663_at	NCAPG	non-SMC condensin I complex, subunit G	NM_022346	64151	Hs.446201, Hs.567567	GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007076: mitotic chromosome condensation, GO:0051301: cell division, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003674: molecular_function, GO:0005515: protein binding		−0.5013	−0.987	−1.4143	−1.434	3.91	5.29	4.79	4.3	3.88	3.86	2
201348_at	GPX3	glutathione peroxidase 3 (plasma)	NM_002084	2878	Hs.386793	GO:0006979: response to oxidative stress, GO:0006982: response to lipid hydroperoxide, GO:0042744: hydrogen peroxide catabolic process, GO:0051289: protein homotetramerization, GO:0005615: extracellular space, GO:0004602: glutathione peroxidase activity, GO:0008134: transcription factor binding, GO:0008430: selenium binding, GO:0016491: oxidoreductase activity	00480: Glutathione metabolism, 00590: Arachidonic acid metabolism	−0.1353	−0.6672	−0.9935	−1.01	11.66	12.26	12.12	11.59	11.26	11.25	2
218355_at	KIF4A	kinesin family member 4A	AF179308	24137	Hs.648326	GO:0006996: organelle organization and biogenesis, GO:0007018: microtubule-based movement, GO:0008089: anterograde axon cargo transport, GO:0005737: cytoplasm, GO:0005875: microtubule associated complex, GO:0005876: spindle microtubule, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003777: microtubule motor activity, GO:0005515: protein binding, GO:0005524: ATP binding		−0.4535	−1.09	−1.2507	−1.2667	2.09	3.35	2.89	2.26	2.1	2.08	2

(*Continued*)

TABLE E2. (*Continued*)

209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2	M57731	2920	Hs.590921	GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0008009: chemokine activity	04060: Cytokine-cytokine receptor interaction	−0.7032	−1.8845	−2.265	−2.5243	3.44	6.27	5.57	4.39	4.01	3.75	2
221009_s_at	ANGPTL4	angiopoietin-like 4	NM_016109	51129	Hs.9613	GO:0001525: angiogenesis, GO:0001666: response to hypoxia, GO:0007165: signal transduction, GO:0007275: multicellular organismal development, GO:0030154: cell differentiation, GO:0043066: negative regulation of apoptosis, GO:0045766: positive regulation of angiogenesis, GO:0051005: negative regulation of lipoprotein lipase activity, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005615: extracellular space, GO:0004857: enzyme inhibitor activity, GO:0005102: receptor binding	03320: PPAR signaling pathway	−0.3609	−1.1136	−1.3308	−1.444	5.75	7.41	7.05	6.29	6.08	5.96	2
204033_at	TRIP13	thyroid hormone receptor interactor 13	NM_004237	9319	Hs.436187	GO:0006366: transcription from RNA polymerase II promoter, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003712: transcription cofactor activity, GO:0005524: ATP binding, GO:0017111: nucleoside-triphosphatase activity		−0.3169	−1.0357	−1.1971	−1.328	3.25	4.51	4.2	3.48	3.32	3.18	2
207828_s_at	CENPF	centromere protein F, 350/400ka (mitosin)	NM_005196	1063	Hs.497741	GO:0000085: G2 phase of mitotic cell cycle, GO:0007067: mitosis, GO:0007094: mitotic cell cycle spindle assembly checkpoint, GO:0008283: cell proliferation, GO:0016202: regulation of striated muscle development, GO:0016481: negative regulation of transcription, GO:0042493: response to drug, GO:0051301: cell division, GO:0051310: metaphase plate congression, GO:0051382: kinetochore assembly, GO:0000776: kinetochore, GO:0000785: chromatin, GO:0000922: spindle pole, GO:0000940: outer kinetochore of condensed chromosome, GO:0000940: outer kinetochore of condensed chromosome, GO:0005634: nucleus, GO:0005635: nuclear envelope, GO:0005694: chromosome, GO:0005737: cytoplasm, GO:0016363: nuclear matrix, GO:0003682: chromatin binding, GO:0008022: protein C-terminus binding, GO:0008134: transcription factor binding, GO:0042803: protein homodimerization activity, GO:0045502: dynein binding, GO:0046982: protein heterodimerization activity		−0.2997	−0.8952	−1.0032	−1.156	5.64	6.64	6.34	5.74	5.64	5.48	2

(*Continued*)

TABLE E2. (*Continued*)

205190_at	PLS1	plastin 1 (I isoform)	NM_002670	5357	Hs.203637	GO:0005737: cytoplasm, GO:0005903: brush border, GO:0015629: actin cytoskeleton, GO:0003779: actin binding, GO:0005200: structural constituent of cytoskeleton, GO:0005509: calcium ion binding, GO:0051015: actin filament binding		−0.213	−0.8355	−1.2112	−1.0497	5.2	5.62	5.41	4.78	4.41	4.57	2
219580_s_at	TMC5	transmembrane channel-like 5	NM_024780	79838	Hs.115838	GO:0016020: membrane, GO:0016021: integral to membrane		−0.2556	−0.6519	−1.0212	−0.9589	4.51	5.5	5.24	4.85	4.48	4.54	2
204470_at	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	NM_001511	2919	Hs.789	GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007242: intracellular signaling cascade, GO:0007399: nervous system development, GO:0008283: cell proliferation, GO:0008285: negative regulation of cell proliferation, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0008009: chemokine activity, GO:0008047: enzyme activator activity, GO:0008083: growth factor activity	04060: Cytokine-cytokine receptor interaction, 05120: Epithelial cell signaling in Helicobacter pylori infection	−1.1885	−2.8817	−3.7286	−3.9317	2.97	7.41	6.22	4.52	3.68	3.47	2
201884_at	CEACAM5	carcinoembryonic antigen-related cell adhesion molecule 5	NM_004363	1048	Hs.466814	GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0048503: GPI anchor binding		−0.4194	−1.2815	−1.6509	−1.7933	4.57	6.52	6.1	5.24	4.87	4.72	2
203649_s_at	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid)	NM_000300	5320	Hs.466804	GO:0006644: phospholipid metabolic process, GO:0016042: lipid catabolic process, GO:0005576: extracellular region, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0016787: hydrolase activity, GO:0047498: calcium-dependent phospholipase A2 activity	00564: Glycerophospholipid metabolism, 00565: Ether lipid metabolism, 00590: Arachidonic acid metabolism, 00591: Linoleic acid metabolism, 04010: MAPK signaling pathway, 04370: VEGF signaling pathway, 04664: Fc epsilon RI signaling pathway, 04730: Long-term depression, 04912: GnRH signaling pathway	−0.6361	−1.6468	−2.2206	−2.1317	9.83	10.46	9.83	8.82	8.24	8.33	2
207165_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	NM_012485	3161	Hs.72550	GO:0006928: cell motility, GO:0005737: cytoplasm, GO:0004872: receptor activity, GO:0005540: hyaluronic acid binding	04512: ECM-receptor interaction	0.0564	−0.8669	−1.1087	−1.5688	4.33	5.28	5.33	4.41	4.17	3.71	2
205242_at	CXCL13	chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	NM_006419	10563	Hs.100431	GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0007267: cell-cell signaling, GO:0048535: lymph node development, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0008009: chemokine activity	04060: Cytokine-cytokine receptor interaction	−0.0495	−1.467	−1.4699	−2.0243	2.4	4.73	4.68	3.27	3.26	2.71	2
209546_s_at	APOL1	apolipoprotein L, 1	AF323540	8542	Hs.114309	GO:0006629: lipid metabolic process, GO:0006869: lipid transport, GO:0008202: steroid metabolic process, GO:0008203: cholesterol metabolic process, GO:0042157: lipoprotein metabolic process, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005319: lipid transporter activity, GO:0008289: lipid binding		0.0876	−0.688	−0.6857	−1.0681	6.34	8.29	8.38	7.61	7.61	7.23	2

(*Continued*)

TABLE E2. (*Continued*)

218755_at	KIF20A	kinesin family member 20A	NM_005733	10112	Hs.73625	GO:0007018: microtubule-based movement, GO:0015031: protein transport, GO:0016192: vesicle-mediated transport, GO:0005794: Golgi apparatus, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0000166: nucleotide binding, GO:0003777: microtubule motor activity, GO:0005215: transporter activity, GO:0005524: ATP binding		−0.2418	−0.8263	−1.0089	−1.2228	3.13	4.39	4.15	3.56	3.38	3.17	2
204034_at	ETHE1	ethylmalonic encephalopathy 1	NM_014297	23474	Hs.7486	GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0008270: zinc ion binding, GO:0016787: hydrolase activity, GO:0046872: metal ion binding		−0.233	−1.0349	−1.348	−2.0556	7.03	8.91	8.68	7.88	7.56	6.85	2
205633_s_at	ALAS1	aminolevulinate, delta-, synthase 1	NM_000688	211	Hs.476308	GO:0006783: heme biosynthetic process, GO:0009058: biosynthetic process, GO:0033014: tetrapyrrole biosynthetic process, GO:0005739: mitochondrion, GO:0003870: 5-aminolevulinate synthase activity, GO:0008415: acyltransferase activity, GO:0016769: transferase activity, transferring nitrogenous groups, GO:0030170: pyridoxal phosphate binding	00260: Glycine, serine and threonine metabolism, 00860: Porphyrin and chlorophyll metabolism	−0.1876	−0.5651	−0.782	−1.1492	9.49	10.56	10.37	9.99	9.78	9.41	2
203418_at	CCNA2	cyclin A2	NM_001237	890	Hs.58974	GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007095: mitotic cell cycle G2/M transition DNA damage checkpoint, GO:0045941: positive regulation of transcription, GO:0051301: cell division, GO:0001939: female pronucleus, GO:0001940: male pronucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005515: protein binding	04110: Cell cycle	−0.3918	−0.9351	−1.0219	−1.7246	2.75	4.24	3.85	3.3	3.22	2.51	2
204408_at	APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2	NM_014481	27301	Hs.659558	GO:0006281: DNA repair, GO:0005622: intracellular, GO:0005739: mitochondrion, GO:0003677: DNA binding, GO:0003906: DNA-(apurinic or apyrimidinic site) lyase activity, GO:0004519: endonuclease activity, GO:0008270: zinc ion binding, GO:0016829: lyase activity		−0.1315	−0.5898	−0.6774	−1.1725	3.82	4.84	4.71	4.25	4.17	3.67	2
219918_s_at	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	NM_018123	259266	Hs.121028	GO:0007049: cell cycle, GO:0007067: mitosis, GO:0051301: cell division, GO:0005737: cytoplasm, GO:0005516: calmodulin binding		−0.2976	−1.0062	−1.2193	−2.1601	7.12	8.39	8.09	7.38	7.17	6.23	2
221521_s_at	GINS2	GINS complex subunit 2 (Psf2 homolog)	BC003186	51659	Hs.433180	GO:0006260: DNA replication, GO:0005634: nucleus, GO:0005515: protein binding		−0.5717	−0.8902	−1.604	−2.0478	5.46	7.27	6.7	6.38	5.67	5.23	2
205349_at	GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	NM_002068	2769	Hs.73797	GO:0006471: protein amino acid ADP-ribosylation, GO:0007165: signal transduction, GO:0007202: phospholipase C activation, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0007207: muscarinic acetylcholine receptor, phospholipase C activating pathway, GO:0005834: heterotrimeric G-protein complex, GO:0005886: plasma membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0004871: signal transducer activity, GO:0005525: GTP binding	04020: Calcium signaling pathway	−0.3827	−0.6491	−1.2173	−1.4597	8.98	10.39	10	9.74	9.17	8.93	2

(*Continued*)

TABLE E2. (*Continued*)

205774_at	F12	coagulation factor XII (Hageman factor)	NM_000505	2161	Hs.1321	GO:0006508: proteolysis, GO:0007596: blood coagulation, GO:0042730: fibrinolysis, GO:0005576: extracellular region, GO:0003805: coagulation factor XIa activity, GO:0003806: coagulation factor XIIa activity, GO:0004252: serine-type endopeptidase activity	04610: Complement and coagulation cascades	−0.4621	−0.5298	−1.0568	−1.2725	6.62	7.98	7.52	7.45	6.92	6.71	2
201714_at	TUBG1	tubulin, gamma 1	NM_001070	7283	Hs.279669	GO:0000212: meiotic spindle organization and biogenesis, GO:0000226: microtubule cytoskeleton organization and biogenesis, GO:0051258: protein polymerization, GO:0000242: pericentriolar material, GO:0000794: condensed nuclear chromosome, GO:0000930: gamma-tubulin complex, GO:0005737: cytoplasm, GO:0005737: cytoplasm, GO:0005816: spindle pole body, GO:0005827: polar microtubule, GO:0005881: cytoplasmic microtubule, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding, GO:0005525: GTP binding		−0.3522	−0.4379	−0.9217	−1.0503	9.21	10.16	9.8	9.72	9.24	9.11	2
205476_at	CCL20	chemokine (C-C motif) ligand 20	NM_004591	6364	Hs.75498	GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0042742: defense response to bacterium, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005515: protein binding, GO:0008009: chemokine activity	04060: Cytokine-cytokine receptor interaction	−1.2682	−1.5567	−3.1133	−3.7083	2.63	6.46	5.2	4.91	3.35	2.76	2
202338_at	TK1	thymidine kinase 1, soluble	NM_003258	7083	Hs.515122	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006260: DNA replication, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004797: thymidine kinase activity, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity	00240: Pyrimidine metabolism	−0.3644	−0.5375	−1.1015	−1.3367	5.14	6.35	5.98	5.81	5.25	5.01	2
219956_at	GALNT6	UDP-N-acetyl-alpha-D-				galactosamine:polypeptide N-acetylgalactosaminyl transferase 6 (GalNAc-T6)	NM_007210	11226	Hs.505575									
	GO:0006493: protein amino acid O-linked	glycosylation, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004653: polypeptide N-				acetylgalactosaminyltransferase activity, GO:0005509: calcium ion binding, GO:0005529: sugar binding, GO:0016757: transferase activity, transferring glycosyl groups, GO:0030145: manganese ion binding	00512: O-Glycan biosynthesis, 01030: Glycan structures - biosynthesis 1	−0.741	−1.0359	−1.9914	−2.4024	5.47	8.11	7.36	7.07	6.11	5.7	2
209372_x_at	TUBB2A	tubulin, beta 2A	BF971587	7280	Hs.654543	GO:0007018: microtubule-based movement, GO:0051258: protein polymerization, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005874: microtubule, GO:0043234: protein complex, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding, GO:0005525: GTP binding	04540: Gap junction, 05130: Pathogenic Escherichia coli infection - EHEC, 05131: Pathogenic Escherichia coli infection - EPEC	−0.6283	−0.5333	−0.9871	−1.3711	8.29	9.36	8.73	8.82	8.37	7.98	2

(*Continued*)

TABLE E2. (*Continued*)

213793_s_at	HOMER1	homer homolog 1 (Drosophila)	BE550452	9456	Hs.591761	GO:0007206: metabotropic glutamate receptor, phospholipase C activating pathway, GO:0007268: synaptic transmission, GO:0005737: cytoplasm, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0030054: cell junction, GO:0045202: synapse, GO:0005515: protein binding		−0.5012	−0.5217	−0.9399	−1.2648	8.42	9.51	9.01	8.99	8.57	8.25	2
207455_at	P2RY1	purinergic receptor P2Y, G-protein coupled, 1	NM_002563	5028	Hs.654526	GO:0007200: G-protein signaling, coupled to IP3 second messenger (phospholipase C activating), GO:0007596: blood coagulation, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0045028: purinergic nucleotide receptor activity, G-protein coupled	04080: Neuroactive ligand-receptor interaction	−0.5616	−0.465	−0.9939	−1.4201	3.35	4.69	4.13	4.22	3.69	3.27	2
209260_at	SFN	stratifin	BC000329	2810	Hs.523718	GO:0000074: regulation of progression through cell cycle, GO:0001836: release of cytochrome c from mitochondria, GO:0006469: negative regulation of protein kinase activity, GO:0007165: signal transduction, GO:0008283: cell proliferation, GO:0008630: DNA damage response, signal transduction resulting in induction of apoptosis, GO:0008632: apoptotic program, GO:0043154: negative regulation of caspase activity, GO:0005615: extracellular space, GO:0005737: cytoplasm, GO:0008426: protein kinase C inhibitor activity, GO:0019904: protein domain specific binding	04110: Cell cycle, 04115: p53 signaling pathway	−0.4129	−0.4086	−0.8448	−1.1133	12.51	13.31	12.9	12.9	12.47	12.2	2

(*Continued*)

TABLE E2. (*Continued*)

201291_s_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	AU159942	7153	Hs.156346	GO:0006260: DNA replication, GO:0006265: DNA topological change, GO:0006266: DNA ligation, GO:0006281: DNA repair, GO:0007059: chromosome segregation, GO:0030263: apoptotic chromosome condensation, GO:0043065: positive regulation of apoptosis, GO:0045870: positive regulation of retroviral genome replication, GO:0048015: phosphoinositide-mediated signaling, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0005694: chromosome, GO:0005730: nucleolus, GO:0005737: cytoplasm, GO:0005814: centriole, GO:0009330: DNA topoisomerase complex (ATP-hydrolyzing), GO:0019035: viral integration complex, GO:0000166: nucleotide binding, GO:0003682: chromatin binding, GO:0003918: DNA topoisomerase (ATP-hydrolyzing) activity, GO:0005080: protein kinase C binding, GO:0005524: ATP binding, GO:0008022: protein C-terminus binding, GO:0008094: DNA-dependent ATPase activity, GO:0008144: drug binding, GO:0042803: protein homodimerization activity, GO:0042826: histone deacetylase binding, GO:0043130: ubiquitin binding, GO:0046982: protein heterodimerization activity	−0.6796	−1.0374	−1.452	−2.0753	7.56	8.86	8.18	7.82	7.41	6.79	2
205436_s_at	H2AFX	H2A histone family, member X	NM_002105	3014	Hs.477879	GO:0000724: double-strand break repair via homologous recombination, GO:0006281: DNA repair, GO:0006310: DNA recombination, GO:0006334: nucleosome assembly, GO:0007001: chromosome organization and biogenesis (sensu Eukaryota), GO:0007049: cell cycle, GO:0007126: meiosis, GO:0007283: spermatogenesis, GO:0000786: nucleosome, GO:0005634: nucleus, GO:0005657: replication fork, GO:0005694: chromosome, GO:0003684: damaged DNA binding, GO:0005515: protein binding	−0.4533	−0.6101	−0.8969	−1.3502	7.97	9.03	8.58	8.42	8.13	7.68	2
203747_at	AQP3	aquaporin 3 (Gill blood group)	NM_004925	360	Hs.234642	GO:0006810: transport, GO:0007588: excretion, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005215: transporter activity	−0.456	−0.6336	−0.8286	−1.2607	10.55	11.23	10.78	10.6	10.41	9.97	2

(*Continued*)

TABLE E2. (*Continued*)

204768_s_at	FEN1	flap structure-specific endonuclease 1	NM_004111	2237	Hs.409065	GO:0006260: DNA replication, GO:0006302: double-strand break repair, GO:0009650: UV protection, GO:0048015: phosphoinositide-mediated signaling, GO:0005634: nucleus, GO:0000287: magnesium ion binding, GO:0003684: damaged DNA binding, GO:0003690: double-stranded DNA binding, GO:0004519: endonuclease activity, GO:0004523: ribonuclease H activity, GO:0005515: protein binding, GO:0008309: double-stranded DNA specific exodeoxyribonuclease activity, GO:0008409: 5'-3' exonuclease activity, GO:0016787: hydrolase activity, GO:0017108: 5'-flap endonuclease activity, GO:0030145: manganese ion binding		−0.4822	−0.6577	−0.9057	−1.3869	5.1	6.3	5.82	5.64	5.4	4.92	2
203974_at	HDHD1A	haloacid dehalogenase-like hydrolase domain containing 1A	NM_012080	8226	Hs.185910	GO:0008152: metabolic process, GO:0005575: cellular_component, GO:0003824: catalytic activity		−0.0491	−0.5406	−1.1048	−1.2891	5.68	7.1	7.05	6.56	6	5.81	2
1431_at	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	J02843	1571	Hs.12907	GO:0006118: electron transport, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0004497: monooxygenase activity, GO:0005506: iron ion binding, GO:0019825: oxygen binding, GO:0020037: heme binding, GO:0046872: metal ion binding, GO:0050381: unspecific monooxygenase activity	00590: Arachidonic acid metabolism, 00591: Linoleic acid metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	−0.1588	−0.5161	−0.945	−1.1956	6.15	7.2	7.04	6.68	6.25	6	2
201201_at	CSTB	cystatin B (stefin B)	NM_000100	1476	Hs.695	GO:0008344: adult locomotory behavior, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0004869: cysteine protease inhibitor activity, GO:0005515: protein binding		−0.1307	−0.4363	−0.8383	−1.0892	12.76	13.84	13.71	13.41	13.01	12.75	2
213421_x_at	PRSS3	protease, serine, 3 (mesotrypsin)	AW007273	5646	Hs.654513	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007586: digestion, GO:0031638: zymogen activation, GO:0043542: endothelial cell migration, GO:0005615: extracellular space, GO:0004252: serine-type endopeptidase activity, GO:0004295: trypsin activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0008233: peptidase activity	04080: Neuroactive ligand-receptor interaction	−0.2463	−0.5643	−1.3374	−1.3391	9.74	11.32	11.07	10.76	9.98	9.98	2
215395_x_at	TRY6	trypsinogen C	U66061	154754	Hs.661703			−0.3155	−0.5343	−1.2977	−1.3077	7.58	9.12	8.8	8.58	7.82	7.81	2
204715_at	PANX1	pannexin 1	NM_015368	24145	Hs.591976	GO:0005921: gap junction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030054: cell junction		−0.2358	−0.5818	−1.1691	−1.2086	5.98	7.04	6.8	6.45	5.87	5.83	2
208002_s_at	ACOT7	acyl-CoA thioesterase 7	NM_007274	11332	Hs.126137	GO:0006629: lipid metabolic process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0000062: acyl-CoA binding, GO:0016290: palmitoyl-CoA hydrolase activity, GO:0016787: hydrolase activity		−0.16	−0.4123	−1.0553	−1.0397	8	9.2	9.04	8.78	8.14	8.16	2
216470_x_at	TRY6	trypsinogen C	AF009664	154754	Hs.661703			−0.3502	−0.5497	−1.4045	−1.4887	6.11	7.78	7.43	7.23	6.37	6.29	2
219555_s_at	CENPN	centromere protein N	NM_018455	55839	Hs.660033	GO:0000775: chromosome, pericentric region, GO:0005694: chromosome		−0.3763	−0.7522	−1.6531	−1.7277	4.34	6.03	5.65	5.28	4.38	4.3	2

(*Continued*)

TABLE E2. (*Continued*)

203573_s_at	RABGGTA	Rab geranylgeranyltransferase, alpha subunit	NM_004581	5875	Hs.377992	GO:0006464: protein modification process, GO:0007601: visual perception, GO:0018346: protein amino acid prenylation, GO:0004663: Rab-protein geranylgeranyltransferase activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0008318: protein prenyltransferase activity, GO:0016740: transferase activity, GO:0046872: metal ion binding		−0.1497	−0.5924	−1.1875	−1.2676	6.87	8.29	8.14	7.7	7.11	7.03	2
218392_x_at	SFXN1	sideroflexin 1	NM_022754	94081	Hs.369440	GO:0006812: cation transport, GO:0006826: iron ion transport, GO:0030218: erythrocyte differentiation, GO:0005739: mitochondrion, GO:0005743: mitochondrial inner membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0008324: cation transmembrane transporter activity		−0.174	−0.5484	−1.066	−1.1719	6.15	7.74	7.57	7.2	6.68	6.57	2
208937_s_at	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	D13889	3397	Hs.504609	GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007275: multicellular organismal development, GO:0016481: negative regulation of transcription, GO:0043433: negative regulation of transcription factor activity, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005515: protein binding, GO:0016564: transcription repressor activity	04350: TGF-beta signaling pathway	−0.1988	−0.5596	−0.9667	−1.0975	10.42	11.79	11.59	11.23	10.82	10.69	2
213680_at	KRT6C	keratin 6C	AI831452	286887	Hs.654613	GO:0007010: cytoskeleton organization and biogenesis, GO:0005882: intermediate filament, GO:0005198: structural molecule activity	01430: Cell Communication	−0.3185	−0.7918	−1.4596	−1.7415	12.4	14.2	13.88	13.41	12.74	12.46	2
202833_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	NM_000295	5265	Hs.525557	GO:0006953: acute-phase response, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding	04610: Complement and coagulation cascades	−0.3935	−1.3253	−2.2843	−2.6748	3.22	6.15	5.76	4.82	3.87	3.47	2
203021_at	SLPI	secretory leukocyte peptidase inhibitor	NM_003064	6590	Hs.517070	GO:0005576: extracellular region, GO:0004867: serine-type endopeptidase inhibitor activity		−0.1881	−0.5668	−0.9762	−1.1709	11.43	12.73	12.55	12.17	11.76	11.56	2
214710_s_at	CCNB1	cyclin B1	BE407516	891	Hs.23960	GO:0000074: regulation of progression through cell cycle, GO:0000086: G2/M transition of mitotic cell cycle, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0051301: cell division, GO:0005575: cellular_component, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005515: protein binding	04110: Cell cycle, 04115: p53 signaling pathway	−0.5204	−1.2339	−2.3366	−2.89	5.2	7.81	7.29	6.58	5.47	4.92	2
202705_at	CCNB2	cyclin B2	NM_004701	9133	Hs.194698	GO:0000074: regulation of progression through cell cycle, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0051301: cell division, GO:0005634: nucleus, GO:0015630: microtubule cytoskeleton, GO:0005515: protein binding	04110: Cell cycle, 04115: p53 signaling pathway	−0.207	−0.7951	−1.528	−1.8574	7.02	8.68	8.47	7.88	7.15	6.82	2

(*Continued*)

TABLE E2. (*Continued*)

202712_s_at	CKMT1B	creatine kinase, mitochondrial 1B	NM_020990	1159	Hs.425633	GO:0005739: mitochondrion, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004111: creatine kinase activity, GO:0005524: ATP binding	00330: Arginine and proline metabolism	−0.237	−0.6254	−1.1956	−1.4118	10.21	11.77	11.53	11.14	10.57	10.36	2
205847_at	PRSS22	protease, serine, 22	NM_022119	64063	Hs.459709	GO:0006508: proteolysis, GO:0004252: serine-type endopeptidase activity, GO:0008233: peptidase activity		−0.2594	−1.0041	−1.8484	−2.2931	6.94	9.01	8.75	8	7.16	6.71	2
213523_at	CCNE1	cyclin E1	AI671049	898	Hs.244723	GO:0000074: regulation of progression through cell cycle, GO:0000082: G1/S transition of mitotic cell cycle, GO:0007049: cell cycle, GO:0030521: androgen receptor signaling pathway, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0051301: cell division, GO:0005634: nucleus, GO:0003713: transcription coactivator activity, GO:0005515: protein binding, GO:0050681: androgen receptor binding	04110: Cell cycle, 04115: p53 signaling pathway, 05215: Prostate cancer, 05222: Small cell lung cancer	−0.1786	−0.7297	−1.5245	−1.7898	4.78	6.66	6.48	5.93	5.14	4.87	2
215808_at	KLK10	kallikrein-related peptidase 10	AK026045	5655	Hs.275464	GO:0006508: proteolysis, GO:0007049: cell cycle, GO:0045786: negative regulation of progression through cell cycle, GO:0005576: extracellular region, GO:0004252: serine-type endopeptidase activity		−0.4892	−1.2267	−2.7488	−3.3886	3.15	6.89	6.4	5.66	4.14	3.5	2
202671_s_at	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	NM_003681	8566	Hs.284491	GO:0008615: pyridoxine biosynthetic process, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0008270: zinc ion binding, GO:0008478: pyridoxal kinase activity, GO:0016740: transferase activity, GO:0046872: metal ion binding	00750: Vitamin B6 metabolism	−0.162	−0.4876	−1.0502	−1.324	7.32	8.52	8.36	8.03	7.47	7.2	2
214205_x_at	GLRX3	glutaredoxin 3	AK022131	10539	Hs.42644	GO:0045454: cell redox homeostasis, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0009055: electron carrier activity, GO:0015035: protein disulfide oxidoreductase activity		−0.149	−0.4318	−0.9005	−1.1046	8.44	9.53	9.38	9.1	8.63	8.42	2
207463_x_at	PRSS3	protease, serine, 3 (mesotrypsin)	NM_002771	5646	Hs.654513	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007586: digestion, GO:0031638: zymogen activation, GO:0043542: endothelial cell migration, GO:0005615: extracellular space, GO:0004252: serine-type endopeptidase activity, GO:0004295: trypsin activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0008233: peptidase activity	04080: Neuroactive ligand-receptor interaction	−0.2788	−0.6006	−1.4637	−1.595	9.45	11.14	10.86	10.54	9.68	9.55	2
205829_at	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	NM_000413	3292	Hs.654385, Hs.655222	GO:0006703: estrogen biosynthetic process, GO:0008152: metabolic process, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0005737: cytoplasm, GO:0004303: estradiol 17-beta-dehydrogenase activity, GO:0004303: estradiol 17-beta-dehydrogenase activity, GO:0016491: oxidoreductase activity		−0.2646	−0.764	−2.1381	−2.3301	3.82	6.15	5.88	5.38	4.01	3.82	2

(*Continued*)

TABLE E2. (*Continued*)

208813_at	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	BC000498	2805	Hs.500756	GO:0006520: amino acid metabolic process, GO:0006533: aspartate catabolic process, GO:0009058: biosynthetic process, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0004069: aspartate transaminase activity, GO:0030170: pyridoxal phosphate binding	00251: Glutamate metabolism, 00252: Alanine and aspartate metabolism, 00272: Cysteine metabolism, 00330: Arginine and proline metabolism, 00350: Tyrosine metabolism, 00360: Phenylalanine metabolism, 00400: Phenylalanine, tyrosine and tryptophan biosynthesis, 00401: Novobiocin biosynthesis, 00710: Carbon fixation, 00950: Alkaloid biosynthesis I	−0.1304	−0.3734	−1.018	−1.161	8.95	9.87	9.74	9.5	8.85	8.71	2
210048_at	NAPG	N-ethylmaleimide-sensitive factor attachment protein, gamma	BC001889	8774	Hs.464622	GO:0006461: protein complex assembly, GO:0006886: intracellular protein transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0006891: intra-Golgi vesicle-mediated transport, GO:0006944: membrane fusion, GO:0050821: protein stabilization, GO:0005624: membrane fraction, GO:0005739: mitochondrion, GO:0005783: endoplasmic reticulum, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0005515: protein binding		−0.3133	−0.5213	−0.7972	−1.1415	4.22	5.42	5.11	4.9	4.63	4.28	2
212656_at	TSFM	Ts translation elongation factor, mitochondrial	AF110399	10102	Hs.632704	GO:0006414: translational elongation, GO:0005622: intracellular, GO:0005739: mitochondrion, GO:0003711: transcription elongation regulator activity, GO:0003746: translation elongation factor activity		−0.1871	−0.4881	−0.7947	−1.0505	7.33	8.2	8.01	7.71	7.4	7.15	2
203554_x_at	PTTG1	pituitary tumor-transforming 1	NM_004219	9232	Hs.350966	GO:0006259: DNA metabolic process, GO:0006281: DNA repair, GO:0006366: transcription from RNA polymerase II promoter, GO:0007049: cell cycle, GO:0007059: chromosome segregation, GO:0007067: mitosis, GO:0007283: spermatogenesis, GO:0045143: homologous chromosome segregation, GO:0051276: chromosome organization and biogenesis, GO:0051301: cell division, GO:0005575: cellular_component, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005737: cytoplasm, GO:0003674: molecular_function, GO:0003700: transcription factor activity, GO:0004869: cysteine protease inhibitor activity, GO:0005515: protein binding	04110: Cell cycle	−0.2853	−0.7702	−1.1586	−1.5013	8.96	10.31	10.02	9.54	9.15	8.81	2
218960_at	TMPRSS4	transmembrane protease, serine 4	NM_016425	56649	Hs.161985	GO:0006508: proteolysis, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004252: serine-type endopeptidase activity, GO:0005044: scavenger receptor activity, GO:0008233: peptidase activity		−0.5282	−1.2051	−1.9524	−2.6927	4.5	7.52	6.99	6.32	5.57	4.83	2

(*Continued*)

TABLE E2. (*Continued*)

205595_at	DSG3	desmoglein 3 (pemphigus vulgaris antigen)	NM_001944	1830	Hs.1925	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005911: intercellular junction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding	01430: Cell Communication	−0.4336	−0.8898	−1.3644	−1.9295	10.5	12.1	11.67	11.21	10.74	10.17	2
210119_at	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	U73191	3772	Hs.411299	GO:0006811: ion transport, GO:0006813: potassium ion transport, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005242: inward rectifier potassium channel activity, GO:0005244: voltage-gated ion channel activity, GO:0005267: potassium channel activity, GO:0030955: potassium ion binding		−0.6153	−1.301	−1.9758	−2.7713	4.81	7.97	7.35	6.67	5.99	5.2	2
209408_at	KIF2C	kinesin family member 2C	U63743	11004	Hs.69360	GO:0007018: microtubule-based movement, GO:0007067: mitosis, GO:0008283: cell proliferation, GO:0030951: establishment and/or maintenance of microtubule cytoskeleton polarity, GO:0000775: chromosome, pericentric region, GO:0005737: cytoplasm, GO:0005871: kinesin complex, GO:0005874: microtubule, GO:0000166: nucleotide binding, GO:0003777: microtubule motor activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0019237: centromeric DNA binding		−0.4741	−0.6326	−0.834	−1.0035	3.6	4.58	4.1	3.94	3.74	3.57	2
216244_at	IL1RN	interleukin 1 receptor antagonist	BE563442	3557	Hs.81134	GO:0006629: lipid metabolic process, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0030073: insulin secretion, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005152: interleukin-1 receptor antagonist activity, GO:0005515: protein binding		−0.7689	−1.1587	−1.5926	−1.9389	6.48	8.53	7.77	7.38	6.94	6.6	2

(*Continued*)

TABLE E2. (*Continued*)

202067_s_at	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	AI861942	3949	Hs.213289	GO:0006493: protein amino acid O-linked glycosylation, GO:0006629: lipid metabolic process, GO:0006869: lipid transport, GO:0006897: endocytosis, GO:0008202: steroid metabolic process, GO:0008203: cholesterol metabolic process, GO:0030299: cholesterol absorption, GO:0030301: cholesterol transport, GO:0042157: lipoprotein metabolic process, GO:0042632: cholesterol homeostasis, GO:0005768: endosome, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004872: receptor activity, GO:0004888: transmembrane receptor activity, GO:0005041: low-density lipoprotein receptor activity, GO:0005319: lipid transporter activity, GO:0005509: calcium ion binding, GO:0008034: lipoprotein binding		−0.9173	−1.328	−1.8198	−1.9834	3.84	5.72	4.8	4.39	3.9	3.74	2
203821_at	HBEGF	heparin-binding EGF-like growth factor	NM_001945	1839	Hs.799	GO:0007165: signal transduction, GO:0007173: epidermal growth factor receptor signaling pathway, GO:0007517: muscle development, GO:0008016: regulation of heart contraction, GO:0035313: wound healing, spreading of epidermal cells, GO:0048661: positive regulation of smooth muscle cell proliferation, GO:0051549: positive regulation of keratinocyte migration, GO:0005615: extracellular space, GO:0005887: integral to plasma membrane, GO:0009986: cell surface, GO:0016020: membrane, GO:0004872: receptor activity, GO:0005154: epidermal growth factor receptor binding, GO:0008083: growth factor activity, GO:0008201: heparin binding	04012: ErbB signaling pathway, 04912: GnRH signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection	−1.0553	−1.2862	−1.8458	−2.1303	6.55	8.55	7.5	7.27	6.71	6.42	2
218585_s_at	DTL	denticleless homolog (Drosophila)	AK001261	51514	Hs.656473	GO:0006260: DNA replication, GO:0006512: ubiquitin cycle, GO:0006974: response to DNA damage stimulus, GO:0005737: cytoplasm, GO:0005515: protein binding		−0.4463	−0.7346	−1.0529	−1.1341	5.94	7.05	6.6	6.31	6	5.91	2
203023_at	HSPC111	hypothetical protein HSPC111	NM_016391	51491	Hs.652195			−0.487	−0.5931	−0.8689	−1.023	7.39	8.13	7.64	7.53	7.26	7.1	2

(*Continued*)

TABLE E2. (*Continued*)

204908_s_at	BCL3	B-cell CLL/lymphoma 3	NM_005178	602	Hs.31210	GO:0000060: protein import into nucleus, translocation, GO:0002268: follicular dendritic cell differentiation, GO:0002315: marginal zone B cell differentiation, GO:0002455: humoral immune response mediated by circulating immunoglobulin, GO:0002467: germinal center formation, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006974: response to DNA damage stimulus, GO:0007249: I-kappaB kinase/NF-kappaB cascade, GO:0009615: response to virus, GO:0010225: response to UV-C, GO:0016481: negative regulation of transcription, GO:0030198: extracellular matrix organization and biogenesis, GO:0032729: positive regulation of interferon-gamma production, GO:0042088: T-helper 1 type immune response, GO:0042345: regulation of NF-kappaB import into nucleus, GO:0042536: negative regulation of tumor necrosis factor biosynthetic process, GO:0042742: defense response to bacterium, GO:0042771: DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis, GO:0042832: defense response to protozoan, GO:0043066: negative regulation of apoptosis, GO:0045064: T-helper 2 cell differentiation, GO:0045082: positive regulation of interleukin-10 biosynthetic process, GO:0045415: negative regulation of interleukin-8 biosynthetic process, GO:0045727: positive regulation of protein biosynthetic process, GO:0045941: positive regulation of transcription, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0048536: spleen development, GO:0051101: regulation of DNA binding, GO:0051457: maintenance of protein localization in nucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0032996: Bcl3-Bcl10 complex, GO:0033257: Bcl3/NF-kappaB2 complex, GO:0008134: transcription factor binding, GO:0030528: transcription regulator activity, GO:0030674: protein binding, bridging	−0.4685	−0.5843	−0.8937	−1.0216	6.32	7.49	7.02	6.9	6.59	6.46	2
222039_at	LOC146909	hypothetical protein LOC146909	AA292789	146909	Hs.135094		−0.5548	−0.812	−1.2332	−1.4098	6.33	7.5	6.94	6.68	6.26	6.09	2

(*Continued*)

TABLE E2. (*Continued*)

201531_at	ZFP36	zinc finger protein 36, C3H type, homolog (mouse)	NM_003407	7538	Hs.534052, Hs.690222	GO:0006402: mRNA catabolic process, GO:0007243: protein kinase cascade, GO:0043488: regulation of mRNA stability, GO:0045638: negative regulation of myeloid cell differentiation, GO:0050728: negative regulation of inflammatory response, GO:0050779: RNA destabilization, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0003677: DNA binding, GO:0003727: single-stranded RNA binding, GO:0003729: mRNA binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.4693	−0.6305	−0.9633	−1.1821	9.54	10.48	10.01	9.85	9.52	9.3	2
202095_s_at	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	NM_001168	332	Hs.514527	GO:0000086: G2/M transition of mitotic cell cycle, GO:0000910: cytokinesis, GO:0006915: apoptosis, GO:0006916: anti-apoptosis, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0031503: protein complex localization, GO:0031503: protein complex localization, GO:0031536: positive regulation of exit from mitosis, GO:0031577: spindle checkpoint, GO:0043154: negative regulation of caspase activity, GO:0045931: positive regulation of progression through mitotic cell cycle, GO:0051303: establishment of chromosome localization, GO:0000775: chromosome, pericentric region, GO:0005622: intracellular, GO:0005694: chromosome, GO:0005737: cytoplasm, GO:0005814: centriole, GO:0005829: cytosol, GO:0005876: spindle microtubule, GO:0005881: cytoplasmic microtubule, GO:0030496: midbody, GO:0031021: interphase microtubule organizing center, GO:0043234: protein complex, GO:0043234: protein complex, GO:0004869: cysteine protease inhibitor activity, GO:0008017: microtubule binding, GO:0008270: zinc ion binding, GO:0042803: protein homodimerization activity, GO:0043027: caspase inhibitor activity, GO:0046872: metal ion binding, GO:0046982: protein heterodimerization activity, GO:0048037: cofactor binding	05210: Colorectal cancer	−0.4495	−0.591	−0.8869	−1.1097	4.47	5.58	5.13	4.98	4.69	4.47	2
203233_at	IL4R	interleukin 4 receptor	NM_000418	3566	Hs.513457	GO:0006955: immune response, GO:0007165: signal transduction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004872: receptor activity, GO:0004896: hematopoietin/interferon-class (D200-domain) cytokine receptor activity, GO:0004913: interleukin-4 receptor activity, GO:0005057: receptor signaling protein activity, GO:0005515: protein binding	04060: Cytokine-cytokine receptor interaction, 04630: Jak-STAT signaling pathway, 04640: Hematopoietic cell lineage	−0.3138	−0.6943	−1.002	−1.085	8.5	9.91	9.6	9.22	8.91	8.83	2

(*Continued*)

TABLE E2. (*Continued*)

211806_s_at	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	D87291	3772	Hs.411299	GO:0006811: ion transport, GO:0006813: potassium ion transport, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005242: inward rectifier potassium channel activity, GO:0005244: voltage-gated ion channel activity, GO:0005267: potassium channel activity, GO:0030955: potassium ion binding		−0.3131	−0.7077	−1.0496	−1.1399	3.54	4.78	4.46	4.07	3.73	3.64	2
221539_at	EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	AB044548	1978	Hs.411641	GO:0008286: insulin receptor signaling pathway, GO:0045947: negative regulation of translational initiation, GO:0005515: protein binding, GO:0008190: eukaryotic initiation factor 4E binding	04012: ErbB signaling pathway, 04150: mTOR signaling pathway, 04910: Insulin signaling pathway, 05221: Acute myeloid leukemia	−0.3255	−0.5416	−0.9622	−1.0028	7.22	8.44	8.11	7.89	7.47	7.43	2
212236_x_at	KRT17	keratin 17	Z19574	3872	Hs.2785	GO:0008150: biological_process, GO:0008544: epidermis development, GO:0005575: cellular_component, GO:0005882: intermediate filament, GO:0005882: intermediate filament, GO:0005198: structural molecule activity, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding	01430: Cell Communication	−0.4631	−0.9466	−1.5944	−1.5624	12.02	13.89	13.43	12.95	12.3	12.33	2
220780_at	PLA2G3	phospholipase A2, group III	NM_015715	50487	Hs.149623	GO:0006644: phospholipid metabolic process, GO:0016042: lipid catabolic process, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005509: calcium ion binding, GO:0016787: hydrolase activity, GO:0047498: calcium-dependent phospholipase A2 activity	00564: Glycerophospholipid metabolism, 00565: Ether lipid metabolism, 00590: Arachidonic acid metabolism, 00591: Linoleic acid metabolism, 04010: MAPK signaling pathway, 04370: VEGF signaling pathway, 04664: Fc epsilon RI signaling pathway, 04730: Long-term depression, 04912: GnRH signaling pathway	−0.692	−0.9108	−1.636	−1.5741	8.46	9.92	9.23	9.01	8.29	8.35	2
205239_at	AREG	amphiregulin (schwannoma-derived growth factor)	NM_001657	374	Hs.270833	GO:0007267: cell-cell signaling, GO:0008283: cell proliferation, GO:0005615: extracellular space, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005125: cytokine activity, GO:0008083: growth factor activity	04012: ErbB signaling pathway	−0.6756	−1.3233	−2.6505	−3.1254	4.72	7.4	6.72	6.07	4.75	4.27	2

(*Continued*)

TABLE E2. (*Continued*)

200815_s_at	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	L13386	5048	Hs.77318	GO:0000132: establishment of mitotic spindle orientation, GO:0000226: microtubule cytoskeleton organization and biogenesis, GO:0001675: acrosome formation, GO:0001764: neuron migration, GO:0006810: transport, GO:0006928: cell motility, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007165: signal transduction, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0007405: neuroblast proliferation, GO:0008090: retrograde axon cargo transport, GO:0016042: lipid catabolic process, GO:0030154: cell differentiation, GO:0047496: vesicle transport along microtubule, GO:0051301: cell division, GO:0000235: astral microtubule, GO:0000776: kinetochore, GO:0005635: nuclear envelope, GO:0005737: cytoplasm, GO:0005813: centrosome, GO:0005856: cytoskeleton, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0005938: cell cortex, GO:0016020: membrane, GO:0008017: microtubule binding, GO:0045502: dynein binding	00565: Ether lipid metabolism	−0.2567	−0.5539	−0.954	−1.1194	8.31	9.41	9.15	8.86	8.46	8.29	2
212290_at	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	AA527433	6541	Hs.14846	GO:0006520: amino acid metabolic process, GO:0006810: transport, GO:0006865: amino acid transport, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0015171: amino acid transmembrane transporter activity, GO:0015174: basic amino acid transmembrane transporter activity		−0.3037	−0.6367	−1.0665	−1.3118	6.38	8.18	7.87	7.54	7.11	6.87	2
214091_s_at	GPX3	glutathione peroxidase 3 (plasma)	AW149846	2878	Hs.386793	GO:0006979: response to oxidative stress, GO:0006982: response to lipid hydroperoxide, GO:0042744: hydrogen peroxide catabolic process, GO:0051289: protein homotetramerization, GO:0005615: extracellular space, GO:0004602: glutathione peroxidase activity, GO:0008134: transcription factor binding, GO:0008430: selenium binding, GO:0016491: oxidoreductase activity	00480: Glutathione metabolism, 00590: Arachidonic acid metabolism	−0.1002	−0.6258	−1.0326	−1.1783	11.5	12.12	12.01	11.49	11.08	10.94	2
219911_s_at	SLCO4A1	solute carrier organic anion transporter family, member 4A1	NM_016354	28231	Hs.235782	GO:0006811: ion transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005215: transporter activity		−0.09	−0.6594	−1.1187	−1.3292	7.77	8.68	8.59	8.02	7.56	7.35	2

(*Continued*)

TABLE E2. (*Continued*)

209976_s_at	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	AF182276	1571	Hs.12907	GO:0006118: electron transport, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0004497: monooxygenase activity, GO:0005506: iron ion binding, GO:0019825: oxygen binding, GO:0020037: heme binding, GO:0046872: metal ion binding, GO:0050381: unspecific monooxygenase activity	00590: Arachidonic acid metabolism, 00591: Linoleic acid metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	−0.0257	−0.7657	−1.166	−1.4045	4.47	5.64	5.61	4.87	4.47	4.23	2
211429_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	AF119873	5265	Hs.525557	GO:0006953: acute-phase response, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding	04610: Complement and coagulation cascades	−0.1606	−1.4056	−2.1136	−2.5915	4.93	8.07	7.91	6.66	5.96	5.48	2
36564_at	RNF19B	ring finger protein 19B	W27419	127544	Hs.591504	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.1889	−0.6039	−0.918	−1.0301	6.33	7.39	7.2	6.79	6.47	6.36	2
203234_at	UPP1	uridine phosphorylase 1	NM_003364	7378	Hs.488240	GO:0009116: nucleoside metabolic process, GO:0009166: nucleotide catabolic process, GO:0005737: cytoplasm, GO:0004850: uridine phosphorylase activity, GO:0016757: transferase activity, transferring glycosyl groups	00240: Pyrimidine metabolism	−0.5788	−1.7325	−2.5328	−2.9256	5.99	9.26	8.68	7.53	6.72	6.33	2
205015_s_at	TGFA	transforming growth factor, alpha	NM_003236	7039	Hs.170009	GO:0000074: regulation of progression through cell cycle, GO:0000187: activation of MAPK activity, GO:0001525: angiogenesis, GO:0008283: cell proliferation, GO:0045741: positive regulation of epidermal growth factor receptor activity, GO:0045840: positive regulation of mitosis, GO:0050679: positive regulation of epithelial cell proliferation, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0001948: glycoprotein binding, GO:0004708: MAP kinase kinase activity, GO:0004871: signal transducer activity, GO:0005155: epidermal growth factor receptor activating ligand activity, GO:0008083: growth factor activity	04012: ErbB signaling pathway, 05211: Renal cell carcinoma, 05212: Pancreatic cancer, 05214: Glioma, 05215: Prostate cancer, 05223: Non-small cell lung cancer	−0.2837	−0.8139	−1.2549	−1.4894	2.62	4.25	3.97	3.44	3	2.76	2
219270_at	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)	NM_024111	79094	Hs.155569	GO:0005515: protein binding		−0.6112	−1.8803	−2.8773	−3.1617	4.8	8.04	7.43	6.16	5.16	4.88	2

(*Continued*)

TABLE E2. (*Continued*)

221245_s_at	FZD5	frizzled homolog 5 (Drosophila)	NM_030804	7855	Hs.17631	GO:0007164: establishment of tissue polarity, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007275: multicellular organismal development, GO:0016055: Wnt receptor signaling pathway, GO:0048469: cell maturation, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004872: receptor activity, GO:0004926: non-G-protein coupled 7TM receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0005515: protein binding	04310: Wnt signaling pathway, 04916: Melanogenesis, 05210: Colorectal cancer, 05217: Basal cell carcinoma	−0.3159	−0.9967	−1.3402	−1.6195	7.05	8.65	8.33	7.65	7.31	7.03	2
202954_at	UBE2C	ubiquitin-conjugating enzyme E2C	NM_007019	11065	Hs.93002	GO:0006464: protein modification process, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0007049: cell cycle, GO:0007051: spindle organization and biogenesis, GO:0007067: mitosis, GO:0008054: cyclin catabolic process, GO:0016567: protein ubiquitination, GO:0031536: positive regulation of exit from mitosis, GO:0048015: phosphoinositide-mediated signaling, GO:0051301: cell division, GO:0004842: ubiquitin-protein ligase activity, GO:0016874: ligase activity, GO:0019787: small conjugating protein ligase activity	04120: Ubiquitin mediated proteolysis	−0.2235	−0.8533	−1.1099	−1.5415	8.11	9.2	8.98	8.35	8.09	7.66	2
204162_at	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	NM_006101	10403	Hs.414407	GO:0000070: mitotic sister chromatid segregation, GO:0007049: cell cycle, GO:0007051: spindle organization and biogenesis, GO:0048015: phosphoinositide-mediated signaling, GO:0051301: cell division, GO:0000775: chromosome, pericentric region, GO:0005634: nucleus, GO:0005515: protein binding		−0.4389	−0.9588	−1.1739	−1.6297	4.45	6.05	5.62	5.1	4.88	4.42	2
201860_s_at	PLAT	plasminogen activator, tissue	NM_000930	5327	Hs.491582	GO:0006464: protein modification process, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007596: blood coagulation, GO:0005576: extracellular region, GO:0008233: peptidase activity, GO:0008243: plasminogen activator activity	04610: Complement and coagulation cascades	−0.362	−1.7675	−2.4973	−3.1125	6.46	10	9.64	8.23	7.5	6.89	2

(*Continued*)

TABLE E2. (*Continued*)

203180_at	ALDH1A3	aldehyde dehydrogenase 1 family, member A3	NM_000693	220	Hs.459538	GO:0006066: alcohol metabolic process, GO:0006629: lipid metabolic process, GO:0008152: metabolic process, GO:0005737: cytoplasm, GO:0004028: 3-chloroallyl aldehyde dehydrogenase activity, GO:0004030: aldehyde dehydrogenase [NAD(P)+] activity, GO:0016491: oxidoreductase activity	00010: Glycolysis / Gluconeogenesis, 00053: Ascorbate and aldarate metabolism, 00071: Fatty acid metabolism, 00120: Bile acid biosynthesis, 00220: Urea cycle and metabolism of amino groups, 00280: Valine, leucine and isoleucine degradation, 00310: Lysine degradation, 00340: Histidine metabolism, 00350: Tyrosine metabolism, 00360: Phenylalanine metabolism, 00380: Tryptophan metabolism, 00410: beta-Alanine metabolism, 00561: Glycerolipid metabolism, 00620: Pyruvate metabolism, 00640: Propanoate metabolism, 00650: Butanoate metabolism, 00903: Limonene and pinene degradation, 00980: Metabolism of xenobiotics by cytochrome P450	−0.4443	−1.6899	−2.3069	−2.8084	4.37	7.55	7.11	5.86	5.24	4.74	2
209236_at	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	AL389886	9962	Hs.516866	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006810: transport, GO:0006811: ion transport, GO:0006814: sodium ion transport, GO:0015851: nucleobase transport, GO:0015993: molecular hydrogen transport, GO:0019852: L-ascorbic acid metabolic process, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005215: transporter activity, GO:0008523: sodium-dependent multivitamin transmembrane transporter activity, GO:0015205: nucleobase transmembrane transporter activity, GO:0015293: symporter activity, GO:0031402: sodium ion binding		−0.219	−1.0013	−0.9589	−1.5893	7.58	9.34	9.12	8.33	8.38	7.75	2
216952_s_at	LMNB2	lamin B2	M94363	84823	Hs.538286	GO:0008150: biological_process, GO:0005638: lamin filament, GO:0016020: membrane, GO:0005198: structural molecule activity	01430: Cell Communication	−0.2227	−0.7985	−0.8792	−1.21	4.43	5.42	5.2	4.62	4.54	4.21	2
218035_s_at	FLJ20273	RNA-binding protein	NM_019027	54502	Hs.518727	GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding		−0.1347	−0.6469	−0.76	−1.098	9.2	9.85	9.72	9.2	9.09	8.75	2
204962_s_at	CENPA	centromere protein A	NM_001809	1058	Hs.1594	GO:0006334: nucleosome assembly, GO:0007001: chromosome organization and biogenesis (sensu Eukaryota), GO:0000775: chromosome, pericentric region, GO:0000786: nucleosome, GO:0005634: nucleus, GO:0005694: chromosome, GO:0003677: DNA binding, GO:0003682: chromatin binding		−0.3373	−1.0234	−1.1164	−1.5766	5.03	6.09	5.75	5.06	4.97	4.51	2
206364_at	KIF14	kinesin family member 14	NM_014875	9928	Hs.3104	GO:0007018: microtubule-based movement, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0000166: nucleotide binding, GO:0003777: microtubule motor activity, GO:0005524: ATP binding		−0.3362	−0.8874	−1.0176	−1.4028	3.47	4.68	4.34	3.79	3.66	3.28	2

(*Continued*)

TABLE E2. (*Continued*)

205157_s_at	KRT17	keratin 17	NM_000422	3872	Hs.2785	GO:0008150: biological_process, GO:0008544: epidermis development, GO:0005575: cellular_component, GO:0005882: intermediate filament, GO:0005882: intermediate filament, GO:0005198: structural molecule activity, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding	01430: Cell Communication	−0.5552	−1.1772	−2.0446	−2.0813	11.87	14.27	13.71	13.1	12.23	12.19	2
212022_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	AU132185	4288	Hs.80976	GO:0000074: regulation of progression through cell cycle, GO:0007049: cell cycle, GO:0008283: cell proliferation, GO:0005730: nucleolus, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding		−0.5637	−1.033	−1.5048	−1.7757	5.31	6.99	6.43	5.96	5.49	5.22	2
204767_s_at	FEN1	flap structure-specific endonuclease 1	BC000323	2237	Hs.409065	GO:0006260: DNA replication, GO:0006302: double-strand break repair, GO:0009650: UV protection, GO:0048015: phosphoinositide-mediated signaling, GO:0005634: nucleus, GO:0000287: magnesium ion binding, GO:0003684: damaged DNA binding, GO:0003690: double-stranded DNA binding, GO:0004519: endonuclease activity, GO:0004523: ribonuclease H activity, GO:0005515: protein binding, GO:0008309: double-stranded DNA specific exodeoxyribonuclease activity, GO:0008409: 5'-3' exonuclease activity, GO:0016787: hydrolase activity, GO:0017108: 5'-flap endonuclease activity, GO:0030145: manganese ion binding		−0.3323	−0.6377	−1.0016	−1.1609	6.51	7.67	7.33	7.03	6.67	6.51	2
210827_s_at	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	U73844	1999	Hs.67928	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0006954: inflammatory response, GO:0007275: multicellular organismal development, GO:0030855: epithelial cell differentiation, GO:0060056: mammary gland involution, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0003713: transcription coactivator activity, GO:0005515: protein binding, GO:0016564: transcription repressor activity, GO:0043565: sequence-specific DNA binding		−0.5277	−1.0017	−1.6156	−1.8499	4.37	6.32	5.79	5.32	4.7	4.47	2

(*Continued*)

TABLE E2. (*Continued*)

203764_at	DLG7	discs, large homolog 7 (Drosophila)	NM_014750	9787	Hs.77695	GO:0000087: M phase of mitotic cell cycle, GO:0000087: M phase of mitotic cell cycle, GO:0007049: cell cycle, GO:0007079: mitotic chromosome movement towards spindle pole, GO:0007267: cell-cell signaling, GO:0008283: cell proliferation, GO:0045842: positive regulation of mitotic metaphase/anaphase transition, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0031616: spindle pole centrosome, GO:0031616: spindle pole centrosome, GO:0004721: phosphoprotein phosphatase activity, GO:0004721: phosphoprotein phosphatase activity, GO:0005515: protein binding		−0.7075	−1.5294	−2.1728	−2.678	3.59	6.21	5.5	4.68	4.03	3.53	2
204493_at	BID	BH3 interacting domain death agonist	NM_001196	637	Hs.591054	GO:0001836: release of cytochrome c from mitochondria, GO:0008625: induction of apoptosis via death domain receptors, GO:0043065: positive regulation of apoptosis, GO:0051402: neuron apoptosis, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005829: cytosol, GO:0016020: membrane, GO:0005123: death receptor binding, GO:0005515: protein binding	04115: p53 signaling pathway, 04210: Apoptosis, 04650: Natural killer cell mediated cytotoxicity	−0.3626	−0.7695	−1.0278	−1.2163	2.86	4.22	3.86	3.45	3.2	3.01	2
222037_at	MCM4	minichromosome maintenance complex component 4	AI859865	4173	Hs.460184	GO:0006260: DNA replication, GO:0006268: DNA unwinding during replication, GO:0006270: DNA replication initiation, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003678: DNA helicase activity, GO:0003697: single-stranded DNA binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008094: DNA-dependent ATPase activity, GO:0017111: nucleoside-triphosphatase activity	04110: Cell cycle	−0.3225	−0.6249	−0.8929	−1.0695	4.72	5.56	5.23	4.93	4.66	4.49	2
200935_at	CALR	calreticulin	NM_004343	811	Hs.515162	GO:0006355: regulation of transcription, DNA-dependent, GO:0006457: protein folding, GO:0006611: protein export from nucleus, GO:0006874: cellular calcium ion homeostasis, GO:0042981: regulation of apoptosis, GO:0005578: proteinaceous extracellular matrix, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0005788: endoplasmic reticulum lumen, GO:0005829: cytosol, GO:0003677: DNA binding, GO:0005509: calcium ion binding, GO:0005529: sugar binding, GO:0008270: zinc ion binding, GO:0051082: unfolded protein binding	04612: Antigen processing and presentation	−0.2919	−0.7033	−1.0617	−1.2067	5.88	6.82	6.53	6.12	5.76	5.61	2

(*Continued*)

TABLE E2. (*Continued*)

202870_s_at	CDC20	cell division cycle 20 homolog (S. cerevisiae)	NM_001255	991	Hs.524947	GO:0000074: regulation of progression through cell cycle, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0051301: cell division, GO:0005819: spindle, GO:0005515: protein binding	04110: Cell cycle, 04120: Ubiquitin mediated proteolysis	−0.767	−1.4982	−2.3056	−2.841	5.1	7.55	6.78	6.05	5.24	4.71	2
212657_s_at	IL1RN	interleukin 1 receptor antagonist	AW083357	3557	Hs.81134	GO:0006629: lipid metabolic process, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0030073: insulin secretion, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005152: interleukin-1 receptor antagonist activity, GO:0005515: protein binding		−0.4016	−0.7157	−1.1378	−1.3591	10.89	12.12	11.72	11.41	10.98	10.76	2
213572_s_at	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	AI554300	1992	Hs.381167	GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity		−0.4857	−0.8261	−1.3408	−1.7487	8.42	10.2	9.71	9.37	8.86	8.45	2
218498_s_at	ERO1L	ERO1-like (S. cerevisiae)	NM_014584	30001	Hs.592304	GO:0006118: electron transport, GO:0006457: protein folding, GO:0006464: protein modification process, GO:0006810: transport, GO:0009266: response to temperature stimulus, GO:0030968: unfolded protein response, GO:0051085: chaperone cofactor-dependent protein folding, GO:0005624: membrane fraction, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016491: oxidoreductase activity	05110: Cholera - Infection	−0.3781	−0.7926	−1.1017	−1.7033	6.98	8.44	8.06	7.64	7.34	6.73	2
202779_s_at	UBE2S	ubiquitin-conjugating enzyme E2S	NM_014501	27338	Hs.396393, Hs.592114	GO:0006464: protein modification process, GO:0006464: protein modification process, GO:0006512: ubiquitin cycle, GO:0004842: ubiquitin-protein ligase activity, GO:0016874: ligase activity, GO:0019787: small conjugating protein ligase activity		−0.342	−0.7392	−0.985	−1.5133	7.36	8.64	8.3	7.9	7.66	7.13	2
203256_at	CDH3	cadherin 3, type 1, P-cadherin (placental)	NM_001793	1001	Hs.461074	GO:0007156: homophilic cell adhesion, GO:0007601: visual perception, GO:0050896: response to stimulus, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding	04514: Cell adhesion molecules (CAMs)	−0.4171	−0.9795	−1.3059	−1.9105	8.84	11.04	10.62	10.06	9.73	9.13	2
204641_at	NEK2	NIMA (never in mitosis gene a)-related kinase 2	NM_002497	4751	Hs.153704	GO:0006468: protein amino acid phosphorylation, GO:0007049: cell cycle, GO:0007088: regulation of mitosis, GO:0007126: meiosis, GO:0051301: cell division, GO:0005737: cytoplasm, GO:0005813: centrosome, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity		−0.4548	−1.336	−1.7474	−2.3714	4.17	6.08	5.62	4.74	4.33	3.71	2

(*Continued*)

TABLE E2. (*Continued*)

205014_at	FGFBP1	fibroblast growth factor binding protein 1	NM_005130	9982	Hs.1690	GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0008285: negative regulation of cell proliferation, GO:0005615: extracellular space, GO:0016020: membrane, GO:0008201: heparin binding, GO:0019838: growth factor binding		−0.7461	−1.1725	−1.8611	−2.0404	9.78	11.28	10.54	10.11	9.42	9.24	2
209803_s_at	PHLDA2	pleckstrin homology-like domain, family A, member 2	AF001294	7262	Hs.154036	GO:0006349: imprinting, GO:0006915: apoptosis, GO:0009887: organ morphogenesis, GO:0005737: cytoplasm		−0.5871	−0.7458	−1.3866	−1.5123	9.94	11.07	10.48	10.32	9.68	9.55	2
216532_x_at			AL138831	643450				−0.2622	−0.5433	−0.7727	−1.0676	6.73	7.71	7.44	7.16	6.93	6.64	2
205402_x_at	PRSS2	protease, serine, 2 (trypsin 2)	NM_002770	5645	Hs.622865	GO:0006508: proteolysis, GO:0007586: digestion, GO:0030307: positive regulation of cell growth, GO:0030574: collagen catabolic process, GO:0030574: collagen catabolic process, GO:0045785: positive regulation of cell adhesion, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0031012: extracellular matrix, GO:0004295: trypsin activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0008233: peptidase activity	04080: Neuroactive ligand-receptor interaction	−0.2943	−0.5362	−1.0939	−1.0621	3.6	4.75	4.46	4.21	3.66	3.69	2
209100_at	IFRD2	interferon-related developmental regulator 2	BC001327	7866	Hs.315177, Hs.534543	GO:0008283: cell proliferation, GO:0030154: cell differentiation, GO:0005575: cellular_component, GO:0003674: molecular_function		−0.3494	−0.5204	−0.9135	−1.0047	7.6	8.65	8.3	8.13	7.73	7.64	2
214011_s_at	HSPC111	hypothetical protein HSPC111	BE314601	51491	Hs.652195			−0.4244	−0.551	−0.9221	−1.2092	9.16	9.92	9.49	9.37	9	8.71	2
201693_s_at	EGR1	early growth response 1	NM_001964	1958	Hs.326035	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0030217: T cell differentiation, GO:0045941: positive regulation of transcription, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.8165	−0.9094	−1.5779	−1.8728	5.14	6.77	5.96	5.86	5.2	4.9	2
217185_s_at	LOC442240	similar to zinc finger protein 259	Z95118	442240	Hs.626676			−0.5915	−0.5899	−0.9841	−1.273	5.17	6.36	5.77	5.77	5.37	5.08	2
203499_at	EPHA2	EPH receptor A2	NM_004431	1969	Hs.171596	GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007275: multicellular organismal development, GO:0030182: neuron differentiation, GO:0048013: ephrin receptor signaling pathway, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0004713: protein-tyrosine kinase activity, GO:0004872: receptor activity, GO:0005003: ephrin receptor activity, GO:0005524: ATP binding, GO:0016740: transferase activity	04360: Axon guidance	−0.5587	−1.0183	−1.4034	−1.8733	6.69	8.57	8.01	7.55	7.16	6.69	2

(*Continued*)

TABLE E2. (*Continued*)

204351_at	S100P	S100 calcium binding protein P	NM_005980	6286	Hs.2962	GO:0043542: endothelial cell migration, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000287: magnesium ion binding, GO:0005509: calcium ion binding, GO:0048306: calcium-dependent protein binding	−0.2433	−1.1348	−2.123	−2.4214	8.42	10.27	10.03	9.14	8.15	7.85	2
39249_at	AQP3	aquaporin 3 (Gill blood group)	AB001325	360	Hs.234642	GO:0006810: transport, GO:0007588: excretion, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005215: transporter activity	−0.4954	−0.7136	−0.9011	−1.29	11.26	12.01	11.52	11.3	11.11	10.72	2
213984_at	PDS5A	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	AW991219	23244	Hs.331431	GO:0005515: protein binding	−0.5553	−0.6005	−0.8162	−1.1375	4.04	4.88	4.33	4.28	4.07	3.75	2
215760 _s_at	SBNO2	strawberry notch homolog 2 (Drosophila)	AC005390	22904	Hs.408708		−0.5651	−0.669	−0.8828	−1.2325	4.38	5.44	4.88	4.77	4.56	4.21	2
212268_at	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	NM_030666	1992	Hs.381167	GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity	−0.6556	−1.2302	−1.934	−2.6526	7.79	10.56	9.9	9.33	8.62	7.91	2
213007_at	FANCI	Fanconi anemia, complementation group I	W74442	55215	Hs.513126	GO:0006281: DNA repair, GO:0007049: cell cycle, GO:0005694: chromosome, GO:0005515: protein binding	−0.4323	−0.8936	−1.1044	−1.5993	6.28	7.63	7.2	6.74	6.53	6.03	2
216905 _s_at	ST14	suppression of tumorigenicity 14 (colon carcinoma)	U20428	6768	Hs.504315	GO:0006508: proteolysis, GO:0005576: extracellular region, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0019897: extrinsic to plasma membrane, GO:0004252: serine-type endopeptidase activity	−0.3787	−0.7146	−0.9546	−1.2733	6.23	7.47	7.09	6.76	6.52	6.2	2
218796_at	C20orf42	chromosome 20 open reading frame 42	NM_017671	55612	Hs.472054		−0.3456	−0.8963	−1.1798	−1.496	9.79	11.35	11	10.45	10.17	9.85	2
212021 _s_at	MKI67	antigen identified by monoclonal antibody Ki-67	AU132185	4288	Hs.80976	GO:0000074: regulation of progression through cell cycle, GO:0007049: cell cycle, GO:0008283: cell proliferation, GO:0005730: nucleolus, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding	−0.6044	−1.1087	−1.7095	−2.2334	4.31	6.34	5.73	5.23	4.63	4.1	2
212659 _s_at	IL1RN	interleukin 1 receptor antagonist	AW083357	3557	Hs.81134	GO:0006629: lipid metabolic process, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0030073: insulin secretion, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005152: interleukin-1 receptor antagonist activity, GO:0005515: protein binding	−0.5114	−0.9092	−1.2306	−1.7	7.83	9.45	8.94	8.54	8.22	7.75	2
60474_at	C20orf42	chromosome 20 open reading frame 42	AA469071	55612	Hs.472054		−0.4177	−0.9247	−1.2409	−1.637	9.44	11.04	10.62	10.11	9.8	9.4	2

(*Continued*)

TABLE E2. (*Continued*)

205394_at	CHEK1	CHK1 checkpoint homolog (S. pombe)	NM_001274	1111	Hs.24529	GO:0000077: DNA damage checkpoint, GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0000086: G2/M transition of mitotic cell cycle, GO:0006281: DNA repair, GO:0006468: protein amino acid phosphorylation, GO:0007049: cell cycle, GO:0007131: meiotic recombination, GO:0007276: gamete generation, GO:0008285: negative regulation of cell proliferation, GO:0000794: condensed nuclear chromosome, GO:0005634: nucleus, GO:0005657: replication fork, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04110: Cell cycle, 04115: p53 signaling pathway	−0.6557	−0.8683	−1.1627	−1.601	3.57	4.97	4.31	4.1	3.8	3.36	2
205534_at	PCDH7	protocadherin 7	NM_002589	5099	Hs.479439, Hs.570785	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding		−0.4773	−0.768	−1.1364	−1.506	6.96	8.12	7.64	7.35	6.98	6.61	2
220187_at	STEAP4	STEAP family member 4	NM_024636	79689	Hs.521008	GO:0006118: electron transport, GO:0006811: ion transport, GO:0006826: iron ion transport, GO:0045444: fat cell differentiation, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0005506: iron ion binding, GO:0005507: copper ion binding, GO:0016491: oxidoreductase activity, GO:0046872: metal ion binding, GO:0050660: FAD binding		−0.8687	−1.5684	−1.979	−3.0335	5.62	8.43	7.56	6.86	6.45	5.4	2
220865_s_at	PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1	NM_014317	23590	Hs.558468	GO:0006744: ubiquinone biosynthetic process, GO:0008299: isoprenoid biosynthetic process, GO:0008299: isoprenoid biosynthetic process, GO:0000010: trans-hexaprenyltranstransferase activity, GO:0016740: transferase activity, GO:0046982: protein heterodimerization activity		−0.7317	−1.3653	−1.913	−2.7624	4.33	6.76	6.03	5.39	4.85	4	2
219148_at	PBK	PDZ binding kinase	NM_018492	55872	Hs.104741	GO:0006468: protein amino acid phosphorylation, GO:0007067: mitosis, GO:0005575: cellular_component, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity		−0.521	−1.1287	−1.4466	−2.0297	5.85	7.32	6.79	6.19	5.87	5.29	2
219588_s_at	NCAPG2	non-SMC condensin II complex, subunit G2	NM_017760	54892	Hs.18616	GO:0001833: inner cell mass cell proliferation, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007076: mitotic chromosome condensation, GO:0051301: cell division, GO:0005515: protein binding		−0.4161	−0.6153	−0.7235	−1.0621	7.21	8.04	7.63	7.43	7.32	6.98	2

(*Continued*)

TABLE E2. (*Continued*)

206157_at	PTX3	pentraxin-related gene, rapidly induced by IL-1 beta	NM_002852	5806	Hs.591286	GO:0001878: response to yeast, GO:0006954: inflammatory response, GO:0008228: opsonization, GO:0045429: positive regulation of nitric oxide biosynthetic process, GO:0050766: positive regulation of phagocytosis, GO:0005576: extracellular region, GO:0001872: zymosan binding		−0.5352	−1.0099	−1.3176	−1.7889	3.46	5.18	4.64	4.17	3.86	3.39	2
209373_at	MALL	mal, T-cell differentiation protein-like	BC003179	7851	Hs.185055	GO:0042632: cholesterol homeostasis, GO:0000139: Golgi membrane, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0016023: cytoplasmic membrane-bound vesicle, GO:0030136: clathrin-coated vesicle, GO:0045121: lipid raft, GO:0005515: protein binding		−0.301	−0.5117	−0.8121	−1.0722	9.37	10.49	10.19	9.98	9.68	9.42	2
200733 _s_at	PTP4A1	protein tyrosine phosphatase type IVA, member 1	BF576710	7803	Hs.227777	GO:0006470: protein amino acid dephosphorylation, GO:0007049: cell cycle, GO:0007275: multicellular organismal development, GO:0005737: cytoplasm, GO:0005768: endosome, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0004725: protein tyrosine phosphatase activity, GO:0016787: hydrolase activity		−0.3172	−0.5459	−0.8753	−1.1842	10.14	11.14	10.82	10.59	10.26	9.95	2
202068 _s_at	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	NM_000527	3949	Hs.213289	GO:0006493: protein amino acid O-linked glycosylation, GO:0006629: lipid metabolic process, GO:0006869: lipid transport, GO:0006897: endocytosis, GO:0008202: steroid metabolic process, GO:0008203: cholesterol metabolic process, GO:0030299: cholesterol absorption, GO:0030301: cholesterol transport, GO:0042157: lipoprotein metabolic process, GO:0042632: cholesterol homeostasis, GO:0005768: endosome, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004872: receptor activity, GO:0004888: transmembrane receptor activity, GO:0005041: low-density lipoprotein receptor activity, GO:0005319: lipid transporter activity, GO:0005509: calcium ion binding, GO:0008034: lipoprotein binding		−0.6082	−0.982	−1.5472	−2.0666	9.2	10.74	10.13	9.76	9.19	8.67	2
205759 _s_at	SULT2B1	sulfotransferase family, cytosolic, 2B, member 1	NM_004605	6820	Hs.369331	GO:0006629: lipid metabolic process, GO:0008202: steroid metabolic process, GO:0005737: cytoplasm, GO:0004027: alcohol sulfotransferase activity, GO:0016740: transferase activity, GO:0050294: steroid sulfotransferase activity	00150: Androgen and estrogen metabolism, 00920: Sulfur metabolism	−0.244	−0.3898	−1.0088	−1.2146	10.11	11.32	11.08	10.93	10.31	10.11	2
212769_at	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	AI567426	7090	Hs.287362	GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0009887: organ morphogenesis, GO:0016055: Wnt receptor signaling pathway, GO:0005634: nucleus, GO:0005515: protein binding		−0.2105	−0.4442	−1.077	−1.2654	6.47	8.14	7.93	7.7	7.07	6.88	2

(*Continued*)

TABLE E2. (*Continued*)

209825_s_at	UCK2	uridine-cytidine kinase 2	BC002906	7371	Hs.458360	GO:0008150: biological_process, GO:0009058: biosynthetic process, GO:0005575: cellular_component, GO:0000166: nucleotide binding, GO:0003674: molecular_function, GO:0004849: uridine kinase activity, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity	00240: Pyrimidine metabolism	−0.4632	−0.6324	−1.2672	−1.7661	6.81	8.2	7.74	7.57	6.93	6.43	2
219347_at	NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	NM_018283	55270	Hs.144407	GO:0000287: magnesium ion binding, GO:0016787: hydrolase activity, GO:0030145: manganese ion binding		−0.2736	−0.4151	−0.8781	−1.1284	8.29	9.1	8.83	8.69	8.22	7.97	2
207622_s_at	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	NM_005692	10061	Hs.654958	GO:0006810: transport, GO:0005740: mitochondrial envelope, GO:0043190: ATP-binding cassette (ABC) transporter complex, GO:0000166: nucleotide binding, GO:0005215: transporter activity, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0016887: ATPase activity		−0.3212	−0.4305	−0.8468	−1.0997	8.23	9.09	8.77	8.66	8.24	7.99	2
209247_s_at	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	BC001661	10061	Hs.654958	GO:0006810: transport, GO:0005740: mitochondrial envelope, GO:0043190: ATP-binding cassette (ABC) transporter complex, GO:0000166: nucleotide binding, GO:0005215: transporter activity, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0016887: ATPase activity		−0.2413	−0.3393	−0.7551	−1.0305	7.83	8.72	8.48	8.38	7.96	7.69	2
202613_at	CTPS	CTP synthase	NM_001905	1503	Hs.473087	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006221: pyrimidine nucleotide biosynthetic process, GO:0006241: CTP biosynthetic process, GO:0006541: glutamine metabolic process, GO:0042493: response to drug, GO:0005575: cellular_component, GO:0003883: CTP synthase activity, GO:0003883: CTP synthase activity, GO:0005515: protein binding, GO:0016874: ligase activity	00240: Pyrimidine metabolism	−0.2761	−0.4472	−0.8271	−1.1102	7.1	8.12	7.84	7.67	7.29	7.01	2
204881_s_at	UGCG	UDP-glucose ceramide glucosyltransferase	NM_003358	7357	Hs.304249, Hs.593014	GO:0006679: glucosylceramide biosynthetic process, GO:0006688: glycosphingolipid biosynthetic process, GO:0008544: epidermis development, GO:0005615: extracellular space, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0008120: ceramide glucosyltransferase activity, GO:0016757: transferase activity, transferring glycosyl groups	00600: Sphingolipid metabolism, 01031: Glycan structures - biosynthesis 2	−0.3601	−0.4872	−1.0397	−1.4057	10.29	11.52	11.61	11.03	10.48	10.11	2

(*Continued*)

TABLE E2. (*Continued*)

201473_at	JUNB	jun B proto-oncogene	NM_002229	3726	Hs.25292	GO:0000074: regulation of progression through cell cycle, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0009987: cellular process, GO:0000785: chromatin, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0003713: transcription coactivator activity, GO:0003714: transcription corepressor activity, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity		−0.4082	−0.58	−1.1623	−1.525	8.85	10.15	9.74	9.57	8.98	8.62	2
202107_s_at	MCM2	minichromosome maintenance complex component 2	NM_004526	4171	Hs.477481	GO:0006260: DNA replication, GO:0006268: DNA unwinding during replication, GO:0006270: DNA replication initiation, GO:0006334: nucleosome assembly, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007049: cell cycle, GO:0000785: chromatin, GO:0005634: nucleus, GO:0005664: nuclear origin of replication recognition complex, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003688: DNA replication origin binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008094: DNA-dependent ATPase activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	04110: Cell cycle	−0.3326	−0.4665	−0.8986	−1.2089	8.7	9.51	9.18	9.05	8.62	8.31	2
211015_s_at	HSPA4	heat shock 70kDa protein 4	L12723	3308	Hs.90093	GO:0006986: response to unfolded protein, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0005524: ATP binding		−0.2465	−0.4499	−0.8454	−1.1436	9.71	10.76	10.52	10.31	9.92	9.62	2
214226_at	POL3S	polyserase 3	AA528252	339105	Hs.569575			−0.5594	−0.9825	−1.9147	−2.4864	3.6	5.72	5.16	4.74	3.8	3.23	2
201695_s_at	NP	nucleoside phosphorylase	NM_000270	4860	Hs.75514	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006304: DNA modification, GO:0004731: purine-nucleoside phosphorylase activity	00230: Purine metabolism, 00240: Pyrimidine metabolism, 00760: Nicotinate and nicotinamide metabolism	−0.4233	−0.9355	−1.6878	−2.2436	7.55	9.7	9.28	8.77	8.01	7.46	2
204826_at	CCNF	cyclin F	NM_001761	899	Hs.1973	GO:0000320: re-entry into mitotic cell cycle, GO:0001890: placenta development, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0051301: cell division, GO:0005634: nucleus, GO:0005515: protein binding		−0.2609	−0.5385	−0.9749	−1.2482	4.94	6.13	5.87	5.59	5.16	4.88	2
209344_at	TPM4	tropomyosin 4	BC002827	7171	Hs.631618	GO:0006928: cell motility, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005862: muscle thin filament tropomyosin, GO:0003779: actin binding, GO:0008307: structural constituent of muscle		−0.3615	−0.3869	−0.8418	−1.2153	8.8	9.62	9.26	9.24	8.78	8.41	2
219998_at	HSPC159	galectin-related protein	NM_014181	29094	Hs.372208	GO:0005622: intracellular, GO:0005529: sugar binding		−0.3441	−0.2829	−0.8338	−1.1658	8.93	9.45	9.11	9.17	8.62	8.29	2
218516_s_at	IMPAD1	inositol monophosphatase domain containing 1	NM_017813	54928	Hs.591872, Hs.595255	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000287: magnesium ion binding, GO:0008934: inositol-1(or 4)-monophosphatase activity, GO:0016787: hydrolase activity		−0.3615	−0.2892	−0.7275	−1.009	7.29	8.34	7.98	8.05	7.61	7.33	2

(*Continued*)

TABLE E2. (*Continued*)

220238_s_at	KLHL7	kelch-like 7 (Drosophila)	NM_018846	55975	Hs.654817	GO:0005730: nucleolus, GO:0005515: protein binding		−0.3277	−0.2865	−0.7761	−1.0039	5.87	6.49	6.16	6.2	5.71	5.48	2
208965_s_at	PYHIN1	pyrin and HIN domain family, member 1	BG256677	149628	Hs.380250			0.0018	−0.1642	−0.5888	−1.6874	8.84	10.35	10.35	10.19	9.76	8.66	3
218900_at	CNNM4	cyclin M4	NM_020184	26504	Hs.656229			0.3047	−0.0669	−0.7842	−1.8738	5.03	7.11	7.42	7.04	6.33	5.24	3
218986_s_at	FLJ20035	hypothetical protein FLJ20035	NM_017631	55601	Hs.591710	GO:0003676: nucleic acid binding, GO:0005524: ATP binding, GO:0008026: ATP-dependent helicase activity, GO:0016787: hydrolase activity		0.1931	0.0013	−0.4698	−1.1291	8.78	9.89	10.08	9.89	9.42	8.76	3
207655_s_at	BLNK	B-cell linker	NM_013314	29760	Hs.665244	GO:0006954: inflammatory response, GO:0006959: humoral immune response, GO:0007242: intracellular signaling cascade, GO:0007242: intracellular signaling cascade, GO:0007516: hemocyte development, GO:0030183: B cell differentiation, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0005068: transmembrane receptor protein tyrosine kinase adaptor protein activity, GO:0005070: SH3/SH2 adaptor activity	04662: B cell receptor signaling pathway	0.1715	0.0323	−0.3794	−1.0092	8.05	9.37	9.55	9.41	8.99	8.36	3
208191_x_at	PSG4	pregnancy specific beta-1-glycoprotein 4	NM_002780	5672	Hs.654468	GO:0006952: defense response, GO:0007565: female pregnancy, GO:0005576: extracellular region, GO:0005615: extracellular space		0.1998	0.0433	−0.4297	−1.0514	4.13	5	5.2	5.04	4.57	3.94	3
217188_s_at	C14orf1	chromosome 14 open reading frame 1	AC007182	11161	Hs.15106	GO:0008150: biological_process, GO:0016126: sterol biosynthetic process, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030133: transport vesicle, GO:0003674: molecular_function		0.1334	−0.0804	−0.4443	−1.1563	7.96	8.32	8.45	8.23	7.87	7.16	3
218622_at	NUP37	nucleoporin 37kDa	NM_024057	79023	Hs.444276	GO:0006605: protein targeting, GO:0015031: protein transport, GO:0051028: mRNA transport, GO:0005643: nuclear pore		0.0892	−0.0541	−0.4187	−1.0596	8.05	8.57	8.66	8.52	8.15	7.51	3
202266_at	TTRAP	TRAF and TNF receptor associated protein	NM_016614	51567	Hs.403010	GO:0007166: cell surface receptor linked signal transduction, GO:0003714: transcription corepressor activity		0.1054	−0.051	−0.3722	−1.0143	10.39	11.11	11.22	11.06	10.74	10.1	3
211367_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	U13699	834	Hs.2490	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007165: signal transduction, GO:0042981: regulation of apoptosis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0008234: cysteine-type peptidase activity, GO:0008656: caspase activator activity, GO:0030693: caspase activity, GO:0030693: caspase activity	01510: Neurodegenerative Disorders, 05040: Huntington's disease, 05050: Dentatorubropallidoluysian atrophy (DRPLA)	0.199	−0.05	−0.5295	−1.4633	7.99	9.19	9.39	9.14	8.66	7.73	3
210732_s_at	LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)	AL136105	3964	Hs.4082, Hs.652333	GO:0005615: extracellular space, GO:0005737: cytoplasm, GO:0005529: sugar binding, GO:0005529: sugar binding		0.0961	−0.1138	−0.6592	−1.8446	6.91	8.47	8.57	8.36	7.82	6.63	3
214453_s_at	IFI44	interferon-induced protein 44	NM_006417	10561	Hs.82316	GO:0009615: response to virus, GO:0005737: cytoplasm		0.2397	−0.0294	−0.8687	−2.3465	6.07	9.29	9.53	9.26	8.42	6.94	3

(*Continued*)

TABLE E2. (*Continued*)

200887_s_at	STAT1	signal transducer and activator of transcription 1, 91kDa	NM_007315	6772	Hs.694776	GO:0000074: regulation of progression through cell cycle, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0006919: caspase activation, GO:0007165: signal transduction, GO:0007242: intracellular signaling cascade, GO:0007249: I-kappaB kinase/NF-kappaB cascade, GO:0007260: tyrosine phosphorylation of STAT protein, GO:0007262: STAT protein nuclear translocation, GO:0009615: response to virus, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0004871: signal transducer activity, GO:0005062: hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity, GO:0005509: calcium ion binding, GO:0005515: protein binding	04620: Toll-like receptor signaling pathway, 04630: Jak-STAT signaling pathway, 05212: Pancreatic cancer	0.0664	−0.0462	−0.459	−1.3479	10.52	11.83	11.9	11.79	11.37	10.49	3
202170_s_at	AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	AF151057	60496	Hs.524009	GO:0009059: macromolecule biosynthetic process, GO:0005737: cytoplasm, GO:0000287: magnesium ion binding, GO:0008897: phosphopantetheinyltransferase activity, GO:0016740: transferase activity	00300: Lysine biosynthesis, 00310: Lysine degradation	0.0996	−0.024	−0.4334	−1.251	7.45	8.09	8.19	8.07	7.66	6.84	3
219695_at	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	NM_024703	55512	Hs.368421	GO:0006685: sphingomyelin catabolic process, GO:0007049: cell cycle, GO:0007275: multicellular organismal development, GO:0030072: peptide hormone secretion, GO:0000137: Golgi cis cisterna, GO:0005624: membrane fraction, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000287: magnesium ion binding, GO:0004767: sphingomyelin phosphodiesterase activity, GO:0016787: hydrolase activity	00600: Sphingolipid metabolism	0.1561	−0.0801	−0.5252	−1.5579	8.55	10.13	10.28	10.05	9.6	8.57	3
222262_s_at	ETNK1	ethanolamine kinase 1	AL137750	55500	Hs.29464	GO:0006646: phosphatidylethanolamine biosynthetic process, GO:0005737: cytoplasm, GO:0004305: ethanolamine kinase activity, GO:0016301: kinase activity, GO:0016740: transferase activity	00564: Glycerophospholipid metabolism	0.1806	−0.0615	−0.3745	−1.2211	4.39	5.27	5.46	5.21	4.9	4.05	3
211366_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	U13698	834	Hs.2490	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007165: signal transduction, GO:0042981: regulation of apoptosis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0008234: cysteine-type peptidase activity, GO:0008656: caspase activator activity, GO:0030693: caspase activity, GO:0030693: caspase activity	01510: Neurodegenerative Disorders, 05040: Huntington's disease, 05050: Dentatorubropallidoluysian atrophy (DRPLA)	0.1493	−0.0904	−0.4055	−1.287	8.08	9.06	9.21	8.97	8.66	7.78	3

(*Continued*)

TABLE E2. (*Continued*)

211368_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	U13700	834	Hs.2490	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007165: signal transduction, GO:0042981: regulation of apoptosis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0008234: cysteine-type peptidase activity, GO:0008656: caspase activator activity, GO:0030693: caspase activity, GO:0030693: caspase activity	01510: Neurodegenerative Disorders, 05040: Huntington's disease, 05050: Dentatorubropallidoluysian atrophy (DRPLA)	0.1536	−0.0234	−0.3293	−1.0708	8.59	9.42	9.58	9.4	9.09	8.35	3
203560_at	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	NM_003878	8836	Hs.78619	GO:0006541: glutamine metabolic process, GO:0005764: lysosome, GO:0008238: exopeptidase activity, GO:0008464: gamma-glutamyl hydrolase activity, GO:0016787: hydrolase activity	00790: Folate biosynthesis	0.1046	0.0746	−0.3978	−1.1017	10.05	11.2	11.3	11.27	10.8	10.1	3
203767_s_at	STS	steroid sulfatase (microsomal), isozyme S	AI122754	412	Hs.522578	GO:0006629: lipid metabolic process, GO:0006706: steroid catabolic process, GO:0007565: female pregnancy, GO:0008152: metabolic process, GO:0008544: epidermis development, GO:0005624: membrane fraction, GO:0005764: lysosome, GO:0005768: endosome, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0005794: Golgi apparatus, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0004773: steryl-sulfatase activity, GO:0005509: calcium ion binding, GO:0016787: hydrolase activity	00150: Androgen and estrogen metabolism	0.3379	0.0639	−0.4037	−1.5128	8.3	9.79	10.12	9.85	9.38	8.27	3
202578_s_at	DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	NM_018332	55308	Hs.656037	GO:0006605: protein targeting, GO:0015031: protein transport, GO:0051028: mRNA transport, GO:0005643: nuclear pore, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003723: RNA binding, GO:0005524: ATP binding, GO:0008026: ATP-dependent helicase activity, GO:0016787: hydrolase activity	00500: Starch and sucrose metabolism, 00790: Folate biosynthesis	0.2596	0.1478	−0.3014	−1.2304	5.79	6.19	6.45	6.34	5.89	4.96	3
202687_s_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	NM_003810	8743	Hs.478275	GO:0006915: apoptosis, GO:0006917: induction of apoptosis, GO:0006955: immune response, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004871: signal transducer activity, GO:0005125: cytokine activity, GO:0005164: tumor necrosis factor receptor binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	04060: Cytokine-cytokine receptor interaction, 04210: Apoptosis, 04650: Natural killer cell mediated cytotoxicity	0.2725	0.0584	−0.2736	−1.1382	9.86	10.96	11.24	11.02	10.69	9.83	3

(*Continued*)

TABLE E2. (*Continued*)

219369_s_at	OTUB2	OTU domain, ubiquitin aldehyde binding 2	NM_023112	78990	Hs.278815	GO:0006512: ubiquitin cycle, GO:0006519: amino acid and derivative metabolic process, GO:0005575: cellular_component, GO:0008234: cysteine-type peptidase activity, GO:0016289: CoA hydrolase activity		0.177	0.0992	−0.5186	−1.5553	7.38	9.07	9.24	9.17	8.55	7.51	3
221107_at	CHRNA9	cholinergic receptor, nicotinic, alpha 9	NM_017581	55584	Hs.272278	GO:0006811: ion transport, GO:0006816: calcium ion transport, GO:0016021: integral to membrane, GO:0030054: cell junction, GO:0045202: synapse, GO:0045211: postsynaptic membrane, GO:0004889: nicotinic acetylcholine-activated cation-selective channel activity, GO:0005216: ion channel activity, GO:0005230: extracellular ligand-gated ion channel activity, GO:0005262: calcium channel activity, GO:0005509: calcium ion binding, GO:0030594: neurotransmitter receptor activity		0.5272	0.2512	−0.8042	−2.8722	3.86	7.49	8.02	7.74	6.69	4.62	3
214490_at	ARSF	arylsulfatase F	NM_004042	416	Hs.101674	GO:0008152: metabolic process, GO:0004065: arylsulfatase activity, GO:0005509: calcium ion binding, GO:0016787: hydrolase activity		0.5922	0.112	−1.0327	−3.3727	4.99	8.67	9.27	8.79	7.64	5.3	3
218582_at	5-Mar	membrane-associated ring finger (C3HC4) 5	NM_017824	54708	Hs.573490	GO:0006512: ubiquitin cycle, GO:0005739: mitochondrion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019867: outer membrane, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016874: ligase activity, GO:0046872: metal ion binding		0.2226	0.0119	−0.3536	−1.1498	7.5	8.14	8.36	8.15	7.79	6.99	3
213933_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	AW242315	5733	Hs.445000	GO:0006351: transcription, DNA-dependent, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0008150: biological_process, GO:0008219: cell death, GO:0005635: nuclear envelope, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004879: ligand-dependent nuclear receptor activity, GO:0004957: prostaglandin E receptor activity, GO:0004957: prostaglandin E receptor activity, GO:0004957: prostaglandin E receptor activity	04020: Calcium signaling pathway, 04080: Neuroactive ligand-receptor interaction	0.247	0.1359	−0.3673	−1.5453	9.4	10.31	10.56	10.45	9.94	8.76	3
214279_s_at	NDRG2	NDRG family member 2	W74452	57447	Hs.525205	GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0030154: cell differentiation, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0003674: molecular_function		0.3202	0.1502	−0.2731	−1.2256	9.47	9.89	10.21	10.04	9.61	8.66	3

(*Continued*)

TABLE E2. (*Continued*)

211561_x_at	MAPK14	mitogen-activated protein kinase 14	L35253	1432	Hs.588289	GO:0006468: protein amino acid phosphorylation, GO:0006928: cell motility, GO:0006935: chemotaxis, GO:0006950: response to stress, GO:0007166: cell surface receptor linked signal transduction, GO:0007243: protein kinase cascade, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004707: MAP kinase activity, GO:0004708: MAP kinase kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008339: MP kinase activity, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04370: VEGF signaling pathway, 04620: Toll-like receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 04670: Leukocyte transendothelial migration, 04912: GnRH signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection	0.2659	0.0503	−0.6785	−2.2679	5.28	7.06	7.32	7.11	6.38	4.79	3
211834_s_at	TP63	tumor protein p63	AB042841	8626	Hs.137569	GO:0006350: transcription, GO:0006915: apoptosis, GO:0006917: induction of apoptosis, GO:0007219: Notch signaling pathway, GO:0007275: multicellular organismal development, GO:0045747: positive regulation of Notch signaling pathway, GO:0045892: negative regulation of transcription, DNA-dependent, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0051289: protein homotetramerization, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0016563: transcription activator activity, GO:0016563: transcription activator activity, GO:0016564: transcription repressor activity, GO:0042802: identical protein binding, GO:0046872: metal ion binding		0.322	−0.0476	−0.7463	−2.6714	4.63	6.85	7.17	6.8	6.1	4.18	3
206643_at	HAL	histidine ammonia-lyase	NM_002108	3034	Hs.190783	GO:0006548: histidine catabolic process, GO:0009058: biosynthetic process, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0004397: histidine ammonia-lyase activity, GO:0016211: ammonia ligase activity, GO:0016829: lyase activity	00340: Histidine metabolism, 00910: Nitrogen metabolism	0.2866	0.0725	−0.4142	−1.6264	10.67	12.5	12.79	12.57	12.09	10.87	3
210830_s_at	PON2	paraoxonase 2	AF001602	5445	Hs.530077	GO:0005576: extracellular region, GO:0016020: membrane, GO:0004063: aryldialkylphosphatase activity, GO:0004064: arylesterase activity, GO:0016787: hydrolase activity	00361: gamma-Hexachlorocyclohexane degradation, 00363: Bisphenol A degradation	0.2084	−0.0161	−0.3966	−1.1187	9.9	10.93	11.13	10.91	10.53	9.81	3
205832_at	CPA4	carboxypeptidase A4	NM_016352	51200	Hs.93764	GO:0006508: proteolysis, GO:0016573: histone acetylation, GO:0005575: cellular_component, GO:0004180: carboxypeptidase activity, GO:0004182: carboxypeptidase A activity, GO:0008237: metallopeptidase activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.1624	0.0598	−0.3971	−1.2051	7.99	9.25	9.42	9.31	8.86	8.05	3
206133_at	XAF1	XIAP associated factor-1	NM_017523	54739	Hs.441975	GO:0008270: zinc ion binding		0.153	0.0512	−0.9427	−2.6475	5.51	8.34	8.49	8.39	7.39	5.69	3
204439_at	IFI44L	interferon-induced protein 44-like	NM_006820	10964	Hs.389724			0.2596	0.0957	−0.9304	−2.349	7.05	9.75	10.01	9.84	8.82	7.4	3

(*Continued*)

TABLE E2. (*Continued*)

204702_s_at	NFE2L3	nuclear factor (erythroid-derived 2)-like 3	NM_004289	9603	Hs.404741, Hs.651505	GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003713: transcription coactivator activity, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity	0.2587	0.1328	−0.5538	−1.7191	7.16	8.58	8.84	8.71	8.03	6.86	3
216125_s_at	RANBP9	RAN binding protein 9	AF064606	10048	Hs.306242	GO:0006461: protein complex assembly, GO:0007020: microtubule nucleation, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005875: microtubule associated complex, GO:0005515: protein binding, GO:0008536: Ran GTPase binding	0.1869	−0.0052	−0.356	−1.3868	7.43	8.63	8.82	8.63	8.28	7.24	3
221698_s_at	CLEC7A	C-type lectin domain family 7, member A	AF313468	64581	Hs.143929	GO:0006910: phagocytosis, recognition, GO:0006954: inflammatory response, GO:0009756: carbohydrate mediated signaling, GO:0042110: T cell activation, GO:0042832: defense response to protozoan, GO:0045087: innate immune response, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005529: sugar binding, GO:0005529: sugar binding, GO:0008329: pattern recognition receptor activity, GO:0042287: MHC protein binding	0.2497	0.0113	−0.4388	−1.7884	6.94	9.63	9.88	9.64	9.19	7.84	3
200798_x_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	NM_021960	4170	Hs.632486	GO:0001709: cell fate determination, GO:0006916: anti-apoptosis, GO:0007275: multicellular organismal development, GO:0008632: apoptotic program, GO:0019725: cellular homeostasis, GO:0030154: cell differentiation, GO:0042981: regulation of apoptosis, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding, GO:0015266: protein channel activity, GO:0046982: protein heterodimerization activity	−0.2201	−0.4173	−0.662	−2.023	10.11	11.24	11.02	10.82	10.57	9.21	3
212365_at	MYO1B	myosin IB	BF215996	4430	Hs.439620	GO:0016459: myosin complex, GO:0000166: nucleotide binding, GO:0003774: motor activity, GO:0003779: actin binding, GO:0005516: calmodulin binding, GO:0005524: ATP binding	−0.1799	−0.3246	−0.5198	−1.4478	7.78	9.24	9.06	8.91	8.72	7.79	3
205240_at	GPSM2	G-protein signaling modulator 2 (AGS3-like, C. elegans)	NM_013296	29899	Hs.584901	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0005737: cytoplasm, GO:0005096: GTPase activator activity, GO:0005488: binding, GO:0042802: identical protein binding	−0.0915	−0.2747	−0.4498	−1.2582	8.9	9.53	9.43	9.25	9.08	8.27	3

(*Continued*)

TABLE E2. (*Continued*)

210018_x_at	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	AB026118	10892	Hs.601217	GO:0002726: positive regulation of T cell cytokine production, GO:0006508: proteolysis, GO:0006512: ubiquitin cycle, GO:0006916: anti-apoptosis, GO:0006952: defense response, GO:0007250: activation of NF-kappaB-inducing kinase, GO:0042981: regulation of apoptosis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0050852: T cell receptor signaling pathway, GO:0050870: positive regulation of T cell activation, GO:0051168: nuclear export, GO:0051259: protein oligomerization, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0032449: CBM complex, GO:0004842: ubiquitin-protein ligase activity, GO:0004871: signal transducer activity, GO:0008233: peptidase activity, GO:0019209: kinase activator activity, GO:0030693: caspase activity, GO:0043621: protein self-association	04660: T cell receptor signaling pathway, 04662: B cell receptor signaling pathway	−0.1841	−0.4488	−0.7752	−2.014	6.97	8.1	7.92	7.65	7.33	6.09	3
214895_s_at	ADAM10	ADAM metallopeptidase domain 10	AU135154	102	Hs.578508	GO:0001701: in utero embryonic development, GO:0006468: protein amino acid phosphorylation, GO:0007162: negative regulation of cell adhesion, GO:0007162: negative regulation of cell adhesion, GO:0007219: Notch signaling pathway, GO:0007229: integrin-mediated signaling pathway, GO:0007267: cell-cell signaling, GO:0051089: constitutive protein ectodomain proteolysis, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0005798: Golgi-associated vesicle, GO:0005886: plasma membrane, GO:0009986: cell surface, GO:0016021: integral to membrane, GO:0004222: metalloendopeptidase activity, GO:0005178: integrin binding, GO:0008270: zinc ion binding, GO:0019901: protein kinase binding, GO:0042803: protein homodimerization activity, GO:0046872: metal ion binding	05120: Epithelial cell signaling in Helicobacter pylori infection	−0.0012	−0.3695	−0.4425	−1.588	6.25	7.29	7.29	6.92	6.85	5.7	3
201435_s_at	EIF4E	eukaryotic translation initiation factor 4E	AW268640	1977	Hs.249718	GO:0006413: translational initiation, GO:0006417: regulation of translation, GO:0005737: cytoplasm, GO:0016281: eukaryotic translation initiation factor 4F complex, GO:0000339: RNA cap binding, GO:0003743: translation initiation factor activity, GO:0005515: protein binding		−0.0422	−0.2253	−0.5227	−1.7312	9.62	10.69	10.64	10.46	10.16	8.95	3

(*Continued*)

TABLE E2. (*Continued*)

217960_s_at	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	NM_020243	56993	Hs.595072	GO:0006626: protein targeting to mitochondrion, GO:0015031: protein transport, GO:0043681: protein import into mitochondrion, GO:0005739: mitochondrion, GO:0005742: mitochondrial outer membrane translocase complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019867: outer membrane, GO:0004872: receptor activity, GO:0005515: protein binding		−0.1012	−0.3639	−0.5234	−1.5413	7.76	8.77	8.66	8.4	8.24	7.22	3
221765_at	UGCG	UDP-glucose ceramide glucosyltransferase	AI378044	7357	Hs.304249, Hs.593014	GO:0006679: glucosylceramide biosynthetic process, GO:0006688: glycosphingolipid biosynthetic process, GO:0008544: epidermis development, GO:0005615: extracellular space, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0008120: ceramide glucosyltransferase activity, GO:0016757: transferase activity, transferring glycosyl groups	00600: Sphingolipid metabolism, 01031: Glycan structures - biosynthesis 2	−0.0642	−0.7187	−1.05	−3.1276	7.08	9.59	9.53	8.88	8.54	6.47	3
213501_at	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	T62985	51	Hs.464137	GO:0006118: electron transport, GO:0006629: lipid metabolic process, GO:0006635: fatty acid beta-oxidation, GO:0006693: prostaglandin metabolic process, GO:0007283: spermatogenesis, GO:0005739: mitochondrion, GO:0005777: peroxisome, GO:0005778: peroxisomal membrane, GO:0003995: acyl-CoA dehydrogenase activity, GO:0003997: acyl-CoA oxidase activity, GO:0009053: electron donor activity, GO:0050660: FAD binding	00071: Fatty acid metabolism, 03320: PPAR signaling pathway	−0.0168	−0.1634	−0.3359	−1.0302	5.55	6.24	6.22	6.08	5.9	5.21	3
206075_s_at	CSNK2A1	casein kinase 2, alpha 1 polypeptide	NM_001895	1457	Hs.644056	GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0016055: Wnt receptor signaling pathway, GO:0005634: nucleus, GO:0005886: plasma membrane, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004682: protein kinase CK2 activity, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0047485: protein N-terminus binding	04310: Wnt signaling pathway, 04520: Adherens junction, 04530: Tight junction	−0.0746	−0.2457	−0.5463	−1.6677	7.06	7.9	7.83	7.66	7.36	6.24	3
206113_s_at	RAB5A	RAB5A, member RAS oncogene family	NM_004162	5868	Hs.475663	GO:0006897: endocytosis, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0001726: ruffle, GO:0005769: early endosome, GO:0005886: plasma membrane, GO:0030139: endocytic vesicle, GO:0045121: lipid raft, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005525: GTP binding	05030: Amyotrophic lateral sclerosis (ALS)	−0.1158	−0.3414	−0.7948	−2.24	8.83	10.45	10.33	10.11	9.65	8.21	3

(*Continued*)

TABLE E2. (*Continued*)

209457_at	DUSP5	dual specificity phosphatase 5	U16996	1847	Hs.2128	GO:0006470: protein amino acid dephosphorylation, GO:0006470: protein amino acid dephosphorylation, GO:0004725: protein tyrosine phosphatase activity, GO:0016787: hydrolase activity, GO:0016791: phosphoric monoester hydrolase activity, GO:0017017: MAP kinase tyrosine/serine/threonine phosphatase activity	04010: MAPK signaling pathway	−0.0804	−0.3177	−0.4726	−1.6106	5.94	6.96	6.88	6.64	6.49	5.35	3
217811_at	SELT	selenoprotein T	NM_016275	51714	Hs.369052	GO:0001514: selenocysteine incorporation, GO:0045454: cell redox homeostasis, GO:0008430: selenium binding		−0.0804	−0.2642	−0.5185	−1.5491	10.05	10.78	10.7	10.52	10.26	9.23	3
200900_s_at	M6PR	mannose-6-phosphate receptor (cation dependent)	AI583537	4074	Hs.134084	GO:0006810: transport, GO:0006898: receptor-mediated endocytosis, GO:0008333: endosome to lysosome transport, GO:0015761: mannose transport, GO:0005764: lysosome, GO:0005770: late endosome, GO:0005887: integral to plasma membrane, GO:0009986: cell surface, GO:0016020: membrane, GO:0004888: transmembrane receptor activity, GO:0005515: protein binding, GO:0005537: mannose binding, GO:0015578: mannose transmembrane transporter activity		−0.0451	−0.2608	−0.3892	−1.2418	8.09	8.79	8.75	8.53	8.4	7.55	3
206788_s_at	CBFB	core-binding factor, beta subunit	AF294326	865	Hs.460988	GO:0001649: osteoblast differentiation, GO:0006366: transcription from RNA polymerase II promoter, GO:0008150: biological_process, GO:0030098: lymphocyte differentiation, GO:0030099: myeloid cell differentiation, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0048469: cell maturation, GO:0005575: cellular_component, GO:0005634: nucleus, GO:0003674: molecular_function, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0003713: transcription coactivator activity, GO:0005515: protein binding		−0.0749	−0.2398	−0.411	−1.2871	6.15	7.13	7.05	6.89	6.71	5.84	3
203276_at	LMNB1	lamin B1	NM_005573	4001	Hs.89497	GO:0005634: nucleus, GO:0005638: lamin filament, GO:0016020: membrane, GO:0005198: structural molecule activity, GO:0005198: structural molecule activity	01430: Cell Communication	−0.3223	−0.6671	−0.7146	−1.8969	7.1	8.39	8.07	7.73	7.68	6.5	3

(*Continued*)

TABLE E2. (*Continued*)

201514_s_at	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	NM_005754	10146	Hs.587054	GO:0006810: transport, GO:0007265: Ras protein signal transduction, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003677: DNA binding, GO:0003723: RNA binding, GO:0004003: ATP-dependent DNA helicase activity, GO:0004004: ATP-dependent RNA helicase activity, GO:0004386: helicase activity, GO:0004519: endonuclease activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016787: hydrolase activity		−0.2015	−0.4037	−0.5007	−1.0685	8.52	9.24	9.04	8.83	8.74	8.17	3
215207_x_at	LOC729148	similar to lethal (2) k00619 CG4775-PA	BF695847	729148	Hs.632805			−0.1949	−0.4259	−0.5096	−1.0432	4.69	5.45	5.26	5.03	4.94	4.41	3
219272_at	TRIM62	tripartite motif-containing 62	NM_018207	55223	Hs.656006	GO:0005622: intracellular, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0965	−0.2796	−0.8396	−1.1366	5.58	6.69	6.6	6.41	5.85	5.56	3
206472_s_at	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	NM_005078	7090	Hs.287362	GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0009887: organ morphogenesis, GO:0016055: Wnt receptor signaling pathway, GO:0005634: nucleus, GO:0005515: protein binding		−0.1562	−0.3569	−0.9777	−1.3764	7.23	8.87	8.72	8.52	7.9	7.5	3
206604_at	OVOL1	ovo-like 1 (Drosophila)	NM_004561	5017	Hs.134434	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0000239: pachytene, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007283: spermatogenesis, GO:0007498: mesoderm development, GO:0008544: epidermis development, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.133	−0.2442	−0.7938	−1.0601	6.02	7.02	6.89	6.78	6.23	5.96	3
219554_at	RHCG	Rh family, C glycoprotein	NM_016321	51458	Hs.459284	GO:0006810: transport, GO:0015696: ammonium transport, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005215: transporter activity, GO:0008519: ammonium transmembrane transporter activity, GO:0030506: ankyrin binding		−0.4601	−1.8083	−4.5392	−6.0967	3.91	10.36	9.9	8.55	5.82	4.26	3
221779_at	MICALL1	MICAL-like 1	AB051455	85377	Hs.517610	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0994	−0.3991	−1.006	−1.3478	8.6	10.16	10.06	9.76	9.15	8.81	3
203127_s_at	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	BC005123	9517	Hs.435661	GO:0009058: biosynthetic process, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004758: serine C-palmitoyltransferase activity, GO:0008415: acyltransferase activity, GO:0016769: transferase activity, transferring nitrogenous groups, GO:0030170: pyridoxal phosphate binding	00600: Sphingolipid metabolism	−0.2386	−0.9649	−2.2973	−3.2403	4.99	8.44	8.2	7.48	6.15	5.2	3

(*Continued*)

TABLE E2. (*Continued*)

204858_s_at	ECGF1	endothelial cell growth factor 1 (platelet-derived)	NM_001953	1890	Hs.592212	GO:0000002: mitochondrial genome maintenance, GO:0001525: angiogenesis, GO:0006206: pyrimidine base metabolic process, GO:0006220: pyrimidine nucleotide metabolic process, GO:0006260: DNA replication, GO:0006935: chemotaxis, GO:0007166: cell surface receptor linked signal transduction, GO:0007267: cell-cell signaling, GO:0007275: multicellular organismal development, GO:0008152: metabolic process, GO:0030154: cell differentiation, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0005161: platelet-derived growth factor receptor binding, GO:0008083: growth factor activity, GO:0009032: thymidine phosphorylase activity, GO:0016757: transferase activity, transferring glycosyl groups	00230: Purine metabolism, 00240: Pyrimidine metabolism, 05219: Bladder cancer	−0.1844	−0.8178	−2.0302	−2.9778	7.37	10.86	10.68	10.05	8.83	7.89	3
210020_x_at	CALML3	calmodulin-like 3	M58026	810	Hs.239600	GO:0005509: calcium ion binding	04020: Calcium signaling pathway, 04070: Phosphatidylinositol signaling system, 04720: Long-term potentiation, 04740: Olfactory transduction, 04910: Insulin signaling pathway, 04912: GnRH signaling pathway, 04916: Melanogenesis, 05040: Huntington's disease, 05214: Glioma	0.012	−0.0985	−0.8113	−1.1023	11.78	13.29	13.3	13.19	12.48	12.19	3
211136_s_at	CLPTM1	cleft lip and palate associated transmembrane protein 1	BC004865	1209	Hs.444441	GO:0007275: multicellular organismal development, GO:0030154: cell differentiation, GO:0005887: integral to plasma membrane, GO:0016020: membrane		−0.0725	0.1641	−0.4592	−1.0626	8.77	9.32	9.24	9.48	8.86	8.25	3
206686_at	PDK1	pyruvate dehydrogenase kinase, isozyme 1	NM_002610	5163	Hs.470633	GO:0005975: carbohydrate metabolic process, GO:0006006: glucose metabolic process, GO:0007264: small GTPase mediated signal transduction, GO:0018106: peptidyl-histidine phosphorylation, GO:0005739: mitochondrion, GO:0004673: protein histidine kinase activity, GO:0004740: [pyruvate dehydrogenase (lipoamide)] kinase activity, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity	04660: T cell receptor signaling pathway, 04664: Fc epsilon RI signaling pathway	−0.337	−0.0988	−0.4512	−1.0441	4.34	5.33	4.99	5.23	4.88	4.29	3
222309_at	C6orf62	chromosome 6 open reading frame 62	AW972292	81688	Hs.519930	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0003674: molecular_function		−0.404	−0.1392	−0.6606	−1.32	6.28	7.2	6.8	7.06	6.54	5.88	3

(*Continued*)

TABLE E2. (*Continued*)

211919_s_at	CXCR4	chemokine (C-X-C motif) receptor 4	AF348491	7852	Hs.593413	GO:0000187: activation of MAPK activity, GO:0001569: patterning of blood vessels, GO:0001667: ameboidal cell migration, GO:0001764: neuron migration, GO:0006915: apoptosis, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0007281: germ cell development, GO:0007420: brain development, GO:0008045: motor axon guidance, GO:0008354: germ cell migration, GO:0009615: response to virus, GO:0030334: regulation of cell migration, GO:0042098: T cell proliferation, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0030426: growth cone, GO:0031252: leading edge, GO:0001584: rhodopsin-like receptor activity, GO:0003779: actin binding, GO:0005515: protein binding, GO:0015026: coreceptor activity, GO:0016493: C-C chemokine receptor activity, GO:0016494: C-X-C chemokine receptor activity, GO:0032027: myosin light chain binding	04060: Cytokine-cytokine receptor interaction, 04360: Axon guidance, 04670: Leukocyte transendothelial migration	0.4121	−0.788	−0.99	−2.4458	2.66	5.78	6.19	4.99	4.79	3.33	3
220285_at	FAM108B1	family with sequence similarity 108, member B1	NM_016014	51104	Hs.380389	GO:0016787: hydrolase activity		0.1905	−0.4522	−0.5557	−1.1389	2.54	3.7	3.89	3.25	3.15	2.56	3
220528_at	VNN3	vanin 3	NM_018399	55350	Hs.183656	GO:0006807: nitrogen compound metabolic process, GO:0008150: biological_process, GO:0005575: cellular_component, GO:0016020: membrane, GO:0016811: hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides, GO:0017159: pantetheinase activity, GO:0048503: GPI anchor binding	00760: Nicotinate and nicotinamide metabolism, 00930: Caprolactam degradation	0.3188	−0.3233	−0.9306	−1.4184	3.82	5.26	5.58	4.94	4.33	3.84	3
206912_at	FOXE1	forkhead box E1 (thyroid transcription factor 2)	NM_004473	2304	Hs.159234	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0009653: anatomical structure morphogenesis, GO:0030878: thyroid gland development, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0060022: hard palate development, GO:0060023: soft palate development, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0043565: sequence-specific DNA binding		0.2758	−0.387	−0.7295	−1.1147	3.27	4.42	4.7	4.03	3.69	3.31	3

(*Continued*)

TABLE E2. (*Continued*)

216316_x_at	GK	glycerol kinase	X78713	2710	Hs.1466	GO:0005975: carbohydrate metabolic process, GO:0006072: glycerol-3-phosphate metabolic process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity	00561: Glycerolipid metabolism, 03320: PPAR signaling pathway	0.4807	−0.6879	−1.6673	−2.5341	2.98	5.43	5.91	4.74	3.77	2.9	3
219316_s_at	FLVCR2	feline leukemia virus subgroup C cellular receptor family, member 2	NM_017791	55640	Hs.509966, Hs.615289	GO:0006810: transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005215: transporter activity		0.2689	−0.2914	−0.9304	−1.2711	3.81	5.06	5.33	4.77	4.13	3.79	3
220249_at	HYAL4	hyaluronoglucosaminidase 4	NM_012269	23553	Hs.28673	GO:0005975: carbohydrate metabolic process, GO:0006027: glycosaminoglycan catabolic process, GO:0007342: fusion of sperm to egg plasma membrane, GO:0008152: metabolic process, GO:0003824: catalytic activity, GO:0004415: hyaluronoglucosaminidase activity		0.4615	−0.6297	−1.9069	−2.5166	3.44	6.23	6.69	5.6	4.32	3.71	3
219684_at	RTP4	receptor (chemosensory) transporter protein 4	NM_022147	64108	Hs.43388	GO:0001580: detection of chemical stimulus during sensory perception of bitter taste, GO:0006612: protein targeting to membrane, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding		0.5095	−0.1046	−0.839	−1.2675	2.53	4.33	4.83	4.22	3.49	3.06	3
221416_at	PLA2G2F	phospholipase A2, group IIF	NM_022819	64600	Hs.302034	GO:0006644: phospholipid metabolic process, GO:0008150: biological_process, GO:0016042: lipid catabolic process, GO:0005576: extracellular region, GO:0004623: phospholipase A2 activity, GO:0005509: calcium ion binding, GO:0016787: hydrolase activity	00564: Glycerophospholipid metabolism, 00565: Ether lipid metabolism, 00590: Arachidonic acid metabolism, 00591: Linoleic acid metabolism, 04010: MAPK signaling pathway, 04370: VEGF signaling pathway, 04664: Fc epsilon RI signaling pathway, 04730: Long-term depression, 04912: GnRH signaling pathway	0.2831	−0.4759	−1.284	−1.4076	2.51	3.99	4.27	3.52	2.71	2.58	3
212481_s_at	TPM4	tropomyosin 4	AI214061	7171	Hs.631618	GO:0006928: cell motility, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005862: muscle thin filament tropomyosin, GO:0003779: actin binding, GO:0008307: structural constituent of muscle		−0.3422	−0.3717	−0.8117	−1.3243	8.41	9.49	9.15	9.12	8.68	8.17	3
200730_s_at	PTP4A1	protein tyrosine phosphatase type IVA, member 1	BF576710	7803	Hs.227777	GO:0006470: protein amino acid dephosphorylation, GO:0007049: cell cycle, GO:0007275: multicellular organismal development, GO:0005737: cytoplasm, GO:0005768: endosome, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0004725: protein tyrosine phosphatase activity, GO:0016787: hydrolase activity		−0.3817	−1.0337	−1.2357	−2.9993	7.3	9.57	9.18	8.53	8.33	6.57	3

(*Continued*)

TABLE E2. (*Continued*)

217678_at	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	AA488687	23657	Hs.390594	GO:0006461: protein complex assembly, GO:0006810: transport, GO:0006865: amino acid transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0015171: amino acid transmembrane transporter activity, GO:0015327: cystine:glutamate antiporter activity		−0.3136	−0.4314	−0.9414	−1.5256	6.92	8.78	8.47	8.35	7.84	7.25	3
218349 _s_at	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	AA824298	55055	Hs.21331	GO:0000776: kinetochore		−0.5494	−0.6869	−1.3699	−2.5047	3.73	5.75	5.2	5.07	4.38	3.25	3
208910 _s_at	C1QBP	complement component 1, q subcomponent binding protein	L04636	708	Hs.555866	GO:0006955: immune response, GO:0005739: mitochondrion, GO:0005759: mitochondrial matrix, GO:0005886: plasma membrane, GO:0005515: protein binding		−0.2384	−0.3631	−0.6338	−1.247	10.5	11.32	11.08	10.96	10.69	10.07	3
209024 _s_at	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	AI472757	10492	Hs.571177	GO:0006397: mRNA processing, GO:0008380: RNA splicing, GO:0005634: nucleus, GO:0005681: spliceosome, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0008143: poly(A) binding		−0.2603	−0.2804	−0.5949	−1.0536	9.78	10.54	10.28	10.26	9.94	9.48	3
213741 _s_at	KPNA1	karyopherin alpha 1 (importin alpha 5)	BF575685	3836	Hs.161008	GO:0000018: regulation of DNA recombination, GO:0006607: NLS-bearing substrate import into nucleus, GO:0006886: intracellular protein transport, GO:0005634: nucleus, GO:0005643: nuclear pore, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0008139: nuclear localization sequence binding, GO:0008565: protein transporter activity		−0.2806	−0.4004	−0.6487	−1.2929	7.48	8.23	7.95	7.83	7.58	6.94	3
214168 _s_at	TJP1	tight junction protein 1 (zona occludens 1)	AA813018	7082	Hs.510833	GO:0007043: intercellular junction assembly, GO:0005624: membrane fraction, GO:0005918: septate junction, GO:0005923: tight junction, GO:0005923: tight junction, GO:0016020: membrane, GO:0016323: basolateral plasma membrane, GO:0030054: cell junction, GO:0005515: protein binding, GO:0005515: protein binding	04520: Adherens junction, 04530: Tight junction, 04540: Gap junction, 05120: Epithelial cell signaling in Helicobacter pylori infection	−0.2909	−0.3756	−0.7183	−1.4518	6.66	8.37	8.08	8	7.65	6.92	3
203362 _s_at	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	NM_002358	4085	Hs.591697	GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007093: mitotic cell cycle checkpoint, GO:0051301: cell division, GO:0000776: kinetochore, GO:0005515: protein binding	04110: Cell cycle	−0.4155	−0.6301	−1.1278	−2.1538	7.62	8.94	8.52	8.31	7.81	6.78	3

(*Continued*)

TABLE E2. (*Continued*)

204678_s_at	KCNK1	potassium channel, subfamily K, member 1	U90065	3775	Hs.208544	GO:0006811: ion transport, GO:0006813: potassium ion transport, GO:0006813: potassium ion transport, GO:0005624: membrane fraction, GO:0008076: voltage-gated potassium channel complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005216: ion channel activity, GO:0005242: inward rectifier potassium channel activity, GO:0005244: voltage-gated ion channel activity, GO:0005267: potassium channel activity, GO:0030955: potassium ion binding		−0.1985	−0.3913	−0.614	−1.1139	5.9	6.54	6.34	6.15	5.92	5.42	3
219099_at	C12orf5	chromosome 12 open reading frame 5	NM_020375	57103	Hs.504545	GO:0008152: metabolic process, GO:0005622: intracellular, GO:0016853: isomerase activity		−0.4022	−0.6205	−1.0241	−1.9614	6.62	8.42	8.02	7.8	7.39	6.46	3
220620_at	CRCT1	cysteine-rich C-terminal 1	NM_019060	54544	Hs.110196	GO:0005515: protein binding		−0.1115	−0.2906	−0.7796	−1.2243	10.5	11.91	11.8	11.62	11.13	10.68	3
217785_s_at	YKT6	YKT6 v-SNARE homolog (S. cerevisiae)	NM_006555	10652	Hs.520794	GO:0006888: ER to Golgi vesicle-mediated transport, GO:0006903: vesicle targeting, GO:0006904: vesicle docking during exocytosis, GO:0015031: protein transport, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0031410: cytoplasmic vesicle, GO:0016740: transferase activity, GO:0019706: protein-cysteine S-palmitoleyltransferase activity	04130: SNARE interactions in vesicular transport	−0.3607	−0.4885	−0.8985	−1.6985	5.31	7.07	6.71	6.58	6.17	5.37	3
217924_at	C6orf106	chromosome 6 open reading frame 106	AL523965	64771	Hs.643498			−0.1567	−0.2725	−0.6483	−1.6456	5.98	7.29	7.14	7.02	6.64	5.65	3
204751_x_at	DSC2	desmocollin 2	NM_004949	1824	Hs.95612	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005911: intercellular junction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding	01430: Cell Communication	−0.5208	−1.4057	−2.0876	−4.1698	7.95	11.37	10.85	9.96	9.28	7.2	3
205220_at	GPR109B	G protein-coupled receptor 109B	NM_006018	8843	Hs.458425	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0045028: purinergic nucleotide receptor activity, G-protein coupled		0.0314	−0.2796	−0.7151	−1.0813	9.6	10.42	10.45	10.14	9.7	9.34	3
201537_s_at	DUSP3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	AL048503	1845	Hs.181046	GO:0006470: protein amino acid dephosphorylation, GO:0006470: protein amino acid dephosphorylation, GO:0004725: protein tyrosine phosphatase activity, GO:0008138: protein tyrosine/serine/threonine phosphatase activity, GO:0016787: hydrolase activity, GO:0016791: phosphoric monoester hydrolase activity	04010: MAPK signaling pathway	−0.1957	−0.409	−0.6302	−1.2376	5.32	6.1	5.9	5.69	5.47	4.86	3
204747_at	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	NM_001549	3437	Hs.47338	GO:0006955: immune response, GO:0008150: biological_process, GO:0005575: cellular_component, GO:0005488: binding		0.0529	−0.1171	−0.7455	−1.2002	7.16	8.85	8.91	8.74	8.11	7.65	3

(*Continued*)

TABLE E2. (*Continued*)

210559_s_at	CDC2	cell division cycle 2, G1 to S and G2 to M	D88357	983	Hs.334562	GO:0000074: regulation of progression through cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0006916: anti-apoptosis, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007089: traversing start control point of mitotic cell cycle, GO:0051301: cell division, GO:0005634: nucleus, GO:0005876: spindle microtubule, GO:0030496: midbody, GO:0000166: nucleotide binding, GO:0004693: cyclin-dependent protein kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04110: Cell cycle, 04115: p53 signaling pathway, 04540: Gap junction	−0.343	−0.8147	−1.204	−2.3713	6.16	7.75	7.4	6.93	6.54	5.38	3
210834_s_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	AL031429	5733	Hs.445000	GO:0006351: transcription, DNA-dependent, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0008150: biological_process, GO:0008219: cell death, GO:0005635: nuclear envelope, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004879: ligand-dependent nuclear receptor activity, GO:0004957: prostaglandin E receptor activity, GO:0004957: prostaglandin E receptor activity, GO:0004957: prostaglandin E receptor activity	04020: Calcium signaling pathway, 04080: Neuroactive ligand-receptor interaction	0.2979	−0.1425	−0.9414	−1.4474	3.01	4.75	5.05	4.6	3.81	3.3	3
209507_at	RPA3	replication protein A3, 14kDa	BC005264	6119	Hs.487540	GO:0006260: DNA replication, GO:0006281: DNA repair, GO:0005662: DNA replication factor A complex, GO:0003697: single-stranded DNA binding		−0.1235	−0.3151	−0.5983	−1.0065	8.73	9.35	9.22	9.03	8.75	8.34	3
212379_at	GART	phosphoribosylglycinamide formyltransferase,				phosphoribosylglycinamide synthetase, phosphori-bosylaminoimidazole synthetase	BE966876	2618	Hs.473648										
	GO:0006164: purine nucleotide	biosynthetic process, GO:0006189: 'de novo' IMP biosynthetic process, GO:0006412: translation, GO:0009058: biosynthetic process, GO:0009113: purine base biosynthetic process, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003824: catalytic activity, GO:0004637: phosphoribosylamine-glycine ligase activity, GO:0004641:				phosphoribosylformylglycinamidine cyclo-ligase activity, GO:0004644: phosphoribosylglycinamide formyltransferase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008168: methyltransferase activity, GO:0016740: transferase activity, GO:0016874: ligase activity	00230: Purine metabolism, 00670: One carbon pool by folate	−0.2282	−0.4089	−0.9865	−1.6351	6.13	7.3	7.07	6.89	6.31	5.66	3
218951_s_at	PLCXD1	phosphatidylinositol-specific phospholipase C, X domain containing 1	NM_018390	55344	Hs.522568	GO:0007242: intracellular signaling cascade, GO:0004629: phospholipase C activity		−0.1897	−0.4495	−1.0257	−1.6281	8.69	10.28	10.09	9.83	9.26	8.65	3

(*Continued*)

TABLE E2. (*Continued*)

219389_at	SUSD4	sushi domain containing 4	NM_017982	55061	Hs.497841	GO:0016020: membrane, GO:0016021: integral to membrane		0.0715	−0.1629	−0.6868	−1.038	5.07	6.48	6.56	6.32	5.8	5.45	3
212378_at	GART	phosphoribosylglycinamide formyltransferase, phosphoribosyl-glycinamide synthetase, phosphoribosyl-aminoimidazole synthetase	NM_000819	2618	Hs.473648	GO:0006164: purine nucleotide biosynthetic process, GO:0006189: 'de novo' IMP biosynthetic process, GO:0006412: translation, GO:0009058: biosynthetic process, GO:0009113: purine base biosynthetic process, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003824: catalytic activity, GO:0004637: phosphoribosylamine-glycine ligase activity, GO:0004641: phosphoribosylformylglycinamidine cyclo-ligase activity, GO:0004644: phosphoribosylglycinamide formyltransferase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008168: methyltransferase activity, GO:0016740: transferase activity, GO:0016874: ligase activity	00230: Purine metabolism, 00670: One carbon pool by folate	−0.1472	−0.3322	−0.8232	−1.2717	7.71	8.56	8.42	8.23	7.74	7.29	3
212737_at	GM2A	GM2 ganglioside activator	AL513583	2760	Hs.483873	GO:0006687: glycosphingolipid metabolic process, GO:0006689: ganglioside catabolic process, GO:0007611: learning and/or memory, GO:0009313: oligosaccharide catabolic process, GO:0019377: glycolipid catabolic process, GO:0019915: sequestering of lipid, GO:0030149: sphingolipid catabolic process, GO:0050877: neurological process, GO:0050885: regulation of balance, GO:0005739: mitochondrion, GO:0005764: lysosome, GO:0004563: beta-N-acetylhexosaminidase activity, GO:0030290: sphingolipid activator protein activity		0.0553	−0.5149	−1.1845	−1.8511	10.73	12.85	12.91	12.34	11.67	11	3
211715_s_at	BDH1	3-hydroxybutyrate dehydrogenase, type 1	BC005844	622	Hs.274539	GO:0008152: metabolic process, GO:0008152: metabolic process, GO:0005739: mitochondrion, GO:0005743: mitochondrial inner membrane, GO:0005759: mitochondrial matrix, GO:0003858: 3-hydroxybutyrate dehydrogenase activity, GO:0003858: 3-hydroxybutyrate dehydrogenase activity, GO:0016491: oxidoreductase activity	00072: Synthesis and degradation of ketone bodies, 00650: Butanoate metabolism	0.0092	−0.333	−0.6445	−1.1188	7.75	8.89	8.9	8.56	8.24	7.77	3

(*Continued*)

TABLE E2. (*Continued*)

211788 _s_at	TREX2	three prime repair exonuclease 2	AF319573	11219	Hs.644635	GO:0006281: DNA repair, GO:0042177: negative regulation of protein catabolic process, GO:0043161: proteasomal ubiquitin-dependent protein catabolic process, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0005622: intracellular, GO:0000287: magnesium ion binding, GO:0004527: exonuclease activity, GO:0008296: 3'-5'-exodeoxyribonuclease activity, GO:0008853: exodeoxyribonuclease III activity, GO:0016787: hydrolase activity, GO:0031996: thioesterase binding, GO:0031996: thioesterase binding		0.2976	−0.6907	−2.3337	−3.7106	2.43	6.81	7.11	6.12	4.47	3.1	3
210357 _s_at	SMOX	spermine oxidase	BC000669	54498	Hs.433337	GO:0006118: electron transport, GO:0046208: spermine catabolic process, GO:0005737: cytoplasm, GO:0016491: oxidoreductase activity, GO:0046592: polyamine oxidase activity		−0.2361	−0.4621	−1.1378	−1.8186	7.62	9.44	9.2	8.98	8.3	7.62	3
211622 _s_at	ARF3	ADP-ribosylation factor 3	M33384	377	Hs.119177	GO:0006888: ER to Golgi vesicle-mediated transport, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0005622: intracellular, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding	05110: Cholera - Infection	−0.0156	−0.1717	−0.9844	−1.4993	5.2	6.66	6.65	6.49	5.68	5.16	3
209679 _s_at	LOC57228	small trans-membrane and glycosylated protein	BC003379	57228	Hs.652389			0.027	−0.1922	−0.7884	−1.3507	8.73	9.98	10.01	9.79	9.19	8.63	3
209744 _x_at	ITCH	itchy homolog E3 ubiquitin protein ligase (mouse)	AB056663	83737	Hs.632272	GO:0001558: regulation of cell growth, GO:0006464: protein modification process, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0006954: inflammatory response, GO:0046718: entry of virus into host cell, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0004842: ubiquitin-protein ligase activity, GO:0005515: protein binding, GO:0016874: ligase activity	04120: Ubiquitin mediated proteolysis, 05050: Dentatorubropallidoluysian atrophy (DRPLA)	0.0736	−0.3004	−0.7562	−1.2002	4.68	5.89	5.96	5.59	5.13	4.69	3
209093 _s_at	GBA	glucosidase, beta; acid (includes glucosylceramidase)	K02920	2629	Hs.282997	GO:0005975: carbohydrate metabolic process, GO:0006629: lipid metabolic process, GO:0006665: sphingolipid metabolic process, GO:0007040: lysosome organization and biogenesis, GO:0008152: metabolic process, GO:0005764: lysosome, GO:0016020: membrane, GO:0003824: catalytic activity, GO:0004348: glucosylceramidase activity, GO:0016798: hydrolase activity, acting on glycosyl bonds, GO:0043169: cation binding	00460: Cyanoamino acid metabolism, 00500: Starch and sucrose metabolism, 00600: Sphingolipid metabolism, 00940: Phenylpropanoid biosynthesis, 01032: Glycan structures - degradation	0.069	−0.428	−1.2807	−1.9933	7.84	10.15	10.21	9.72	8.87	8.15	3

(*Continued*)

TABLE E2. (*Continued*)

209186_at	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	M23114	488	Hs.506759	GO:0002026: cardiac inotropy, GO:0006812: cation transport, GO:0006816: calcium ion transport, GO:0006874: cellular calcium ion homeostasis, GO:0006984: ER-nuclear signaling pathway, GO:0007155: cell adhesion, GO:0008152: metabolic process, GO:0008544: epidermis development, GO:0015992: proton transport, GO:0045822: negative regulation of heart contraction, GO:0005624: membrane fraction, GO:0005789: endoplasmic reticulum membrane, GO:0005792: microsome, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016529: sarcoplasmic reticulum, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0005388: calcium-transporting ATPase activity, GO:0005509: calcium ion binding, GO:0005524: ATP binding, GO:0016787: hydrolase activity, GO:0016820: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, GO:0048155: S100 alpha binding	04020: Calcium signaling pathway	−0.1391	−0.2746	−0.6961	−1.126	11.59	12.38	12.24	12.1	11.68	11.25	3
207008_at	IL8RB	interleukin 8 receptor, beta	NM_001557	3579	Hs.846	GO:0006915: apoptosis, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006968: cellular defense response, GO:0007200: G-protein signaling, coupled to IP3 second messenger (phospholipase C activating), GO:0008284: positive regulation of cell proliferation, GO:0030593: neutrophil chemotaxis, GO:0042119: neutrophil activation, GO:0005622: intracellular, GO:0005887: integral to plasma membrane, GO:0009986: cell surface, GO:0016020: membrane, GO:0042629: mast cell granule, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004918: interleukin-8 receptor activity	04060: Cytokine-cytokine receptor interaction, 05120: Epithelial cell signaling in Helicobacter pylori infection	−0.0733	−0.3299	−1.1696	−1.8166	6.05	8.38	8.3	8.05	7.21	6.56	3
207992_s_at	AMPD3	adenosine monophosphate deaminase (isoform E)	NM_000480	272	Hs.501890	GO:0006196: AMP catabolic process, GO:0009117: nucleotide metabolic process, GO:0009168: purine ribonucleoside monophosphate biosynthetic process, GO:0003876: AMP deaminase activity, GO:0016787: hydrolase activity	00230: Purine metabolism	0.0591	−0.3697	−0.7897	−1.29	7.82	9.17	9.23	8.8	8.38	7.88	3
206421_s_at	SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	NM_003784	8710	Hs.138202	GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity		−0.0698	−0.49	−1.0346	−1.6552	10.69	12.11	12.04	11.62	11.07	10.45	3

(*Continued*)

TABLE E2. (*Continued*)

206553_at	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	NM_002535	4939	Hs.414332	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006401: RNA catabolic process, GO:0006955: immune response, GO:0005739: mitochondrion, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0001730: 2'-5'-oligoadenylate synthetase activity, GO:0003723: RNA binding, GO:0005524: ATP binding, GO:0016740: transferase activity		−0.0981	−0.3701	−1.0466	−1.6447	3.12	4.98	4.88	4.61	3.93	3.33	3
205064_at	SPRR1B	small proline-rich protein 1B (cornifin)	NM_003125	6699	Hs.1076	GO:0008544: epidermis development, GO:0018149: peptide cross-linking, GO:0030216: keratinocyte differentiation, GO:0031424: keratinization, GO:0001533: cornified envelope, GO:0005737: cytoplasm, GO:0005882: intermediate filament, GO:0005198: structural molecule activity, GO:0030674: protein binding, bridging		−0.1584	−0.35	−0.8422	−1.3789	12.64	14.2	14.05	13.86	13.36	12.83	3
205590_at	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	NM_005739	10125	Hs.591127	GO:0007265: Ras protein signal transduction, GO:0051056: regulation of small GTPase mediated signal transduction, GO:0005622: intracellular, GO:0005624: membrane fraction, GO:0005088: Ras guanyl-nucleotide exchange factor activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0008289: lipid binding	04010: MAPK signaling pathway, 04660: T cell receptor signaling pathway	0.026	−0.2827	−0.6119	−1.0556	8.49	9.53	9.55	9.25	8.92	8.47	3
204415_at	IFI6	interferon, alpha-inducible protein 6	NM_022873	2537	Hs.510635, Hs.511731, Hs.523847	GO:0001836: release of cytochrome c from mitochondria, GO:0006916: anti-apoptosis, GO:0006955: immune response, GO:0043154: negative regulation of caspase activity, GO:0051902: negative regulation of mitochondrial depolarization, GO:0005739: mitochondrion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding		−0.3667	−0.6305	−1.9477	−3.0656	7.08	10.47	10.11	9.84	8.53	7.41	3
204478_s_at	RABIF	RAB interacting factor	U74324	5877	Hs.90875	GO:0006944: membrane fusion, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.1064	−0.2762	−0.8265	−1.2814	6.75	7.87	7.77	7.6	7.05	6.59	3
203665_at	HMOX1	heme oxygenase (decycling) 1	NM_002133	3162	Hs.517581	GO:0006788: heme oxidation, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005624: membrane fraction, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0004392: heme oxygenase (decyclizing) activity, GO:0004871: signal transducer activity, GO:0005506: iron ion binding, GO:0016491: oxidoreductase activity, GO:0046872: metal ion binding	00860: Porphyrin and chlorophyll metabolism	0.1426	−0.2745	−0.8354	−1.4768	8.37	10.09	10.23	9.81	9.25	8.61	3

(*Continued*)

TABLE E2. (*Continued*)

203740_at	MPHOSPH6	M-phase phosphoprotein 6	NM_005792	10200	Hs.344400	GO:0000074: regulation of progression through cell cycle, GO:0000087: M phase of mitotic cell cycle, GO:0005737: cytoplasm, GO:0005515: protein binding		−0.1287	−0.4364	−0.978	−1.6339	9.4	11.01	10.88	10.57	10.03	9.37	3
202788_at	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	NM_004635	7867	Hs.234521	GO:0006468: protein amino acid phosphorylation, GO:0006950: response to stress, GO:0007165: signal transduction, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004708: MAP kinase kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04370: VEGF signaling pathway	−0.0128	−0.1928	−0.6185	−1.0073	10.1	11.17	11.16	10.98	10.55	10.16	3
202831_at	GPX2	glutathione peroxidase 2 (gastrointestinal)	NM_002083	2877	Hs.2704	GO:0006979: response to oxidative stress, GO:0005737: cytoplasm, GO:0004602: glutathione peroxidase activity, GO:0008430: selenium binding, GO:0009055: electron carrier activity	00480: Glutathione metabolism, 00590: Arachidonic acid metabolism	0.0653	−0.6605	−1.4772	−2.2976	5.27	8.01	8.08	7.35	6.54	5.72	3
201243_s_at	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	NM_001677	481	Hs.291196	GO:0006811: ion transport, GO:0006813: potassium ion transport, GO:0006814: sodium ion transport, GO:0005890: sodium:potassium-exchanging ATPase complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005391: sodium:potassium-exchanging ATPase activity, GO:0030955: potassium ion binding, GO:0031402: sodium ion binding		0.0305	−0.2603	−0.7307	−1.1893	11.88	12.6	12.63	12.34	11.87	11.41	3
201274_at	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5	NM_002790	5686	Hs.485246	GO:0006511: ubiquitin-dependent protein catabolic process, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0005839: proteasome core complex (sensu Eukaryota), GO:0004298: threonine endopeptidase activity	03050: Proteasome	−0.0525	−0.3458	−0.7379	−1.2267	8.89	9.95	9.9	9.61	9.21	8.72	3
200734_s_at	ARF3	ADP-ribosylation factor 3	BG341906	377	Hs.119177	GO:0006888: ER to Golgi vesicle-mediated transport, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0005622: intracellular, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding	05110: Cholera - Infection	−0.0955	−0.2696	−0.8358	−1.2383	8.33	9.52	9.43	9.25	8.69	8.28	3
200776_s_at	LOC151579	similar to basic leucine zipper and W2 domains 1	AL518328	151579	Hs.529231			−0.33	−0.5483	−1.0294	−2.0275	10.4	11.81	11.48	11.26	10.78	9.78	3
220664_at	SPRR2C	small proline-rich protein 2C	NM_006518	6702	Hs.592363	GO:0007566: embryo implantation, GO:0008544: epidermis development, GO:0009411: response to UV, GO:0030216: keratinocyte differentiation, GO:0042698: menstrual cycle, GO:0051258: protein polymerization, GO:0001533: cornified envelope, GO:0005737: cytoplasm, GO:0003676: nucleic acid binding, GO:0005198: structural molecule activity, GO:0046872: metal ion binding, GO:0046983: protein dimerization activity		−0.2038	−0.9789	−3.2291	−5.22	7.97	13.44	13.24	12.46	10.21	8.22	3

(*Continued*)

TABLE E2. (*Continued*)

220944_at	PGLYRP4	peptidoglycan recognition protein 4	NM_020393	57115	Hs.58356	GO:0009253: peptidoglycan catabolic process, GO:0016045: detection of bacterium, GO:0045087: innate immune response, GO:0050830: defense response to Gram-positive bacterium, GO:0005622: intracellular, GO:0016020: membrane, GO:0005515: protein binding, GO:0008745: N-acetylmuramoyl-L-alanine amidase activity, GO:0016019: peptidoglycan receptor activity	0.2539	−0.1798	−1.0754	−1.753	6.31	8.24	8.49	8.06	7.16	6.48	3
220239_at	KLHL7	kelch-like 7 (Drosophila)	NM_018846	55975	Hs.654817	GO:0005730: nucleolus, GO:0005515: protein binding	0.0224	−0.119	−0.6264	−1.0553	5.85	6.41	6.44	6.29	5.79	5.36	3
220318_at	EPN3	epsin 3	NM_017957	55040	Hs.670090	GO:0005737: cytoplasm, GO:0031410: cytoplasmic vesicle, GO:0008289: lipid binding	−0.0641	−0.3608	−1.1773	−2.0166	6.11	8.15	8.08	7.79	6.97	6.13	3
219799 _s_at	DHRS9	dehydrogenase/reductase (SDR family) member 9	NM_005771	10170	Hs.179608	GO:0008152: metabolic process, GO:0008209: androgen metabolic process, GO:0008209: androgen metabolic process, GO:0030855: epithelial cell differentiation, GO:0042448: progesterone metabolic process, GO:0042572: retinol metabolic process, GO:0042904: 9-cis-retinoic acid biosynthetic process, GO:0042904: 9-cis-retinoic acid biosynthetic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0005792: microsome, GO:0016020: membrane, GO:0030176: integral to endoplasmic reticulum membrane, GO:0030176: integral to endoplasmic reticulum membrane, GO:0004022: alcohol dehydrogenase activity, GO:0004022: alcohol dehydrogenase activity, GO:0004745: retinol dehydrogenase activity, GO:0004745: retinol dehydrogenase activity, GO:0016491: oxidoreductase activity, GO:0016854: racemase and epimerase activity, GO:0047035: 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity, GO:0047035: 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity	0.0238	−0.5508	−1.2324	−1.9448	5.99	7.8	7.82	7.24	6.56	5.85	3
220013_at	ABHD9	abhydrolase domain containing 9	NM_024794	79852	Hs.156457	GO:0006725: aromatic compound metabolic process, GO:0016787: hydrolase activity	−0.0376	−0.2218	−0.776	−1.2435	9.93	11.21	11.17	10.98	10.43	9.96	3
219352_at	HERC6	hect domain and RLD 6	NM_017912	55008	Hs.529317	GO:0006464: protein modification process, GO:0006512: ubiquitin cycle, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0004842: ubiquitin-protein ligase activity, GO:0016874: ligase activity	0.0237	−0.5422	−2.1085	−3.6584	5.53	9.97	10	9.43	7.86	6.31	3
219795_at	SLC6A14	solute carrier family 6 (amino acid transporter), member 14	NM_007231	11254	Hs.522109	GO:0006520: amino acid metabolic process, GO:0006836: neurotransmitter transport, GO:0006865: amino acid transport, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005328: neurotransmitter:sodium symporter activity, GO:0015171: amino acid transmembrane transporter activity, GO:0015293: symporter activity	−0.3801	−1.1472	−2.7149	−4.2559	8.03	11.71	11.33	10.57	9	7.46	3

(*Continued*)

TABLE E2. (*Continued*)

218890_x_at	MRPL35	mitochondrial ribosomal protein L35	NM_016622	51318	Hs.433439	GO:0006412: translation, GO:0005739: mitochondrion, GO:0005761: mitochondrial ribosome, GO:0030529: ribonucleoprotein complex, GO:0003735: structural constituent of ribosome, GO:0045182: translation regulator activity		0.1464	−0.2047	−0.8676	−1.4883	6.66	7.82	7.97	7.61	6.95	6.33	3
219015_s_at	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	BC005336	55849	Hs.659791	GO:0005975: carbohydrate metabolic process, GO:0030259: lipid glycosylation, GO:0016758: transferase activity, transferring hexosyl groups, GO:0030246: carbohydrate binding	00510: N-Glycan biosynthesis, 01030: Glycan structures - biosynthesis 1	−0.2553	−0.2297	−0.8312	−2.1069	6.2	7.3	7.05	7.07	6.47	5.2	3
218817_at	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	NM_021928	60559	Hs.42194	GO:0006465: signal peptide processing, GO:0005783: endoplasmic reticulum, GO:0005787: signal peptidase complex, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0009003: signal peptidase activity	00310: Lysine degradation, 00780: Biotin metabolism	−0.0355	−0.3567	−1.0374	−1.6935	3.94	5.48	5.45	5.13	4.45	3.79	3
218856_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	NM_016629	27242	Hs.443577	GO:0006915: apoptosis, GO:0007165: signal transduction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0005515: protein binding	04060: Cytokine-cytokine receptor interaction	−0.0943	−0.3459	−0.7567	−1.2199	7.47	9.3	9.21	8.95	8.54	8.08	3
218542_at	CEP55	centrosomal protein 55kDa	NM_018131	55165	Hs.14559	GO:0007049: cell cycle, GO:0007067: mitosis, GO:0051301: cell division		−0.3426	−0.8136	−1.1987	−2.2196	4.98	6.72	6.37	5.9	5.52	4.5	3
218719_s_at	GINS3	GINS complex subunit 3 (Psf3 homolog)	NM_022770	64785	Hs.47125			−0.0037	−0.145	−0.7614	−1.3069	4.28	5.61	5.61	5.47	4.85	4.31	3
218400_at	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	NM_006187	4940	Hs.528634	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006955: immune response, GO:0005792: microsome, GO:0003723: RNA binding, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0016779: nucleotidyltransferase activity		−0.0076	−0.4164	−1.5573	−2.6043	6.46	9.69	9.68	9.28	8.13	7.09	3
218512_at	WDR12	WD repeat domain 12	NM_018256	55759	Hs.73291			−0.133	−0.3383	−0.6972	−1.067	7.96	8.8	8.67	8.47	8.11	7.74	3
217315_s_at	KLK13	kallikrein-related peptidase 13	AL050220	26085	Hs.165296	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0005576: extracellular region, GO:0005737: cytoplasm, GO:0004252: serine-type endopeptidase activity, GO:0004252: serine-type endopeptidase activity, GO:0005515: protein binding, GO:0008233: peptidase activity		−0.1919	−1.2919	−3.0025	−4.6405	4.34	9.11	8.92	7.82	6.11	4.47	3
217475_s_at	LIMK2	LIM domain kinase 2	AC002073	3985	Hs.474596	GO:0006468: protein amino acid phosphorylation, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004672: protein kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008270: zinc ion binding, GO:0016740: transferase activity, GO:0046872: metal ion binding	04360: Axon guidance, 04810: Regulation of actin cytoskeleton	0.0793	−0.2632	−0.714	−1.1241	5.63	6.53	6.61	6.27	5.82	5.41	3

(*Continued*)

TABLE E2. (*Continued*)

215891_s_at	GM2A	GM2 ganglioside activator	X61094	2760	Hs.483873	GO:0006687: glycosphingolipid metabolic process, GO:0006689: ganglioside catabolic process, GO:0007611: learning and/or memory, GO:0009313: oligosaccharide catabolic process, GO:0019377: glycolipid catabolic process, GO:0019915: sequestering of lipid, GO:0030149: sphingolipid catabolic process, GO:0050877: neurological process, GO:0050885: regulation of balance, GO:0005739: mitochondrion, GO:0005764: lysosome, GO:0004563: beta-N-acetylhexosaminidase activity, GO:0030290: sphingolipid activator protein activity		0.1151	−1.2219	−2.4302	−4.5408	4.5	9.5	9.62	8.28	7.07	4.96	3
215966_x_at	GK3P	glycerol kinase 3 pseudogene	AA292874	2713	Hs.654557	GO:0005975: carbohydrate metabolic process, GO:0006072: glycerol-3-phosphate metabolic process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004370: glycerol kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity		0.1302	−0.7199	−1.5512	−2.4467	4.96	7.58	7.71	6.86	6.02	5.13	3
213696_s_at	MED8	mediator complex subunit 8	AA421957	112950	Hs.301756	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0000119: mediator complex, GO:0004872: receptor activity		−0.1433	−0.5009	−1.1378	−2.0274	7.44	9.28	9.14	8.78	8.14	7.25	3
213710_s_at			AL523275					−0.2267	−0.305	−0.6177	−1.0771	7.32	7.55	7.32	7.25	6.93	6.47	3
208012_x_at	SP110	SP110 nuclear body protein	NM_004509	3431	Hs.145150	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0045454: cell redox homeostasis, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0005062: hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.2067	−0.006	−0.5142	−1.0079	7.16	8.3	8.5	8.29	7.78	7.29	3
208967_s_at	AK2	adenylate kinase 2	U39945	204	Hs.470907	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0005739: mitochondrion, GO:0005743: mitochondrial inner membrane, GO:0000166: nucleotide binding, GO:0004017: adenylate kinase activity, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0019206: nucleoside kinase activity	00230: Purine metabolism	−0.062	−0.3133	−0.7031	−1.1031	9.15	10.11	10.05	9.8	9.41	9.01	3
205513_at	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	NM_001062	6947	Hs.2012	GO:0006811: ion transport, GO:0006824: cobalt ion transport, GO:0015889: cobalamin transport, GO:0015087: cobalt ion transmembrane transporter activity, GO:0031419: cobalamin binding, GO:0050897: cobalt ion binding		−0.022	−1.5334	−5.3007	−7.9084	3.88	12.4	12.38	10.87	7.1	4.49	3

(*Continued*)

TABLE E2. (*Continued*)

205863_at	S100A12	S100 calcium binding protein A12	NM_005621	6283	Hs.19413	GO:0006805: xenobiotic metabolic process, GO:0006954: inflammatory response, GO:0042742: defense response to bacterium, GO:0050832: defense response to fungus, GO:0005626: insoluble fraction, GO:0005829: cytosol, GO:0005509: calcium ion binding, GO:0008270: zinc ion binding		0.1155	−1.3388	−4.9461	−7.1078	2.8	10.98	11.1	9.65	6.04	3.88	3
204058_at	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	AL049699	4199	Hs.21160	GO:0005975: carbohydrate metabolic process, GO:0006108: malate metabolic process, GO:0006741: NADP biosynthetic process, GO:0009725: response to hormone stimulus, GO:0009743: response to carbohydrate stimulus, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0004473: malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity, GO:0004473: malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity, GO:0009055: electron carrier activity, GO:0030145: manganese ion binding, GO:0043531: ADP binding, GO:0046872: metal ion binding, GO:0050661: NADP binding, GO:0051287: NAD binding	00620: Pyruvate metabolism, 00710: Carbon fixation, 03320: PPAR signaling pathway	−0.0373	−0.2537	−0.7759	−1.1754	10.21	11.0411	10.79	10.26	9.86	3
204385_at	KYNU	kynureninase (L-kynurenine hydrolase)	NM_003937	8942	Hs.470126	GO:0006569: tryptophan catabolic process, GO:0008152: metabolic process, GO:0009435: NAD biosynthetic process, GO:0005737: cytoplasm, GO:0008233: peptidase activity, GO:0008483: transaminase activity, GO:0016787: hydrolase activity, GO:0030170: pyridoxal phosphate binding, GO:0030429: kynureninase activity	00380: Tryptophan metabolism	0.0308	−1.0317	−2.381	−4.2639	3.85	8.84	8.88	7.81	6.46	4.58	3
218448_at	C20orf11	chromosome 20 open reading frame 11	NM_017896	54994	Hs.353013	GO:0005515: protein binding		−0.0266	−0.3124	−0.6784	−1.0137	9.59	10.65	10.63	10.34	9.98	9.64	3
218943_s_at	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	NM_014314	23586	Hs.190622	GO:0009615: response to virus, GO:0045087: innate immune response, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008026: ATP-dependent helicase activity, GO:0016787: hydrolase activity, GO:0017111: nucleoside-triphosphatase activity		−0.0427	−0.4359	−1.2525	−1.8872	6.88	8.93	8.89	8.49	7.68	7.04	3

(*Continued*)

TABLE E2. (*Continued*)

219095_at	PLA2G4B	phospholipase A2, group IVB (cytosolic)	NM_005090	8681	Hs.198161	GO:0006954: inflammatory response, GO:0007567: parturition, GO:0016042: lipid catabolic process, GO:0019369: arachidonic acid metabolic process, GO:0019722: calcium-mediated signaling, GO:0046475: glycerophospholipid catabolic process, GO:0005576: extracellular region, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005768: endosome, GO:0005829: cytosol, GO:0016020: membrane, GO:0004622: lysophospholipase activity, GO:0005509: calcium ion binding, GO:0005544: calcium-dependent phospholipid binding, GO:0016787: hydrolase activity, GO:0047498: calcium-dependent phospholipase A2 activity		−0.0181	−0.4798	−1.1725	−1.6454	8.85	10.52	10.51	10.05	9.35	8.88	3
219691_at	SAMD9	sterile alpha motif domain containing 9	NM_017654	54809	Hs.65641			−0.0557	−0.8265	−1.8501	−2.7219	5.23	8.31	8.25	7.48	6.46	5.59	3
214512_s_at	SUB1	SUB1 homolog (S. cerevisiae)	NM_006713	10923	Hs.229641	GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0005667: transcription factor complex, GO:0003677: DNA binding, GO:0003697: single-stranded DNA binding, GO:0003713: transcription coactivator activity, GO:0005515: protein binding		−0.1959	−0.437	−0.7261	−1.2782	11.15	12.29	12.09	11.85	11.56	11.01	3
214583_at	RSC1A1	regulatory solute carrier protein, family 1, member 1	AI268381	6248	Hs.145049, Hs.657818	GO:0006810: transport, GO:0051051: negative regulation of transport, GO:0008200: ion channel inhibitor activity		0.006	−0.2778	−0.7701	−1.2088	5.26	6.4	6.4	6.12	5.63	5.19	3
217919_s_at	MRPL42	mitochondrial ribosomal protein L42	AL136659	28977	Hs.199579	GO:0006412: translation, GO:0005739: mitochondrion, GO:0005763: mitochondrial small ribosomal subunit, GO:0030529: ribonucleoprotein complex, GO:0003735: structural constituent of ribosome		0.062	−0.1568	−0.6045	−1.7051	8.2	9.3	9.36	9.14	8.69	7.59	3
208456_s_at	RRAS2	related RAS viral (r-ras) oncogene homolog 2	NM_012250	22800	Hs.502004	GO:0007265: Ras protein signal transduction, GO:0009987: cellular process, GO:0005622: intracellular, GO:0005783: endoplasmic reticulum, GO:0005886: plasma membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding	04010: MAPK signaling pathway, 04530: Tight junction, 04810: Regulation of actin cytoskeleton	−0.1916	−0.2348	−0.3938	−1.0556	5.9	6.63	6.44	6.4	6.24	5.57	3
208539_x_at	SPRR2D	small proline-rich protein 2D	NM_006945	6703	Hs.505327	GO:0007566: embryo implantation, GO:0008544: epidermis development, GO:0030216: keratinocyte differentiation, GO:0031424: keratinization, GO:0042698: menstrual cycle, GO:0001533: cornified envelope, GO:0005737: cytoplasm, GO:0005198: structural molecule activity		−0.0086	−0.235	−1.0834	−2.9082	13.13	15.59	15.59	15.36	14.51	12.69	3

(*Continued*)

TABLE E2. (*Continued*)

213927_at	MAP3K9	mitogen-activated protein kinase kinase kinase 9	AV753204	4293	Hs.445496, Hs.593542	GO:0007257: activation of JNK activity, GO:0046777: protein amino acid autophosphorylation, GO:0005575: cellular_component, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004706: JUN kinase kinase kinase activity, GO:0004708: MAP kinase kinase activity, GO:0004713: protein-tyrosine kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0042803: protein homodimerization activity		0.0224	−0.1132	−0.5637	−1.4096	8.27	9.45	9.47	9.34	8.88	8.04	3
216804 _s_at	PDLIM5	PDZ and LIM domain 5	AK027217	10611	Hs.480311	GO:0005624: membrane fraction, GO:0005829: cytosol, GO:0015629: actin cytoskeleton, GO:0003779: actin binding, GO:0005080: protein kinase C binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0042805: actinin binding, GO:0046872: metal ion binding		−0.1713	−0.2164	−0.4325	−1.0838	9.08	9.41	9.24	9.2	8.98	8.33	3
209363 _s_at	MED21	mediator complex subunit 21	U46837	9412	Hs.286145	GO:0006350: transcription, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0000119: mediator complex, GO:0005665: DNA-directed RNA polymerase II, core complex, GO:0003702: RNA polymerase II transcription factor activity, GO:0003713: transcription coactivator activity, GO:0003899: DNA-directed RNA polymerase activity, GO:0005515: protein binding		0.0264	−0.0724	−0.406	−1.0627	6.88	7.59	7.62	7.52	7.19	6.53	3
211075 _s_at	CD47	CD47 molecule	Z25521	961	Hs.446414	GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0008228: opsonization, GO:0008284: positive regulation of cell proliferation, GO:0022409: positive regulation of cell-cell adhesion, GO:0050766: positive regulation of phagocytosis, GO:0050870: positive regulation of T cell activation, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005515: protein binding	04512: ECM-receptor interaction	−0.0456	−0.3328	−0.8232	−1.5667	10.23	11.84	11.8	11.51	11.02	10.28	3
207181 _s_at	CASP7	caspase 7, apoptosis-related cysteine peptidase	NM_001227	840	Hs.9216	GO:0001836: release of cytochrome c from mitochondria, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007507: heart development, GO:0008632: apoptotic program, GO:0009411: response to UV, GO:0005737: cytoplasm, GO:0005789: endoplasmic reticulum membrane, GO:0031966: mitochondrial membrane, GO:0005515: protein binding, GO:0008234: cysteine-type peptidase activity, GO:0030693: caspase activity	01510: Neurodegenerative Disorders, 04210: Apoptosis, 05010: Alzheimer's disease, 05050: Dentatorubropallidoluysian atrophy (DRPLA)	−0.0472	−0.225	−0.4387	−1.0822	8.13	8.85	8.8	8.63	8.41	7.77	3

(*Continued*)

TABLE E2. (*Continued*)

207387_s_at	GK	glycerol kinase	NM_000167	2710	Hs.1466	GO:0005975: carbohydrate metabolic process, GO:0006072: glycerol-3-phosphate metabolic process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity	00561: Glycerolipid metabolism, 03320: PPAR signaling pathway	0.1462	−0.6962	−1.3597	−3.4357	5.23	8.34	8.49	7.65	6.98	4.91	3
206164_at	CLCA2	chloride channel, calcium activated, family member 2	NM_006536	9635	Hs.241551	GO:0006810: transport, GO:0005887: integral to plasma membrane, GO:0005254: chloride channel activity	04740: Olfactory transduction	−0.1086	−0.2212	−0.5447	−1.2671	11.31	12.32	12.21	12.1	11.78	11.05	3
206166_s_at	CLCA2	chloride channel, calcium activated, family member 2	AF043977	9635	Hs.241551	GO:0006810: transport, GO:0005887: integral to plasma membrane, GO:0005254: chloride channel activity	04740: Olfactory transduction	−0.0757	−0.3576	−0.6929	−1.7213	10.97	12.5	12.42	12.14	11.8	10.77	3
216607_s_at	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	U40053	1595	Hs.417077		00100: Biosynthesis of steroids	−0.0891	−0.4047	−0.7435	−1.9791	8.79	9.83	9.74	9.43	9.09	7.85	3
217388_s_at	KYNU	kynureninase (L-kynurenine hydrolase)	D55639	8942	Hs.470126	GO:0006569: tryptophan catabolic process, GO:0008152: metabolic process, GO:0009435: NAD biosynthetic process, GO:0005737: cytoplasm, GO:0008233: peptidase activity, GO:0008483: transaminase activity, GO:0016787: hydrolase activity, GO:0030170: pyridoxal phosphate binding, GO:0030429: kynureninase activity	00380: Tryptophan metabolism	0.0191	−0.6804	−1.926	−4.1734	4.53	11.05	11.07	10.37	9.12	6.87	3
209208_at	MPDU1	mannose-P-dolichol utilization defect 1	AF059752	9526	Hs.632249	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding		0.1117	−0.1224	−0.3606	−1.0178	7.42	8.27	8.38	8.14	7.9	7.25	3
209872_s_at	PKP3	plakophilin 3	BF001503	11187	Hs.534395	GO:0007155: cell adhesion, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0030057: desmosome, GO:0005198: structural molecule activity, GO:0005515: protein binding		−0.2447	−0.3495	−0.8959	−1.8627	8.45	9.74	9.5	9.39	8.84	7.88	3
203125_x_at	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	AF046997	4891	Hs.505545	GO:0006810: transport, GO:0006811: ion transport, GO:0006826: iron ion transport, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005215: transporter activity, GO:0005381: iron ion transmembrane transporter activity, GO:0005506: iron ion binding		0.2531	−0.0734	−0.3637	−1.1031	4.41	5.34	5.59	5.26	4.97	4.23	3
203972_s_at	PEX3	peroxisomal biogenesis factor 3	AB035307	8504	Hs.7277	GO:0007031: peroxisome organization and biogenesis, GO:0007031: peroxisome organization and biogenesis, GO:0005777: peroxisome, GO:0005779: integral to peroxisomal membrane, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005515: protein binding		0.0009	−0.2276	−0.6007	−1.6097	9	9.75	9.76	9.53	9.15	8.14	3

(*Continued*)

TABLE E2. (*Continued*)

214070_s_at	ATP10B	ATPase, Class V, type 10B	AW006935	23120	Hs.109358	GO:0006810: transport, GO:0015914: phospholipid transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004012: phospholipid-translocating ATPase activity, GO:0005524: ATP binding, GO:0015662: ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, GO:0016787: hydrolase activity		0.2355	−0.1871	−0.5325	−1.5079	7.87	9.58	9.82	9.39	9.05	8.07	3
217202_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	U08626	2752	Hs.518525	GO:0001505: regulation of neurotransmitter levels, GO:0006542: glutamine biosynthetic process, GO:0006807: nitrogen compound metabolic process, GO:0005737: cytoplasm, GO:0004356: glutamate-ammonia ligase activity, GO:0016874: ligase activity	00251: Glutamate metabolism, 00550: Peptidoglycan biosynthesis, 00910: Nitrogen metabolism	0.112	−0.3011	−0.7001	−1.7208	8.69	10.22	10.33	9.92	9.52	8.5	3
209949_at	NCF2	neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2)	BC001606	4688	Hs.587558	GO:0006801: superoxide metabolic process, GO:0006968: cellular defense response, GO:0001669: acrosome, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0005488: binding, GO:0005515: protein binding, GO:0009055: electron carrier activity	04670: Leukocyte transendothelial migration	0.1263	−0.265	−0.4362	−1.4216	6.6	7.67	7.8	7.41	7.24	6.25	3
209970_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	M87507	834	Hs.2490	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007165: signal transduction, GO:0042981: regulation of apoptosis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0008234: cysteine-type peptidase activity, GO:0008656: caspase activator activity, GO:0030693: caspase activity, GO:0030693: caspase activity	01510: Neurodegenerative Disorders, 05040: Huntington's disease, 05050: Dentatorubropallidoluysian atrophy (DRPLA)	0.1834	−0.114	−0.3815	−1.1428	8.28	9.18	9.36	9.06	8.79	8.03	3
209142_s_at	UBE2G1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	BC002775	7326	Hs.462035	GO:0006464: protein modification process, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0004842: ubiquitin-protein ligase activity, GO:0016874: ligase activity		0.0798	−0.2291	−0.5178	−1.2634	9.95	10.94	11.02	10.72	10.43	9.68	3
209456_s_at	FBXW11	F-box and WD repeat domain containing 11	AB033281	23291	Hs.484138	GO:0016055: Wnt receptor signaling pathway, GO:0016567: protein ubiquitination, GO:0000151: ubiquitin ligase complex, GO:0005737: cytoplasm, GO:0004842: ubiquitin-protein ligase activity, GO:0005515: protein binding	04120: Ubiquitin mediated proteolysis, 04310: Wnt signaling pathway, 04340: Hedgehog signaling pathway	0.0131	−0.412	−0.8711	−2.3481	5.26	7.29	7.31	6.88	6.42	4.94	3

(*Continued*)

TABLE E2. (*Continued*)

206302_s_at	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	NM_019094	11163	Hs.591008	GO:0007242: intracellular signaling cascade, GO:0009187: cyclic nucleotide metabolic process, GO:0019722: calcium-mediated signaling, GO:0019935: cyclic-nucleotide-mediated signaling, GO:0046831: regulation of RNA export from nucleus, GO:0046907: intracellular transport, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0000287: magnesium ion binding, GO:0008486: diphosphoinositol-polyphosphate diphosphatase activity, GO:0016787: hydrolase activity, GO:0030145: manganese ion binding		0.1361	−0.2503	−0.5642	−1.6762	8.5	9.8710	9.62	9.3	8.19	3
206748_s_at	SPAG9	sperm associated antigen 9	NM_003971	9043	Hs.463439, Hs.593620	GO:0007283: spermatogenesis, GO:0005737: cytoplasm, GO:0016021: integral to membrane		−0.0613	−0.1606	−0.634	−1.4179	6.89	7.86	7.8	7.7	7.22	6.44	3
201487_at	CTSC	cathepsin C	NM_001814	1075	Hs.128065, Hs.656121	GO:0006508: proteolysis, GO:0006955: immune response, GO:0005764: lysosome, GO:0004197: cysteine-type endopeptidase activity, GO:0004214: dipeptidyl-peptidase I activity, GO:0008234: cysteine-type peptidase activity, GO:0031404: chloride ion binding		0.0804	−0.243	−0.4728	−1.3027	10.34	11.81	11.89	11.57	11.34	10.51	3
201739_at	SGK	serum/glucocorticoid regulated kinase	NM_005627	6446	Hs.510078	GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0006814: sodium ion transport, GO:0006915: apoptosis, GO:0006974: response to DNA damage stimulus, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity		0.0515	−0.2649	−0.5761	−1.3178	11.32	12.46	12.51	12.2	11.89	11.14	3
200803_s_at	TEGT	testis enhanced gene transcript (BAX inhibitor 1)	NM_003217	7009	Hs.35052	GO:0006915: apoptosis, GO:0043066: negative regulation of apoptosis, GO:0005626: insoluble fraction, GO:0005634: nucleus, GO:0005783: endoplasmic reticulum, GO:0005887: integral to plasma membrane, GO:0016020: membrane		0.0573	−0.1967	−0.496	−1.3447	11.45	12.01	12.06	11.81	11.51	10.66	3
200806_s_at	HSPD1	heat shock 60kDa protein 1 (chaperonin)	BE256479	3329	Hs.595053, Hs.632539	GO:0006457: protein folding, GO:0006457: protein folding, GO:0006986: response to unfolded protein, GO:0030150: protein import into mitochondrial matrix, GO:0042981: regulation of apoptosis, GO:0044267: cellular protein metabolic process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0051082: unfolded protein binding, GO:0051082: unfolded protein binding, GO:0051087: chaperone binding	04940: Type I diabetes mellitus, 05060: Prion disease	−0.1896	−0.389	−0.6222	−1.4957	10.54	11.08	10.89	10.69	10.46	9.58	3

(*Continued*)

TABLE E2. (*Continued*)

200648_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	NM_002065	2752	Hs.518525	GO:0001505: regulation of neurotransmitter levels, GO:0006542: glutamine biosynthetic process, GO:0006807: nitrogen compound metabolic process, GO:0005737: cytoplasm, GO:0004356: glutamate-ammonia ligase activity, GO:0016874: ligase activity	00251: Glutamate metabolism, 00550: Peptidoglycan biosynthesis, 00910: Nitrogen metabolism	0.1023	−0.4026	−0.7409	−1.8411	10.12	11.61	11.72	11.21	10.87	9.77	3
200669_s_at	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	NM_003340	7323	Hs.518773	GO:0006464: protein modification process, GO:0006464: protein modification process, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0004842: ubiquitin-protein ligase activity, GO:0005515: protein binding, GO:0016874: ligase activity, GO:0019787: small conjugating protein ligase activity	04120: Ubiquitin mediated proteolysis	−0.0279	−0.2019	−0.3961	−1.0796	11.04	11.72	11.69	11.51	11.32	10.64	3
217028_at	CXCR4	chemokine (C-X-C motif) receptor 4	AJ224869	7852	Hs.593413	GO:0000187: activation of MAPK activity, GO:0001569: patterning of blood vessels, GO:0001667: ameboidal cell migration, GO:0001764: neuron migration, GO:0006915: apoptosis, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0007281: germ cell development, GO:0007420: brain development, GO:0008045: motor axon guidance, GO:0008354: germ cell migration, GO:0009615: response to virus, GO:0030334: regulation of cell migration, GO:0042098: T cell proliferation, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0030426: growth cone, GO:0031252: leading edge, GO:0001584: rhodopsin-like receptor activity, GO:0003779: actin binding, GO:0005515: protein binding, GO:0015026: coreceptor activity, GO:0016493: C-C chemokine receptor activity, GO:0016494: C-X-C chemokine receptor activity, GO:0032027: myosin light chain binding	04060: Cytokine-cytokine receptor interaction, 04360: Axon guidance, 04670: Leukocyte transendothelial migration	0.0914	−0.4205	−0.8809	−2.397	5	8.26	8.35	7.84	7.38	5.86	3
218095_s_at	TMEM165	transmembrane protein 165	BC003545	55858	Hs.479766	GO:0016020: membrane, GO:0016021: integral to membrane		0.0686	−0.2171	−0.5059	−1.109	10.4	11.38	11.45	11.17	10.88	10.27	3
214697_s_at	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	AW190873	9991	Hs.269988	GO:0006397: mRNA processing, GO:0009653: anatomical structure morphogenesis, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003723: RNA binding, GO:0003723: RNA binding		0.0913	−0.2497	−0.7724	−2.3008	6.42	8.36	8.45	8.11	7.59	6.06	3

(*Continued*)

TABLE E2. (*Continued*)

216640_s_at	PDIA6	protein disulfide isomerase family A, member 6	AK026926	10130	Hs.212102	GO:0006457: protein folding, GO:0045454: cell redox homeostasis, GO:0005783: endoplasmic reticulum, GO:0005793: ER-Golgi intermediate compartment, GO:0003756: protein disulfide isomerase activity, GO:0005515: protein binding, GO:0016853: isomerase activity		−0.1805	−0.2852	−0.4955	−1.0592	10.46	11.1	10.91	10.81	10.6	10.04	3
213060_s_at	CHI3L2	chitinase 3-like 2	U58515	1117	Hs.514840	GO:0005975: carbohydrate metabolic process, GO:0006032: chitin catabolic process, GO:0005615: extracellular space, GO:0004568: chitinase activity, GO:0016787: hydrolase activity, GO:0043169: cation binding		0.2914	−0.4468	−1.6127	−4.2711	6.79	10.28	10.57	9.84	8.67	6.01	3
213320_at	PRMT3	protein arginine methyltransferase 3	AL551971	10196	Hs.152337	GO:0008152: metabolic process, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0003676: nucleic acid binding, GO:0008168: methyltransferase activity, GO:0008270: zinc ion binding, GO:0016274: protein-arginine N-methyltransferase activity, GO:0016740: transferase activity, GO:0046872: metal ion binding	00150: Androgen and estrogen metabolism, 00340: Histidine metabolism, 00350: Tyrosine metabolism, 00380: Tryptophan metabolism, 00440: Aminophosphonate metabolism, 00450: Selenoamino acid metabolism, 00626: Naphthalene and anthracene degradation	0.0317	−0.2613	−0.4794	−1.178	7.26	7.77	7.8	7.51	7.29	6.59	3
210951_x_at	RAB27A	RAB27A, member RAS oncogene family	AF125393	5873	Hs.654978	GO:0006605: protein targeting, GO:0007264: small GTPase mediated signal transduction, GO:0007596: blood coagulation, GO:0015031: protein transport, GO:0016192: vesicle-mediated transport, GO:0030318: melanocyte differentiation, GO:0032400: melanosome localization, GO:0032402: melanosome transport, GO:0043316: cytotoxic T cell degranulation, GO:0043320: natural killer cell degranulation, GO:0043473: pigmentation, GO:0001750: photoreceptor outer segment, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0030141: secretory granule, GO:0030425: dendrite, GO:0042470: melanosome, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0031489: myosin V binding		0.111	−0.4442	−1.1753	−3.2742	7.39	9.74	9.85	9.3	8.57	6.47	3
211676_s_at	IFNGR1	interferon gamma receptor 1	AF056979	3459	Hs.520414	GO:0007165: signal transduction, GO:0009615: response to virus, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004872: receptor activity, GO:0004906: interferon-gamma receptor activity, GO:0019955: cytokine binding	04060: Cytokine-cytokine receptor interaction, 04630: Jak-STAT signaling pathway, 04650: Natural killer cell mediated cytotoxicity	0.0923	−0.2188	−0.3392	−1.1313	10.39	11.36	11.45	11.14	11.02	10.22	3
210594_x_at	MPZL1	myelin protein zero-like 1	AF239756	9019	Hs.493919	GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007267: cell-cell signaling, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005198: structural molecule activity, GO:0005515: protein binding	04514: Cell adhesion molecules (CAMs)	0.0039	−0.277	−0.5057	−1.3954	5.96	7.17	7.17	6.89	6.66	5.77	3
210638_s_at	FBXO9	F-box protein 9	AF176704	26268	Hs.216653	GO:0016567: protein ubiquitination, GO:0000151: ubiquitin ligase complex, GO:0004842: ubiquitin-protein ligase activity		0.1061	−0.1645	−0.4677	−1.1038	9.92	10.82	10.93	10.65	10.35	9.72	3

(*Continued*)

TABLE E2. (*Continued*)

207098_s_at	MFN1	mitofusin 1	NM_017927	55669	Hs.478383	GO:0008053: mitochondrial fusion, GO:0008150: biological_process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019867: outer membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding, GO:0016787: hydrolase activity	0.0303	−0.1547	−0.4679	−1.3198	8.9	9.66	9.69	9.5	9.19	8.34	3
209520_s_at	NCBP1	nuclear cap binding protein subunit 1, 80kDa	BC001450	4686	Hs.595669, Hs.686479	GO:0006379: mRNA cleavage, GO:0006406: mRNA export from nucleus, GO:0006810: transport, GO:0008380: RNA splicing, GO:0016070: RNA metabolic process, GO:0031442: positive regulation of mRNA 3'-end processing, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0000339: RNA cap binding, GO:0005515: protein binding	0.147	−0.217	−0.5972	−1.8553	6.31	7.59	7.74	7.38	7	5.74	3
204905_s_at	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	NM_004280	9521	Hs.631818	GO:0006412: translation, GO:0008285: negative regulation of cell proliferation, GO:0043065: positive regulation of apoptosis, GO:0043517: positive regulation of DNA damage response, signal transduction by p53 class mediator, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005515: protein binding	−0.2272	−0.3057	−0.633	−1.074	9.1	9.57	9.34	9.26	8.93	8.49	3
205126_at	VRK2	vaccinia related kinase 2	NM_006296	7444	Hs.694816	GO:0046777: protein amino acid autophosphorylation, GO:0005624: membrane fraction, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	−0.0945	−0.3209	−0.5636	−1.2966	8.35	9.12	9.03	8.8	8.56	7.83	3
221962_s_at	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	AI829920	7328	Hs.643548	GO:0006464: protein modification process, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0004842: ubiquitin-protein ligase activity, GO:0016874: ligase activity, GO:0019787: small conjugating protein ligase activity	0.011	−0.266	−0.7616	−1.8603	6.95	8.75	8.76	8.49	7.99	6.89	3
200889_s_at	SSR1	signal sequence receptor, alpha (translocon-associated protein alpha)	NM_003144	6745	Hs.114033	GO:0006613: cotranslational protein targeting to membrane, GO:0008284: positive regulation of cell proliferation, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005048: signal sequence binding, GO:0005509: calcium ion binding	−0.1872	−0.2568	−0.5524	−1.424	9.48	10.56	10.38	10.31	10.01	9.14	3
200987_x_at	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	AA758755	10197	Hs.152978	GO:0000502: proteasome complex (sensu Eukaryota), GO:0005829: cytosol, GO:0008537: proteasome activator complex, GO:0008538: proteasome activator activity, GO:0042802: identical protein binding	−0.2278	−0.3452	−0.903	−1.6526	7.64	8.89	8.66	8.54	7.98	7.23	3
219648_at	MREG	melanoregulin	NM_018000	55686	Hs.281680, Hs.693918	GO:0016020: membrane	0.0559	−0.1643	−0.4342	−1.1126	10.14	11.13	11.19	10.97	10.7	10.02	3

(*Continued*)

TABLE E2. (*Continued*)

219960_s_at	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	NM_015984	51377	Hs.591458	GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0005622: intracellular, GO:0005829: cytosol, GO:0043234: protein complex, GO:0004221: ubiquitin thiolesterase activity, GO:0005515: protein binding, GO:0008234: cysteine-type peptidase activity, GO:0016787: hydrolase activity		−0.0332	−0.0537	−0.4499	−1.0811	8.73	9.28	9.24	9.22	8.83	8.19	3
214435_x_at	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	NM_005402	5898	Hs.6906	GO:0006935: chemotaxis, GO:0007165: signal transduction, GO:0007264: small GTPase mediated signal transduction, GO:0005622: intracellular, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005525: GTP binding	05212: Pancreatic cancer	−0.2744	−0.3859	−0.5349	−1.2155	8.8	9.65	9.38	9.27	9.12	8.44	3
214446_at	ELL2	elongation factor, RNA polymerase II, 2	NM_012081	22936	Hs.592742	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006368: RNA elongation from RNA polymerase II promoter, GO:0008023: transcription elongation factor complex, GO:0003702: RNA polymerase II transcription factor activity		−0.3688	−0.6199	−1.3186	−2.8069	5.01	7.43	7.06	6.81	6.11	4.62	3
212102_s_at	KPNA6	karyopherin alpha 6 (importin alpha 7)	BG403834	23633	Hs.470588	GO:0006607: NLS-bearing substrate import into nucleus, GO:0006886: intracellular protein transport, GO:0005634: nucleus, GO:0005643: nuclear pore, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0008565: protein transporter activity		−0.1595	−0.3262	−0.5198	−1.2935	5.24	5.96	5.8	5.64	5.44	4.67	3
212219_at	PSME4	proteasome (prosome, macropain) activator subunit 4	D38521	23198	Hs.413801	GO:0007275: multicellular organismal development, GO:0007283: spermatogenesis, GO:0030154: cell differentiation, GO:0005829: cytosol, GO:0043234: protein complex		0.0785	−0.2521	−0.3288	−1.0238	8.61	9.2	9.27	8.94	8.87	8.17	3
204240_s_at	SMC2	structural maintenance of chromosomes 2	NM_006444	10592	Hs.119023	GO:0006259: DNA metabolic process, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007076: mitotic chromosome condensation, GO:0051276: chromosome organization and biogenesis, GO:0051301: cell division, GO:0000228: nuclear chromosome, GO:0000796: condensin complex, GO:0000796: condensin complex, GO:0005694: chromosome, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0046982: protein heterodimerization activity		−0.1996	−0.294	−0.5705	−1.5955	5.75	6.61	6.41	6.31	6.04	5.01	3
204614_at	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	NM_002575	5055	Hs.594481	GO:0006916: anti-apoptosis, GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0008243: plasminogen activator activity		−0.0864	−0.2983	−0.5415	−1.2306	10.69	11.44	11.35	11.14	10.9	10.21	3
202430_s_at	PLSCR1	phospholipid scramblase 1	NM_021105	5359	Hs.130759	GO:0009615: response to virus, GO:0017121: phospholipid scrambling, GO:0030168: platelet activation, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0017128: phospholipid scramblase activity		0.0979	−0.1432	−0.4352	−1.2967	9.04	10.15	10.25	10.01	9.72	8.86	3

(*Continued*)

TABLE E2. (*Continued*)

202626 _s_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	AI356412	4067	Hs.491767	GO:0006468: protein amino acid phosphorylation, GO:0007242: intracellular signaling cascade, GO:0008284: positive regulation of cell proliferation, GO:0009725: response to hormone stimulus, GO:0030218: erythrocyte differentiation, GO:0042531: positive regulation of tyrosine phosphorylation of STAT protein, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004716: receptor signaling protein tyrosine kinase activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04662: B cell receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 04730: Long-term depression, 05120: Epithelial cell signaling in Helicobacter pylori infection	−0.0538	−0.5519	−0.9151	−1.8868	4.28	6.55	6.5	6	5.64	4.67	3
202269 _x_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	NM_002053	2633	Hs.62661	GO:0006955: immune response, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding, GO:0005525: GTP binding		−0.3674	−0.4126	−0.7589	−1.7199	8.44	10.21	9.84	9.79	9.45	8.49	3
202352 _s_at	PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	AI446530	5718	Hs.646575	GO:0005829: cytosol, GO:0005838: proteasome regulatory particle (sensu Eukaryota), GO:0005515: protein binding	03050: Proteasome	−0.1522	−0.2723	−0.6857	−1.2808	9.53	10.43	10.28	10.16	9.74	9.15	3
201048 _x_at	RAB6A	RAB6A, member RAS oncogene family	NM_002869	5870	Hs.12152, Hs.503222, Hs.535586	GO:0006888: ER to Golgi vesicle-mediated transport, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding		−0.2454	−0.4488	−0.7478	−1.8131	6.04	7.38	7.14	6.93	6.64	5.57	3
201195 _s_at	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	AB018009	8140	Hs.513797	GO:0006520: amino acid metabolic process, GO:0006810: transport, GO:0006810: transport, GO:0006865: amino acid transport, GO:0015804: neutral amino acid transport, GO:0005886: plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0015171: amino acid transmembrane transporter activity, GO:0015175: neutral amino acid transmembrane transporter activity, GO:0042605: peptide antigen binding		−0.4735	−0.6866	−1.0765	−2.5433	7.85	10.22	9.75	9.53	9.14	7.68	3
204761_at	USP6NL	USP6 N-terminal like	NM_014688	9712	Hs.498661	GO:0008150: biological_process, GO:0032313: regulation of Rab GTPase activity, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0003674: molecular_function, GO:0005096: GTPase activator activity, GO:0005097: Rab GTPase activator activity		−0.064	−0.1571	−0.6483	−1.2056	8.27	9.19	9.13	9.04	8.55	7.99	3

(*Continued*)

TABLE E2. (*Continued*)

204809_at	CLPX	ClpX caseinolytic peptidase X homolog (E. coli)	NM_006660	10845	Hs.113823	GO:0006457: protein folding, GO:0015031: protein transport, GO:0005739: mitochondrion, GO:0005743: mitochondrial inner membrane, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008270: zinc ion binding, GO:0042623: ATPase activity, coupled, GO:0046872: metal ion binding		−0.0681	−0.1645	−0.5342	−1.1751	9.98	10.74	10.68	10.58	10.21	9.57	3
203358 _s_at	EZH2	enhancer of zeste homolog 2 (Drosophila)	NM_004456	2146	Hs.444082	GO:0006325: establishment and/or maintenance of chromatin architecture, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0035098: ESC/E(Z) complex, GO:0003677: DNA binding, GO:0003677: DNA binding, GO:0005515: protein binding, GO:0042054: histone methyltransferase activity		−0.2466	−0.1706	−0.4083	−1.0938	7.22	7.88	7.63	7.71	7.47	6.79	3
203770 _s_at	STS	steroid sulfatase (microsomal), isozyme S	NM_000351	412	Hs.522578	GO:0006629: lipid metabolic process, GO:0006706: steroid catabolic process, GO:0007565: female pregnancy, GO:0008152: metabolic process, GO:0008544: epidermis development, GO:0005624: membrane fraction, GO:0005764: lysosome, GO:0005768: endosome, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0005794: Golgi apparatus, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0004773: steryl-sulfatase activity, GO:0005509: calcium ion binding, GO:0016787: hydrolase activity	00150: Androgen and estrogen metabolism	0.2278	−0.2219	−0.6216	−1.3419	5.67	6.8	7.02	6.57	6.18	5.45	3
211906 _s_at	SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	AB046400	6318	Hs.123035	GO:0006955: immune response, GO:0030162: regulation of proteolysis, GO:0005576: extracellular region, GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding		−0.0545	−0.5635	−2.553	−5.9912	7.88	14.95	14.9	14.39	12.4	8.96	3
212009 _s_at	STIP1	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	AL553320	10963	Hs.337295	GO:0006950: response to stress, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0005488: binding		−0.3398	−0.3299	−0.8459	−1.7255	7.97	9.03	8.69	8.7	8.18	7.3	3
209853 _s_at	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	BC001423	10197	Hs.152978	GO:0000502: proteasome complex (sensu Eukaryota), GO:0005829: cytosol, GO:0008537: proteasome activator complex, GO:0008538: proteasome activator activity, GO:0042802: identical protein binding		−0.1736	−0.3489	−1.0911	−1.6656	7.59	8.87	8.7	8.52	7.78	7.21	3
210186 _s_at	FKBP1A	FK506 binding protein 1A, 12kDa	BC005147	2280	Hs.471933	GO:0006457: protein folding, GO:0006457: protein folding, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005737: cytoplasm, GO:0003755: peptidyl-prolyl cis-trans isomerase activity, GO:0004872: receptor activity, GO:0005515: protein binding, GO:0016853: isomerase activity		−0.0519	−0.0969	−0.551	−1.3503	8.4	9.02	8.97	8.92	8.47	7.67	3

(*Continued*)

TABLE E2. (*Continued*)

207126_x_at	UGT1A1	UDP glucuronosyltransferase 1 family, polypeptide A1	NM_000463	54658	Hs.654499	GO:0006789: bilirubin conjugation, GO:0007586: digestion, GO:0008152: metabolic process, GO:0008210: estrogen metabolic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0015020: glucuronosyltransferase activity	00040: Pentose and glucuronate interconversions, 00150: Androgen and estrogen metabolism, 00500: Starch and sucrose metabolism, 00860: Porphyrin and chlorophyll metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	−0.0397	−0.2014	−0.6465	−1.5007	8.26	9.18	9.14	8.98	8.53	7.68	3
207356_at	DEFB4	defensin, beta 4	NM_004942	1673	Hs.105924	GO:0006935: chemotaxis, GO:0006955: immune response, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0042742: defense response to bacterium, GO:0005576: extracellular region		−0.1025	−0.943	−3.2521	−6.2217	7.96	14.84	14.74	13.9	11.59	8.62	3
206628_at	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	NM_000343	6523	Hs.1964	GO:0001656: metanephros development, GO:0006811: ion transport, GO:0006814: sodium ion transport, GO:0015758: glucose transport, GO:0050892: intestinal absorption, GO:0005887: integral to plasma membrane, GO:0005903: brush border, GO:0016020: membrane, GO:0016324: apical plasma membrane, GO:0005215: transporter activity, GO:0005351: sugar:hydrogen ion symporter activity, GO:0005412: glucose:sodium symporter activity, GO:0031402: sodium ion binding		0.0216	−0.6055	−2.0286	−3.2509	5.48	8.39	8.41	7.78	6.36	5.14	3
206911_at	TRIM25	tripartite motif-containing 25	NM_005082	7706	Hs.528952	GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.0559	−0.1219	−0.4934	−1.1132	3.45	4.72	4.77	4.6	4.23	3.61	3
210138_at	RGS20	regulator of G-protein signaling 20	AF074979	8601	Hs.368733	GO:0008277: regulation of G-protein coupled receptor protein signaling pathway, GO:0009968: negative regulation of signal transduction, GO:0016020: membrane, GO:0004871: signal transducer activity, GO:0005096: GTPase activator activity, GO:0005515: protein binding		−0.0808	−0.2698	−1.0527	−2.6461	4.02	6.73	6.65	6.47	5.68	4.09	3
210317_s_at	YWHAE	tyrosine 3-monooxygenase/ tryptophan 5-monooxygenase activation protein, epsilon polypeptide	U28936	7531	Hs.513851	GO:0007242: intracellular signaling cascade, GO:0005737: cytoplasm, GO:0019899: enzyme binding, GO:0019904: protein domain specific binding	04110: Cell cycle	−0.1859	−0.0643	−0.9416	−1.7767	7.54	8.25	8.06	8.18	7.31	6.47	3

(*Continued*)

TABLE E2. (*Continued*)

205016_at	TGFA	transforming growth factor, alpha	NM_003236	7039	Hs.170009	GO:0000074: regulation of progression through cell cycle, GO:0000187: activation of MAPK activity, GO:0001525: angiogenesis, GO:0008283: cell proliferation, GO:0045741: positive regulation of epidermal growth factor receptor activity, GO:0045840: positive regulation of mitosis, GO:0050679: positive regulation of epithelial cell proliferation, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0001948: glycoprotein binding, GO:0004708: MAP kinase kinase activity, GO:0004871: signal transducer activity, GO:0005155: epidermal growth factor receptor activating ligand activity, GO:0008083: growth factor activity	04012: ErbB signaling pathway, 05211: Renal cell carcinoma, 05212: Pancreatic cancer, 05214: Glioma, 05215: Prostate cancer, 05223: Non-small cell lung cancer	−0.0024	−0.4141	−1.0589	−2.0403	8.29	9.8	9.8	9.39	8.74	7.76	3
205483_s_at	ISG15	ISG15 ubiquitin-like modifier	NM_005101	9636	Hs.458485	GO:0006464: protein modification process, GO:0006512: ubiquitin cycle, GO:0006955: immune response, GO:0007267: cell-cell signaling, GO:0009615: response to virus, GO:0032020: ISG15-protein conjugation, GO:0048525: negative regulation of viral life cycle, GO:0005615: extracellular space, GO:0005737: cytoplasm, GO:0001730: 2'-5'-oligoadenylate synthetase activity, GO:0003725: double-stranded RNA binding, GO:0005515: protein binding		0.0913	−0.5202	−1.7193	−2.4411	7.88	11	11.09	10.48	9.28	8.56	3
206562_s_at	CSNK1A1	casein kinase 1, alpha 1	NM_001892	1452	Hs.529862, Hs.654547	GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0016055: Wnt receptor signaling pathway, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004681: casein kinase I activity, GO:0005524: ATP binding, GO:0016740: transferase activity	04310: Wnt signaling pathway, 04340: Hedgehog signaling pathway	−0.1727	−0.2769	−0.7374	−1.7449	10.71	11.98	11.81	11.7	11.24	10.23	3
206605_at	P11	26 serine protease	NM_006025	8909	Hs.997	GO:0006508: proteolysis, GO:0007565: female pregnancy, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005737: cytoplasm, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0004252: serine-type endopeptidase activity, GO:0008083: growth factor activity		−0.0971	−0.1746	−0.7522	−1.2187	8.69	9.44	9.34	9.26	8.69	8.22	3

(*Continued*)

TABLE E2. (*Continued*)

206491_s_at	NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha	NM_003827	8775	Hs.126938	GO:0006886: intracellular protein transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0006891: intra-Golgi vesicle-mediated transport, GO:0006944: membrane fusion, GO:0007420: brain development, GO:0030182: neuron differentiation, GO:0045176: apical protein localization, GO:0005783: endoplasmic reticulum, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0005488: binding, GO:0005515: protein binding, GO:0019905: syntaxin binding		−0.0454	−0.0308	−0.5532	−1.0142	9.77	10.46	10.42	10.43	9.91	9.45	3
206561_s_at	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	NM_020299	57016	Hs.116724	GO:0006081: aldehyde metabolic process, GO:0007586: digestion, GO:0008202: steroid metabolic process, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0004033: aldo-keto reductase activity, GO:0016491: oxidoreductase activity	00051: Fructose and mannose metabolism, 00052: Galactose metabolism, 00120: Bile acid biosynthesis, 00260: Glycine, serine and threonine metabolism, 00310: Lysine degradation, 00363: Bisphenol A degradation, 00591: Linoleic acid metabolism, 00625: Tetrachloroethene degradation, 00650: Butanoate metabolism	−0.2477	−0.9244	−2.1414	−4.5634	6.86	12.03	11.78	11.1	9.88	7.46	3
206303_s_at	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	NM_019094	11163	Hs.591008	GO:0007242: intracellular signaling cascade, GO:0009187: cyclic nucleotide metabolic process, GO:0019722: calcium-mediated signaling, GO:0019935: cyclic-nucleotide-mediated signaling, GO:0046831: regulation of RNA export from nucleus, GO:0046907: intracellular transport, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0000287: magnesium ion binding, GO:0008486: diphosphoinositol-polyphosphate diphosphatase activity, GO:0016787: hydrolase activity, GO:0030145: manganese ion binding		−0.1415	−0.5472	−0.9	−1.9732	3.75	5.49	5.35	4.94	4.59	3.52	3
206409_at	TIAM1	T-cell lymphoma invasion and metastasis 1	NM_003253	7074	Hs.517228	GO:0007165: signal transduction, GO:0007264: small GTPase mediated signal transduction, GO:0035023: regulation of Rho protein signal transduction, GO:0048013: ephrin receptor signaling pathway, GO:0050772: positive regulation of axonogenesis, GO:0005622: intracellular, GO:0005886: plasma membrane, GO:0005057: receptor signaling protein activity, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0005515: protein binding, GO:0005543: phospholipid binding, GO:0046875: ephrin receptor binding	04810: Regulation of actin cytoskeleton	0.027	−0.2264	−0.5882	−1.2467	6.81	7.66	7.69	7.44	7.07	6.41	3
206177_s_at	ARG1	arginase, liver	NM_000045	383	Hs.440934	GO:0000050: urea cycle, GO:0006527: arginine catabolic process, GO:0005737: cytoplasm, GO:0004053: arginase activity, GO:0016787: hydrolase activity, GO:0030145: manganese ion binding, GO:0046872: metal ion binding	00220: Urea cycle and metabolism of amino groups, 00330: Arginine and proline metabolism	0.1136	−0.1684	−0.8018	−1.7987	11.71	13.63	13.75	13.47	12.83	11.84	3
206193_s_at	CDSN	corneodesmosin	NM_001264	1041	Hs.556031			−0.0408	−0.0236	−0.6601	−1.1484	11.97	12.92	12.88	12.9	12.26	11.77	3

(*Continued*)

TABLE E2. (*Continued*)

205990_s_at	WNT5A	wingless-type MMTV integration site family, member 5A	NM_003392	7474	Hs.643085	GO:0007165: signal transduction, GO:0007223: Wnt receptor signaling pathway, calcium modulating pathway, GO:0007254: JNK cascade, GO:0007267: cell-cell signaling, GO:0009653: anatomical structure morphogenesis, GO:0009790: embryonic development, GO:0030324: lung development, GO:0030326: embryonic limb morphogenesis, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0004871: signal transducer activity, GO:0005102: receptor binding	04310: Wnt signaling pathway, 04340: Hedgehog signaling pathway, 04916: Melanogenesis, 05217: Basal cell carcinoma	−0.0778	−0.2397	−0.9729	−2.3974	6.9	10.48	10.4	10.24	9.51	8.09	3
206125_s_at	KLK8	kallikrein-related peptidase 8	NM_007196	11202	Hs.104570	GO:0006508: proteolysis, GO:0007399: nervous system development, GO:0004252: serine-type endopeptidase activity, GO:0008233: peptidase activity		−0.1351	−0.2063	−0.6678	−1.205	10.71	11.9	11.76	11.69	11.23	10.69	3
205822_s_at	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	NM_002130	3157	Hs.397729	GO:0006084: acetyl-CoA metabolic process, GO:0006629: lipid metabolic process, GO:0006695: cholesterol biosynthetic process, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0004421: hydroxymethylglutaryl-CoA synthase activity, GO:0016740: transferase activity	00072: Synthesis and degradation of ketone bodies, 00280: Valine, leucine and isoleucine degradation, 00650: Butanoate metabolism	−0.0269	−0.9364	−1.2328	−3.1195	7.33	9.33	9.3	8.39	8.1	6.21	3
205844_at	VNN1	vanin 1	NM_004666	8876	Hs.12114, Hs.683856	GO:0006807: nitrogen compound metabolic process, GO:0006928: cell motility, GO:0016020: membrane, GO:0016811: hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides, GO:0048503: GPI anchor binding	00770: Pantothenate and CoA biosynthesis	0.6204	−0.288	−1.2168	−2.5115	3.79	7.42	8.04	7.13	6.2	4.9	3

(*Continued*)

TABLE E2. (*Continued*)

205767_at	EREG	epiregulin	NM_001432	2069	Hs.115263	GO:0000074: regulation of progression through cell cycle, GO:0001525: angiogenesis, GO:0001550: ovarian cumulus expansion, GO:0001556: oocyte maturation, GO:0001819: positive regulation of cytokine production, GO:0007143: female meiosis, GO:0007173: epidermal growth factor receptor signaling pathway, GO:0007267: cell-cell signaling, GO:0007275: multicellular organismal development, GO:0009299: mRNA transcription, GO:0009887: organ morphogenesis, GO:0016481: negative regulation of transcription, GO:0019221: cytokine and chemokine mediated signaling pathway, GO:0030216: keratinocyte differentiation, GO:0030728: ovulation, GO:0042060: wound healing, GO:0042327: positive regulation of phosphorylation, GO:0042327: positive regulation of phosphorylation, GO:0042700: luteinizing hormone signaling pathway, GO:0043616: keratinocyte proliferation, GO:0045089: positive regulation of innate immune response, GO:0045410: positive regulation of interleukin-6 biosynthetic process, GO:0045740: positive regulation of DNA replication, GO:0045740: positive regulation of DNA replication, GO:0045741: positive regulation of epidermal growth factor receptor activity, GO:0045840: positive regulation of mitosis, GO:0045860: positive regulation of protein kinase activity, GO:0048146: positive regulation of fibroblast proliferation, GO:0048160: primary follicle stage, oogenesis, GO:0048661: positive regulation of smooth muscle cell proliferation, GO:0050680: negative regulation of epithelial cell proliferation, GO:0051151: negative regulation of smooth muscle cell differentiation, GO:0005615: extracellular space, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005154: epidermal growth factor receptor binding, GO:0005154: epidermal growth factor receptor binding, GO:0005515: protein binding, GO:0008083: growth factor activity, GO:0046982: protein heterodimerization activity	04012: ErbB signaling pathway	−0.1461	−0.2928	−0.7822	−1.5969	9.4	10.52	10.37	10.23	9.74	8.92	3
205778_at	KLK7	kallikrein-related peptidase 7	NM_005046	5650	Hs.151254	GO:0006508: proteolysis, GO:0008544: epidermis development, GO:0004252: serine-type endopeptidase activity		−0.1431	−0.2897	−0.5744	−1.1551	11.8	12.94	12.79	12.65	12.36	11.78	3

(*Continued*)

TABLE E2. (*Continued*)

205724_at	PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	NM_000299	5317	Hs.497350	GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0007275: multicellular organismal development, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005882: intermediate filament, GO:0030054: cell junction, GO:0030057: desmosome, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0019215: intermediate filament binding, GO:0030280: structural constituent of epidermis		−0.3244	−0.348	−1.1964	−2.534	8.23	9.9	9.58	9.55	8.71	7.37	3
205729_at	OSMR	oncostatin M receptor	NM_003999	9180	Hs.120658	GO:0007166: cell surface receptor linked signal transduction, GO:0008283: cell proliferation, GO:0005900: oncostatin-M receptor complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004924: oncostatin-M receptor activity	04060: Cytokine-cytokine receptor interaction, 04630: Jak-STAT signaling pathway	−0.1318	−0.8176	−1.013	−2.6237	6.03	8.14	8.01	7.33	7.13	5.52	3
205552_s_at	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	NM_002534	4938	Hs.524760	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006955: immune response, GO:0009615: response to virus, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0003723: RNA binding, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0016779: nucleotidyltransferase activity		0.0974	−0.1686	−1.5331	−3.1658	6.19	9.78	9.87	9.61	8.24	6.61	3
205569_at	LAMP3	lysosomal-associated membrane protein 3	NM_014398	27074	Hs.518448	GO:0008283: cell proliferation, GO:0005765: lysosomal membrane, GO:0016020: membrane, GO:0016021: integral to membrane		0.1503	−0.2189	−1.0376	−2.1847	7.95	10.14	10.29	9.92	9.1	7.95	3
204972_at	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	NM_016817	4939	Hs.414332	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006401: RNA catabolic process, GO:0006955: immune response, GO:0005739: mitochondrion, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0001730: 2'-5'-oligoadenylate synthetase activity, GO:0003723: RNA binding, GO:0005524: ATP binding, GO:0016740: transferase activity		0.0601	−0.3903	−1.7827	−3.8079	4.37	9.21	9.27	8.82	7.42	5.4	3

(*Continued*)

TABLE E2. (*Continued*)

204995_at	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	AL567411	8851	Hs.500015	GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0001764: neuron migration, GO:0007158: neuron adhesion, GO:0007213: acetylcholine receptor signaling, muscarinic pathway, GO:0007411: axon guidance, GO:0007413: axonal fasciculation, GO:0007420: brain development, GO:0007420: brain development, GO:0008283: cell proliferation, GO:0009790: embryonic development, GO:0031175: neurite development, GO:0035235: ionotropic glutamate receptor signaling pathway, GO:0043525: positive regulation of neuron apoptosis, GO:0045664: regulation of neuron differentiation, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0016533: cyclin-dependent protein kinase 5 activator complex, GO:0030424: axon, GO:0030426: growth cone, GO:0031594: neuromuscular junction, GO:0043025: cell soma, GO:0043197: dendritic spine, GO:0043292: contractile fiber, GO:0004672: protein kinase activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005515: protein binding, GO:0016534: cyclin-dependent protein kinase 5 activator activity, GO:0043539: protein serine/threonine kinase activator activity, GO:0045296: cadherin binding	−0.2871	−0.4767	−1.2704	−2.55	5.06	7.4	7.11	6.92	6.13	4.85	3
204841_s_at	EEA1	early endosome antigen 1	NM_003566	8411	Hs.567367	GO:0006906: vesicle fusion, GO:0016189: synaptic vesicle to endosome fusion, GO:0045022: early endosome to late endosome transport, GO:0005622: intracellular, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0005769: early endosome, GO:0005829: cytosol, GO:0016020: membrane, GO:0019897: extrinsic to plasma membrane, GO:0003676: nucleic acid binding, GO:0005516: calmodulin binding, GO:0005545: phosphatidylinositol binding, GO:0008270: zinc ion binding, GO:0030742: GTP-dependent protein binding, GO:0042803: protein homodimerization activity, GO:0046872: metal ion binding	0.0035	−0.0311	−0.4968	−1.0317	5.31	5.93	5.93	5.9	5.43	4.9	3

(*Continued*)

TABLE E2. (*Continued*)

204967_at	SHROOM2	shroom family member 2	NM_001649	357	Hs.567236	GO:0000902: cell morphogenesis, GO:0002089: lens morphogenesis in camera-type eye, GO:0007275: multicellular organismal development, GO:0007420: brain development, GO:0008057: eye pigment granule organization and biogenesis, GO:0016477: cell migration, GO:0032401: establishment of melanosome localization, GO:0032438: melanosome organization and biogenesis, GO:0043482: cellular pigment accumulation, GO:0043583: ear development, GO:0045176: apical protein localization, GO:0051017: actin filament bundle formation, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005874: microtubule, GO:0005886: plasma membrane, GO:0005913: cell-cell adherens junction, GO:0005923: tight junction, GO:0016324: apical plasma membrane, GO:0030054: cell junction, GO:0030864: cortical actin cytoskeleton, GO:0008013: beta-catenin binding, GO:0015280: amiloride-sensitive sodium channel activity, GO:0051015: actin filament binding		0.245	−0.0671	−0.8785	−1.3615	5.39	6.97	7.21	6.9	6.09	5.61	3
204527_at	MYO5A	myosin VA (heavy chain 12, myoxin)	NM_000259	4644	Hs.21213	GO:0006810: transport, GO:0008150: biological_process, GO:0030048: actin filament-based movement, GO:0001726: ruffle, GO:0005737: cytoplasm, GO:0016459: myosin complex, GO:0016459: myosin complex, GO:0030426: growth cone, GO:0043005: neuron projection, GO:0000146: microfilament motor activity, GO:0000166: nucleotide binding, GO:0003674: molecular_function, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0051015: actin filament binding		−0.0447	−0.3439	−0.8019	−1.6503	7.07	8.53	8.49	8.19	7.73	6.88	3
204532_x_at	UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A9	NM_021027	54600	Hs.654499	GO:0008152: metabolic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0015020: glucuronosyltransferase activity	00040: Pentose and glucuronate interconversions, 00150: Androgen and estrogen metabolism, 00500: Starch and sucrose metabolism, 00860: Porphyrin and chlorophyll metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	−0.0936	−0.2231	−0.8234	−1.7591	7.51	8.59	8.5	8.37	7.77	6.83	3
204444_at	KIF11	kinesin family member 11	NM_004523	3832	Hs.8878	GO:0007018: microtubule-based movement, GO:0007049: cell cycle, GO:0007052: mitotic spindle organization and biogenesis, GO:0007067: mitosis, GO:0007100: mitotic centrosome separation, GO:0051300: spindle pole body organization and biogenesis, GO:0051301: cell division, GO:0000922: spindle pole, GO:0005871: kinesin complex, GO:0005876: spindle microtubule, GO:0000166: nucleotide binding, GO:0003777: microtubule motor activity, GO:0005524: ATP binding		−0.235	−0.5877	−1.0729	−2.1045	6.83	7.98	7.75	7.39	6.91	5.88	3

(*Continued*)

TABLE E2. (*Continued*)

204465_s_at	INA	internexin neuronal intermediate filament protein, alpha	NM_004692	9118	Hs.500916	GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0030154: cell differentiation, GO:0045104: intermediate filament cytoskeleton organization and biogenesis, GO:0005883: neurofilament, GO:0005200: structural constituent of cytoskeleton	01430: Cell Communication	−0.0217	0.0406	−0.6994	−1.2766	4.74	6.15	6.13	6.19	5.45	4.87	3
204147_s_at	TFDP1	transcription factor Dp-1	NM_007111	7027	Hs.79353	GO:0000074: regulation of progression through cell cycle, GO:0000074: regulation of progression through cell cycle, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007049: cell cycle, GO:0008283: cell proliferation, GO:0005667: transcription factor complex, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0003713: transcription coactivator activity	04110: Cell cycle, 04350: TGF-beta signaling pathway	−0.1546	−0.3617	−0.5852	−1.3224	5.66	6.56	6.4	6.19	5.97	5.23	3
204224_s_at	GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)	NM_000161	2643	Hs.86724	GO:0006559: L-phenylalanine catabolic process, GO:0006729: tetrahydrobiopterin biosynthetic process, GO:0006809: nitric oxide biosynthetic process, GO:0019438: aromatic compound biosynthetic process, GO:0042133: neurotransmitter metabolic process, GO:0005737: cytoplasm, GO:0003934: GTP cyclohydrolase I activity, GO:0003934: GTP cyclohydrolase I activity, GO:0005515: protein binding, GO:0016787: hydrolase activity	00790: Folate biosynthesis	0.0631	−0.1332	−0.5073	−1.1527	8.8	9.83	9.89	9.7	9.32	8.68	3
204059_s_at	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	NM_002395	4199	Hs.21160	GO:0005975: carbohydrate metabolic process, GO:0006108: malate metabolic process, GO:0006741: NADP biosynthetic process, GO:0009725: response to hormone stimulus, GO:0009743: response to carbohydrate stimulus, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0004473: malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity, GO:0004473: malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity, GO:0009055: electron carrier activity, GO:0030145: manganese ion binding, GO:0043531: ADP binding, GO:0046872: metal ion binding, GO:0050661: NADP binding, GO:0051287: NAD binding	00620: Pyruvate metabolism, 00710: Carbon fixation, 03320: PPAR signaling pathway	0.0168	−0.2791	−0.7747	−1.4847	10.65	11.6	11.62	11.32	10.83	10.12	3
204128_s_at	RFC3	replication factor C (activator 1) 3, 38kDa	BC000149	5983	Hs.115474	GO:0000731: DNA synthesis during DNA repair, GO:0006271: DNA strand elongation during DNA replication, GO:0005663: DNA replication factor C complex, GO:0005663: DNA replication factor C complex, GO:0000166: nucleotide binding, GO:0003689: DNA clamp loader activity, GO:0005515: protein binding, GO:0016887: ATPase activity		−0.1502	−0.4275	−0.7322	−1.7267	5.1	6.02	5.87	5.6	5.29	4.3	3

(*Continued*)

TABLE E2. (*Continued*)

203798_s_at	VSNL1	visinin-like 1	NM_003385	7447	Hs.444212	GO:0005509: calcium ion binding	−0.3085	−0.739	−1.4335	−2.5267	6.83	9.41	9.1	8.67	7.97	6.88	3
203964_at	NMI	N-myc (and STAT) interactor	NM_004688	9111	Hs.54483	GO:0006366: transcription from RNA polymerase II promoter, GO:0006954: inflammatory response, GO:0007259: JAK-STAT cascade, GO:0005737: cytoplasm, GO:0003712: transcription cofactor activity, GO:0005515: protein binding	−0.1102	−0.213	−0.6153	−1.1408	9.35	10.44	10.33	10.22	9.82	9.3	3
203779_s_at	MPZL2	myelin protein zero-like 2	NM_005797	10205	Hs.116651	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0009653: anatomical structure morphogenesis, GO:0005856: cytoskeleton, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding	−0.3355	−0.7129	−1.5671	−3.7664	6.67	10.1	9.76	9.38	8.53	6.33	3
203780_at	MPZL2	myelin protein zero-like 2	AF275945	10205	Hs.116651	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0009653: anatomical structure morphogenesis, GO:0005856: cytoskeleton, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding	−0.2001	−0.3829	−0.7749	−1.7762	10.49	12.11	11.91	11.73	11.33	10.33	3
203691_at	PI3	peptidase inhibitor 3, skin-derived (SKALP)	NM_002638	5266	Hs.112341	GO:0007620: copulation, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding	−0.0956	−0.8079	−2.5046	−5.0262	8.87	14.6	14.51	13.8	12.1	9.58	3
203699_s_at	DIO2	deiodinase, iodothyronine, type II	U53506	1734	Hs.202354, Hs.694871	GO:0001514: selenocysteine incorporation, GO:0006590: thyroid hormone generation, GO:0042446: hormone biosynthetic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004800: thyroxine 5'-deiodinase activity, GO:0004800: thyroxine 5'-deiodinase activity, GO:0008430: selenium binding, GO:0008430: selenium binding	0.318	−0.3187	−1.0734	−2.3315	3.43	6.61	6.93	6.3	5.54	4.28	3
203471_s_at	PLEK	pleckstrin	NM_002664	5341	Hs.468840	GO:0007242: intracellular signaling cascade, GO:0005509: calcium ion binding	−0.0393	−0.4736	−0.5599	−1.3211	4	5.51	5.47	5.04	4.95	4.19	3
203641_s_at	COBLL1	COBL-like 1	NM_014900	22837	Hs.470457		0.2187	−0.3917	−0.7769	−1.6638	5.89	7.02	7.24	6.63	6.24	5.36	3

(*Continued*)

TABLE E2. (*Continued*)

203311_s_at	ARF6	ADP-ribosylation factor 6	NM_001663	382	Hs.525330, Hs.593068, Hs.694988	GO:0006888: ER to Golgi vesicle-mediated transport, GO:0006928: cell motility, GO:0007155: cell adhesion, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0016192: vesicle-mediated transport, GO:0030838: positive regulation of actin filament polymerization, GO:0030866: cortical actin cytoskeleton organization and biogenesis, GO:0031529: ruffle organization and biogenesis, GO:0035020: regulation of Rac protein signal transduction, GO:0048261: negative regulation of receptor mediated endocytosis, GO:0001726: ruffle, GO:0005622: intracellular, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0005768: endosome, GO:0005886: plasma membrane, GO:0005938: cell cortex, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding	05110: Cholera - Infection	−0.1935	−0.301	−0.4375	−1.0389	8.78	9.5	9.31	9.2	9.06	8.46	3
203360_s_at	MYCBP	c-myc binding protein	D50692	26292	Hs.591506	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0003713: transcription coactivator activity, GO:0005515: protein binding		−0.1782	−0.1776	−0.5788	−1.3387	7.74	8.5	8.32	8.32	7.92	7.16	3
203207_s_at	MTFR1	mitochondrial fission regulator 1	BF214329	9650	Hs.654531	GO:0005739: mitochondrion, GO:0005886: plasma membrane		−0.0596	−0.0722	−0.4005	−1.0764	7.29	7.69	7.63	7.62	7.29	6.61	3
203293_s_at	LMAN1	lectin, mannose-binding, 1	NM_005570	3998	Hs.465295	GO:0006457: protein folding, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0007596: blood coagulation, GO:0015031: protein transport, GO:0000139: Golgi membrane, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005793: ER-Golgi intermediate compartment, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030017: sarcomere, GO:0005529: sugar binding, GO:0005537: mannose binding, GO:0051082: unfolded protein binding		−0.2032	−0.1077	−0.4682	−1.1112	3.98	4.92	4.72	4.82	4.46	3.81	3
203032_s_at	FH	fumarate hydratase	NM_000143	2271	Hs.592490	GO:0006099: tricarboxylic acid cycle, GO:0006106: fumarate metabolic process, GO:0007049: cell cycle, GO:0045786: negative regulation of progression through cell cycle, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0045239: tricarboxylic acid cycle enzyme complex, GO:0004333: fumarate hydratase activity, GO:0016829: lyase activity	00020: Citrate cycle (TCA cycle), 00720: Reductive carboxylate cycle (CO2 fixation), 05211: Renal cell carcinoma	−0.1141	−0.0551	−0.5965	−1.013	7.87	8.54	8.43	8.49	7.95	7.53	3

(*Continued*)

TABLE E2. (*Continued*)

203148_s_at	TRIM14	tripartite motif-containing 14	NM_014788	9830	Hs.575631	GO:0007386: compartment specification, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.0161	−0.3505	−0.9859	−1.8259	7.79	9.73	9.74	9.38	8.74	7.9	3
202886_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	M65254	5519	Hs.584790	GO:0000158: protein phosphatase type 2A activity, GO:0003823: antigen binding, GO:0005488: binding, GO:0005515: protein binding, GO:0046982: protein heterodimerization activity	04310: Wnt signaling pathway, 04350: TGF-beta signaling pathway, 04530: Tight junction, 04730: Long-term depression	−0.1871	−0.4352	−0.6371	−1.4239	6.47	7.02	6.83	6.58	6.38	5.6	3
202889_x_at	MAP7	microtubule-associated protein 7	T62571	9053	Hs.486548	GO:0000226: microtubule cytoskeleton organization and biogenesis, GO:0007163: establishment and/or maintenance of cell polarity, GO:0005737: cytoplasm, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0016020: membrane, GO:0005198: structural molecule activity		−0.0596	−0.0663	−0.4346	−1.1246	6.42	7.32	7.26	7.25	6.88	6.19	3
202805_s_at	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	NM_004996	4363	Hs.391464	GO:0006810: transport, GO:0006810: transport, GO:0042493: response to drug, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0005215: transporter activity, GO:0005215: transporter activity, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0016887: ATPase activity, GO:0016887: ATPase activity, GO:0042626: ATPase activity, coupled to transmembrane movement of substances, GO:0042626: ATPase activity, coupled to transmembrane movement of substances	02010: ABC transporters - General	−0.0431	−0.2658	−0.6669	−1.3217	4.26	5.84	5.79	5.57	5.17	4.52	3
202869_at	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	NM_016816	4938	Hs.524760	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006955: immune response, GO:0009615: response to virus, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0003723: RNA binding, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0016779: nucleotidyltransferase activity		0.1456	−0.1457	−1.5859	−3.1584	4.49	8.53	8.68	8.39	6.95	5.38	3
202697_at	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	NM_007006	11051	Hs.528834	GO:0006397: mRNA processing, GO:0005813: centrosome, GO:0042382: paraspeckles, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0016787: hydrolase activity		0.0073	−0.1402	−0.5511	−1.3303	8.06	8.93	8.93	8.79	8.38	7.6	3
202787_s_at	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	NM_004635	7867	Hs.234521	GO:0006468: protein amino acid phosphorylation, GO:0006950: response to stress, GO:0007165: signal transduction, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004708: MAP kinase kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04370: VEGF signaling pathway	0.0547	−0.2528	−0.7255	−1.3645	8.01	9.39	9.44	9.14	8.66	8.02	3

(*Continued*)

TABLE E2. (*Continued*)

202604_x_at	ADAM10	ADAM metallopeptidase domain 10	NM_001110	102	Hs.578508	GO:0001701: in utero embryonic development, GO:0006468: protein amino acid phosphorylation, GO:0007162: negative regulation of cell adhesion, GO:0007162: negative regulation of cell adhesion, GO:0007219: Notch signaling pathway, GO:0007229: integrin-mediated signaling pathway, GO:0007267: cell-cell signaling, GO:0051089: constitutive protein ectodomain proteolysis, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0005798: Golgi-associated vesicle, GO:0005886: plasma membrane, GO:0009986: cell surface, GO:0016021: integral to membrane, GO:0004222: metalloendopeptidase activity, GO:0005178: integrin binding, GO:0008270: zinc ion binding, GO:0019901: protein kinase binding, GO:0042803: protein homodimerization activity, GO:0046872: metal ion binding	05120: Epithelial cell signaling in Helicobacter pylori infection	−0.002	−0.4875	−0.7072	−1.7891	3.6	5.02	5.02	4.54	4.32	3.24	3
202693_s_at	STK17A	serine/threonine kinase 17a	NM_004760	9263	Hs.655413	GO:0006468: protein amino acid phosphorylation, GO:0006915: apoptosis, GO:0006917: induction of apoptosis, GO:0007243: protein kinase cascade, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity		−0.1513	−0.3589	−0.5679	−1.2527	8.25	9	8.85	8.65	8.44	7.75	3
202446_s_at	PLSCR1	phospholipid scramblase 1	AI825926	5359	Hs.130759	GO:0009615: response to virus, GO:0017121: phospholipid scrambling, GO:0030168: platelet activation, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0017128: phospholipid scramblase activity		0.0339	−0.2714	−0.7347	−1.5399	9.03	10.47	10.5	10.2	9.73	8.93	3
202595_s_at	LEPROTL1	leptin receptor overlapping transcript-like 1	BC000642	23484	Hs.146585	GO:0016020: membrane, GO:0016021: integral to membrane		0.02	−0.0818	−0.5811	−1.1653	9.07	10.15	10.17	10.06	9.57	8.98	3
202357_s_at	CFB	complement factor B	NM_001710	629	Hs.69771	GO:0006508: proteolysis, GO:0006956: complement activation, GO:0006957: complement activation, alternative pathway, GO:0005576: extracellular region, GO:0001848: complement binding, GO:0003812: alternative-complement-pathway C3/C5 convertase activity, GO:0004252: serine-type endopeptidase activity, GO:0008233: peptidase activity	04610: Complement and coagulation cascades	0.1282	−0.5839	−0.9512	−1.7158	6.8	8.6	8.73	8.02	7.65	6.89	3
202411_at	IFI27	interferon, alpha-inducible protein 27	NM_005532	3429	Hs.532634	GO:0006955: immune response, GO:0008150: biological_process, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003674: molecular_function		0.005	−0.1895	−0.7508	−1.7325	11.41	13.77	13.77	13.58	13.02	12.03	3

(*Continued*)

TABLE E2. (*Continued*)

202195 _s_at	TMED5	transmembrane emp24 protein transport domain containing 5	NM_016040	50999	Hs.482873	GO:0006810: transport, GO:0005783: endoplasmic reticulum, GO:0005793: ER-Golgi intermediate compartment, GO:0016020: membrane, GO:0016021: integral to membrane	−0.1437	−0.1937	−0.5604	−1.0742	7.5	8.25	8.11	8.06	7.69	7.18	3
202236 _s_at	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	NM_003051	6566	Hs.75231	GO:0006810: transport, GO:0015711: organic anion transport, GO:0015728: mevalonate transport, GO:0005624: membrane fraction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0005215: transporter activity, GO:0005515: protein binding, GO:0015130: mevalonate transmembrane transporter activity, GO:0015293: symporter activity, GO:0015355: secondary active monocarboxylate transmembrane transporter activity	−0.3914	−0.5523	−0.8325	−1.8625	8.71	10.11	9.72	9.56	9.28	8.25	3
201946 _s_at	CCT2	chaperonin containing TCP1, subunit 2 (beta)	AL545982	10576	Hs.189772	GO:0000074: regulation of progression through cell cycle, GO:0006457: protein folding, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0005832: chaperonin-containing T-complex, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0051082: unfolded protein binding	−0.2058	−0.3333	−0.7437	−1.6019	9.96	10.86	10.66	10.53	10.12	9.26	3
202064 _s_at	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	AF052059	6400	Hs.181300	GO:0007219: Notch signaling pathway, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005488: binding	−0.0956	−0.2843	−0.6379	−1.2117	3.65	4.77	4.67	4.48	4.13	3.56	3
201821 _s_at	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	NM_006335	10440	Hs.20716	GO:0006626: protein targeting to mitochondrion, GO:0005739: mitochondrion, GO:0005744: mitochondrial inner membrane presequence translocase complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0015450: protein transmembrane transporter activity	−0.114	−0.1539	−0.4568	−1.0363	9.6	10.21	10.1	10.06	9.75	9.17	3

(*Continued*)

TABLE E2. (*Continued*)

201848_s_at	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	U15174	664	Hs.144873	GO:0001666: response to hypoxia, GO:0006309: DNA fragmentation during apoptosis, GO:0006338: chromatin remodeling, GO:0006800: oxygen and reactive oxygen species metabolic process, GO:0006916: anti-apoptosis, GO:0006917: induction of apoptosis, GO:0008219: cell death, GO:0008219: cell death, GO:0008634: negative regulation of survival gene product activity, GO:0045837: negative regulation of membrane potential, GO:0046902: regulation of mitochondrial membrane permeability, GO:0051402: neuron apoptosis, GO:0051607: defense response to virus, GO:0005634: nucleus, GO:0005635: nuclear envelope, GO:0005654: nucleoplasm, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005739: mitochondrion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030425: dendrite, GO:0031307: integral to mitochondrial outer membrane, GO:0031966: mitochondrial membrane, GO:0031966: mitochondrial membrane, GO:0042803: protein homodimerization activity, GO:0046982: protein heterodimerization activity	0.0196	−0.2258	−0.6784	−1.2616	8.43	9.36	9.38	9.13	8.68	8.1	3
201732_s_at	CLCN3	chloride channel 3	NM_001829	1182	Hs.481186	GO:0006811: ion transport, GO:0006821: chloride transport, GO:0006885: regulation of pH, GO:0048388: endosomal lumen acidification, GO:0005769: early endosome, GO:0005769: early endosome, GO:0005770: late endosome, GO:0005770: late endosome, GO:0005794: Golgi apparatus, GO:0005794: Golgi apparatus, GO:0009986: cell surface, GO:0012506: vesicle membrane, GO:0012506: vesicle membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005244: voltage-gated ion channel activity, GO:0005247: voltage-gated chloride channel activity, GO:0005515: protein binding, GO:0030165: PDZ domain binding, GO:0030165: PDZ domain binding, GO:0031404: chloride ion binding, GO:0042803: protein homodimerization activity, GO:0046982: protein heterodimerization activity, GO:0046982: protein heterodimerization activity	−0.1269	−0.4453	−0.9151	−1.8281	7.26	8.71	8.59	8.27	7.8	6.89	3

(*Continued*)

TABLE E2. (*Continued*)

201733_at	CLCN3	chloride channel 3	AA902971	1182	Hs.481186	GO:0006811: ion transport, GO:0006821: chloride transport, GO:0006885: regulation of pH, GO:0048388: endosomal lumen acidification, GO:0005769: early endosome, GO:0005769: early endosome, GO:0005770: late endosome, GO:0005770: late endosome, GO:0005794: Golgi apparatus, GO:0005794: Golgi apparatus, GO:0009986: cell surface, GO:0012506: vesicle membrane, GO:0012506: vesicle membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005244: voltage-gated ion channel activity, GO:0005247: voltage-gated chloride channel activity, GO:0005515: protein binding, GO:0030165: PDZ domain binding, GO:0030165: PDZ domain binding, GO:0031404: chloride ion binding, GO:0042803: protein homodimerization activity, GO:0046982: protein heterodimerization activity, GO:0046982: protein heterodimerization activity		−0.1127	−0.3589	−0.7775	−1.8099	7.58	8.84	8.73	8.48	8.07	7.03	3
201629_s_at	ACP1	acid phosphatase 1, soluble	NM_004300	52	Hs.558296	GO:0006470: protein amino acid dephosphorylation, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0003993: acid phosphatase activity, GO:0004725: protein tyrosine phosphatase activity, GO:0004726: non-membrane spanning protein tyrosine phosphatase activity, GO:0016787: hydrolase activity, GO:0042802: identical protein binding	00361: gamma-Hexachlorocyclohexane degradation, 00740: Riboflavin metabolism, 04520: Adherens junction	−0.1635	−0.1827	−0.5197	−1.0092	8.18	9	8.84	8.82	8.48	7.99	3
201663_s_at	SMC4	structural maintenance of chromosomes 4	NM_005496	10051	Hs.58992	GO:0006259: DNA metabolic process, GO:0007001: chromosome organization and biogenesis (sensu Eukaryota), GO:0007049: cell cycle, GO:0007076: mitotic chromosome condensation, GO:0051301: cell division, GO:0000796: condensin complex, GO:0005634: nucleus, GO:0005694: chromosome, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0046982: protein heterodimerization activity		−0.1766	−0.5233	−0.8921	−1.9858	6.72	7.76	7.58	7.24	6.87	5.77	3
201490_s_at	PPIF	peptidylprolyl isomerase F (cyclophilin F)	NM_005729	10105	Hs.381072	GO:0006457: protein folding, GO:0005624: membrane fraction, GO:0005739: mitochondrion, GO:0003755: peptidyl-prolyl cis-trans isomerase activity, GO:0016853: isomerase activity, GO:0042277: peptide binding		−0.2675	−0.7846	−1.6289	−3.3319	8.05	10.81	10.54	10.03	9.18	7.48	3

(*Continued*)

TABLE E2. (*Continued*)

201523_x_at	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	BE262760	7334	Hs.524630	GO:0000724: double-strand break repair via homologous recombination, GO:0000729: DNA double-strand break processing, GO:0006301: postreplication repair, GO:0006464: protein modification process, GO:0006508: proteolysis, GO:0016574: histone ubiquitination, GO:0031058: positive regulation of histone modification, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0045739: positive regulation of DNA repair, GO:0050852: T cell receptor signaling pathway, GO:0051092: activation of NF-kappaB transcription factor, GO:0051443: positive regulation of ubiquitin ligase activity, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0031372: UBC13-MMS2 complex, GO:0004842: ubiquitin-protein ligase activity, GO:0005515: protein binding, GO:0016874: ligase activity, GO:0043130: ubiquitin binding		−0.0204	−0.3538	−0.6953	−1.8236	8.2	9.56	9.54	9.2	8.86	7.73	3
201469_s_at	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	AI809967	6464	Hs.433795	GO:0000187: activation of MAPK activity, GO:0000187: activation of MAPK activity, GO:0001558: regulation of cell growth, GO:0007176: regulation of epidermal growth factor receptor activity, GO:0007242: intracellular signaling cascade, GO:0008284: positive regulation of cell proliferation, GO:0045840: positive regulation of mitosis, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005886: plasma membrane, GO:0005886: plasma membrane, GO:0005068: transmembrane receptor protein tyrosine kinase adaptor protein activity, GO:0005158: insulin receptor binding, GO:0005159: insulin-like growth factor receptor binding, GO:0005515: protein binding, GO:0005543: phospholipid binding	04012: ErbB signaling pathway, 04510: Focal adhesion, 04650: Natural killer cell mediated cytotoxicity, 04910: Insulin signaling pathway, 05214: Glioma, 05220: Chronic myeloid leukemia	−0.2211	−0.6095	−1.0288	−1.9722	6.94	8.58	8.36	7.97	7.55	6.61	3
201476_s_at	RRM1	ribonucleotide reductase M1 polypeptide	AI692974	6240	Hs.558393	GO:0006260: DNA replication, GO:0005737: cytoplasm, GO:0005971: ribonucleoside-diphosphate reductase complex, GO:0000166: nucleotide binding, GO:0004748: ribonucleoside-diphosphate reductase activity, GO:0005524: ATP binding, GO:0016491: oxidoreductase activity	00230: Purine metabolism, 00240: Pyrimidine metabolism	−0.1551	−0.2025	−0.7342	−1.7327	8.68	9.5	9.34	9.3	8.77	7.77	3
201118_at	PGD	phosphogluconate dehydrogenase	NM_002631	5226	Hs.464071	GO:0006118: electron transport, GO:0009051: pentose-phosphate shunt, oxidative branch, GO:0004616: phosphogluconate dehydrogenase (decarboxylating) activity, GO:0005515: protein binding, GO:0016491: oxidoreductase activity, GO:0050661: NADP binding	00030: Pentose phosphate pathway	−0.0972	−0.3678	−0.6616	−1.257	9.03	10.04	9.94	9.67	9.38	8.78	3

(*Continued*)

TABLE E2. (*Continued*)

201196 _s_at	AMD1	adenosylmethionine decarboxylase 1	M21154	262	Hs.159118	GO:0006597: spermine biosynthetic process, GO:0006597: spermine biosynthetic process, GO:0008295: spermidine biosynthetic process, GO:0008295: spermidine biosynthetic process, GO:0005575: cellular_component, GO:0004014: adenosylmethionine decarboxylase activity, GO:0004014: adenosylmethionine decarboxylase activity, GO:0016829: lyase activity	00220: Urea cycle and metabolism of amino groups, 00271: Methionine metabolism	−0.3694	−0.4029	−0.7941	−1.833	9.47	10.43	10.06	10.03	9.63	8.6	3
201089 _at	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	NM_001693	526	Hs.295917	GO:0006811: ion transport, GO:0015986: ATP synthesis coupled proton transport, GO:0015988: energy coupled proton transport, against electrochemical gradient, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0016469: proton-transporting two-sector ATPase complex, GO:0005524: ATP binding, GO:0008553: hydrogen-exporting ATPase activity, phosphorylative mechanism, GO:0016787: hydrolase activity, GO:0046872: metal ion binding, GO:0046933: hydrogen ion transporting ATP synthase activity, rotational mechanism, GO:0046961: hydrogen ion transporting ATPase activity, rotational mechanism	00190: Oxidative phosphorylation, 05120: Epithelial cell signaling in Helicobacter pylori infection	0.0011	−0.1577	−0.4628	−1.0176	10.5	11.26	11.26	11.1	10.79	10.24	3
201101 _s_at	BCLAF1	BCL2-associated transcription factor 1	BE963370	9774	Hs.486542	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006917: induction of apoptosis, GO:0016481: negative regulation of transcription, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003677: DNA binding, GO:0005515: protein binding, GO:0016564: transcription repressor activity		−0.1353	−0.1821	−0.7396	−1.8188	5.8	7.06	6.92	6.87	6.32	5.24	3
200838 _at	CTSB	cathepsin B	NM_001908	1508	Hs.520898	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0042981: regulation of apoptosis, GO:0050790: regulation of catalytic activity, GO:0005622: intracellular, GO:0005739: mitochondrion, GO:0005764: lysosome, GO:0004197: cysteine-type endopeptidase activity, GO:0004213: cathepsin B activity, GO:0005515: protein binding	04612: Antigen processing and presentation	0.0024	−0.3525	−0.384	−1.0492	11.19	12.3	12.3	11.95	11.92	11.25	3
200841 _s_at	EPRS	glutamyl-prolyl-tRNA synthetase	AI142677	2058	Hs.497788	GO:0006424: glutamyl-tRNA aminoacylation, GO:0006433: prolyl-tRNA aminoacylation, GO:0006461: protein complex assembly, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004818: glutamate-tRNA ligase activity, GO:0004827: proline-tRNA ligase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016874: ligase activity	00251: Glutamate metabolism, 00330: Arginine and proline metabolism, 00860: Porphyrin and chlorophyll metabolism, 00970: Aminoacyl-tRNA biosynthesis	−0.1556	−0.0758	−0.7486	−1.6212	3.34	4.6	4.44	4.52	3.85	2.98	3

(*Continued*)

TABLE E2. (*Continued*)

41469_at	PI3	peptidase inhibitor 3, skin-derived (SKALP)	L10343	5266	Hs.112341	GO:0007620: copulation, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding		−0.042	−0.5981	−2.1328	−4.7421	9.05	14.3	14.26	13.7	12.17	9.56	3
200712_s_at	MAPRE1	microtubule-associated protein, RP/EB family, member 1	NM_012325	22919	Hs.472437	GO:0000074: regulation of progression through cell cycle, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0008283: cell proliferation, GO:0031115: negative regulation of microtubule polymerization, GO:0051301: cell division, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0005819: spindle, GO:0005874: microtubule, GO:0030981: cortical microtubule cytoskeleton, GO:0008022: protein C-terminus binding, GO:0051010: microtubule plus-end binding		−0.23	−0.2057	−0.5962	−1.3984	8.63	9.31	9.08	9.11	8.72	7.91	3
200796_s_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	BF594446	4170	Hs.632486	GO:0001709: cell fate determination, GO:0006916: anti-apoptosis, GO:0007275: multicellular organismal development, GO:0008632: apoptotic program, GO:0019725: cellular homeostasis, GO:0030154: cell differentiation, GO:0042981: regulation of apoptosis, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding, GO:0015266: protein channel activity, GO:0046982: protein heterodimerization activity		−0.4653	−0.4668	−1.5028	−3.0668	5.01	7.88	7.42	7.42	6.38	4.82	3
221903_s_at	CYLD	cylindromatosis (turban tumor syndrome)	BF516433	1540	Hs.578973	GO:0006412: translation, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0007049: cell cycle, GO:0045786: negative regulation of progression through cell cycle, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005840: ribosome, GO:0005856: cytoskeleton, GO:0003735: structural constituent of ribosome, GO:0004221: ubiquitin thiolesterase activity, GO:0008234: cysteine-type peptidase activity		−0.0077	−0.1692	−0.5064	−1.0212	7.08	7.97	7.96	7.8	7.46	6.95	3
266_s_at	CD24	CD24 molecule	L33930	934	Hs.644105, Hs.694721	GO:0006959: humoral immune response, GO:0005886: plasma membrane, GO:0048503: GPI anchor binding	04640: Hematopoietic cell lineage	−0.1516	−0.3333	−0.8911	−1.7307	11.72	13.38	13.23	13.05	12.49	11.65	3
221487_s_at	ENSA	endosulfine alpha	AF067170	2029	Hs.632456	GO:0006810: transport, GO:0007584: response to nutrient, GO:0005737: cytoplasm, GO:0005102: receptor binding, GO:0008200: ion channel inhibitor activity		−0.0468	−0.26	−0.7159	−1.5181	7.49	8.43	8.38	8.17	7.72	6.91	3
221803_s_at	NRBF2	nuclear receptor binding factor 2	AA883074	29982	Hs.449628	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005737: cytoplasm		0.0024	−0.1398	−0.6248	−1.4507	8.44	9.75	9.75	9.61	9.12	8.3	3

(*Continued*)

TABLE E2. (*Continued*)

220892_s_at	PSAT1	phosphoserine aminotransferase 1	NM_021154	29968	Hs.494261	GO:0006564: L-serine biosynthetic process, GO:0008152: metabolic process, GO:0008615: pyridoxine biosynthetic process, GO:0008652: amino acid biosynthetic process, GO:0004648: phosphoserine transaminase activity, GO:0016740: transferase activity, GO:0030170: pyridoxal phosphate binding	00260: Glycine, serine and threonine metabolism, 00750: Vitamin B6 metabolism	−0.0746	−0.1989	−0.5659	−1.4034	9.87	10.52	10.45	10.32	9.96	9.12	3
221113_s_at	WNT16	wingless-type MMTV integration site family, member 16	NM_016087	51384	Hs.272375	GO:0007223: Wnt receptor signaling pathway, calcium modulating pathway, GO:0007267: cell-cell signaling, GO:0007275: multicellular organismal development, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0004871: signal transducer activity, GO:0005201: extracellular matrix structural constituent	04310: Wnt signaling pathway, 04340: Hedgehog signaling pathway, 04916: Melanogenesis, 05217: Basal cell carcinoma	0.1269	−0.2966	−0.6458	−1.3879	5.74	6.53	6.66	6.23	5.88	5.14	3
220322_at	IL1F9	interleukin 1 family, member 9	NM_019618	56300	Hs.211238	GO:0006955: immune response, GO:0007267: cell-cell signaling, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005152: interleukin-1 receptor antagonist activity		−0.1941	−0.7965	−2.2743	−5.0934	8.04	12.8	12.61	12.01	10.53	7.71	3
220724_at	FLJ21511	hypothetical protein FLJ21511	NM_025087	80157	Hs.479703			0.0288	−0.1128	−0.5732	−1.0936	9.38	10.19	10.22	10.08	9.62	9.1	3
219856_at	C1orf116	chromosome 1 open reading frame 116	NM_023938	79098	Hs.32417			−0.0342	−0.1751	−0.778	−1.769	6.84	8.27	8.23	8.09	7.49	6.5	3
220104_at	ZC3HAV1	zinc finger CCCH-type, antiviral 1	NM_020119	56829	Hs.133512	GO:0006471: protein amino acid ADP-ribosylation, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0003950: NAD+ ADP-ribosyltransferase activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0675	−0.2821	−0.5411	−1.0572	5.02	6.02	5.95	5.74	5.48	4.96	3
219630_at	PDZK1IP1	PDZK1 interacting protein 1	NM_005764	10158	Hs.431099	GO:0005576: extracellular region, GO:0016020: membrane, GO:0016021: integral to membrane		0.0219	−0.3776	−1.0203	−2.1149	10.12	12.14	12.16	11.76	11.12	10.02	3
219722_s_at	GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	NM_024307	79153	Hs.289015	GO:0006071: glycerol metabolic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0008889: glycerophosphodiester phosphodiesterase activity, GO:0016787: hydrolase activity		−0.0959	−0.4766	−1.7878	−3.2699	6.26	9.81	9.71	9.33	8.02	6.54	3
219412_at	RAB38	RAB38, member RAS oncogene family	NM_022337	23682	Hs.591975	GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0005575: cellular_component, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding		0.0284	−0.2704	−0.7289	−1.4232	9.92	11.04	11.07	10.77	10.32	9.62	3
219428_s_at	PXMP4	peroxisomal membrane protein 4, 24kDa	NM_007238	11264	Hs.654857	GO:0005624: membrane fraction, GO:0005777: peroxisome, GO:0005778: peroxisomal membrane, GO:0016020: membrane, GO:0016021: integral to membrane		−0.0655	−0.2344	−0.6472	−1.3071	7.57	8.93	8.87	8.7	8.29	7.63	3
219289_at	HEATR3	HEAT repeat containing 3	NM_017939	55027	Hs.647381	GO:0005488: binding		0.0086	−0.3156	−0.4503	−1.0172	7.98	8.81	8.81	8.49	8.35	7.79	3

(*Continued*)

TABLE E2. (*Continued*)

219403_s_at	HPSE	heparanase	AF155510	10855	Hs.44227	GO:0006029: proteoglycan metabolic process, GO:0006954: inflammatory response, GO:0005764: lysosome, GO:0016020: membrane, GO:0000287: magnesium ion binding, GO:0004566: beta-glucuronidase activity, GO:0005509: calcium ion binding, GO:0016787: hydrolase activity	00531: Glycosaminoglycan degradation, 01032: Glycan structures - degradation	−0.0366	−0.6423	−2.204	−5.3236	6.67	11.33	11.29	10.69	9.12	6.01	3
219253_at	TMEM185B	transmembrane protein 185B	NM_024121	79134	Hs.376722	GO:0016020: membrane, GO:0016021: integral to membrane		−0.1448	−0.114	−0.6548	−1.1185	6.15	7.02	6.88	6.91	6.37	5.91	3		
219267_at	GLTP	glycolipid transfer protein	NM_016433	51228	Hs.381256	GO:0046836: glycolipid transport, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0017089: glycolipid transporter activity, GO:0051861: glycolipid binding		−0.0404	−0.1579	−0.5243	−1.0285	11.55	12.7	12.66	12.55	12.18	11.68	3		
219121_s_at	RBM35A	RNA binding motif protein 35A	NM_017697	54845	Hs.487471	GO:0000166: nucleotide binding, GO:0003723: RNA binding		−0.0568	−0.1956	−0.611	−1.5928	10.29	11.04	10.99	10.85	10.43	9.45	3		
219209_at	IFIH1	interferon induced with helicase C domain 1	NM_022168	64135	Hs.163173	GO:0009615: response to virus, GO:0042981: regulation of apoptosis, GO:0045087: innate immune response, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003723: RNA binding, GO:0004386: helicase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016787: hydrolase activity	00500: Starch and sucrose metabolism, 00790: Folate biosynthesis	0.1373	−0.0265	−0.7306	−1.5734	8.78	10.24	10.38	10.22	9.51	8.67	3		
219016_at	FASTKD5	FAST kinase domains 5	NM_021826	60493	Hs.654646	GO:0006915: apoptosis, GO:0004672: protein kinase activity, GO:0005524: ATP binding		−0.0458	−0.1059	−0.4164	−1.0365	6.39	7.1	7.06	7	6.69	6.07	3		
219079_at	CYB5R4	cytochrome b5 reductase 4	NM_016230	51167	Hs.5741	GO:0006118: electron transport, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0004128: cytochrome-b5 reductase activity, GO:0005506: iron ion binding, GO:0016491: oxidoreductase activity, GO:0020037: heme binding		−0.2267	−0.3861	−1.0475	−2.3598	5.57	7.13	6.91	6.75	6.09	4.77	3		
218810_at	ZC3H12A	zinc finger CCCH-type containing 12A	NM_025079	80149	Hs.656294			−0.1897	−0.7683	−2.143	−4.1637	6.37	10.27	10.08	9.5	8.12	6.1	3		
218992_at	C9orf46	chromosome 9 open reading frame 46	NM_018465	55848	Hs.584242	GO:0016020: membrane, GO:0016021: integral to membrane		0.0483	−0.161	−0.4602	−1.0794	8.36	9.23	9.28	9.07	8.77	8.15	3		
218295_s_at	NUP50	nucleoporin 50kDa	AF267865	10762	Hs.475103	GO:0006605: protein targeting, GO:0015031: protein transport, GO:0046907: intracellular transport, GO:0051028: mRNA transport, GO:0005643: nuclear pore, GO:0016021: integral to membrane, GO:0019867: outer membrane, GO:0015288: porin activity		−0.204	−0.4511	−0.9945	−2.3804	5.83	7.72	7.52	7.27	6.73	5.34	3		
218454_at	FLJ22662	hypothetical protein FLJ22662	NM_024829	79887	Hs.131933			0.0728	−0.1683	−0.7471	−1.474	10.61	12.43	12.5	12.26	11.68	10.96	3		
218209_s_at	P15RS	hypothetical protein FLJ10656	NM_018170	55197	Hs.464912	GO:0016301: kinase activity		−0.0743	−0.1908	−0.7435	−1.7731	7.23	8.15	8.08	7.96	7.41	6.38	3		
218254_s_at	SAR1B	SAR1 gene homolog B (S. cerevisiae)	NM_016103	51128	Hs.432984	GO:0006886: intracellular protein transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0007264: small GTPase mediated signal transduction, GO:0005622: intracellular, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0005525: GTP binding		−0.0309	−0.225	−0.5766	−1.1869	9.35	10.19	10.16	9.96	9.61	9	3		

(*Continued*)

TABLE E2. (*Continued*)

218073_s_at	TMEM48	transmembrane protein 48	NM_018087	55706	Hs.476525	GO:0006605: protein targeting, GO:0015031: protein transport, GO:0031081: nuclear pore distribution, GO:0051028: mRNA transport, GO:0051292: nuclear pore complex assembly, GO:0005643: nuclear pore, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0017056: structural constituent of nuclear pore		−0.0567	−0.1666	−0.824	−1.7145	5.58	6.26	6.2	6.09	5.43	4.54	3
218163_at	MCTS1	malignant T cell amplified sequence 1	NM_014060	28985	Hs.102696	GO:0000074: regulation of progression through cell cycle, GO:0008284: positive regulation of cell proliferation, GO:0003723: RNA binding		0.0068	−0.1234	−0.4307	−1.0929	9.39	10.03	10.04	9.91	9.6	8.94	3
217921_at	MAN1A2	mannosidase, alpha, class 1A, member 2	BE543064	10905	Hs.435938	GO:0006491: N-glycan processing, GO:0008152: metabolic process, GO:0005624: membrane fraction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004571: mannosyl-oligosaccharide 1,2-alpha-mannosidase activity, GO:0004571: mannosyl-oligosaccharide 1,2-alpha-mannosidase activity, GO:0005509: calcium ion binding, GO:0016798: hydrolase activity, acting on glycosyl bonds	00510: N-Glycan biosynthesis, 01030: Glycan structures - biosynthesis 1	−0.0873	−0.2542	−0.6238	−1.4099	4.46	5.57	5.48	5.31	4.94	4.16	3
217930_s_at	TOLLIP	toll interacting protein	NM_019009	54472	Hs.368527	GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007242: intracellular signaling cascade, GO:0007267: cell-cell signaling, GO:0016310: phosphorylation, GO:0045321: leukocyte activation, GO:0005737: cytoplasm, GO:0045092: interleukin-18 receptor complex, GO:0045323: interleukin-1 receptor complex, GO:0004871: signal transducer activity, GO:0005121: Toll binding, GO:0005515: protein binding	04620: Toll-like receptor signaling pathway	−0.1742	−0.1803	−0.6454	−1.0657	8.57	9.52	9.35	9.34	8.88	8.46	3
217741_s_at	ZFAND5	zinc finger, AN1-type domain 5	NM_006007	7763	Hs.406096	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0003674: molecular_function, GO:0003677: DNA binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0894	−0.3163	−0.6946	−1.4169	9.99	11.1	11.01	10.79	10.41	9.69	3
217835_x_at	C20orf24	chromosome 20 open reading frame 24	NM_018840	55969	Hs.584985	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0003674: molecular_function, GO:0005515: protein binding		−0.1028	−0.2839	−0.6911	−1.1941	11.28	12.37	12.27	12.09	11.68	11.18	3

(*Continued*)

TABLE E2. (*Continued*)

217294_s_at	ENO1	enolase 1, (alpha)	U88968	2023	Hs.517145	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006096: glycolysis, GO:0006350: transcription, GO:0030308: negative regulation of cell growth, GO:0000015: phosphopyruvate hydratase complex, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0000287: magnesium ion binding, GO:0003700: transcription factor activity, GO:0003714: transcription corepressor activity, GO:0004634: phosphopyruvate hydratase activity, GO:0005515: protein binding, GO:0008243: plasminogen activator activity, GO:0016829: lyase activity	00010: Glycolysis/ Gluconeogenesis	−0.2655	−0.2916	−0.6852	−1.3978	11.76	12.63	12.36	12.34	11.94	11.23	3
217356_s_at	PGK1	phosphoglycerate kinase 1	S81916	5230	Hs.78771	GO:0006096: glycolysis, GO:0016310: phosphorylation, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004618: phosphoglycerate kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity	00010: Glycolysis/ Gluconeogenesis, 00710: Carbon fixation	−0.1013	−0.195	−0.5194	−1.0265	11.87	12.52	12.42	12.32	12	11.49	3
216598_s_at	CCL2	chemokine (C-C motif) ligand 2	S69738	6347	Hs.303649	GO:0006468: protein amino acid phosphorylation, GO:0006874: cellular calcium ion homeostasis, GO:0006916: anti-apoptosis, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006959: humoral immune response, GO:0007155: cell adhesion, GO:0007187: G-protein signaling, coupled to cyclic nucleotide second messenger, GO:0007259: JAK-STAT cascade, GO:0007267: cell-cell signaling, GO:0009887: organ morphogenesis, GO:0019079: viral genome replication, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0016020: membrane, GO:0001664: G-protein-coupled receptor binding, GO:0004672: protein kinase activity, GO:0004871: signal transducer activity, GO:0008009: chemokine activity	04060: Cytokine-cytokine receptor interaction	−0.1339	−0.3418	−0.569	−1.3289	8.15	9.97	9.84	9.63	9.4	8.64	3
216915_s_at	PTPN12	protein tyrosine phosphatase, non-receptor type 12	S69182	5782	Hs.61812	GO:0006470: protein amino acid dephosphorylation, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0004726: non-membrane spanning protein tyrosine phosphatase activity, GO:0016787: hydrolase activity, GO:0017124: SH3 domain binding		−0.383	−0.3734	−0.6119	−1.404	6.19	7.32	6.94	6.95	6.71	5.92	3
216202_s_at	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	U15555	9517	Hs.435661	GO:0009058: biosynthetic process, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004758: serine C-palmitoyltransferase activity, GO:0008415: acyltransferase activity, GO:0016769: transferase activity, transferring nitrogenous groups, GO:0030170: pyridoxal phosphate binding	00600: Sphingolipid metabolism	−0.1466	−0.7978	−2.007	−3.3364	6.27	9.92	9.77	9.12	7.91	6.58	3

(*Continued*)

TABLE E2. (*Continued*)

216258_s_at	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	BE148534	5275	Hs.241407	GO:0009411: response to UV, GO:0030162: regulation of proteolysis, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity		−0.2209	−0.7832	−2.2556	−4.7962	5.69	10.44	10.22	9.65	8.18	5.64	3
215465_at	ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12	AL080207	26154	Hs.134585	GO:0006869: lipid transport, GO:0019725: cellular homeostasis, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0016887: ATPase activity	02010: ABC transporters - General	0.1228	−0.1817	−0.9151	−2.0759	9.69	11.43	11.56	11.25	10.52	9.36	3
215471_s_at	MAP7	microtubule-associated protein 7	AJ242502	9053	Hs.486548	GO:0000226: microtubule cytoskeleton organization and biogenesis, GO:0007163: establishment and/or maintenance of cell polarity, GO:0005737: cytoplasm, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0016020: membrane, GO:0005198: structural molecule activity		−0.0339	0.0058	−0.5158	−1.1797	7.23	7.98	7.95	7.99	7.47	6.8	3
214499_s_at	BCLAF1	BCL2-associated transcription factor 1	AF249273	9774	Hs.486542	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006917: induction of apoptosis, GO:0016481: negative regulation of transcription, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003677: DNA binding, GO:0005515: protein binding, GO:0016564: transcription repressor activity		−0.2483	−0.1553	−0.4981	−1.0993	7.42	8.43	8.18	8.27	7.93	7.33	3
214581_x_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	BE568134	27242	Hs.443577	GO:0006915: apoptosis, GO:0007165: signal transduction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0005515: protein binding	04060: Cytokine-cytokine receptor interaction	−0.1936	−0.5131	−0.9909	−2.3648	6.5	8.66	8.46	8.14	7.67	6.29	3
214076_at	GFOD2	glucose-fructose oxidoreductase domain containing 2	AI697803	81577	Hs.656247	GO:0006118: electron transport, GO:0008152: metabolic process, GO:0016491: oxidoreductase activity		0.1752	−0.068	−0.8221	−1.4538	5.05	6.55	6.73	6.48	5.73	5.1	3
214119_s_at	FKBP1A	FK506 binding protein 1A, 12kDa	AI936769	2280	Hs.471933	GO:0006457: protein folding, GO:0006457: protein folding, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005737: cytoplasm, GO:0003755: peptidyl-prolyl cis-trans isomerase activity, GO:0004872: receptor activity, GO:0005515: protein binding, GO:0016853: isomerase activity		−0.0982	−0.1024	−0.4435	−1.1543	9.86	10.23	10.13	10.13	9.79	9.08	3
213562_s_at	SQLE	squalene epoxidase	BF979497	6713	Hs.71465	GO:0006118: electron transport, GO:0008152: metabolic process, GO:0016126: sterol biosynthetic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004506: squalene monooxygenase activity, GO:0016491: oxidoreductase activity	00100: Biosynthesis of steroids, 00900: Terpenoid biosynthesis	−0.2829	−0.5207	−1.3799	−2.771	7.43	9.43	9.15	8.91	8.05	6.66	3
213851_at	TMEM110	transmembrane protein 110	BG031677	375346	Hs.371222	GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0016021: integral to membrane		−0.003	−0.0387	−0.5037	−1.0062	4.16	4.95	4.94	4.91	4.44	3.94	3
213189_at	MINA	MYC induced nuclear antigen	AI823896	84864	Hs.607776			0.0139	−0.108	−0.5038	−1.0827	9.2	9.75	9.76	9.64	9.25	8.67	3

(*Continued*)

TABLE E2. (*Continued*)

213425_at	WNT5A	wingless-type MMTV integration site family, member 5A	AI968085	7474	Hs.643085	GO:0007165: signal transduction, GO:0007223: Wnt receptor signaling pathway, calcium modulating pathway, GO:0007254: JNK cascade, GO:0007267: cell-cell signaling, GO:0009653: anatomical structure morphogenesis, GO:0009790: embryonic development, GO:0030324: lung development, GO:0030326: embryonic limb morphogenesis, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0004871: signal transducer activity, GO:0005102: receptor binding	04310: Wnt signaling pathway, 04340: Hedgehog signaling pathway, 04916: Melanogenesis, 05217: Basal cell carcinoma	−0.0133	−0.2108	−0.6618	−1.5449	6.16	9.01	9	8.8	8.35	7.47	3
212942_s_at	KIAA1199	KIAA1199	AB033025	57214	Hs.459088	GO:0007605: sensory perception of sound		−0.061	−0.3558	−0.679	−1.4385	4.79	6.27	6.2	5.91	5.59	4.83	3
212978_at	LRRC8B	leucine rich repeat containing 8 family, member B	AU146004	23507	Hs.482017, Hs.632420	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding		0.0938	−0.2664	−0.6565	−1.5379	8.7	9.74	9.84	9.48	9.09	8.21	3
212531_at	LCN2	lipocalin 2 (oncogene 24p3)	NM_005564	3934	Hs.204238	GO:0006810: transport, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0005215: transporter activity, GO:0005488: binding		0.0204	−0.9124	−2.9907	−5.818	6.53	12.21	12.23	11.3	9.22	6.39	3
212902_at	SEC24A	SEC24 related gene family, member A (S. cerevisiae)	BE645231	10802	Hs.595540	GO:0006886: intracellular protein transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0030127: COPII vesicle coat, GO:0030127: COPII vesicle coat, GO:0003674: molecular_function, GO:0005515: protein binding, GO:0008270: zinc ion binding		−0.1919	−0.483	−1.2384	−2.1201	5.5	7.29	7.1	6.81	6.06	5.17	3
212016_s_at	PTBP1	polypyrimidine tract binding protein 1	AA679988	5725	Hs.172550	GO:0006397: mRNA processing, GO:0006397: mRNA processing, GO:0008380: RNA splicing, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0005730: nucleolus, GO:0030530: heterogeneous nuclear ribonucleoprotein complex, GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0008187: poly-pyrimidine tract binding		−0.3286	−0.4089	−0.7421	−1.7604	8.63	9.71	9.38	9.3	8.96	7.95	3
212125_at	RANGAP1	Ran GTPase activating protein 1	NM_002883	5905	Hs.183800	GO:0007165: signal transduction, GO:0007165: signal transduction, GO:0005625: soluble fraction, GO:0005643: nuclear pore, GO:0005737: cytoplasm, GO:0048471: perinuclear region of cytoplasm, GO:0005096: GTPase activator activity, GO:0005098: Ran GTPase activator activity, GO:0005098: Ran GTPase activator activity, GO:0005515: protein binding, GO:0005515: protein binding		−0.1163	−0.306	−0.5545	−1.1343	8.69	9.46	9.35	9.16	8.91	8.33	3

(*Continued*)

TABLE E2. (*Continued*)

211612 _s_at	IL13RA1	interleukin 13 receptor, alpha 1	U62858	3597	Hs.496646	GO:0007166: cell surface receptor linked signal transduction, GO:0005886: plasma membrane, GO:0005898: interleukin-13 receptor complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004896: hematopoietin/interferon-class (D200-domain) cytokine receptor activity	04060: Cytokine-cytokine receptor interaction, 04630: Jak-STAT signaling pathway	−0.2055	−0.6202	−1.222	−2.8861	6.9	8.87	8.67	8.25	7.65	5.99	3
211681 _s_at	PDLIM5	PDZ and LIM domain 5	AF116705	10611	Hs.480311	GO:0005624: membrane fraction, GO:0005829: cytosol, GO:0015629: actin cytoskeleton, GO:0003779: actin binding, GO:0005080: protein kinase C binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0042805: actinin binding, GO:0046872: metal ion binding		−0.1501	−0.1131	−0.5837	−1.0085	5.85	6.31	6.16	6.2	5.73	5.3	3
211150 _s_at	DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	J03866	1737	Hs.335551	GO:0006085: acetyl-CoA biosynthetic process, GO:0006090: pyruvate metabolic process, GO:0006096: glycolysis, GO:0008152: metabolic process, GO:0005739: mitochondrion, GO:0005967: mitochondrial pyruvate dehydrogenase complex, GO:0045254: pyruvate dehydrogenase complex, GO:0004742: dihydrolipoyllysine-residue acetyltransferase activity, GO:0004742: dihydrolipoyllysine-residue acetyltransferase activity, GO:0005515: protein binding, GO:0008415: acyltransferase activity, GO:0016740: transferase activity, GO:0031405: lipoic acid binding	00010: Glycolysis/Gluconeogenesis, 00252: Alanine and aspartate metabolism, 00620: Pyruvate metabolism	−0.0978	−0.1057	−0.7879	−1.7403	6.67	7.6	7.5	7.49	6.81	5.86	3
211362 _s_at	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	AF169949	5275	Hs.241407	GO:0009411: response to UV, GO:0030162: regulation of proteolysis, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity		−0.2316	−0.8987	−2.3951	−5.0325	4.77	9.94	9.71	9.05	7.55	4.91	3
210852 _s_at	AASS	aminoadipate-semialdehyde synthase	AF229180	10157	Hs.156738	GO:0006118: electron transport, GO:0006554: lysine catabolic process, GO:0051262: protein tetramerization, GO:0005739: mitochondrion, GO:0010010: lysine-ketoglutarate reductase activity, GO:0016491: oxidoreductase activity, GO:0047130: saccharopine dehydrogenase (NADP+, L-lysine-forming) activity, GO:0047131: saccharopine dehydrogenase (NAD+, L-glutamate-forming) activity	00300: Lysine biosynthesis, 00310: Lysine degradation	−0.0365	−0.3441	−0.5315	−1.2118	5.02	6.84	6.81	6.5	6.31	5.63	3
210935 _s_at	WDR1	WD repeat domain 1	AF274954	9948	Hs.128548	GO:0007605: sensory perception of sound, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0003779: actin binding, GO:0005515: protein binding		−0.2506	−0.404	−0.8148	−1.608	8.73	9.83	9.58	9.42	9.01	8.22	3

(*Continued*)

TABLE E2. (*Continued*)

210663 _s_at	KYNU	kynureninase (L-kynurenine hydrolase)	BC000879	8942	Hs.470126	GO:0006569: tryptophan catabolic process, GO:0008152: metabolic process, GO:0009435: NAD biosynthetic process, GO:0005737: cytoplasm, GO:0008233: peptidase activity, GO:0008483: transaminase activity, GO:0016787: hydrolase activity, GO:0030170: pyridoxal phosphate binding, GO:0030429: kynureninase activity	00380: Tryptophan metabolism	0.023	−0.8847	−2.3379	−4.8808	3.06	9.59	9.61	8.71	7.25	4.71	3
210802 _s_at	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	BC002841	27292	Hs.533222	GO:0000154: rRNA modification, GO:0006364: rRNA processing, GO:0000179: rRNA (adenine-N6, N6-)-dimethyltransferase activity, GO:0003723: RNA binding, GO:0008168: methyltransferase activity, GO:0016740: transferase activity		−0.178	−0.3401	−0.595	−1.2893	7.61	8.47	8.29	8.13	7.87	7.18	3
210413 _x_at	SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	U19557	6318	Hs.123035	GO:0006955: immune response, GO:0030162: regulation of proteolysis, GO:0005576: extracellular region, GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding		−0.0977	−0.5521	−2.3008	−4.918	8.53	14.46	14.36	13.9	12.15	9.54	3
210449 _x_at	MAPK14	mitogen-activated protein kinase 14	AF100544	1432	Hs.588289	GO:0006468: protein amino acid phosphorylation, GO:0006928: cell motility, GO:0006935: chemotaxis, GO:0006950: response to stress, GO:0007166: cell surface receptor linked signal transduction, GO:0007243: protein kinase cascade, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004707: MAP kinase activity, GO:0004708: MAP kinase kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008339: MP kinase activity, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04370: VEGF signaling pathway, 04620: Toll-like receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 04670: Leukocyte transendothelial migration, 04912: GnRH signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection	0.1199	−0.2501	−0.8619	−2.0331	4.72	6.62	6.74	6.37	5.76	4.59	3
209882 _at	RIT1	Ras-like without CAAX 1	AF084462	6016	Hs.491234	GO:0007165: signal transduction, GO:0007264: small GTPase mediated signal transduction, GO:0005622: intracellular, GO:0005886: plasma membrane, GO:0000166: nucleotide binding, GO:0005516: calmodulin binding, GO:0005525: GTP binding, GO:0005525: GTP binding		−0.113	−0.4147	−1.0883	−2.2113	4.35	6.39	6.27	5.97	5.3	4.18	3
210087 _s_at	MPZL1	myelin protein zero-like 1	AF095727	9019	Hs.493919	GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007267: cell-cell signaling, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005198: structural molecule activity, GO:0005515: protein binding	04514: Cell adhesion molecules (CAMs)	0.0086	−0.3406	−0.8756	−1.6765	6.1	8.09	8.1	7.75	7.22	6.42	3

(*Continued*)

TABLE E2. (*Continued*)

209761_s_at	SP110	SP110 nuclear body protein	AA969194	3431	Hs.145150	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0045454: cell redox homeostasis, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0005062: hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0185	−0.0254	−0.5531	−1.065	7.61	8.78	8.76	8.76	8.23	7.72	3
209772_s_at	CD24	CD24 molecule	X69397	934	Hs.644105, Hs.694721	GO:0006959: humoral immune response, GO:0005886: plasma membrane, GO:0048503: GPI anchor binding	04640: Hematopoietic cell lineage	−0.2658	−0.7042	−1.8198	−3.3447	8.62	11.94	11.67	11.23	10.12	8.59	3
209231_s_at	DCTN5	dynactin 5 (p25)	BC004191	84516	Hs.435941	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0008415: acyltransferase activity		0.093	−0.279	−0.8261	−1.6629	5.51	7.1	7.19	6.82	6.27	5.43	3
209514_s_at	RAB27A	RAB27A, member RAS oncogene family	BE502030	5873	Hs.654978	GO:0006605: protein targeting, GO:0007264: small GTPase mediated signal transduction, GO:0007596: blood coagulation, GO:0015031: protein transport, GO:0016192: vesicle-mediated transport, GO:0030318: melanocyte differentiation, GO:0032400: melanosome localization, GO:0032402: melanosome transport, GO:0043316: cytotoxic T cell degranulation, GO:0043320: natural killer cell degranulation, GO:0043473: pigmentation, GO:0001750: photoreceptor outer segment, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0030141: secretory granule, GO:0030425: dendrite, GO:0042470: melanosome, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0031489: myosin V binding		0.0655	−0.4965	−1.3256	−3.2204	6.29	9.24	9.3	8.74	7.91	6.02	3
208952_s_at	LARP5	La ribonucleoprotein domain family, member 5	AU154358	23185	Hs.631814	GO:0003723: RNA binding		−0.0934	−0.2973	−0.5109	−1.0662	6.78	7.79	7.69	7.49	7.27	6.72	3
209188_x_at	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	AW516932	1810	Hs.348418	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003714: transcription corepressor activity, GO:0008134: transcription factor binding, GO:0043565: sequence-specific DNA binding		−0.0172	−0.1031	−0.5842	−1.4333	8.1	8.89	8.88	8.79	8.31	7.46	3
208932_at	PPP4C	protein phosphatase 4 (formerly X), catalytic subunit	BC001416	5531	Hs.534338	GO:0000226: microtubule cytoskeleton organization and biogenesis, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005813: centrosome, GO:0004704: NF-kappaB-inducing kinase activity, GO:0004722: protein serine/threonine phosphatase activity, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0016787: hydrolase activity, GO:0030145: manganese ion binding, GO:0046872: metal ion binding		−0.1396	−0.2317	−0.571	−1.3062	9.42	10.19	10.05	9.96	9.62	8.88	3

(*Continued*)

TABLE E2. (*Continued*)

208934_s_at	LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)	AI659005	3964	Hs.4082, Hs.652333	GO:0005615: extracellular space, GO:0005737: cytoplasm, GO:0005529: sugar binding, GO:0005529: sugar binding		0.0235	−0.1016	−0.7587	−1.5506	8.6	9.93	9.96	9.83	9.17	8.38	3
208811_s_at	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	AF080569	10049	Hs.490745	GO:0006457: protein folding, GO:0006986: response to unfolded protein, GO:0043154: negative regulation of caspase activity, GO:0045109: intermediate filament organization, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0048471: perinuclear region of cytoplasm, GO:0001671: ATPase activator activity, GO:0031072: heat shock protein binding, GO:0051087: chaperone binding		−0.1447	−0.2964	−0.5741	−1.2311	10.57	11.47	11.33	11.18	10.9	10.24	3
208905_at	CYCS	cytochrome c, somatic	BC005299	54205	Hs.437060, Hs.617193	GO:0006118: electron transport, GO:0006309: DNA fragmentation during apoptosis, GO:0006810: transport, GO:0006915: apoptosis, GO:0008635: caspase activation via cytochrome c, GO:0045333: cellular respiration, GO:0000159: protein phosphatase type 2A complex, GO:0005634: nucleus, GO:0005739: mitochondrion, GO:0005746: mitochondrial respiratory chain, GO:0005758: mitochondrial intermembrane space, GO:0005829: cytosol, GO:0000158: protein phosphatase type 2A activity, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0020037: heme binding, GO:0045155: electron transporter, transferring electrons from CoQH2-cytochrome c reductase complex and cytochrome c oxidase complex activity, GO:0046872: metal ion binding	04115: p53 signaling pathway, 04210: Apoptosis, 05210: Colorectal cancer, 05222: Small cell lung cancer	−0.0904	−0.2469	−0.5253	−1.0196	12.3	13.05	12.96	12.8	12.52	12.03	3
208708_x_at	EIF5	eukaryotic translation initiation factor 5	AL080102	1983	Hs.433702	GO:0006446: regulation of translational initiation, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0000166: nucleotide binding, GO:0003743: translation initiation factor activity, GO:0003924: GTPase activity, GO:0005525: GTP binding		−0.0722	−0.2518	−0.7237	−1.3915	10.64	11.86	11.79	11.61	11.14	10.47	3
208744_x_at	HSPH1	heat shock 105kDa/110kDa protein 1	D86956	10808	Hs.36927	GO:0006986: response to unfolded protein, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0005524: ATP binding		−0.2324	−0.521	−0.8688	−2.0027	6.94	8.27	8.04	7.75	7.4	6.27	3

(*Continued*)

TABLE E2. (*Continued*)

208621_s_at	VIL2	villin 2 (ezrin)	BF663141	7430	Hs.693594	GO:0007016: cytoskeletal anchoring, GO:0008360: regulation of cell shape, GO:0051017: actin filament bundle formation, GO:0001726: ruffle, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0005856: cytoskeleton, GO:0005884: actin filament, GO:0005902: microvillus, GO:0016020: membrane, GO:0019898: extrinsic to membrane, GO:0019898: extrinsic to membrane, GO:0030863: cortical cytoskeleton, GO:0005198: structural molecule activity, GO:0005488: binding, GO:0008092: cytoskeletal protein binding, GO:0043621: protein self-association, GO:0051015: actin filament binding	04670: Leukocyte transendothelial migration, 04810: Regulation of actin cytoskeleton, 05130: Pathogenic Escherichia coli infection - EHEC, 05131: Pathogenic Escherichia coli infection - EPEC	−0.3679	−0.3019	−0.7258	−1.5461	8.93	9.61	9.25	9.31	8.89	8.07	3
208650_s_at	CD24	CD24 molecule	BG327863	934	Hs.644105, Hs.694721	GO:0006959: humoral immune response, GO:0005886: plasma membrane, GO:0048503: GPI anchor binding	04640: Hematopoietic cell lineage	−0.2227	−0.5119	−1.3924	−2.6953	10.94	13.5	13.28	12.99	12.11	10.81		3
208290_s_at	EIF5	eukaryotic translation initiation factor 5	NM_001969	1983	Hs.433702	GO:0006446: regulation of translational initiation, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0000166: nucleotide binding, GO:0003743: translation initiation factor activity, GO:0003924: GTPase activity, GO:0005525: GTP binding		−0.0416	−0.19	−0.7745	−1.7138	9.8	11.11	11.07	10.92	10.34	9.4		3
208309_s_at	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	NM_006785	10892	Hs.601217	GO:0002726: positive regulation of T cell cytokine production, GO:0006508: proteolysis, GO:0006512: ubiquitin cycle, GO:0006916: anti-apoptosis, GO:0006952: defense response, GO:0007250: activation of NF-kappaB-inducing kinase, GO:0042981: regulation of apoptosis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0050852: T cell receptor signaling pathway, GO:0050870: positive regulation of T cell activation, GO:0051168: nuclear export, GO:0051259: protein oligomerization, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0032449: CBM complex, GO:0004842: ubiquitin-protein ligase activity, GO:0004871: signal transducer activity, GO:0008233: peptidase activity, GO:0019209: kinase activator activity, GO:0030693: caspase activity, GO:0043621: protein self-association	04660: T cell receptor signaling pathway, 04662: B cell receptor signaling pathway	−0.1733	−0.3955	−0.931	−2.124	7.28	8.59	8.42	8.2	7.66	6.47		3
207791_s_at	RAB1A	RAB1A, member RAS oncogene family	NM_004161	5861	Hs.310645	GO:0006888: ER to Golgi vesicle-mediated transport, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0016192: vesicle-mediated transport, GO:0005783: endoplasmic reticulum, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding		−0.0721	−0.1046	−0.4125	−1.102	11.49	12.1	12.03	12	11.69	11		3

(*Continued*)

TABLE E2. (*Continued*)

208103_s_at	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	NM_030920	81611	Hs.656466	GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0016023: cytoplasmic membrane-bound vesicle, GO:0005515: protein binding, GO:0019212: phosphatase inhibitor activity		−0.3389	−0.3712	−0.5707	−1.3306	6.4	7.06	6.72	6.69	6.49	5.73	3
207367_at	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	NM_001676	479	Hs.147111	GO:0006813: potassium ion transport, GO:0008152: metabolic process, GO:0015992: proton transport, GO:0005889: hydrogen:potassium-exchanging ATPase complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0005524: ATP binding, GO:0008900: hydrogen:potassium-exchanging ATPase activity, GO:0016787: hydrolase activity, GO:0016820: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, GO:0030955: potassium ion binding	00190: Oxidative phosphorylation	0.2764	−0.8492	−2.9941	−5.6206	4.85	10.82	11.09	9.97	7.82	5.2	3
207620_s_at	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	NM_003688	8573	Hs.495984	GO:0006468: protein amino acid phosphorylation, GO:0007155: cell adhesion, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0015629: actin cytoskeleton, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004385: guanylate kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity	04530: Tight junction	−0.041	−0.3546	−0.4466	−1.1289	4.96	6.31	6.27	5.96	5.86	5.18	3
214838_at	SFT2D2	SFT2 domain containing 2	AL035297	375035	Hs.645435	GO:0015031: protein transport, GO:0016020: membrane, GO:0016021: integral to membrane		0.1539	−0.0054	−0.5799	−1.1685	6.63	7.92	8.07	7.92	7.34	6.75	3
214959_s_at	API5	apoptosis inhibitor 5	AF229253	8539	Hs.435771	GO:0006915: apoptosis, GO:0006916: anti-apoptosis, GO:0006916: anti-apoptosis, GO:0006916: anti-apoptosis, GO:0005634: nucleus, GO:0005681: spliceosome, GO:0005737: cytoplasm, GO:0017134: fibroblast growth factor binding		−0.0633	−0.1331	−0.5172	−1.3786	7.02	7.78	7.72	7.65	7.26	6.4	3
209720_s_at	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	BC005224	6317	Hs.227948	GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity		−0.1074	−0.3161	−1.4576	−3.9813	9.43	14.36	14.25	14.04	12.9	10.38	3

(*Continued*)

TABLE E2. (*Continued*)

209969_s_at	STAT1	signal transducer and activator of transcription 1, 91kDa	BC002704	6772	Hs.694776	GO:0000074: regulation of progression through cell cycle, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0006919: caspase activation, GO:0007165: signal transduction, GO:0007242: intracellular signaling cascade, GO:0007249: I-kappaB kinase/NF-kappaB cascade, GO:0007260: tyrosine phosphorylation of STAT protein, GO:0007262: STAT protein nuclear translocation, GO:0009615: response to virus, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0004871: signal transducer activity, GO:0005062: hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity, GO:0005509: calcium ion binding, GO:0005515: protein binding	04620: Toll-like receptor signaling pathway, 04630: Jak-STAT signaling pathway, 05212: Pancreatic cancer	0.054	−0.3567	−1.0505	−2.4117	6.94	9.93	9.99	9.58	8.88	7.52	3
219358_s_at	CENTA2	centaurin, alpha 2	NM_018404	55803	Hs.514063	GO:0007507: heart development, GO:0043087: regulation of GTPase activity, GO:0005737: cytoplasm, GO:0005740: mitochondrial envelope, GO:0005886: plasma membrane, GO:0005096: GTPase activator activity, GO:0005546: phosphatidylinositol-4,5-bisphosphate binding, GO:0005547: phosphatidylinositol-3,4,5-triphosphate binding, GO:0008270: zinc ion binding, GO:0030674: protein binding, bridging, GO:0043325: phosphatidylinositol-3,4-bisphosphate binding, GO:0043533: inositol 1,3,4,5 tetrakisphosphate binding, GO:0046872: metal ion binding		−0.1711	−0.4265	−1.0959	−1.9555	8.04	10.09	9.92	9.66	8.99	8.13	3
219858_s_at	FLJ20160	FLJ20160 protein	NM_017694	54842	Hs.418581, Hs.644886			−0.2162	−0.3486	−0.7299	−1.4578	8.07	8.73	8.51	8.38	8	7.27	3
212374_at	FEM1B	fem-1 homolog b (C. elegans)	NM_015322	10116	Hs.362733	GO:0006917: induction of apoptosis, GO:0005575: cellular_component, GO:0004872: receptor activity, GO:0005123: death receptor binding		0.2563	−0.0418	−0.6301	−1.3491	5.7	6.64	6.89	6.59	6.01	5.29	3
212479_s_at	RMND5A	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	AK022815	64795	Hs.75277			0.1133	−0.0461	−0.5865	−1.0893	8.22	9.35	9.46	9.31	8.77	8.26	3

(*Continued*)

TABLE E2. (*Continued*)

35820_at	GM2A	GM2 ganglioside activator	M76477	2760	Hs.483873	GO:0006687: glycosphingolipid metabolic process, GO:0006689: ganglioside catabolic process, GO:0007611: learning and/or memory, GO:0009313: oligosaccharide catabolic process, GO:0019377: glycolipid catabolic process, GO:0019915: sequestering of lipid, GO:0030149: sphingolipid catabolic process, GO:0050877: neurological process, GO:0050885: regulation of balance, GO:0005739: mitochondrion, GO:0005764: lysosome, GO:0004563: beta-N-acetylhexosaminidase activity, GO:0030290: sphingolipid activator protein activity		0.0722	−0.57	−1.2509	−1.925	9.81	12.06	12.13	11.49	10.8	10.13	3
200628_s_at	WARS	tryptophanyl-tRNA synthetase	M61715	7453	Hs.497599	GO:0006436: tryptophanyl-tRNA aminoacylation, GO:0008285: negative regulation of cell proliferation, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004830: tryptophan-tRNA ligase activity, GO:0005524: ATP binding, GO:0016874: ligase activity	00380: Tryptophan metabolism, 00970: Aminoacyl-tRNA biosynthesis	0.0535	−0.3532	−0.5759	−1.1859	6.91	7.99	8.04	7.63	7.41	6.8	3
200664_s_at	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	NM_006145	3337	Hs.515210	GO:0006457: protein folding, GO:0006986: response to unfolded protein, GO:0051085: chaperone cofactor-dependent protein folding, GO:0005737: cytoplasm, GO:0031072: heat shock protein binding, GO:0051082: unfolded protein binding		−0.1509	−0.2674	−0.5218	−1.0071	9.19	10	9.85	9.73	9.48	8.99	3
32069_at	N4BP1	Nedd4 binding protein 1	AB014515	9683	Hs.511839			−0.0994	−0.4366	−0.8575	−1.4133	8.83	10.22	10.13	9.79	9.37	8.81	3
33646_g_at	GM2A	GM2 ganglioside activator	X61094	2760	Hs.483873	GO:0006687: glycosphingolipid metabolic process, GO:0006689: ganglioside catabolic process, GO:0007611: learning and/or memory, GO:0009313: oligosaccharide catabolic process, GO:0019377: glycolipid catabolic process, GO:0019915: sequestering of lipid, GO:0030149: sphingolipid catabolic process, GO:0050877: neurological process, GO:0050885: regulation of balance, GO:0005739: mitochondrion, GO:0005764: lysosome, GO:0004563: beta-N-acetylhexosaminidase activity, GO:0030290: sphingolipid activator protein activity		0.2772	−1.0947	−2.3381	−4.551	3.96	8.71	8.99	7.61	6.37	4.16	3
220599_s_at	CARD14	caspase recruitment domain family, member 14	NM_024110	79092	Hs.655729, Hs.675480	GO:0001934: positive regulation of protein amino acid phosphorylation, GO:0007250: activation of NF-kappaB-inducing kinase, GO:0042981: regulation of apoptosis, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0005515: protein binding, GO:0050700: CARD domain binding		−0.1623	−0.3686	−1.063	−1.8211	7.16	8.66	8.49	8.29	7.59	6.84	3

(*Continued*)

TABLE E2. (*Continued*)

220658_s_at	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	NM_020183	56938	Hs.434269, Hs.663740	GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0048511: rhythmic process, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0004871: signal transducer activity, GO:0030528: transcription regulator activity		−0.3122	−0.6537	−1.7324	−3.0112	5.44	8.51	8.19	7.85	6.77	5.49	3
219990_at	E2F8	E2F transcription factor 8	NM_024680	79733	Hs.523526	GO:0000074: regulation of progression through cell cycle, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005667: transcription factor complex, GO:0003700: transcription factor activity		−0.1989	−0.4308	−0.7835	−1.4575	6.62	7.23	7.03	6.8	6.44	5.77	3
220066_at	NOD2	nucleotide-binding oligomerization domain containing 2	NM_022162	64127	Hs.592072	GO:0001816: cytokine production, GO:0007242: intracellular signaling cascade, GO:0008063: Toll signaling pathway, GO:0016045: detection of bacterium, GO:0032498: detection of muramyl dipeptide, GO:0042742: defense response to bacterium, GO:0042981: regulation of apoptosis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0050718: positive regulation of interleukin-1 beta secretion, GO:0051092: activation of NF-kappaB transcription factor, GO:0051259: protein oligomerization, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0005886: plasma membrane, GO:0031982: vesicle, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0019899: enzyme binding, GO:0019901: protein kinase binding, GO:0032500: muramyl dipeptide binding, GO:0050700: CARD domain binding		−0.1426	−0.3234	−0.7908	−1.4775	8.89	10.29	10.15	9.97	9.5	8.81	3
217834_s_at	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	AL520908	10492	Hs.571177	GO:0006397: mRNA processing, GO:0008380: RNA splicing, GO:0005634: nucleus, GO:0005681: spliceosome, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0008143: poly(A) binding		−0.2039	−0.3807	−0.7812	−1.321	9.36	10.31	10.11	9.93	9.53	8.99	3
218049_s_at	MRPL13	mitochondrial ribosomal protein L13	NM_014078	28998	Hs.333823	GO:0006412: translation, GO:0005622: intracellular, GO:0005739: mitochondrion, GO:0005762: mitochondrial large ribosomal subunit, GO:0005840: ribosome, GO:0003735: structural constituent of ribosome	03010: Ribosome	−0.0878	−0.2333	−0.5418	−1.1857	9.02	9.61	9.53	9.38	9.07	8.43	3

(*Continued*)

TABLE E2. (*Continued*)

217738_at	PBEF1	pre-B-cell colony enhancing factor 1	NM_005746	10135	Hs.489615	GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0008284: positive regulation of cell proliferation, GO:0019363: pyridine nucleotide biosynthetic process, GO:0005737: cytoplasm, GO:0004516: nicotinate phosphoribosyltransferase activity, GO:0005125: cytokine activity, GO:0016757: transferase activity, transferring glycosyl groups, GO:0047280: nicotinamide phosphoribosyltransferase activity	00760: Nicotinate and nicotinamide metabolism	−0.2045	−0.6295	−1.178	−2.2254	9.86	11.36	11.16	10.73	10.18	9.14	3
217739_s_at	PBEF1	pre-B-cell colony enhancing factor 1	NM_005746	10135	Hs.489615	GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0008284: positive regulation of cell proliferation, GO:0019363: pyridine nucleotide biosynthetic process, GO:0005737: cytoplasm, GO:0004516: nicotinate phosphoribosyltransferase activity, GO:0005125: cytokine activity, GO:0016757: transferase activity, transferring glycosyl groups, GO:0047280: nicotinamide phosphoribosyltransferase activity	00760: Nicotinate and nicotinamide metabolism	−0.2198	−0.626	−1.2343	−2.2186	10.73	12.53	12.32	11.91	11.3	10.32	3
216379_x_at	CD24	CD24 molecule	AK000168	934	Hs.644105, Hs.694721	GO:0006959: humoral immune response, GO:0005886: plasma membrane, GO:0048503: GPI anchor binding	04640: Hematopoietic cell lineage	−0.119	−0.3678	−0.9014	−1.6405	12.13	13.79	13.67	13.42	12.88	12.14	3
216684_s_at	SS18	synovial sarcoma translocation, chromosome 18	AF257501	6760	Hs.404263	GO:0005634: nucleus		−0.2013	−0.264	−0.5599	−1.3906	7.76	8.53	8.33	8.26	7.97	7.14	3
211361_s_at	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	AF169949	5275	Hs.241407	GO:0009411: response to UV, GO:0030162: regulation of proteolysis, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity		−0.2013	−0.6705	−1.7565	−2.9866	8.56	11.5	11.29	10.82	9.74	8.51	3
211762_s_at	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	BC005978	3838	Hs.594238	GO:0000018: regulation of DNA recombination, GO:0000072: M phase specific microtubule process, GO:0000085: G2 phase of mitotic cell cycle, GO:0006259: DNA metabolic process, GO:0006606: protein import into nucleus, GO:0006607: NLS-bearing substrate import into nucleus, GO:0006886: intracellular protein transport, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005643: nuclear pore, GO:0005654: nucleoplasm, GO:0005737: cytoplasm, GO:0005737: cytoplasm, GO:0005488: binding, GO:0005515: protein binding, GO:0008139: nuclear localization sequence binding, GO:0008565: protein transporter activity		−0.1851	−0.3906	−0.7932	−1.4361	10	11.08	10.89	10.69	10.28	9.64	3

(*Continued*)

TABLE E2. (*Continued*)

210833_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	AL031429	5733	Hs.445000	GO:0006351: transcription, DNA-dependent, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0008150: biological_process, GO:0008219: cell death, GO:0005635: nuclear envelope, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004879: ligand-dependent nuclear receptor activity, GO:0004957: prostaglandin E receptor activity, GO:0004957: prostaglandin E receptor activity, GO:0004957: prostaglandin E receptor activity	04020: Calcium signaling pathway, 04080: Neuroactive ligand-receptor interaction	0.1578	0.0394	−0.7135	−1.3134	5.27	7.03	7.19	7.07	6.31	5.71	3
210904 _s_at	IL13RA1	interleukin 13 receptor, alpha 1	U81380	3597	Hs.496646	GO:0007166: cell surface receptor linked signal transduction, GO:0005886: plasma membrane, GO:0005898: interleukin-13 receptor complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004896: hematopoietin/interferon-class (D200-domain) cytokine receptor activity	04060: Cytokine-cytokine receptor interaction, 04630: Jak-STAT signaling pathway	−0.1574	−0.4252	−1.2896	−2.7746	7.36	9.31	9.15	8.88	8.02	6.53	3
210652 _s_at	C1orf34	chromosome 1 open reading frame 34	BC004399	22996	Hs.112949	GO:0005488: binding		−0.2881	−0.5776	−1.4877	−2.6196	6.7	9.36	9.08	8.79	7.88	6.74	3
210754 _s_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	M79321	4067	Hs.491767	GO:0006468: protein amino acid phosphorylation, GO:0007242: intracellular signaling cascade, GO:0008284: positive regulation of cell proliferation, GO:0009725: response to hormone stimulus, GO:0030218: erythrocyte differentiation, GO:0042531: positive regulation of tyrosine phosphorylation of STAT protein, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004716: receptor signaling protein tyrosine kinase activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04662: B cell receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 04730: Long-term depression, 05120: Epithelial cell signaling in Helicobacter pylori infection	−0.0248	−0.5095	−0.925	−1.7255	6.17	8.01	7.99	7.51	7.09	6.29	3
210458 _s_at	TANK	TRAF family member-associated NFKB activator	BC003388	10010	Hs.556496	GO:0007165: signal transduction, GO:0007249: I-kappaB kinase/NF-kappaB cascade, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0964	−0.2549	−0.5918	−1.1241	4.84	5.91	5.82	5.66	5.32	4.79	3

(*Continued*)

TABLE E2. (*Continued*)

210589_s_at	GBA	glucosidase, beta; acid (includes glucosylceramidase)	D13287	2629	Hs.282997	GO:0005975: carbohydrate metabolic process, GO:0006629: lipid metabolic process, GO:0006665: sphingolipid metabolic process, GO:0007040: lysosome organization and biogenesis, GO:0008152: metabolic process, GO:0005764: lysosome, GO:0016020: membrane, GO:0003824: catalytic activity, GO:0004348: glucosylceramidase activity, GO:0016798: hydrolase activity, acting on glycosyl bonds, GO:0043169: cation binding	00460: Cyanoamino acid metabolism, 00500: Starch and sucrose metabolism, 00600: Sphingolipid metabolism, 00940: Phenylpropanoid biosynthesis, 01032: Glycan structures - degradation	0.1256	−0.2246	−0.8753	−1.2898	8.96	10.6	10.72	10.37	9.72	9.31	3
209925_at	OCLN	occludin	U53823	4950	Hs.592605	GO:0006461: protein complex assembly, GO:0005886: plasma membrane, GO:0005923: tight junction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030054: cell junction, GO:0005198: structural molecule activity	04514: Cell adhesion molecules (CAMs), 04530: Tight junction, 04670: Leukocyte transendothelial migration, 05130: Pathogenic Escherichia coli infection - EHEC, 05131: Pathogenic Escherichia coli infection - EPEC	−0.0966	−0.3495	−0.9386	−1.6303	5.96	7.23	7.13	6.88	6.29	5.6	3
210058_at	MAPK13	mitogen-activated protein kinase 13	BC000433	5603	Hs.178695	GO:0006468: protein amino acid phosphorylation, GO:0006950: response to stress, GO:0007049: cell cycle, GO:0007243: protein kinase cascade, GO:0000166: nucleotide binding, GO:0004672: protein kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0004707: MAP kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008339: MP kinase activity, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04370: VEGF signaling pathway, 04620: Toll-like receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 04670: Leukocyte transendothelial migration, 04912: GnRH signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection	−0.0808	−0.2479	−0.6541	−1.1747	9.7	10.68	10.6	10.43	10.03	9.51	3
209792_s_at	KLK10	kallikrein-related peptidase 10	BC002710	5655	Hs.275464	GO:0006508: proteolysis, GO:0007049: cell cycle, GO:0045786: negative regulation of progression through cell cycle, GO:0005576: extracellular region, GO:0004252: serine-type endopeptidase activity		−0.2752	−0.577	−1.4417	−2.5253	9.9	12.34	12.06	11.76	10.9	9.81	3
209921_at	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	AB040875	23657	Hs.390594	GO:0006461: protein complex assembly, GO:0006810: transport, GO:0006865: amino acid transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0015171: amino acid transmembrane transporter activity, GO:0015327: cystine:glutamate antiporter activity		−0.0911	−0.511	−1.2368	−2.2419	5.86	8.24	8.15	7.73	7	6	3
209771_x_at	CD24	CD24 molecule	AA761181	934	Hs.644105, Hs.694721	GO:0006959: humoral immune response, GO:0005886: plasma membrane, GO:0048503: GPI anchor binding	04640: Hematopoietic cell lineage	−0.1272	−0.3398	−0.8628	−1.5623	12.2	13.8	13.67	13.46	12.94	12.24	3
209773_s_at	RRM2	ribonucleotide reductase M2 polypeptide	BC001886	6241	Hs.226390	GO:0006260: DNA replication, GO:0009186: deoxyribonucleoside diphosphate metabolic process, GO:0005737: cytoplasm, GO:0004748: ribonucleoside-diphosphate reductase activity, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0016491: oxidoreductase activity	00230: Purine metabolism, 00240: Pyrimidine metabolism, 04115: p53 signaling pathway	−0.4621	−1.1495	−2.2388	−4.5405	5.92	9.45	8.99	8.3	7.21	4.91	3

(*Continued*)

TABLE E2. (*Continued*)

209218_at	SQLE	squalene epoxidase	AF098865	6713	Hs.71465	GO:0006118: electron transport, GO:0008152: metabolic process, GO:0016126: sterol biosynthetic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004506: squalene monooxygenase activity, GO:0016491: oxidoreductase activity	00100: Biosynthesis of steroids, 00900: Terpenoid biosynthesis	−0.1082	−0.2424	−0.7476	−1.221	10.89	11.81	11.7	11.57	11.06	10.59	3
209719 _x_at	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	BC005224	6317	Hs.227948	GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity		−0.0951	−0.4387	−1.6316	−4.0763	8.91	14.21	14.11	13.77	12.58	10.13	3
208651 _x_at	CD24	CD24 molecule	BG327863	934	Hs.644105, Hs.694721	GO:0006959: humoral immune response, GO:0005886: plasma membrane, GO:0048503: GPI anchor binding	04640: Hematopoietic cell lineage	−0.1628	−0.4233	−0.9997	−1.8939	10.85	12.62	12.46	12.2	11.62	10.73	3
209025 _s_at	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	AF037448	10492	Hs.571177	GO:0006397: mRNA processing, GO:0008380: RNA splicing, GO:0005634: nucleus, GO:0005681: spliceosome, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0008143: poly(A) binding		−0.122	−0.3679	−0.7954	−1.6248	9.03	10.17	10.05	9.81	9.38	8.55	3
208126 _s_at	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	NM_000772	1562	Hs.511872	GO:0006118: electron transport, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0004497: monooxygenase activity, GO:0004497: monooxygenase activity, GO:0005506: iron ion binding, GO:0019825: oxygen binding, GO:0020037: heme binding, GO:0046872: metal ion binding, GO:0050381: unspecific monooxygenase activity	00590: Arachidonic acid metabolism, 00591: Linoleic acid metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	0.5173	0.172	−0.859	−1.6233	4.63	6.37	6.89	6.54	5.51	4.75	3
208436 _s_at	IRF7	interferon regulatory factor 7	NM_004030	3665	Hs.166120	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006955: immune response, GO:0009615: response to virus, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0003704: specific RNA polymerase II transcription factor activity	04620: Toll-like receptor signaling pathway	0.0406	−0.3689	−1.3641	−2.1875	7.27	9.7	9.75	9.34	8.34	7.52	3
207381_at	ALOX12B	arachidonate 12-lipoxygenase, 12R type	NM_001139	242	Hs.136574	GO:0006118: electron transport, GO:0006629: lipid metabolic process, GO:0008544: epidermis development, GO:0019370: leukotriene biosynthetic process, GO:0004052: arachidonate 12-lipoxygenase activity, GO:0005506: iron ion binding, GO:0016165: lipoxygenase activity, GO:0016491: oxidoreductase activity, GO:0046872: metal ion binding	00590: Arachidonic acid metabolism	−0.0526	−0.4017	−1.0668	−1.8341	9.55	11.41	11.35	11	10.34	9.57	3

(*Continued*)

TABLE E2. (*Continued*)

207654_x_at	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	NM_001938	1810	Hs.348418	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003714: transcription corepressor activity, GO:0008134: transcription factor binding, GO:0043565: sequence-specific DNA binding	−0.0718	−0.0755	−0.5393	−1.1915	8.16	8.95	8.88	8.87	8.41	7.76	3
207038_at	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	NM_004694	9120	Hs.42645, Hs.463838	GO:0006810: transport, GO:0015718: monocarboxylic acid transport, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005215: transporter activity, GO:0008028: monocarboxylic acid transmembrane transporter activity, GO:0015293: symporter activity	0.2079	−0.0666	−0.8525	−1.3149	3.53	5.56	5.77	5.49	4.71	4.25	3
207254_at	SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1	NM_005073	6564	Hs.436893	GO:0006857: oligopeptide transport, GO:0007586: digestion, GO:0015031: protein transport, GO:0005575: cellular_component, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005215: transporter activity, GO:0015198: oligopeptide transporter activity, GO:0015293: symporter activity, GO:0015333: peptide:hydrogen symporter activity	0.2685	−0.139	−0.5576	−1.051	8.77	9.88	10.14	9.74	9.32	8.83	3
206499_s_at	RCC1	regulator of chromosome condensation 1	NM_001269	1104	Hs.469723	GO:0000082: G1/S transition of mitotic cell cycle, GO:0006323: DNA packaging, GO:0007049: cell cycle, GO:0007052: mitotic spindle organization and biogenesis, GO:0007088: regulation of mitosis, GO:0007090: regulation of S phase of mitotic cell cycle, GO:0051301: cell division, GO:0000790: nuclear chromatin, GO:0000794: condensed nuclear chromosome, GO:0005737: cytoplasm, GO:0003682: chromatin binding, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005087: Ran guanyl-nucleotide exchange factor activity, GO:0005515: protein binding, GO:0042393: histone binding	−0.1616	−0.4406	−0.8546	−1.5865	5.93	7.2	7.04	6.76	6.35	5.62	3
207018_s_at	RAB27B	RAB27B, member RAS oncogene family	NM_004163	5874	Hs.25318	GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding	0.066	−0.1918	−1.1322	−1.8348	5.07	7.1	7.17	6.91	5.97	5.27	3

(*Continued*)

TABLE E2. (*Continued*)

205783_at	KLK13	kallikrein-related peptidase 13	NM_015596	26085	Hs.165296	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0005576: extracellular region, GO:0005737: cytoplasm, GO:0004252: serine-type endopeptidase activity, GO:0004252: serine-type endopeptidase activity, GO:0005515: protein binding, GO:0008233: peptidase activity		−0.3364	−1.4042	−3.0774	−5.3801	4.66	10.44	10.1	9.04	7.36	5.06	3
206034_at	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	NM_002640	5271	Hs.368077	GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding		−0.0932	−0.1209	−0.6178	−1.001	8.57	9.44	9.34	9.31	8.82	8.43	3
205246_at	PEX13	peroxisome biogenesis factor 13	NM_002618	5194	Hs.567316	GO:0015031: protein transport, GO:0016560: protein import into peroxisome matrix, docking, GO:0005624: membrane fraction, GO:0005777: peroxisome, GO:0005778: peroxisomal membrane, GO:0005779: integral to peroxisomal membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding		−0.1478	−0.5115	−1.073	−1.9591	4.81	6.8	6.66	6.29	5.73	4.85	3
205554 _s_at	DNASE1L3	deoxyribonuclease I-like 3	NM_004944	1776	Hs.476453	GO:0006308: DNA catabolic process, GO:0006309: DNA fragmentation during apoptosis, GO:0006915: apoptosis, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0004519: endonuclease activity, GO:0004536: deoxyribonuclease activity, GO:0004536: deoxyribonuclease activity, GO:0005509: calcium ion binding, GO:0016787: hydrolase activity		−0.0292	−0.5083	−0.9027	−1.7797	6.28	8.23	8.2	7.72	7.33	6.45	3
205008_s_at	CIB2	calcium and integrin binding family member 2	NM_006383	10518	Hs.129867	GO:0005509: calcium ion binding, GO:0005515: protein binding		0.1649	−0.0139	−0.7358	−1.1804	5.94	7.01	7.18	7	6.28	5.83	3
205241_at	SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	NM_005138	9997	Hs.658057	GO:0006118: electron transport, GO:0006457: protein folding, GO:0005739: mitochondrion, GO:0005507: copper ion binding, GO:0046872: metal ion binding		−0.1362	−0.4418	−1.161	−1.9776	7.92	10.1	9.97	9.66	8.94	8.12	3
204616_at	UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	NM_006002	7347	Hs.162241	GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0004221: ubiquitin thiolesterase activity, GO:0008234: cysteine-type peptidase activity		−0.0675	−0.257	−0.6672	−1.1035	10.67	11.61	11.54	11.35	10.94	10.51	3
204638_at	ACP5	acid phosphatase 5, tartrate resistant	NM_001611	54	Hs.1211	GO:0005764: lysosome, GO:0016021: integral to membrane, GO:0003993: acid phosphatase activity, GO:0005506: iron ion binding, GO:0016787: hydrolase activity, GO:0046872: metal ion binding	00361: gamma-Hexachlorocyclohexane degradation, 00740: Riboflavin metabolism	0.0212	−0.2904	−0.7245	−1.2766	8.17	9.81	9.83	9.52	9.08	8.53	3
204170 _s_at	CKS2	CDC28 protein kinase regulatory subunit 2	NM_001827	1164	Hs.83758	GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0007049: cell cycle, GO:0007051: spindle organization and biogenesis, GO:0007127: meiosis I, GO:0008283: cell proliferation, GO:0048015: phosphoinositide-mediated signaling, GO:0051301: cell division, GO:0016538: cyclin-dependent protein kinase regulator activity		−0.2643	−0.7443	−1.5148	−2.6812	7.51	9.22	8.96	8.48	7.71	6.54	3

(*Continued*)

TABLE E2. (*Continued*)

204341_at	TRIM16	tripartite motif-containing 16	NM_006470	10626	Hs.123534	GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0116	−0.1659	−0.4418	−1.0499	9.86	10.82	10.81	10.66	10.38	9.77	3
203153_at	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	NM_001548	3434	Hs.20315	GO:0006955: immune response, GO:0008150: biological_process, GO:0005737: cytoplasm, GO:0005488: binding		0.266	0.0891	−1.1034	−1.9675	7.78	10.13	10.4	10.22	9.03	8.17	3
203432_at	TMPO	thymopoietin	AW272611	7112	Hs.11355	GO:0045449: regulation of transcription, GO:0005634: nucleus, GO:0005635: nuclear envelope, GO:0005694: chromosome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003677: DNA binding, GO:0005521: lamin binding		−0.1424	−0.2968	−0.9321	−1.5359	7.06	7.96	7.82	7.66	7.03	6.42	3
202539_s_at	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	NM_000859	3156	Hs.643495	GO:0006629: lipid metabolic process, GO:0006695: cholesterol biosynthetic process, GO:0008354: germ cell migration, GO:0008406: gonad development, GO:0005624: membrane fraction, GO:0005777: peroxisome, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004420: hydroxymethylglutaryl-CoA reductase (NADPH) activity, GO:0016491: oxidoreductase activity	00100: Biosynthesis of steroids	−0.0889	−0.2257	−0.5812	−1.0167	10.45	11.07	10.98	10.84	10.49	10.05	3
202575_at	CRABP2	cellular retinoic acid binding protein 2	NM_001878	1382	Hs.405662	GO:0006355: regulation of transcription, DNA-dependent, GO:0006810: transport, GO:0007165: signal transduction, GO:0008544: epidermis development, GO:0005737: cytoplasm, GO:0005215: transporter activity, GO:0008289: lipid binding, GO:0016918: retinal binding		−0.0804	−0.3687	−1.2267	−2.073	10.16	12.76	12.68	12.39	11.53	10.68	3
202503_s_at	KIAA0101	KIAA0101	NM_014736	9768	Hs.81892	GO:0005739: mitochondrion		−0.3386	−0.6566	−1.3206	−2.3209	7.32	9.01	8.67	8.35	7.68	6.68	3
202533_s_at	DHFR	dihydrofolate reductase	NM_000791	1719	Hs.648635, Hs.654551	GO:0006545: glycine biosynthetic process, GO:0006730: one-carbon compound metabolic process, GO:0009165: nucleotide biosynthetic process, GO:0005575: cellular_component, GO:0004146: dihydrofolate reductase activity, GO:0016491: oxidoreductase activity, GO:0050661: NADP binding	00670: One carbon pool by folate, 00790: Folate biosynthesis	−0.1596	−0.3227	−0.6814	−1.2382	7.02	8.02	7.86	7.7	7.34	6.78	3
202069_s_at	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	NM_005530	3419	Hs.591110	GO:0005975: carbohydrate metabolic process, GO:0006099: tricarboxylic acid cycle, GO:0008152: metabolic process, GO:0005739: mitochondrion, GO:0000287: magnesium ion binding, GO:0004449: isocitrate dehydrogenase (NAD+) activity, GO:0016491: oxidoreductase activity, GO:0016616: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, GO:0030145: manganese ion binding	00020: Citrate cycle (TCA cycle)	−0.1748	−0.5084	−1.0293	−1.8384	9.32	10.73	10.55	10.22	9.7	8.89	3

(*Continued*)

TABLE E2. (*Continued*)

202134_s_at	WWTR1	WW domain containing transcription regulator 1	NM_015472	25937	Hs.477921	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0001649: osteoblast differentiation, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0045599: negative regulation of fat cell differentiation, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0005634: nucleus, GO:0005667: transcription factor complex, GO:0005737: cytoplasm, GO:0003713: transcription coactivator activity, GO:0003714: transcription corepressor activity, GO:0005515: protein binding, GO:0030528: transcription regulator activity		−0.1848	−0.8333	−1.9246	−3.0776	4.43	7.55	7.37	6.72	5.63	4.48	3
201890_at	RRM2	ribonucleotide reductase M2 polypeptide	BE966236	6241	Hs.226390	GO:0006260: DNA replication, GO:0009186: deoxyribonucleoside diphosphate metabolic process, GO:0005737: cytoplasm, GO:0004748: ribonucleoside-diphosphate reductase activity, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0016491: oxidoreductase activity	00230: Purine metabolism, 00240: Pyrimidine metabolism, 04115: p53 signaling pathway	−0.5585	−0.8481	−1.5463	−2.8106	8.45	10.45	9.9	9.61	8.91	7.64	3
202058_s_at	KPNA1	karyopherin alpha 1 (importin alpha 5)	BC002374	3836	Hs.161008	GO:0000018: regulation of DNA recombination, GO:0006607: NLS-bearing substrate import into nucleus, GO:0006886: intracellular protein transport, GO:0005634: nucleus, GO:0005643: nuclear pore, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0008139: nuclear localization sequence binding, GO:0008565: protein transporter activity		−0.1558	−0.3011	−0.9312	−1.6941	6.17	7.32	7.17	7.02	6.39	5.63	3
201735_s_at	CLCN3	chloride channel 3	NM_001829	1182	Hs.481186	GO:0006811: ion transport, GO:0006821: chloride transport, GO:0006885: regulation of pH, GO:0048388: endosomal lumen acidification, GO:0005769: early endosome, GO:0005769: early endosome, GO:0005770: late endosome, GO:0005770: late endosome, GO:0005794: Golgi apparatus, GO:0005794: Golgi apparatus, GO:0009986: cell surface, GO:0012506: vesicle membrane, GO:0012506: vesicle membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005244: voltage-gated ion channel activity, GO:0005247: voltage-gated chloride channel activity, GO:0005515: protein binding, GO:0030165: PDZ domain binding, GO:0030165: PDZ domain binding, GO:0031404: chloride ion binding, GO:0042803: protein homodimerization activity, GO:0046982: protein heterodimerization activity, GO:0046982: protein heterodimerization activity		−0.0758	−0.3782	−0.8439	−1.5692	9.6	10.85	10.78	10.47	10.01	9.28	3
201777_s_at	KIAA0494	KIAA0494	BC002525	9813	Hs.100874	GO:0005509: calcium ion binding		0.0026	−0.0817	−0.4753	−1.0822	4.28	5.22	5.23	5.14	4.75	4.14	3

(*Continued*)

TABLE E2. (*Continued*)

201543_s_at	SAR1A	SAR1 gene homolog A (S. cerevisiae)	NM_020150	56681	Hs.499960	GO:0006886: intracellular protein transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0007264: small GTPase mediated signal transduction, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding		−0.1933	−0.2767	−0.6067	−1.0791	7.65	8.64	8.44	8.36	8.03	7.56	3
201673_s_at	GYS1	glycogen synthase 1 (muscle)	NM_002103	2997	Hs.386225	GO:0005978: glycogen biosynthetic process, GO:0004373: glycogen (starch) synthase activity, GO:0005515: protein binding, GO:0016757: transferase activity, transferring glycosyl groups	00500: Starch and sucrose metabolism, 04910: Insulin signaling pathway	−0.1824	−0.3313	−0.6215	−1.1531	6.58	7.72	7.54	7.39	7.1	6.57	3
217140_s_at	VDAC1	voltage-dependent anion channel 1	AJ002428	7416	Hs.519320	GO:0006820: anion transport, GO:0008632: apoptotic program, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0019867: outer membrane, GO:0046930: pore complex, GO:0005515: protein binding, GO:0008308: voltage-gated ion-selective channel activity, GO:0015288: porin activity	04020: Calcium signaling pathway	−0.1208	−0.2785	−0.6851	−1.184	10	10.67	10.55	10.39	9.98	9.48	3
217272_s_at	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	AJ001698	5275	Hs.241407	GO:0009411: response to UV, GO:0030162: regulation of proteolysis, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0004867: serine-type endopeptidase inhibitor activity		−0.1415	−0.5727	−1.4533	−2.7194	10.11	12.96	12.82	12.39	11.51	10.24	3
213342_at	YAP1	Yes-associated protein 1, 65kDa	AI745185	10413	Hs.503692	GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0005667: transcription factor complex, GO:0005515: protein binding, GO:0005515: protein binding, GO:0016563: transcription activator activity		−0.1201	−0.3944	−0.5465	−1.3774	7.6	8.53	8.41	8.13	7.98	7.15	3
213457_at	MFHAS1	malignant fibrous histiocytoma amplified sequence 1	BF739959	9258	Hs.379414	GO:0007264: small GTPase mediated signal transduction, GO:0005515: protein binding, GO:0005525: GTP binding		−0.1522	−0.3032	−0.6533	−1.1405	5.53	7.22	7.07	6.92	6.57	6.08	3
214681_at	GK	glycerol kinase	AI830490	2710	Hs.1466	GO:0005975: carbohydrate metabolic process, GO:0006072: glycerol-3-phosphate metabolic process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity	00561: Glycerolipid metabolism, 03320: PPAR signaling pathway	0.063	−0.9353	−1.2804	−2.327	5.01	7.25	7.31	6.31	5.97	4.92	3

(*Continued*)

TABLE E2. (*Continued*)

217043_s_at	MFN1	mitofusin 1	U95822	55669	Hs.478383	GO:0008053: mitochondrial fusion, GO:0008150: biological_process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019867: outer membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding, GO:0016787: hydrolase activity		−0.1384	−0.2889	−0.6231	−1.3372	9.18	10.18	10.04	9.89	9.55	8.84	3
208951_at	ALDH7A1	aldehyde dehydrogenase 7 family, member A1	BC002515	501	Hs.483239	GO:0006081: aldehyde metabolic process, GO:0007605: sensory perception of sound, GO:0008152: metabolic process, GO:0005575: cellular_component, GO:0005739: mitochondrion, GO:0004029: aldehyde dehydrogenase (NAD) activity, GO:0004043: L-aminoadipate-semialdehyde dehydrogenase activity, GO:0016491: oxidoreductase activity	00010: Glycolysis / Gluconeogenesis, 00053: Ascorbate and aldarate metabolism, 00071: Fatty acid metabolism, 00120: Bile acid biosynthesis, 00220: Urea cycle and metabolism of amino groups, 00280: Valine, leucine and isoleucine degradation, 00310: Lysine degradation, 00340: Histidine metabolism, 00380: Tryptophan metabolism, 00410: beta-Alanine metabolism, 00561: Glycerolipid metabolism, 00620: Pyruvate metabolism, 00640: Propanoate metabolism, 00650: Butanoate metabolism, 00903: Limonene and pinene degradation	0.031	−0.381	−0.5376	−1.1073	9.62	10.45	10.48	10.07	9.92	9.35	3
209080_x_at	GLRX3	glutaredoxin 3	AF118652	10539	Hs.42644	GO:0045454: cell redox homeostasis, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0009055: electron carrier activity, GO:0015035: protein disulfide oxidoreductase activity		−0.1601	−0.3543	−0.6913	−1.3104	10.07	11.02	10.86	10.67	10.33	9.71	3
221477_s_at	MGC5618	hypothetical protein MGC5618	BC001980	79099				0.1396	−0.5564	−0.9414	−1.5991	8.88	9.96	10.1	9.41	9.02	8.36	3
222223_s_at	IL1F5	interleukin 1 family, member 5 (delta)	AF216693	26525	Hs.516301	GO:0006954: inflammatory response, GO:0006955: immune response, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005152: interleukin-1 receptor antagonist activity		−0.1366	−0.4796	−1.3959	−2.295	10.35	12.63	12.5	12.15	11.24	10.34	3
209653_at	KPNA4	karyopherin alpha 4 (importin alpha 3)	U93240	3840	Hs.288193	GO:0006607: NLS-bearing substrate import into nucleus, GO:0006886: intracellular protein transport, GO:0005634: nucleus, GO:0005643: nuclear pore, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0008565: protein transporter activity		−0.0837	−0.079	−0.6621	−1.4217	4.81	5.64	5.56	5.56	4.98	4.22	3
209727_at	GM2A	GM2 ganglioside activator	M76477	2760	Hs.483873	GO:0006687: glycosphingolipid metabolic process, GO:0006689: ganglioside catabolic process, GO:0007611: learning and/or memory, GO:0009313: oligosaccharide catabolic process, GO:0019377: glycolipid catabolic process, GO:0019915: sequestering of lipid, GO:0030149: sphingolipid catabolic process, GO:0050877: neurological process, GO:0050885: regulation of balance, GO:0005739: mitochondrion, GO:0005764: lysosome, GO:0004563: beta-N-acetylhexosaminidase activity, GO:0030290: sphingolipid activator protein activity		−0.0227	−1.3288	−2.0003	−3.6444	5.73	9.35	9.33	8.02	7.35	5.71	3

(*Continued*)

TABLE E2. (*Continued*)

60528_at	PLA2G4B	phospholipase A2, group IVB (cytosolic)	N71116	8681	Hs.198161	GO:0006954: inflammatory response, GO:0007567: parturition, GO:0016042: lipid catabolic process, GO:0019369: arachidonic acid metabolic process, GO:0019722: calcium-mediated signaling, GO:0046475: glycerophospholipid catabolic process, GO:0005576: extracellular region, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005768: endosome, GO:0005829: cytosol, GO:0016020: membrane, GO:0004622: lysophospholipase activity, GO:0005509: calcium ion binding, GO:0005544: calcium-dependent phospholipid binding, GO:0016787: hydrolase activity, GO:0047498: calcium-dependent phospholipase A2 activity		−0.0109	−0.3964	−1.0533	−1.4798	8.68	10.12	10.11	9.73	9.07	8.64	3
202525_at	PRSS8	protease, serine, 8	NM_002773	5652	Hs.75799	GO:0006508: proteolysis, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0004252: serine-type endopeptidase activity		−0.0599	−0.2895	−0.8055	−1.1491	9.23	10.31	10.25	10.02	9.51	9.16	3
203946_s_at	ARG2	arginase, type II	NM_001172	384	Hs.653205	GO:0000050: urea cycle, GO:0006527: arginine catabolic process, GO:0006809: nitric oxide biosynthetic process, GO:0006941: striated muscle contraction, GO:0005739: mitochondrion, GO:0004053: arginase activity, GO:0016787: hydrolase activity, GO:0030145: manganese ion binding, GO:0046872: metal ion binding	00220: Urea cycle and metabolism of amino groups, 00330: Arginine and proline metabolism	0.1348	−0.3581	−1.4466	−2.3579	3.38	5.99	6.12	5.63	4.54	3.63	3
55081_at	MICALL1	MICAL-like 1	W46406	85377	Hs.517610	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0911	−0.2261	−0.8524	−1.1648	9.57	10.87	10.78	10.64	10.01	9.7	3
202086_at	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	NM_002462	4599	Hs.517307	GO:0006917: induction of apoptosis, GO:0006952: defense response, GO:0006955: immune response, GO:0007165: signal transduction, GO:0009615: response to virus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0005525: GTP binding		−0.129	−0.4504	−1.7328	−2.4938	8.06	11.28	11.15	10.83	9.54	8.78	3
212142_at	MCM4	minichromosome maintenance complex component 4	AI936566	4173	Hs.460184	GO:0006260: DNA replication, GO:0006268: DNA unwinding during replication, GO:0006270: DNA replication initiation, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003678: DNA helicase activity, GO:0003697: single-stranded DNA binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008094: DNA-dependent ATPase activity, GO:0017111: nucleoside-triphosphatase activity	04110: Cell cycle	−0.0442	−0.2564	−0.9045	−1.2825	2.66	3.79	3.75	3.54	2.89	2.51	3

(*Continued*)

TABLE E2. (*Continued*)

211016_x_at	HSPA4	heat shock 70kDa protein 4	BC002526	3308	Hs.90093	GO:0006986: response to unfolded protein, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0005524: ATP binding	−0.3101	−0.5105	−1.1698	−1.7492	5.59	7.55	7.24	7.04	6.38	5.81	3
206004_at	TGM3	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)	NM_003245	7053	Hs.2022	GO:0006464: protein modification process, GO:0018149: peptide cross-linking, GO:0030216: keratinocyte differentiation, GO:0030216: keratinocyte differentiation, GO:0031069: hair follicle morphogenesis, GO:0031424: keratinization, GO:0043163: cell envelope organization and biogenesis, GO:0051262: protein tetramerization, GO:0005737: cytoplasm, GO:0031234: extrinsic to internal side of plasma membrane, GO:0000287: magnesium ion binding, GO:0003810: protein-glutamine gamma-glutamyltransferase activity, GO:0003924: GTPase activity, GO:0005509: calcium ion binding, GO:0005525: GTP binding, GO:0008415: acyltransferase activity, GO:0016746: transferase activity, transferring acyl groups, GO:0019003: GDP binding	−0.307	−0.6158	−1.5221	−2.2376	10.42	12.32	12.01	11.7	10.79	10.08	3
212246_at	MCFD2	multiple coagulation factor deficiency 2	BE880828	90411	Hs.293689	GO:0006888: ER to Golgi vesicle-mediated transport, GO:0015031: protein transport, GO:0005783: endoplasmic reticulum, GO:0005509: calcium ion binding	−0.1772	−0.3949	−0.9501	−1.4175	6.5	7.89	7.71	7.49	6.94	6.47	3
217192_s_at	PRDM1	PR domain containing 1, with ZNF domain	AL022067	639	Hs.436023	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	−0.2692	−0.6885	−1.1671	−1.8269	5.05	7.27	7	6.58	6.1	5.44	3
221896_s_at	HIGD1A	HIG1 domain family, member 1A	BE739519	25994	Hs.7917, Hs.192124, Hs.593134	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0043234: protein complex, GO:0005515: protein binding	−0.1554	−0.3807	−0.7664	−1.1902	11.72	12.74	12.59	12.36	11.98	11.55	3
201489_at	PPIF	peptidylprolyl isomerase F (cyclophilin F)	BC005020	10105	Hs.381072	GO:0006457: protein folding, GO:0005624: membrane fraction, GO:0005739: mitochondrion, GO:0003755: peptidyl-prolyl cis-trans isomerase activity, GO:0016853: isomerase activity, GO:0042277: peptide binding	−0.2622	−0.7011	−1.382	−2.2684	9.36	11.66	11.4	10.96	10.28	9.39	3
201583_s_at	SEC23B	Sec23 homolog B (S. cerevisiae)	NM_006363	10483	Hs.369373, Hs.460238	GO:0006886: intracellular protein transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0016192: vesicle-mediated transport, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0030127: COPII vesicle coat, GO:0048471: perinuclear region of cytoplasm, GO:0005515: protein binding, GO:0008270: zinc ion binding	−0.2437	−0.4652	−0.9301	−1.3644	7.89	8.86	8.61	8.39	7.93	7.49	3

(*Continued*)

TABLE E2. (*Continued*)

214698_at	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	AW190873	9991	Hs.269988	GO:0006397: mRNA processing, GO:0009653: anatomical structure morphogenesis, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003723: RNA binding, GO:0003723: RNA binding		−0.2406	−0.3886	−0.7826	−1.2073	5.65	6.81	6.56	6.42	6.02	5.6	3
215438 _x_at	GSPT1	G1 to S phase transition 1	BE906054	2935	Hs.528780	GO:0000082: G1/S transition of mitotic cell cycle, GO:0000184: mRNA catabolic process, nonsense-mediated decay, GO:0006412: translation, GO:0005622: intracellular, GO:0000166: nucleotide binding, GO:0003747: translation release factor activity, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding		−0.1861	−0.3566	−0.7612	−1.1861	9.64	10.61	10.42	10.25	9.84	9.42	3
209125_at			J00269	140446				−0.2885	−0.662	−1.3202	−2.0356	12.33	14.66	14.37	13.99	13.33	12.62	3
214580 _x_at	KRT6A	keratin 6A	AL569511	3853	Hs.433845	GO:0007010: cytoskeleton organization and biogenesis, GO:0007398: ectoderm development, GO:0005882: intermediate filament, GO:0005882: intermediate filament, GO:0005198: structural molecule activity, GO:0005198: structural molecule activity, GO:0005515: protein binding	01430: Cell Communication	−0.2667	−0.7371	−1.5383	−2.3587	11.97	14.53	14.27	13.8	13	12.18	3
204203_at	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	NM_001806	1054	Hs.429666	GO:0001889: liver development, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006955: immune response, GO:0030183: B cell differentiation, GO:0042267: natural killer cell mediated cytotoxicity, GO:0043353: enucleate erythrocyte differentiation, GO:0043388: positive regulation of DNA binding, GO:0043433: negative regulation of transcription factor activity, GO:0045078: positive regulation of interferon-gamma biosynthetic process, GO:0045739: positive regulation of DNA repair, GO:0051091: positive regulation of transcription factor activity, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0008134: transcription factor binding, GO:0043565: sequence-specific DNA binding, GO:0046982: protein heterodimerization activity		−0.2161	−0.3709	−0.7701	−1.1955	9.01	10.01	9.79	9.64	9.24	8.81	3
207291_at	PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	NM_024081	79056	Hs.471695	GO:0008150: biological_process, GO:0005576: extracellular region, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003674: molecular_function, GO:0005509: calcium ion binding		−0.2483	−0.4869	−0.9736	−1.5302	7.95	9.28	9.03	8.79	8.3	7.75	3
218009 _s_at	PRC1	protein regulator of cytokinesis 1	NM_003981	9055	Hs.567385	GO:0000022: mitotic spindle elongation, GO:0000910: cytokinesis, GO:0007049: cell cycle, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005876: spindle microtubule, GO:0005515: protein binding		−0.2936	−0.6691	−1.0313	−1.6351	8.61	9.57	9.27	8.9	8.54	7.93	3

(*Continued*)

TABLE E2. (*Continued*)

218039_at	NUSAP1	nucleolar and spindle associated protein 1	NM_016359	51203	Hs.615092	GO:0000281: cytokinesis after mitosis, GO:0007076: mitotic chromosome condensation, GO:0040001: establishment of mitotic spindle localization, GO:0045840: positive regulation of mitosis		−0.1425	−0.4656	−0.6633	−1.1421	9.34	9.97	9.83	9.51	9.31	8.83	3
213988_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1	BE971383	6303	Hs.28491	GO:0008152: metabolic process, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0004145: diamine N-acetyltransferase activity, GO:0008415: acyltransferase activity, GO:0016740: transferase activity	00220: Urea cycle and metabolism of amino groups	−0.1616	−0.5086	−0.8338	−1.4897	8.94	10.03	9.86	9.52	9.19	8.54	3
216834_at	RGS1	regulator of G-protein signaling 1	S59049	5996	Hs.75256	GO:0006955: immune response, GO:0007165: signal transduction, GO:0007193: G-protein signaling, adenylate cyclase inhibiting pathway, GO:0009968: negative regulation of signal transduction, GO:0005886: plasma membrane, GO:0004871: signal transducer activity, GO:0005096: GTPase activator activity, GO:0005516: calmodulin binding		−0.5048	−1.2809	−1.8697	−2.9978	2.44	5.86	5.35	4.58	3.99	2.86	3
208901_s_at	TOP1	topoisomerase (DNA) I	J03250	7150	Hs.472737, Hs.592136	GO:0006260: DNA replication, GO:0006265: DNA topological change, GO:0006268: DNA unwinding during replication, GO:0012501: programmed cell death, GO:0016310: phosphorylation, GO:0040016: embryonic cleavage, GO:0042493: response to drug, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0005694: chromosome, GO:0005730: nucleolus, GO:0005737: cytoplasm, GO:0043204: perikaryon, GO:0003682: chromatin binding, GO:0003917: DNA topoisomerase type I activity, GO:0003918: DNA topoisomerase (ATP-hydrolyzing) activity, GO:0005515: protein binding		−0.1505	−0.4631	−0.6451	−1.147	10.01	10.94	10.79	10.48	10.3	9.8	3
212460_at	C14orf147	chromosome 14 open reading frame 147	BE738425	171546	Hs.269909	GO:0016020: membrane, GO:0016021: integral to membrane		−0.1362	−0.5833	−0.9191	−1.6827	10.69	12.1	11.97	11.52	11.18	10.42	3
204146_at	RAD51AP1	RAD51 associated protein 1	BE966146	10635	Hs.591046	GO:0000724: double-strand break repair via homologous recombination, GO:0006281: DNA repair, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003690: double-stranded DNA binding, GO:0003697: single-stranded DNA binding, GO:0003723: RNA binding, GO:0005515: protein binding		−0.0919	−0.395	−0.6147	−1.083	7.14	7.73	7.64	7.34	7.12	6.65	3
204825_at	MELK	maternal embryonic leucine zipper kinase	NM_014791	9833	Hs.184339	GO:0006468: protein amino acid phosphorylation, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity		−0.4529	−0.9257	−1.3982	−2.312	5.89	7.6	7.15	6.67	6.2	5.29	3

(*Continued*)

TABLE E2. (*Continued*)

201888_s_at	IL13RA1	interleukin 13 receptor, alpha 1	NM_001560	3597	Hs.496646	GO:0007166: cell surface receptor linked signal transduction, GO:0005886: plasma membrane, GO:0005898: interleukin-13 receptor complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004896: hematopoietin/interferon-class (D200-domain) cytokine receptor activity	04060: Cytokine-cytokine receptor interaction, 04630: Jak-STAT signaling pathway	−0.1893	−0.7388	−1.0224	−1.8764	6.98	8.57	8.38	7.83	7.55	6.69	3
202934_at	HK2	hexokinase 2	AI761561	3099	Hs.406266, Hs.591588	GO:0000074: regulation of progression through cell cycle, GO:0006096: glycolysis, GO:0046835: carbohydrate phosphorylation, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004396: hexokinase activity, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity	00010: Glycolysis / Gluconeogenesis, 00051: Fructose and mannose metabolism, 00052: Galactose metabolism, 00500: Starch and sucrose metabolism, 00521: Streptomycin biosynthesis, 00530: Aminosugars metabolism	−0.2202	−0.6088	−0.8733	−1.4869	9.08	10.89	10.67	10.28	10.01	9.4	3
201292_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	AL561834	7153	Hs.156346	GO:0006260: DNA replication, GO:0006265: DNA topological change, GO:0006266: DNA ligation, GO:0006281: DNA repair, GO:0007059: chromosome segregation, GO:0030263: apoptotic chromosome condensation, GO:0043065: positive regulation of apoptosis, GO:0045870: positive regulation of retroviral genome replication, GO:0048015: phosphoinositide-mediated signaling, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0005694: chromosome, GO:0005730: nucleolus, GO:0005737: cytoplasm, GO:0005814: centriole, GO:0009330: DNA topoisomerase complex (ATP-hydrolyzing), GO:0019035: viral integration complex, GO:0000166: nucleotide binding, GO:0003682: chromatin binding, GO:0003918: DNA topoisomerase (ATP-hydrolyzing) activity, GO:0005080: protein kinase C binding, GO:0005524: ATP binding, GO:0008022: protein C-terminus binding, GO:0008094: DNA-dependent ATPase activity, GO:0008144: drug binding, GO:0042803: protein homodimerization activity, GO:0042826: histone deacetylase binding, GO:0043130: ubiquitin binding, GO:0046982: protein heterodimerization activity		−0.3368	−0.7565	−1.1479	−1.8278	8.33	9.45	9.11	8.69	8.3	7.62	3
201420_s_at	WDR77	WD repeat domain 77	BF975273	79084	Hs.204773	GO:0004872: receptor activity		−0.1804	−0.4446	−0.6892	−1.0951	7.72	8.72	8.54	8.28	8.03	7.63	3
219296_at	ZDHHC13	zinc finger, DHHC-type containing 13	NM_019028	54503	Hs.188569	GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004871: signal transducer activity, GO:0008270: zinc ion binding, GO:0008415: acyltransferase activity, GO:0016740: transferase activity, GO:0046872: metal ion binding		−0.2401	−0.6077	−0.8796	−1.4917	8.49	9.77	9.53	9.16	8.89	8.28	3

(*Continued*)

TABLE E2. (*Continued*)

33304_at	ISG20	interferon stimulated exonuclease gene 20kDa	U88964	3669	Hs.459265	GO:0000738: DNA catabolic process, exonucleolytic, GO:0006401: RNA catabolic process, GO:0008283: cell proliferation, GO:0009615: response to virus, GO:0005622: intracellular, GO:0005654: nucleoplasm, GO:0016605: PML body, GO:0000175: 3'-5'-exoribonuclease activity, GO:0003723: RNA binding, GO:0004527: exonuclease activity, GO:0008310: single-stranded DNA specific 3'-5' exodeoxyribonuclease activity, GO:0008859: exoribonuclease II activity, GO:0016787: hydrolase activity, GO:0030145: manganese ion binding, GO:0046872: metal ion binding	−0.1895	−0.4765	−0.7655	−1.2299	5.53	6.9	6.71	6.42	6.13	5.67	3
218888_s_at	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	AI335263	81831	Hs.444046	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity	−0.1356	−0.8522	−1.4027	−2.357	2.71	5.08	4.94	4.22	3.67	2.72	3
219503_s_at	TMEM40	transmembrane protein 40	AI087937	55287	Hs.475502	GO:0016020: membrane, GO:0016021: integral to membrane	−0.1903	−0.5112	−0.7633	−1.2969	8.01	9.17	8.98	8.66	8.41	7.87	3
219657_s_at	KLF3	Kruppel-like factor 3 (basic)	AF285837	51274	Hs.298658	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0005622: intracellular, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	−0.1538	−0.4029	−0.6925	−1.1486	7.17	8.44	8.29	8.04	7.75	7.29	3
200750_s_at	RAN	RAN, member RAS oncogene family	AF054183	5901	Hs.10842	GO:0000074: regulation of progression through cell cycle, GO:0006259: DNA metabolic process, GO:0006405: RNA export from nucleus, GO:0006611: protein export from nucleus, GO:0006886: intracellular protein transport, GO:0006913: nucleocytoplasmic transport, GO:0007052: mitotic spindle organization and biogenesis, GO:0007067: mitosis, GO:0007165: signal transduction, GO:0007264: small GTPase mediated signal transduction, GO:0030521: androgen receptor signaling pathway, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0000785: chromatin, GO:0005643: nuclear pore, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003682: chromatin binding, GO:0003713: transcription coactivator activity, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0050681: androgen receptor binding	−0.2018	−0.3595	−0.6625	−1.0836	12.1	12.94	12.74	12.58	12.28	11.86	3

(*Continued*)

TABLE E2. (*Continued*)

201303_at	EIF4A3	eukaryotic translation initiation factor 4A, isoform 3	NM_014740	9775	Hs.389649	GO:0000184: mRNA catabolic process, nonsense-mediated decay, GO:0006364: rRNA processing, GO:0006397: mRNA processing, GO:0008380: RNA splicing, GO:0005681: spliceosome, GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008026: ATP-dependent helicase activity, GO:0016787: hydrolase activity		−0.2078	−0.3934	−0.704	−1.2255	10.69	11.74	11.53	11.34	11.03	10.51	3
216841_s_at	SOD2	superoxide dismutase 2, mitochondrial	X15132	6648	Hs.487046	GO:0000303: response to superoxide, GO:0001315: age-dependent response to reactive oxygen species, GO:0001315: age-dependent response to reactive oxygen species, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006801: superoxide metabolic process, GO:0006801: superoxide metabolic process, GO:0006979: response to oxidative stress, GO:0005739: mitochondrion, GO:0005743: mitochondrial inner membrane, GO:0004784: superoxide dismutase activity, GO:0008383: manganese superoxide dismutase activity, GO:0016491: oxidoreductase activity, GO:0030145: manganese ion binding, GO:0046872: metal ion binding		−0.2612	−1.1268	−1.6345	−2.9164	6.95	9.57	9.31	8.44	7.94	6.65	3
217755_at	HN1	hematological and neurological expressed 1	AF060925	51155	Hs.532803			−0.2549	−0.5609	−0.938	−1.6044	8.6	9.68	9.43	9.12	8.75	8.08	3
209694_at	PTS	6-pyruvoyltetrahydropterin synthase	M97655	5805	Hs.503860	GO:0006520: amino acid metabolic process, GO:0006559: L-phenylalanine catabolic process, GO:0006729: tetrahydrobiopterin biosynthetic process, GO:0007417: central nervous system development, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0003874: 6-pyruvoyltetrahydropterin synthase activity, GO:0008270: zinc ion binding, GO:0016829: lyase activity, GO:0042802: identical protein binding, GO:0046872: metal ion binding	00790: Folate biosynthesis	−0.1868	−0.358	−0.6206	−1.0376	9.88	10.46	10.27	10.1	9.84	9.42	3
216243_s_at	IL1RN	interleukin 1 receptor antagonist	BE563442	3557	Hs.81134	GO:0006629: lipid metabolic process, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0030073: insulin secretion, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005152: interleukin-1 receptor antagonist activity, GO:0005515: protein binding		−0.409	−0.7103	−1.3227	−2.3403	9	10.75	10.34	10.04	9.43	8.41	3
203797_at	VSNL1	visinin-like 1	AF039555	7447	Hs.444212	GO:0005509: calcium ion binding		−0.2428	−0.4735	−0.8979	−1.46	9.13	10.54	10.29	10.06	9.64	9.08	3

(*Continued*)

TABLE E2. (*Continued*)

204026_s_at	ZWINT	ZW10 interactor	NM_007057	11130	Hs.591363	GO:0000070: mitotic sister chromatid segregation, GO:0007049: cell cycle, GO:0007051: spindle organization and biogenesis, GO:0007093: mitotic cell cycle checkpoint, GO:0048015: phosphoinositide-mediated signaling, GO:0051301: cell division, GO:0051649: establishment of cellular localization, GO:0000776: kinetochore, GO:0047485: protein N-terminus binding		−0.3618	−0.6287	−1.0746	−1.7758	8.42	9.62	9.26	8.99	8.54	7.84	3
201912_s_at	GSPT1	G1 to S phase transition 1	NM_002094	2935	Hs.528780	GO:0000082: G1/S transition of mitotic cell cycle, GO:0000184: mRNA catabolic process, nonsense-mediated decay, GO:0006412: translation, GO:0005622: intracellular, GO:0000166: nucleotide binding, GO:0003747: translation release factor activity, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding		−0.2659	−0.519	−0.8163	−1.486	9.54	10.77	10.51	10.25	9.96	9.29	3
203214_x_at	CDC2	cell division cycle 2, G1 to S and G2 to M	NM_001786	983	Hs.334562	GO:0000074: regulation of progression through cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0006916: anti-apoptosis, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007089: traversing start control point of mitotic cell cycle, GO:0051301: cell division, GO:0005634: nucleus, GO:0005876: spindle microtubule, GO:0030496: midbody, GO:0000166: nucleotide binding, GO:0004693: cyclin-dependent protein kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04110: Cell cycle, 04115: p53 signaling pathway, 04540: Gap junction	−0.4675	−0.8441	−1.4854	−2.4543	5.29	7.31	6.84	6.46	5.82	4.85	3
204733_at	KLK6	kallikrein-related peptidase 6	NM_002774	5653	Hs.79361	GO:0006508: proteolysis, GO:0007417: central nervous system development, GO:0009611: response to wounding, GO:0016540: protein autoprocessing, GO:0030574: collagen catabolic process, GO:0042246: tissue regeneration, GO:0042445: hormone metabolic process, GO:0042552: myelination, GO:0042982: amyloid precursor protein metabolic process, GO:0045595: regulation of cell differentiation, GO:0005576: extracellular region, GO:0005737: cytoplasm, GO:0004252: serine-type endopeptidase activity, GO:0004293: tissue kallikrein activity, GO:0005515: protein binding, GO:0008233: peptidase activity		−0.4312	−2.5491	−5.0227	−6.7749	3.11	10.55	10.12	8.01	5.53	3.78	3
213797_at	RSAD2	radical S-adenosyl methionine domain containing 2	AI337069	91543	Hs.17518	GO:0003824: catalytic activity, GO:0051536: iron-sulfur cluster binding		−0.0553	−1.1964	−2.3129	−2.9731	3.27	6.63	6.58	5.43	4.32	3.66	3

(*Continued*)

TABLE E2. (*Continued*)

208727_s_at	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	BC003682	998	Hs.693589	GO:0007097: nuclear migration, GO:0007163: establishment and/or maintenance of cell polarity, GO:0007264: small GTPase mediated signal transduction, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0030225: macrophage differentiation, GO:0031274: positive regulation of pseudopodium formation, GO:0031333: negative regulation of protein complex assembly, GO:0043552: positive regulation of phosphoinositide 3-kinase activity, GO:0046847: filopodium formation, GO:0051301: cell division, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0030175: filopodium, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding, GO:0030742: GTP-dependent protein binding	04010: MAPK signaling pathway, 04360: Axon guidance, 04370: VEGF signaling pathway, 04510: Focal adhesion, 04520: Adherens junction, 04530: Tight junction, 04660: T cell receptor signaling pathway, 04670: Leukocyte transendothelial migration, 04810: Regulation of actin cytoskeleton, 04912: GnRH signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection, 05130: Pathogenic Escherichia coli infection - EHEC, 05131: Pathogenic Escherichia coli infection - EPEC, 05211: Renal cell carcinoma, 05212: Pancreatic cancer	−0.0136	−0.3271	−0.7755	−1.0118	7.76	8.69	8.68	8.37	7.92	7.68	3
220230_s_at	CYB5R2	cytochrome b5 reductase 2	NM_016229	51700	Hs.414362	GO:0006118: electron transport, GO:0016126: sterol biosynthetic process, GO:0004128: cytochrome-b5 reductase activity, GO:0016491: oxidoreductase activity, GO:0050660: FAD binding, GO:0051287: NAD binding		−0.0609	−0.3994	−0.9312	−1.1829	8.95	10	9.94	9.6	9.07	8.81	3
219225_at	PGBD5	piggyBac transposable element derived 5	NM_024554	79605	Hs.520463	GO:0016020: membrane, GO:0016021: integral to membrane		0.2501	−0.6895	−1.4589	−2.0324	2.3	4.62	4.87	3.93	3.16	2.58	3
207602_at	TMPRSS11D	transmembrane protease, serine 11D	NM_004262	9407	Hs.132195	GO:0006508: proteolysis, GO:0007585: respiratory gaseous exchange, GO:0005576: extracellular region, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004252: serine-type endopeptidase activity, GO:0008233: peptidase activity		0.1044	−1.3229	−3.0695	−4.1569	3.1	8.39	8.49	7.06	5.32	4.23	3
212527_at	D15Wsu75e	DNA segment, Chr 15, Wayne State University 75, expressed	BF057059	27351	Hs.570455			0.0454	−0.3934	−0.9435	−1.2985	6.9	8.18	8.23	7.79	7.24	6.89	3
203128_at	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	NM_004863	9517	Hs.435661	GO:0009058: biosynthetic process, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004758: serine C-palmitoyltransferase activity, GO:0008415: acyltransferase activity, GO:0016769: transferase activity, transferring nitrogenous groups, GO:0030170: pyridoxal phosphate binding	00600: Sphingolipid metabolism	0.08	−0.4333	−0.9529	−1.2886	4.86	6.59	6.67	6.16	5.64	5.3	3
204580_at	MMP12	matrix metallopeptidase 12 (macrophage elastase)	NM_002426	4321	Hs.1695	GO:0000270: peptidoglycan metabolic process, GO:0006508: proteolysis, GO:0006928: cell motility, GO:0005578: proteinaceous extracellular matrix, GO:0004234: macrophage elastase activity, GO:0005509: calcium ion binding, GO:0008270: zinc ion binding		0.3128	−0.8871	−2.0143	−2.7534	2.85	5.79	6.1	4.9	3.77	3.04	3

(*Continued*)

TABLE E2. (*Continued*)

215977_x_at	GK	glycerol kinase	X68285	2710	Hs.1466	GO:0005975: carbohydrate metabolic process, GO:0006072: glycerol-3-phosphate metabolic process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity	00561: Glycerolipid metabolism, 03320: PPAR signaling pathway	0.0788	−1.3073	−2.4115	−3.3955	3.1	6.8	6.88	5.49	4.39	3.4	3
217167_x_at	GK	glycerol kinase	AJ252550	2710	Hs.1466	GO:0005975: carbohydrate metabolic process, GO:0006072: glycerol-3-phosphate metabolic process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity	00561: Glycerolipid metabolism, 03320: PPAR signaling pathway	0.2691	−1.1443	−1.9788	−2.8908	2.79	5.7	5.97	4.55	3.72	2.81	3
214088_s_at	FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group)	AW080549	2525	Hs.169238	GO:0005975: carbohydrate metabolic process, GO:0006486: protein amino acid glycosylation, GO:0005624: membrane fraction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016757: transferase activity, transferring glycosyl groups, GO:0017060: 3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase activity	00601: Glycosphingolipid biosynthesis - lactoseries, 00602: Glycosphingolipid biosynthesis - neo-lactoseries, 01031: Glycan structures - biosynthesis 2	−0.0658	−0.3073	−1.1884	−1.3673	3.38	4.98	4.92	4.68	3.8	3.62	3
205660_at	OASL	2'-5'-oligoadenylate synthetase-like	NM_003733	8638	Hs.118633	GO:0006464: protein modification process, GO:0006955: immune response, GO:0008150: biological_process, GO:0005730: nucleolus, GO:0005737: cytoplasm, GO:0003677: DNA binding, GO:0003725: double-stranded RNA binding, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0046966: thyroid hormone receptor binding		−0.1751	−1.2833	−4.2209	−5.1808	2.85	8.51	8.34	7.23	4.29	3.33	3
210797_s_at	OASL	2'-5'-oligoadenylate synthetase-like	AF063612	8638	Hs.118633	GO:0006464: protein modification process, GO:0006955: immune response, GO:0008150: biological_process, GO:0005730: nucleolus, GO:0005737: cytoplasm, GO:0003677: DNA binding, GO:0003725: double-stranded RNA binding, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0046966: thyroid hormone receptor binding		−0.359	−1.121	−3.4462	−4.3167	4.04	9.12	8.76	8	5.68	4.81	3
219680_at	NLRX1	NLR family member X1	NM_024618	79671	Hs.524082			−0.1902	−0.4297	−1.0434	−1.4032	7.71	9.22	9.03	8.79	8.18	7.82	3
218562_s_at	TMEM57	transmembrane protein 57	NM_018202	55219	Hs.189782	GO:0005634: nucleus, GO:0016020: membrane, GO:0016021: integral to membrane		−0.1501	−0.3359	−0.8036	−1.0348	7.22	8.51	8.36	8.17	7.71	7.47	3
219395_at	RBM35B	RNA binding motif protein 35B	NM_024939	80004	Hs.436585, Hs.592053	GO:0000166: nucleotide binding, GO:0003723: RNA binding		−0.129	−0.3093	−0.7882	−1.0306	9.39	10.4	10.27	10.09	9.61	9.37	3

(*Continued*)

TABLE E2. (*Continued*)

212141_at	MCM4	minichromosome maintenance complex component 4	AA604621	4173	Hs.460184	GO:0006260: DNA replication, GO:0006268: DNA unwinding during replication, GO:0006270: DNA replication initiation, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003678: DNA helicase activity, GO:0003697: single-stranded DNA binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008094: DNA-dependent ATPase activity, GO:0017111: nucleoside-triphosphatase activity	04110: Cell cycle	−0.2969	−0.624	−1.255	−1.7284	6.91	8	7.71	7.38	6.75	6.27	3
203616_at	POLB	polymerase (DNA directed), beta	NM_002690	5423	Hs.654484	GO:0006261: DNA-dependent DNA replication, GO:0006281: DNA repair, GO:0006916: anti-apoptosis, GO:0008219: cell death, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005876: spindle microtubule, GO:0000287: magnesium ion binding, GO:0003890: beta DNA polymerase activity, GO:0008017: microtubule binding, GO:0016740: transferase activity, GO:0016829: lyase activity, GO:0031402: sodium ion binding, GO:0043565: sequence-specific DNA binding	03030: DNA polymerase	−0.1772	−0.3743	−0.8111	−1.0669	9.06	10.06	9.88	9.68	9.24	8.99	3
204268_at	S100A2	S100 calcium binding protein A2	NM_005978	6273	Hs.516484	GO:0043542: endothelial cell migration, GO:0005575: cellular_component, GO:0005509: calcium ion binding		−0.2712	−0.5538	−1.1316	−1.5062	12.98	14.37	14.1	13.82	13.24	12.86	3
214599_at	IVL	involucrin	NM_005547	3713	Hs.516439	GO:0010224: response to UV-B, GO:0018149: peptide cross-linking, GO:0018153: isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine, GO:0030216: keratinocyte differentiation, GO:0031424: keratinization, GO:0001533: cornified envelope, GO:0005737: cytoplasm, GO:0005198: structural molecule activity, GO:0030674: protein binding, bridging		−0.2658	−0.2701	−0.819	−1.1868	11.13	12.48	12.21	12.21	11.66	11.29	3
212432_at	GRPEL1	GrpE-like 1, mitochondrial (E. coli)	AL542571	80273	Hs.443723	GO:0006457: protein folding, GO:0030150: protein import into mitochondrial matrix, GO:0005739: mitochondrion, GO:0005759: mitochondrial matrix, GO:0000774: adenyl-nucleotide exchange factor activity, GO:0042803: protein homodimerization activity, GO:0051082: unfolded protein binding, GO:0051087: chaperone binding		−0.2585	−0.3597	−0.9388	−1.4549	8.02	9.04	8.78	8.68	8.1	7.58	3
216641_s_at	LAD1	ladinin 1	U58994	3898	Hs.519035	GO:0005604: basement membrane, GO:0005198: structural molecule activity		−0.2911	−0.3648	−1.026	−1.4807	9.57	10.57	10.28	10.21	9.54	9.09	3
213796_at	SPRR1A	small proline-rich protein 1A	AI923984	6698	Hs.46320	GO:0008544: epidermis development, GO:0018149: peptide cross-linking, GO:0030216: keratinocyte differentiation, GO:0031424: keratinization, GO:0001533: cornified envelope, GO:0005737: cytoplasm, GO:0005198: structural molecule activity, GO:0030674: protein binding, bridging		−0.3208	−0.4774	−1.3937	−2.0003	11.98	13.98	13.66	13.5	12.58	11.98	3

(*Continued*)

TABLE E2. (*Continued*)

37152_at	PPARD	peroxisome proliferator-activated receptor delta	L07592	5467	Hs.485196	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006006: glucose metabolic process, GO:0006091: generation of precursor metabolites and energy, GO:0006350: transcription, GO:0006629: lipid metabolic process, GO:0006635: fatty acid beta-oxidation, GO:0006635: fatty acid beta-oxidation, GO:0006915: apoptosis, GO:0007566: embryo implantation, GO:0008203: cholesterol metabolic process, GO:0008283: cell proliferation, GO:0008283: cell proliferation, GO:0008366: axon ensheathment, GO:0008544: epidermis development, GO:0009062: fatty acid catabolic process, GO:0015758: glucose transport, GO:0015908: fatty acid transport, GO:0045600: positive regulation of fat cell differentiation, GO:0046697: decidualization, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003707: steroid hormone receptor activity, GO:0005504: fatty acid binding, GO:0008270: zinc ion binding, GO:0016564: transcription repressor activity, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding	03320: PPAR signaling pathway, 04310: Wnt signaling pathway, 05221: Acute myeloid leukemia	−0.2705	−0.3366	−1.0756	−1.4301	7.9	9.55	9.28	9.21	8.47	8.12	3
205194_at	PSPH	phosphoserine phosphatase	NM_004577	5723	Hs.512656	GO:0006564: L-serine biosynthetic process, GO:0008152: metabolic process, GO:0008652: amino acid biosynthetic process, GO:0000287: magnesium ion binding, GO:0004647: phosphoserine phosphatase activity, GO:0005515: protein binding, GO:0016787: hydrolase activity	00260: Glycine, serine and threonine metabolism	−0.2188	−0.2775	−0.7716	−1.0061	5.93	7.18	6.96	6.9	6.41	6.17	3
213427_at	RPP40	ribonuclease P/MRP 40kDa subunit	NM_006638	10799	Hs.511756	GO:0008033: tRNA processing, GO:0005634: nucleus, GO:0005655: nucleolar ribonuclease P complex, GO:0004526: ribonuclease P activity, GO:0005515: protein binding, GO:0016787: hydrolase activity		−0.3234	−0.5149	−1.3192	−1.7859	6.04	7.2	6.88	6.69	5.88	5.42	3
214549_x_at	SPRR1A	small proline-rich protein 1A	NM_005987	6698	Hs.46320	GO:0008544: epidermis development, GO:0018149: peptide cross-linking, GO:0030216: keratinocyte differentiation, GO:0031424: keratinization, GO:0001533: cornified envelope, GO:0005737: cytoplasm, GO:0005198: structural molecule activity, GO:0030674: protein binding, bridging		−0.3419	−0.5919	−1.4854	−2.1033	12.05	14.39	14.05	13.8	12.91	12.29	3
218880_at	FOSL2	FOS-like antigen 2	NM_024530	2355	Hs.220971, Hs.596972	GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0008219: cell death, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity		−0.2715	−0.4555	−1.0894	−1.4574	7.46	8.88	8.61	8.42	7.79	7.42	3

(*Continued*)

TABLE E2. (*Continued*)

210164_at	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	J03189	3002	Hs.1051	GO:0006508: proteolysis, GO:0006915: apoptosis, GO:0006922: cleavage of lamin, GO:0019835: cytolysis, GO:0001772: immunological synapse, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0004252: serine-type endopeptidase activity, GO:0004278: granzyme B activity, GO:0005515: protein binding, GO:0008233: peptidase activity	04650: Natural killer cell mediated cytotoxicity, 04940: Type I diabetes mellitus	−0.3382	−0.5465	−1.3023	−1.8338	2.46	4.47	4.13	3.92	3.17	2.63	3
213137_s_at	PTPN2	protein tyrosine phosphatase, non-receptor type 2	AI828880	5771	Hs.654527	GO:0006470: protein amino acid dephosphorylation, GO:0006470: protein amino acid dephosphorylation, GO:0008286: insulin receptor signaling pathway, GO:0005737: cytoplasm, GO:0004725: protein tyrosine phosphatase activity, GO:0004725: protein tyrosine phosphatase activity, GO:0004872: receptor activity, GO:0005515: protein binding, GO:0016787: hydrolase activity, GO:0016791: phosphoric monoester hydrolase activity		−0.2042	−0.2965	−0.73	−1.0109	8.49	9.36	9.15	9.06	8.63	8.35	3
210608_s_at	FUT2	fucosyltransferase 2 (secretor status included)	BC001899	2524	Hs.579928	GO:0005975: carbohydrate metabolic process, GO:0006486: protein amino acid glycosylation, GO:0006486: protein amino acid glycosylation, GO:0042355: L-fucose catabolic process, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030173: integral to Golgi membrane, GO:0008107: galactoside 2-alpha-L-fucosyltransferase activity, GO:0008417: fucosyltransferase activity, GO:0016757: transferase activity, transferring glycosyl groups	00601: Glycosphingolipid biosynthesis - lactoseries, 00602: Glycosphingolipid biosynthesis - neo-lactoseries, 00603: Glycosphingolipid biosynthesis - globoseries, 01031: Glycan structures - biosynthesis 2	−0.3459	−0.6769	−1.1845	−1.7127	3.7	5.45	5.11	4.78	4.27	3.74	3
209714_s_at	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	AF213033	1033	Hs.84113	GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0000082: G1/S transition of mitotic cell cycle, GO:0007049: cell cycle, GO:0007050: cell cycle arrest, GO:0008285: negative regulation of cell proliferation, GO:0016311: dephosphorylation, GO:0004725: protein tyrosine phosphatase activity, GO:0005515: protein binding, GO:0008138: protein tyrosine/serine/threonine phosphatase activity, GO:0016787: hydrolase activity		−0.5276	−1.0012	−1.7788	−2.5853	5.44	7.25	6.72	6.25	5.47	4.67	3
209800_at	KRT16	keratin 16 (focal non-epidermolytic palmoplantar keratoderma)	AF061812	3868	Hs.655160	GO:0007010: cytoskeleton organization and biogenesis, GO:0008283: cell proliferation, GO:0008544: epidermis development, GO:0045104: intermediate filament cytoskeleton organization and biogenesis, GO:0005882: intermediate filament, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding	01430: Cell Communication	−0.7595	−1.574	−2.791	−4.0366	10.11	14.28	13.52	12.71	11.49	10.25	3

(*Continued*)

TABLE E2. (*Continued*)

203213_at	CDC2	cell division cycle 2, G1 to S and G2 to M	AL524035	983	Hs.334562	GO:0000074: regulation of progression through cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0006916: anti-apoptosis, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007089: traversing start control point of mitotic cell cycle, GO:0051301: cell division, GO:0005634: nucleus, GO:0005876: spindle microtubule, GO:0030496: midbody, GO:0000166: nucleotide binding, GO:0004693: cyclin-dependent protein kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04110: Cell cycle, 04115: p53 signaling pathway, 04540: Gap junction	−0.4227	−0.8521	−1.4003	−2.1543	7.96	9.42	8.99	8.56	8.02	7.26	3
204331_s_at	MRPS12	mitochondrial ribosomal protein S12	AA587905	6183	Hs.411125	GO:0006412: translation, GO:0005622: intracellular, GO:0005739: mitochondrion, GO:0005761: mitochondrial ribosome, GO:0005840: ribosome, GO:0015935: small ribosomal subunit, GO:0003735: structural constituent of ribosome, GO:0005515: protein binding		−0.2619	−0.5732	−0.9118	−1.3437	8.44	9.58	9.32	9.01	8.67	8.24	3
209626_s_at	OSBPL3	oxysterol binding protein-like 3	AY008372	26031	Hs.520259	GO:0006869: lipid transport, GO:0008202: steroid metabolic process, GO:0005515: protein binding		−0.3128	−1.1739	−1.9096	−2.6732	5	7.56	7.25	6.39	5.65	4.89	3
218384_at	CARHSP1	calcium regulated heat stable protein 1, 24kDa	NM_014316	23589	Hs.632184	GO:0006355: regulation of transcription, DNA-dependent, GO:0007242: intracellular signaling cascade, GO:0005737: cytoplasm, GO:0003677: DNA binding, GO:0019902: phosphatase binding		−0.3627	−1.0697	−1.7959	−2.4553	8.53	11.22	10.86	10.15	9.43	8.77	3
204656_at	SHB	Src homology 2 domain containing adaptor protein B	AL138752	6461	Hs.521482	GO:0001525: angiogenesis, GO:0006915: apoptosis, GO:0007242: intracellular signaling cascade, GO:0007275: multicellular organismal development, GO:0030154: cell differentiation, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0005070: SH3/SH2 adaptor activity		−0.0885	−0.4541	−0.6679	−1.0392	4.95	5.94	5.86	5.49	5.28	4.9	3
215223_s_at	SOD2	superoxide dismutase 2, mitochondrial	W46388	6648	Hs.487046	GO:0000303: response to superoxide, GO:0001315: age-dependent response to reactive oxygen species, GO:0001315: age-dependent response to reactive oxygen species, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006801: superoxide metabolic process, GO:0006801: superoxide metabolic process, GO:0006979: response to oxidative stress, GO:0005739: mitochondrion, GO:0005743: mitochondrial inner membrane, GO:0004784: superoxide dismutase activity, GO:0008383: manganese superoxide dismutase activity, GO:0016491: oxidoreductase activity, GO:0030145: manganese ion binding, GO:0046872: metal ion binding		−0.4123	−1.6519	−2.5768	−4.1032	6.99	10.5	10.09	8.85	7.93	6.4	3

(*Continued*)

TABLE E2. (*Continued*)

212729 _at	DLG3	discs, large homolog 3 (neuroendocrine-dlg, Drosophila)	AI916274	1741	Hs.522680	GO:0008285: negative regulation of cell proliferation, GO:0005575: cellular_component, GO:0004385: guanylate kinase activity, GO:0005515: protein binding, GO:0005515: protein binding		−0.1116	−0.3835	−0.8251	−1.1618	5.48	6.32	6.21	5.94	5.49	5.16	3
208992 _s_at	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	BC000627	6774	Hs.463059	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006355: regulation of transcription, DNA-dependent, GO:0006928: cell motility, GO:0006953: acute-phase response, GO:0007165: signal transduction, GO:0007242: intracellular signaling cascade, GO:0007259: JAK-STAT cascade, GO:0007399: nervous system development, GO:0019221: cytokine and chemokine mediated signaling pathway, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0004871: signal transducer activity, GO:0005062: hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity, GO:0005509: calcium ion binding, GO:0008134: transcription factor binding	04630: Jak-STAT signaling pathway, 04920: Adipocytokine signaling pathway, 05212: Pancreatic cancer, 05221: Acute myeloid leukemia	−0.2046	−0.6078	−1.1012	−1.6933	10.21	11.6	11.4	10.99	10.5	9.91	3
217497 _at	ECGF1	endothelial cell growth factor 1 (platelet-derived)	AW613387	1890	Hs.592212	GO:0000002: mitochondrial genome maintenance, GO:0001525: angiogenesis, GO:0006206: pyrimidine base metabolic process, GO:0006220: pyrimidine nucleotide metabolic process, GO:0006260: DNA replication, GO:0006935: chemotaxis, GO:0007166: cell surface receptor linked signal transduction, GO:0007267: cell-cell signaling, GO:0007275: multicellular organismal development, GO:0008152: metabolic process, GO:0030154: cell differentiation, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0005161: platelet-derived growth factor receptor binding, GO:0008083: growth factor activity, GO:0009032: thymidine phosphorylase activity, GO:0016757: transferase activity, transferring glycosyl groups	00230: Purine metabolism, 00240: Pyrimidine metabolism, 05219: Bladder cancer	−0.133	−0.6623	−1.2358	−1.9173	7.3	10.09	9.95	9.42	8.85	8.17	3
209126 _x_at	KRT6B	keratin 6B	L42612	3854	Hs.654613	GO:0007398: ectoderm development, GO:0005882: intermediate filament, GO:0005200: structural constituent of cytoskeleton	01430: Cell Communication	−0.3436	−0.8998	−1.6211	−2.3436	12.47	14.91	14.57	14.01	13.29	12.57	3
218120 _s_at	HMOX2	heme oxygenase (decycling) 2	NM_002134	3163	Hs.284279	GO:0006788: heme oxidation, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0004392: heme oxygenase (decyclizing) activity, GO:0005506: iron ion binding, GO:0009055: electron carrier activity, GO:0046872: metal ion binding	00860: Porphyrin and chlorophyll metabolism	−0.1412	−0.3954	−0.7758	−1.0892	9.3	10.58	10.44	10.19	9.81	9.49	3

(*Continued*)

TABLE E2. (*Continued*)

203755_at	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	NM_001211	701	Hs.631699	GO:0006468: protein amino acid phosphorylation, GO:0006915: apoptosis, GO:0007049: cell cycle, GO:0007051: spindle organization and biogenesis, GO:0007067: mitosis, GO:0007093: mitotic cell cycle checkpoint, GO:0008283: cell proliferation, GO:0045786: negative regulation of progression through cell cycle, GO:0048015: phosphoinositide-mediated signaling, GO:0051301: cell division, GO:0000776: kinetochore, GO:0000776: kinetochore, GO:0000940: outer kinetochore of condensed chromosome, GO:0005680: anaphase-promoting complex, GO:0005737: cytoplasm, GO:0051233: spindle midzone, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04110: Cell cycle	−0.2009	−0.6743	−1.2249	−1.8008	5.07	6.32	6.12	5.65	5.1	4.52	3
206008_at	TGM1	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)	NM_000359	7051	Hs.508950	GO:0006464: protein modification process, GO:0009887: organ morphogenesis, GO:0018149: peptide cross-linking, GO:0030216: keratinocyte differentiation, GO:0031424: keratinization, GO:0043163: cell envelope organization and biogenesis, GO:0001533: cornified envelope, GO:0005913: cell-cell adherens junction, GO:0016020: membrane, GO:0031224: intrinsic to membrane, GO:0003810: protein-glutamine gamma-glutamyltransferase activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0008415: acyltransferase activity, GO:0016740: transferase activity		−0.3358	−0.9149	−1.8336	−2.6268	8.44	11.15	10.82	10.24	9.32	8.53	3
219978_s_at	NUSAP1	nucleolar and spindle associated protein 1	NM_018454	51203	Hs.615092	GO:0000281: cytokinesis after mitosis, GO:0007076: mitotic chromosome condensation, GO:0040001: establishment of mitotic spindle localization, GO:0045840: positive regulation of mitosis		−0.1519	−0.7767	−1.3245	−1.866	5.73	7.41	7.26	6.63	6.09	5.54	3
202018_s_at	LTF	lactotransferrin	NM_002343	4057	Hs.529517	GO:0006811: ion transport, GO:0006826: iron ion transport, GO:0006879: cellular iron ion homeostasis, GO:0006959: humoral immune response, GO:0042742: defense response to bacterium, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0004252: serine-type endopeptidase activity, GO:0008199: ferric iron binding, GO:0008233: peptidase activity, GO:0046872: metal ion binding		−0.3259	−1.6815	−2.9663	−4.3699	5.89	10.97	10.64	9.29	8	6.6	3

(*Continued*)

TABLE E2. (*Continued*)

202070_s_at	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	NM_005530	3419	Hs.591110	GO:0005975: carbohydrate metabolic process, GO:0006099: tricarboxylic acid cycle, GO:0008152: metabolic process, GO:0005739: mitochondrion, GO:0000287: magnesium ion binding, GO:0004449: isocitrate dehydrogenase (NAD+) activity, GO:0016491: oxidoreductase activity, GO:0016616: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, GO:0030145: manganese ion binding	00020: Citrate cycle (TCA cycle)	−0.1243	−0.5569	−0.9938	−1.5128	8.11	9.4	9.27	8.84	8.4	7.88	3
204601_at	N4BP1	Nedd4 binding protein 1	NM_014664	9683	Hs.511839			−0.1423	−0.7129	−1.2627	−1.7551	6.02	7.74	7.6	7.03	6.48	5.98	3
204822_at	TTK	TTK protein kinase	NM_003318	7272	Hs.169840	GO:0000074: regulation of progression through cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0007052: mitotic spindle organization and biogenesis, GO:0007094: mitotic cell cycle spindle assembly checkpoint, GO:0008284: positive regulation of cell proliferation, GO:0005819: spindle, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004713: protein-tyrosine kinase activity, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity		−0.0967	−0.6894	−1.1101	−1.5766	3.39	4.59	4.5	3.9	3.48	3.02	3
205034_at	CCNE2	cyclin E2	NM_004702	9134	Hs.567387	GO:0000074: regulation of progression through cell cycle, GO:0000075: cell cycle checkpoint, GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0006270: DNA replication initiation, GO:0007049: cell cycle, GO:0051301: cell division, GO:0005634: nucleus, GO:0005515: protein binding, GO:0016538: cyclin-dependent protein kinase regulator activity	04110: Cell cycle, 04115: p53 signaling pathway, 05215: Prostate cancer, 05222: Small cell lung cancer	−0.4992	−0.6225	−1.0382	−1.6273	5.01	6.37	5.87	5.75	5.34	4.75	3
205909_at	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	NM_002692	5427	Hs.162777	GO:0006260: DNA replication, GO:0006281: DNA repair, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003893: epsilon DNA polymerase activity, GO:0016740: transferase activity	00230: Purine metabolism, 00240: Pyrimidine metabolism, 03030: DNA polymerase	−0.4356	−0.5532	−0.8734	−1.4727	5.01	5.92	5.48	5.37	5.04	4.45	3
219037_at	RRP15	ribosomal RNA processing 15 homolog (S. cerevisiae)	NM_016052	51018	Hs.660109	GO:0005515: protein binding		−0.3171	−0.3683	−0.6166	−1.1169	8.1	8.57	8.26	8.21	7.96	7.46	3
201872_s_at	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	NM_002940	6059	Hs.12013	GO:0006118: electron transport, GO:0006401: RNA catabolic process, GO:0006457: protein folding, GO:0009615: response to virus, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0008428: ribonuclease inhibitor activity, GO:0009055: electron carrier activity, GO:0016887: ATPase activity, GO:0051536: iron-sulfur cluster binding		−0.2763	−0.3759	−0.5333	−1.0637	10.07	10.55	10.27	10.17	10.02	9.49	3
219006_at	C6orf66	chromosome 6 open reading frame 66	NM_014165	29078	Hs.591333			−0.3953	−0.4432	−0.7128	−1.3067	8.32	8.93	8.54	8.49	8.22	7.63	3

(*Continued*)

TABLE E2. (*Continued*)

204244 _s_at	DBF4	DBF4 homolog (S. cerevisiae)	NM_006716	10926	Hs.485380	GO:0000074: regulation of progression through cell cycle, GO:0000082: G1/S transition of mitotic cell cycle, GO:0006260: DNA replication, GO:0007049: cell cycle, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0005515: protein binding, GO:0008047: enzyme activator activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	04110: Cell cycle	−0.5477	−0.5695	−0.8272	−1.5233	6.95	7.88	7.34	7.31	7.06	6.36	3
221305 _s_at	UGT1A8	UDP glucuronosyltransferase 1 family, polypeptide A8	NM_019076	54576	Hs.654499	GO:0008152: metabolic process, GO:0008152: metabolic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0008194: UDP-glycosyltransferase activity, GO:0015020: glucuronosyltransferase activity, GO:0016758: transferase activity, transferring hexosyl groups	00040: Pentose and glucuronate interconversions, 00150: Androgen and estrogen metabolism, 00500: Starch and sucrose metabolism, 00860: Porphyrin and chlorophyll metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	−0.6533	−1.0544	−1.5108	−2.5621	2.52	5.01	4.36	3.96	3.5	2.45	3
214155 _s_at	LARP4	La ribonucleoprotein domain family, member 4	AI743740	113251	Hs.653274	GO:0003676: nucleic acid binding, GO:0003723: RNA binding		−0.5512	−0.7369	−0.9613	−1.7529	5.92	7.13	6.58	6.4	6.17	5.38	3
217808 _s_at	MAPKAP1	mitogen-activated protein kinase associated protein 1	NM_024117	79109	Hs.495138	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0016301: kinase activity, GO:0017016: Ras GTPase binding		−0.2504	−0.3997	−0.5796	−1.0683	6.35	7.2	6.95	6.8	6.62	6.13	3
200731 _s_at	PTP4A1	protein tyrosine phosphatase type IVA, member 1	AW165960	7803	Hs.227777	GO:0006470: protein amino acid dephosphorylation, GO:0007049: cell cycle, GO:0007275: multicellular organismal development, GO:0005737: cytoplasm, GO:0005768: endosome, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0004725: protein tyrosine phosphatase activity, GO:0016787: hydrolase activity		−0.4462	−0.6582	−1.0148	−1.6444	8.62	9.63	9.19	8.98	8.62	7.99	3
204109 _s_at	NFYA	nuclear transcription factor Y, alpha	BF445142	4800	Hs.10441	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0005634: nucleus, GO:0016602: CCAAT-binding factor complex, GO:0003700: transcription factor activity, GO:0005515: protein binding	04612: Antigen processing and presentation	−0.2982	−0.4446	−0.656	−1.1742	3.62	4.5	4.2	4.05	3.84	3.32	3
202589 _at	TYMS	thymidylate synthetase	NM_001071	7298	Hs.592338	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006231: dTMP biosynthetic process, GO:0006260: DNA replication, GO:0006281: DNA repair, GO:0009157: deoxyribonucleoside monophosphate biosynthetic process, GO:0009165: nucleotide biosynthetic process, GO:0048015: phosphoinositide-mediated signaling, GO:0004799: thymidylate synthase activity, GO:0008168: methyltransferase activity, GO:0016740: transferase activity	00240: Pyrimidine metabolism, 00670: One carbon pool by folate	−0.4704	−0.5915	−0.8251	−1.3591	8.75	9.74	9.27	9.15	8.92	8.38	3

(*Continued*)

TABLE E2. (*Continued*)

206108 _s_at	SFRS6	splicing factor, arginine/ serine-rich 6	NM_006275	6431	Hs.6891	GO:0006376: mRNA splice site selection, GO:0006397: mRNA processing, GO:0008380: RNA splicing, GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005515: protein binding		−0.5997	−1.0341	−1.2539	−2.1591	4.54	6.31	5.71	5.28	5.06	4.15	3
212612 _at	RCOR1	REST corepressor 1	D31888	23186	Hs.510521	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0016568: chromatin modification, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0005515: protein binding		−0.2724	−0.4376	−0.5604	−1.0202	9.94	10.33	10.06	9.89	9.77	9.31	3
216388 _s_at	LTB4R	leukotriene B4 receptor	U33448	1241	Hs.655431	GO:0006928: cell motility, GO:0006936: muscle contraction, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007165: signal transduction, GO:0007200: G-protein signaling, coupled to IP3 second messenger (phospholipase C activating), GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004872: receptor activity, GO:0004974: leukotriene receptor activity	04080: Neuroactive ligand-receptor interaction	−0.3319	−0.4819	−0.7413	−1.1278	9.1	9.98	9.65	9.5	9.24	8.86	3
205895 _s_at	NOLC1	nucleolar and coiled-body phosphoprotein 1	NM_004741	9221	Hs.523238	GO:0006364: rRNA processing, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0005730: nucleolus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005525: GTP binding		−0.4146	−0.5621	−0.9494	−1.3865	6.12	7.08	6.67	6.52	6.13	5.69	3
206653 _at	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	BF062139	10622	Hs.282387	GO:0006350: transcription, GO:0006359: regulation of transcription from RNA polymerase III promoter, GO:0005666: DNA-directed RNA polymerase III complex, GO:0003899: DNA-directed RNA polymerase activity		−0.3553	−0.541	−0.8528	−1.278	5.44	6.72	6.37	6.18	5.87	5.44	3
203622 _s_at	PNO1	partner of NOB1 homolog (S. cerevisiae)	NM_020143	56902	Hs.262858	GO:0005730: nucleolus, GO:0003723: RNA binding		−0.3507	−0.4268	−0.8156	−1.2633	8.54	9.19	8.84	8.76	8.37	7.92	3
218360 _at	RAB22A	RAB22A, member RAS oncogene family	NM_020673	57403	Hs.529044	GO:0006897: endocytosis, GO:0007032: endosome organization and biogenesis, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0005769: early endosome, GO:0005886: plasma membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005525: GTP binding		−0.3919	−0.4646	−0.868	−1.3591	8.31	9.3	8.91	8.84	8.44	7.95	3
219959 _at	MOCOS	molybdenum cofactor sulfurase	NM_017947	55034	Hs.405028	GO:0006777: Mo-molybdopterin cofactor biosynthetic process, GO:0008152: metabolic process, GO:0043545: molybdopterin cofactor metabolic process, GO:0005575: cellular_component, GO:0008265: Mo-molybdopterin cofactor sulfurase activity, GO:0008483: transaminase activity, GO:0016829: lyase activity, GO:0030151: molybdenum ion binding, GO:0030170: pyridoxal phosphate binding		−0.5316	−0.542	−0.7826	−1.2553	4.47	5.34	4.81	4.8	4.56	4.08	3

(*Continued*)

TABLE E2. (*Continued*)

218782_s_at	ATAD2	ATPase family, AAA domain containing 2	NM_014109	29028	Hs.370834	GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0017111: nucleoside-triphosphatase activity		−0.3543	−0.5575	−0.6399	−1.0498	2.9	3.71	3.35	3.15	3.07	2.66	3
219787_s_at	ECT2	epithelial cell transforming sequence 2 oncogene	NM_018098	1894	Hs.518299	GO:0007242: intracellular signaling cascade, GO:0035023: regulation of Rho protein signal transduction, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005622: intracellular, GO:0004871: signal transducer activity, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0005515: protein binding		−0.5172	−0.8607	−0.8673	−1.5913	7.92	8.77	8.25	7.91	7.9	7.18	3
205419_at	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	NM_004951	1880	Hs.784	GO:0006955: immune response, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0045028: purinergic nucleotide receptor activity, G-protein coupled		−0.316	−0.4519	−0.4194	−1.1752	6.23	7.82	7.5	7.37	7.4	6.64	3
205891_at	ADORA2B	adenosine A2b receptor	NM_000676	136	Hs.167046	GO:0000187: activation of MAPK activity, GO:0006968: cellular defense response, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007190: adenylate cyclase activation, GO:0007254: JNK cascade, GO:0007588: excretion, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0001584: rhodopsin-like receptor activity, GO:0001612: A2B adenosine receptor activity, G-protein coupled, GO:0004872: receptor activity	04020: Calcium signaling pathway, 04080: Neuroactive ligand-receptor interaction	−0.4827	−0.5588	−0.682	−1.4263	7.14	7.58	7.09	7.02	6.9	6.15	3
205287_s_at	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	NM_003222	7022	Hs.473152	GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007267: cell-cell signaling, GO:0030154: cell differentiation, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0046983: protein dimerization activity		−0.4607	−0.6128	−0.566	−1.1669	4.78	6.02	5.56	5.4	5.45	4.85	3
206932_at	CH25H	cholesterol 25-hydroxylase	NM_003956	9023	Hs.47357	GO:0006629: lipid metabolic process, GO:0008152: metabolic process, GO:0008203: cholesterol metabolic process, GO:0016126: sterol biosynthetic process, GO:0005624: membrane fraction, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005506: iron ion binding, GO:0008395: steroid hydroxylase activity, GO:0046872: metal ion binding		−0.5397	−0.5628	−0.6057	−1.299	3.98	5.94	5.4	5.37	5.33	4.64	3

(*Continued*)

TABLE E2. (*Continued*)

218881_s_at	FOSL2	FOS-like antigen 2	NM_024530	2355	Hs.220971, Hs.596972	GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0008219: cell death, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity		−0.3153	−0.5211	−0.4912	−1.1003	4.75	5.68	5.37	5.16	5.19	4.58	3
202431_s_at	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	NM_002467	4609	Hs.202453	GO:0001836: release of cytochrome c from mitochondria, GO:0006309: DNA fragmentation during apoptosis, GO:0006355: regulation of transcription, DNA-dependent, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006879: cellular iron ion homeostasis, GO:0006919: caspase activation, GO:0007050: cell cycle arrest, GO:0008284: positive regulation of cell proliferation, GO:0008629: induction of apoptosis by intracellular signals, GO:0008633: activation of pro-apoptotic gene products, GO:0008634: negative regulation of survival gene product activity, GO:0009314: response to radiation, GO:0042981: regulation of apoptosis, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005819: spindle, GO:0003677: DNA binding, GO:0003700: transcription factor activity, GO:0005515: protein binding	04010: MAPK signaling pathway, 04012: ErbB signaling pathway, 04310: Wnt signaling pathway, 04350: TGF-beta signaling pathway, 04630: Jak-STAT signaling pathway, 05210: Colorectal cancer, 05213: Endometrial cancer, 05216: Thyroid cancer, 05219: Bladder cancer, 05220: Chronic myeloid leukemia, 05221: Acute myeloid leukemia, 05222: Small cell lung cancer	−0.3059	−0.4327	−0.5103	−1.1034	9.85	10.55	10.25	10.12	10.04	9.45	3
206102_at	GINS1	GINS complex subunit 1 (Psf1 homolog)	NM_021067	9837	Hs.658464	GO:0006260: DNA replication, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005515: protein binding		−0.4355	−0.7506	−0.7867	−1.7241	6.18	7.11	6.67	6.36	6.32	5.39	3

(*Continued*)

TABLE E2. (*Continued*)

210480_s_at	MYO6	myosin VI	U90236	4646	Hs.149387	GO:0006886: intracellular protein transport, GO:0006897: endocytosis, GO:0006897: endocytosis, GO:0007605: sensory perception of sound, GO:0007605: sensory perception of sound, GO:0008150: biological_process, GO:0030048: actin filament-based movement, GO:0030048: actin filament-based movement, GO:0030330: DNA damage response, signal transduction by p53 class mediator, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0051046: regulation of secretion, GO:0001726: ruffle, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0005737: cytoplasm, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0005938: cell cortex, GO:0016020: membrane, GO:0016461: unconventional myosin complex, GO:0016461: unconventional myosin complex, GO:0016591: DNA-directed RNA polymerase II, holoenzyme, GO:0031941: filamentous actin, GO:0031941: filamentous actin, GO:0031965: nuclear membrane, GO:0045334: clathrin-coated endocytic vesicle, GO:0048471: perinuclear region of cytoplasm, GO:0048471: perinuclear region of cytoplasm, GO:0000166: nucleotide binding, GO:0003774: motor activity, GO:0003774: motor activity, GO:0005516: calmodulin binding, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0042803: protein homodimerization activity, GO:0043531: ADP binding, GO:0051015: actin filament binding, GO:0051015: actin filament binding, GO:0060001: minus-end directed microfilament motor activity		0.1583	0.3657	−0.1754	−1.46	6.7	7.57	7.73	7.94	7.4	6.11	4
206667_s_at	SCAMP1	secretory carrier membrane protein 1	AF005037	9522	Hs.482587	GO:0006892: post-Golgi vesicle-mediated transport, GO:0015031: protein transport, GO:0005624: membrane fraction, GO:0016020: membrane, GO:0016021: integral to membrane		0.2243	0.4257	−0.4074	−2.2793	5.4	6.6	6.82	7.02	6.19	4.32	4
218748_s_at	EXOC5	exocyst complex component 5	NM_006544	10640	Hs.655158	GO:0006887: exocytosis, GO:0006892: post-Golgi vesicle-mediated transport, GO:0015031: protein transport, GO:0048278: vesicle docking, GO:0005737: cytoplasm, GO:0005737: cytoplasm		0.0843	0.2635	−0.3425	−2.3523	6.89	7.81	7.89	8.07	7.47	5.46	4
201337_s_at	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)	NM_004781	9341	Hs.66708	GO:0006461: protein complex assembly, GO:0006904: vesicle docking during exocytosis, GO:0006944: membrane fusion, GO:0017156: calcium ion-dependent exocytosis, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019717: synaptosome, GO:0030054: cell junction, GO:0045202: synapse	04130: SNARE interactions in vesicular transport	0.0694	0.1293	−0.2195	−1.2093	10.2	10.53	10.6	10.66	10.31	9.32	4

(*Continued*)

TABLE E2. (*Continued*)

218549_s_at	FAM82B	family with sequence similarity 82, member B	AK000672	51115	Hs.145386	GO:0005488: binding	0.0861	0.1251	−0.2133	−1.0651	8.07	8.35	8.43	8.47	8.13	7.28	4
206134_at	ADAMDEC1	ADAM-like, decysin 1	NM_014479	27299	Hs.521459	GO:0006508: proteolysis, GO:0007162: negative regulation of cell adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0016021: integral to membrane, GO:0004222: metalloendopeptidase activity, GO:0005178: integrin binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	1.1743	0.6222	0.3506	−1.4797	3.7	7.33	8.51	7.96	7.68	5.85	4
201683_x_at	TOX4	TOX high mobility group box family member 4	BE783632	9878	Hs.555910	GO:0006355: regulation of transcription, DNA-dependent, GO:0000785: chromatin, GO:0005634: nucleus, GO:0003677: DNA binding	0.3226	0.2494	−0.2729	−1.0796	6.56	7.43	7.75	7.68	7.15	6.35	4
214059_at	IFI44	interferon-induced protein 44	BE049439	10561	Hs.82316	GO:0009615: response to virus, GO:0005737: cytoplasm	0.7682	0.6863	−0.1504	−1.4555	5.29	7.67	8.44	8.36	7.52	6.22	4
211090_s_at	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Z25435	8899	Hs.159014	GO:0006397: mRNA processing, GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0008380: RNA splicing, GO:0005681: spliceosome, GO:0000166: nucleotide binding, GO:0004672: protein kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	0.0384	0.0649	−0.2326	−1.7818	9.06	9.48	9.52	9.55	9.25	7.7	4
201775_s_at	ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1	AA676790	64756	Hs.100874	GO:0006461: protein complex assembly, GO:0005739: mitochondrion, GO:0005515: protein binding	0.0671	0.0653	−0.1829	−1.3376	8.52	8.89	8.96	8.96	8.71	7.56	4
203087_s_at	KIF2A	kinesin heavy chain member 2A	NM_004520	3796	Hs.558351	GO:0007018: microtubule-based movement, GO:0005856: cytoskeleton, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0000166: nucleotide binding, GO:0003777: microtubule motor activity, GO:0005524: ATP binding	0.0808	0.0454	−0.1817	−1.7281	6.98	8.15	8.23	8.2	7.97	6.42	4
213875_x_at	C6orf62	chromosome 6 open reading frame 62	BG252842	81688	Hs.519930	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0003674: molecular_function	0.164	0.2279	−0.1533	−2.1327	8.26	9	9.17	9.23	8.85	6.87	4
217777_s_at	PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	NM_016395	51495	Hs.512973	GO:0007249: I-kappaB kinase/NF-kappaB cascade, GO:0007257: activation of JNK activity, GO:0007264: small GTPase mediated signal transduction, GO:0005096: GTPase activator activity, GO:0005515: protein binding	0.2101	0.2172	0.018	−1.029	7.3	6.92	7.13	7.13	6.94	5.89	4

(*Continued*)

TABLE E2. (*Continued*)

200604 _s_at	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	M18468	5573	Hs.280342, Hs.659124	GO:0001707: mesoderm formation, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007242: intracellular signaling cascade, GO:0005952: cAMP-dependent protein kinase complex, GO:0031594: neuromuscular junction, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0008603: cAMP-dependent protein kinase regulator activity, GO:0008603: cAMP-dependent protein kinase regulator activity, GO:0016301: kinase activity, GO:0030552: cAMP binding	04210: Apoptosis, 04910: Insulin signaling pathway	0.1693	0.1257	−0.0478	−1.8381	9.42	9.99	10.16	10.12	9.95	8.16	4
200729 _s_at	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	BE566290	10097	Hs.393201, Hs.643727	GO:0006928: cell motility, GO:0005737: cytoplasm, GO:0005885: Arp2/3 protein complex, GO:0005198: structural molecule activity, GO:0005515: protein binding		0.0878	0.0447	−0.0477	−1.0274	11	11.29	11.38	11.34	11.25	10.27	4
203007 _x_at	LYPLA1	lysophospholipase I	AF077198	10434	Hs.435850	GO:0006629: lipid metabolic process, GO:0006631: fatty acid metabolic process, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0004622: lysophospholipase activity, GO:0016787: hydrolase activity	00564: Glycerophospholipid metabolism	0.1647	0.1348	−0.1443	−1.1943	9.86	10.66	10.82	10.79	10.51	9.46	4
208653 _s_at	CD164	CD164 molecule, sialomucin	AF299343	8763	Hs.520313	GO:0006955: immune response, GO:0007155: cell adhesion, GO:0007157: heterophilic cell adhesion, GO:0007162: negative regulation of cell adhesion, GO:0007165: signal transduction, GO:0007275: multicellular organismal development, GO:0008285: negative regulation of cell proliferation, GO:0008285: negative regulation of cell proliferation, GO:0030097: hemopoiesis, GO:0005624: membrane fraction, GO:0005625: soluble fraction, GO:0005768: endosome, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005887: integral to plasma membrane		0.1904	0.1647	−0.1196	−1.4205	9.74	10.01	10.2	10.18	9.89	8.59	4
210915 _x_at	TRBC1	T cell receptor beta constant 1	M15564	28639	Hs.654496	GO:0006955: immune response, GO:0016020: membrane, GO:0004872: receptor activity, GO:0005515: protein binding		0.8238	0.4434	0.53	−1.4607	4.46	7.24	8.07	7.69	7.77	5.78	4

(*Continued*)

TABLE E2. (*Continued*)

212588_at	PTPRC	protein tyrosine phosphatase, receptor type, C	Y00062	5788	Hs.654514	GO:0001915: negative regulation of T cell mediated cytotoxicity, GO:0001960: negative regulation of cytokine and chemokine mediated signaling pathway, GO:0006469: negative regulation of protein kinase activity, GO:0006469: negative regulation of protein kinase activity, GO:0006470: protein amino acid dephosphorylation, GO:0006470: protein amino acid dephosphorylation, GO:0007166: cell surface receptor linked signal transduction, GO:0030217: T cell differentiation, GO:0042100: B cell proliferation, GO:0042102: positive regulation of T cell proliferation, GO:0045860: positive regulation of protein kinase activity, GO:0050852: T cell receptor signaling pathway, GO:0050852: T cell receptor signaling pathway, GO:0050853: B cell receptor signaling pathway, GO:0050857: positive regulation of antigen receptor-mediated signaling pathway, GO:0051209: release of sequestered calcium ion into cytosol, GO:0051607: defense response to virus, GO:0051726: regulation of cell cycle, GO:0005887: integral to plasma membrane, GO:0005925: focal adhesion, GO:0016020: membrane, GO:0004725: protein tyrosine phosphatase activity, GO:0004725: protein tyrosine phosphatase activity, GO:0004872: receptor activity, GO:0005001: transmembrane receptor protein tyrosine phosphatase activity, GO:0016787: hydrolase activity, GO:0016791: phosphoric monoester hydrolase activity, GO:0019901: protein kinase binding, GO:0019901: protein kinase binding	04514: Cell adhesion molecules (CAMs), 04660: T cell receptor signaling pathway	0.4551	0.2354	0.276	−1.2378	8.63	9.76	10.22	10.04	8.52	4
201299_s_at	MOBKL1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	NM_018221	55233	Hs.196437	GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.0959	0.2344	0.1733	−1.7422	7.76	8.17	8.27	8.41	8.34	6.43	4
201399_s_at	TRAM1	translocation associated membrane protein 1	BC000687	23471	Hs.491988	GO:0006605: protein targeting, GO:0006613: cotranslational protein targeting to membrane, GO:0015031: protein transport, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity		0.1347	0.1166	0.077	−1.2421	10	10.36	10.5	10.48	10.44	9.12	4
200727_s_at	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	AA699583	10097	Hs.393201, Hs.643727	GO:0006928: cell motility, GO:0005737: cytoplasm, GO:0005885: Arp2/3 protein complex, GO:0005198: structural molecule activity, GO:0005515: protein binding		0.3008	−0.2083	0.0231	−2.1843	5.7	7.4	7.7	7.19	7.42	5.21	4
201295_s_at	WSB1	WD repeat and SOCS box-containing 1	BF111821	26118	Hs.446017	GO:0007242: intracellular signaling cascade, GO:0008150: biological_process, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0003674: molecular_function		0.0339	0.1014	0.1017	−1.5236	7.93	8.17	8.21	8.27	8.27	6.65	4

(*Continued*)

TABLE E2. (*Continued*)

220386_s_at	EML4	echinoderm microtubule associated protein like 4	NM_019063	27436	Hs.593614	GO:0007017: microtubule-based process, GO:0007067: mitosis, GO:0005737: cytoplasm, GO:0005874: microtubule, GO:0003674: molecular_function, GO:0005515: protein binding		0.1286	−0.0461	−0.0091	−1.266	7.74	8.11	8.24	8.06	8.1	6.84	4
221081_s_at	DENND2D	DENN/MADD domain containing 2D	NM_024901	79961	Hs.557850			0.1307	−0.0041	−0.0329	−1.0103	8.15	8.7	8.83	8.69	8.66	7.68	4
219492_at	CHIC2	cysteine-rich hydrophobic domain 2	NM_012110	26511	Hs.335393	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0005794: Golgi apparatus, GO:0005798: Golgi-associated vesicle, GO:0005886: plasma membrane, GO:0031410: cytoplasmic vesicle, GO:0003674: molecular_function		0.1343	−0.0589	−0.1065	−1.2271	9.8	10.52	10.65	10.46	10.41	9.29	4
220330_s_at	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	NM_022136	64092	Hs.473341, Hs.570423	GO:0001784: phosphotyrosine binding		0.2402	−0.3581	−0.2203	−2.2687	4.2	7.1	7.34	6.75	6.88	4.83	4
214483_s_at	ARFIP1	ADP-ribosylation factor interacting protein 1 (arfaptin 1)	AF124489	27236	Hs.416089	GO:0006886: intracellular protein transport, GO:0008150: biological_process, GO:0050708: regulation of protein secretion, GO:0000139: Golgi membrane, GO:0005829: cytosol, GO:0003674: molecular_function		0.1795	0.0076	0.06	−1.493	6.25	6.66	6.84	6.67	6.72	5.17	4
214786_at	MAP3K1	mitogen-activated protein kinase kinase kinase 1	AA361361	4214	Hs.657756	GO:0006468: protein amino acid phosphorylation, GO:0007179: transforming growth factor beta receptor signaling pathway, GO:0008637: apoptotic mitochondrial changes, GO:0030334: regulation of cell migration, GO:0030838: positive regulation of actin filament polymerization, GO:0042060: wound healing, GO:0005575: cellular_component, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004674: protein serine/threonine kinase activity, GO:0004709: MAP kinase kinase kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008270: zinc ion binding, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04912: GnRH signaling pathway	0.1488	0.2302	0.1785	−1.1206	5.94	6.41	6.56	6.65	6.59	5.29	4
212835_at	KIAA0157	KIAA0157	AA777641	23172	Hs.280695	GO:0005515: protein binding		0.3152	0.0652	0.1073	−1.0628	6.19	6.43	6.75	6.5	6.54	5.37	4
213975_s_at	LYZ	lysozyme (renal amyloidosis)	AV711904	4069	Hs.524579	GO:0006954: inflammatory response, GO:0008152: metabolic process, GO:0016998: cell wall catabolic process, GO:0019835: cytolysis, GO:0042742: defense response to bacterium, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0003796: lysozyme activity, GO:0005515: protein binding, GO:0016798: hydrolase activity, acting on glycosyl bonds		0.3319	0.1426	0.061	−1.0736	10.55	12.31	12.64	12.45	12.37	11.24	4
212008_at	UBXD2	UBX domain containing 2	N29889	23190	Hs.591242			0.1455	0.0083	−0.1344	−1.8871	8.69	9.15	9.29	9.15	9.01	7.26	4
212409_s_at	TOR1AIP1	torsin A interacting protein 1	AK021613	26092	Hs.496459	GO:0016020: membrane, GO:0016021: integral to membrane		0.2049	0.1794	0.0063	−1.1181	7.52	7.57	7.78	7.75	7.58	6.45	4

(*Continued*)

TABLE E2. (*Continued*)

210959_s_at	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	AF113128	6715	Hs.552	GO:0006702: androgen biosynthetic process, GO:0007267: cell-cell signaling, GO:0007530: sex determination, GO:0007548: sex differentiation, GO:0030154: cell differentiation, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003865: 3-oxo-5-alpha-steroid 4-dehydrogenase activity, GO:0009055: electron carrier activity	00120: Bile acid biosynthesis, 00150: Androgen and estrogen metabolism, 05215: Prostate cancer	0.4408	−0.0067	−0.0387	−1.0519	7.79	7.7	8.14	7.69	7.66	6.65	4
211559_s_at	CCNG2	cyclin G2	L49506	901	Hs.13291	GO:0000074: regulation of progression through cell cycle, GO:0000075: cell cycle checkpoint, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0051301: cell division, GO:0005737: cytoplasm	04115: p53 signaling pathway	0.6057	0.2982	−0.0853	−1.9235	6.72	7.17	7.77	7.47	7.08	5.25	4
209284_s_at	C3orf63	chromosome 3 open reading frame 63	AI922509	23272	Hs.116877			0.0787	−0.0818	−0.1086	−1.165	8.27	8.57	8.64	8.48	8.46	7.4	4
210148_at	HIPK3	homeodomain interacting protein kinase 3	AF305239	10114	Hs.201918	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006915: apoptosis, GO:0006916: anti-apoptosis, GO:0018105: peptidyl-serine phosphorylation, GO:0018107: peptidyl-threonine phosphorylation, GO:0043508: negative regulation of JNK activity, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0019901: protein kinase binding		0.0281	0.264	−0.0665	−2.4002	6.77	7.68	7.7	7.94	7.61	5.28	4
207339_s_at	LTB	lymphotoxin beta (TNF superfamily, member 3)	NM_002341	4050	Hs.376208	GO:0006955: immune response, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0005575: cellular_component, GO:0005615: extracellular space, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005125: cytokine activity, GO:0005164: tumor necrosis factor receptor binding	04060: Cytokine-cytokine receptor interaction	0.4218	0.1053	0.0734	−1.012	4.02	5.55	5.97	5.66	5.62	4.54	4
207549_x_at	CD46	CD46 molecule, complement regulatory protein	NM_002389	4179	Hs.510402	GO:0006958: complement activation, classical pathway, GO:0007338: single fertilization, GO:0045087: innate immune response, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0004872: receptor activity	04610: Complement and coagulation cascades	0.2467	0.2123	−0.0101	−1.4381	7.4	7.62	7.87	7.83	7.61	6.18	4
205836_s_at	YTHDC2	YTH domain containing 2	NM_022828	64848	Hs.231942	GO:0004386: helicase activity		0.2159	0.2986	0.0653	−1.0086	7.7	7.81	8.03	8.11	7.88	6.8	4

(*Continued*)

TABLE E2. (*Continued*)

207238 _s_at	PTPRC	protein tyrosine phosphatase, receptor type, C	NM_002838	5788	Hs.654514	GO:0001915: negative regulation of T cell mediated cytotoxicity, GO:0001960: negative regulation of cytokine and chemokine mediated signaling pathway, GO:0006469: negative regulation of protein kinase activity, GO:0006469: negative regulation of protein kinase activity, GO:0006470: protein amino acid dephosphorylation, GO:0006470: protein amino acid dephosphorylation, GO:0007166: cell surface receptor linked signal transduction, GO:0030217: T cell differentiation, GO:0042100: B cell proliferation, GO:0042102: positive regulation of T cell proliferation, GO:0045860: positive regulation of protein kinase activity, GO:0050852: T cell receptor signaling pathway, GO:0050852: T cell receptor signaling pathway, GO:0050853: B cell receptor signaling pathway, GO:0050857: positive regulation of antigen receptor-mediated signaling pathway, GO:0051209: release of sequestered calcium ion into cytosol, GO:0051607: defense response to virus, GO:0051726: regulation of cell cycle, GO:0005887: integral to plasma membrane, GO:0005925: focal adhesion, GO:0016020: membrane, GO:0004725: protein tyrosine phosphatase activity, GO:0004725: protein tyrosine phosphatase activity, GO:0004872: receptor activity, GO:0005001: transmembrane receptor protein tyrosine phosphatase activity, GO:0016787: hydrolase activity, GO:0016791: phosphoric monoester hydrolase activity, GO:0019901: protein kinase binding, GO:0019901: protein kinase binding	04514: Cell adhesion molecules (CAMs), 04660: T cell receptor signaling pathway	0.4819	−0.0294	0.217	−1.3236	6.21	7.72	8.2	7.69	7.94	6.4	4
205269 _at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	AI123251	3937	Hs.304475	GO:0006955: immune response, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007242: intracellular signaling cascade, GO:0045576: mast cell activation, GO:0050663: cytokine secretion, GO:0005737: cytoplasm, GO:0005515: protein binding	04650: Natural killer cell mediated cytotoxicity, 04660: T cell receptor signaling pathway, 04664: Fc epsilon RI signaling pathway	0.3464	−0.083	0.0648	−1.0656	5.81	7.23	7.58	7.15	7.3	6.17	4
205732 _s_at	NCOA2	nuclear receptor coactivator 2	NM_006540	10499	Hs.446678	GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0005634: nucleus, GO:0003713: transcription coactivator activity, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0030528: transcription regulator activity, GO:0035257: nuclear hormone receptor binding		0.2507	0.3633	−0.0104	−1.0788	3.86	4.49	4.74	4.85	4.48	3.41	4

(*Continued*)

TABLE E2. (*Continued*)

204174_at	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	NM_001629	241	Hs.507658	GO:0006954: inflammatory response, GO:0019370: leukotriene biosynthetic process, GO:0005624: membrane fraction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005488: binding, GO:0008047: enzyme activator activity		0.4161	0.151	0.0241	−1.3017	6.91	7.8	8.21	7.95	7.82	6.5	4
204716_at	CCDC6	coiled-coil domain containing 6	NM_005436	8030	Hs.591360	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding	05216: Thyroid cancer	−0.0054	0.1673	0.0325	−1.3679	8.17	8.64	8.64	8.81	8.67	7.27	4
204007_at	FCGR3B	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	J04162	2215	Hs.372679	GO:0006955: immune response, GO:0016020: membrane, GO:0004872: receptor activity, GO:0019864: IgG binding, GO:0048503: GPI anchor binding	04650: Natural killer cell mediated cytotoxicity	0.6699	0.1996	0.0525	−1.4616	5.29	6.81	7.48	7.01	6.86	5.35	4
204057_at	IRF8	interferon regulatory factor 8	AI073984	3394	Hs.137427	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006955: immune response, GO:0030099: myeloid cell differentiation, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003705: RNA polymerase II transcription factor activity, enhancer binding		0.519	0.2135	0.0583	−1.1437	6.5	7.91	8.43	8.13	7.97	6.77	4
203553_s_at	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	NM_006575	11183	Hs.130491	GO:0006468: protein amino acid phosphorylation, GO:0006950: response to stress, GO:0007243: protein kinase cascade, GO:0007257: activation of JNK activity, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005083: small GTPase regulator activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity		0.1179	0.1352	0.1385	−1.0025	9.52	9.59	9.71	9.73	9.73	8.59	4
203915_at	CXCL9	chemokine (C-X-C motif) ligand 9	NM_002416	4283	Hs.77367	GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0006968: cellular defense response, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007267: cell-cell signaling, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0008009: chemokine activity	04060: Cytokine-cytokine receptor interaction, 04620: Toll-like receptor signaling pathway	0.3993	−0.1534	0.0458	−2.0437	3.99	5.89	6.29	5.73	5.93	3.84	4

(*Continued*)

TABLE E2. (*Continued*)

202647 _s_at	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	NM_002524	4893	Hs.486502	GO:0000074: regulation of progression through cell cycle, GO:0007264: small GTPase mediated signal transduction, GO:0005622: intracellular, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding	04010: MAPK signaling pathway, 04012: ErbB signaling pathway, 04360: Axon guidance, 04370: VEGF signaling pathway, 04530: Tight junction, 04540: Gap junction, 04650: Natural killer cell mediated cytotoxicity, 04660: T cell receptor signaling pathway, 04662: B cell receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 04720: Long-term potentiation, 04730: Long-term depression, 04810: Regulation of actin cytoskeleton, 04910: Insulin signaling pathway, 04912: GnRH signaling pathway, 04916: Melanogenesis, 05211: Renal cell carcinoma, 05213: Endometrial cancer, 05214: Glioma, 05215: Prostate cancer, 05216: Thyroid cancer, 05218: Melanoma, 05219: Bladder cancer, 05220: Chronic myeloid leukemia, 05221: Acute myeloid leukemia, 05223: Non-small cell lung cancer	−0.0502	0.1329	0.0202	−1.4719	7.45	7.97	7.92	8.1	7.99	6.5	4
203416 _at	CD53	CD53 molecule	NM_000560	963	Hs.443057	GO:0007165: signal transduction, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane		0.3316	−0.1708	−0.0722	−1.2337	8.06	9.24	9.57	9.06	9.16	8	4
201856 _s_at	ZFR	zinc finger RNA binding protein	BC000376	51663	Hs.435231	GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0008270: zinc ion binding		0.0263	−0.1001	−0.1398	−1.6275	5.23	5.96	5.99	5.86	5.82	4.33	4
202516 _s_at	DLG1	discs, large homolog 1 (Drosophila)	NM_004087	1739	Hs.292549	GO:0001935: endothelial cell proliferation, GO:0007015: actin filament organization, GO:0007163: establishment and/or maintenance of cell polarity, GO:0016337: cell-cell adhesion, GO:0030866: cortical actin cytoskeleton organization and biogenesis, GO:0031575: G1/S transition checkpoint, GO:0045930: negative regulation of progression through mitotic cell cycle, GO:0005783: endoplasmic reticulum, GO:0005886: plasma membrane, GO:0005911: intercellular junction, GO:0016323: basolateral plasma membrane, GO:0045202: synapse, GO:0004385: guanylate kinase activity, GO:0004721: phosphoprotein phosphatase activity, GO:0005515: protein binding, GO:0008022: protein C-terminus binding, GO:0008092: cytoskeletal protein binding, GO:0015459: potassium channel regulator activity, GO:0019901: protein kinase binding, GO:0019902: phosphatase binding		−0.0253	0.1039	−0.1184	−1.3123	7.45	7.71	7.69	7.82	7.6	6.4	4

(*Continued*)

TABLE E2. (*Continued*)

217496_s_at	IDE	insulin-degrading enzyme	AA918442	3416	Hs.500546	GO:0006508: proteolysis, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0007548: sex differentiation, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0005777: peroxisome, GO:0004231: insulysin activity, GO:0004871: signal transducer activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	05010: Alzheimer's disease	0.2973	0.3233	−0.0513	−1.0783	10.81	11.85	12.15	12.18	11.8	10.77	4
217521_at			N54942					0.3295	0.3139	−0.2133	−1.3557	8.04	9.86	10.19	10.17	9.65	8.5	4
211574_s_at	CD46	CD46 molecule, complement regulatory protein	D84105	4179	Hs.510402	GO:0006958: complement activation, classical pathway, GO:0007338: single fertilization, GO:0045087: innate immune response, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0004872: receptor activity	04610: Complement and coagulation cascades	0.2757	0.2049	−0.1487	−1.2016	6.85	7.1	7.37	7.3	6.95	5.89	4
212720_at	PAPOLA	poly(A) polymerase alpha	AI670847	10914	Hs.253726	GO:0006350: transcription, GO:0006378: mRNA polyadenylation, GO:0006397: mRNA processing, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003723: RNA binding, GO:0004652: polynucleotide adenylyltransferase activity, GO:0016740: transferase activity		0.0557	0.1252	−0.0684	−1.5338	7.89	8.39	8.44	8.51	8.32	6.86	4
209629_s_at	NXT2	nuclear transport factor 2-like export factor 2	AK023289	55916	Hs.25010	GO:0006810: transport, GO:0015031: protein transport, GO:0051028: mRNA transport, GO:0005622: intracellular, GO:0005737: cytoplasm		0.5481	0.3954	−0.0667	−1.5223	5.66	6.12	6.67	6.52	6.05	4.6	4
211547_s_at	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	L13387	5048	Hs.77318	GO:0000132: establishment of mitotic spindle orientation, GO:0000226: microtubule cytoskeleton organization and biogenesis, GO:0001675: acrosome formation, GO:0001764: neuron migration, GO:0006810: transport, GO:0006928: cell motility, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007165: signal transduction, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0007405: neuroblast proliferation, GO:0008090: retrograde axon cargo transport, GO:0016042: lipid catabolic process, GO:0030154: cell differentiation, GO:0047496: vesicle transport along microtubule, GO:0051301: cell division, GO:0000235: astral microtubule, GO:0000776: kinetochore, GO:0005635: nuclear envelope, GO:0005737: cytoplasm, GO:0005813: centrosome, GO:0005856: cytoskeleton, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0005938: cell cortex, GO:0016020: membrane, GO:0008017: microtubule binding, GO:0045502: dynein binding	00565: Ether lipid metabolism	0.2304	0.24	0.0996	−1.2933	7.74	7.99	8.22	8.23	8.09	6.7	4

(*Continued*)

TABLE E2. (*Continued*)

204393 _s_at	ACPP	acid phosphatase, prostate	NM_001099	55	Hs.433060	GO:0000074: regulation of progression through cell cycle, GO:0005576: extracellular region, GO:0003993: acid phosphatase activity, GO:0004725: protein tyrosine phosphatase activity, GO:0016787: hydrolase activity	00361: gamma-Hexachlorocyclohexane degradation, 00740: Riboflavin metabolism	0.5012	0.4176	−0.1318	−1.1983	9.7	10.99	11.49	11.41	10.86	9.79	4
205159 _at	CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	AV756141	1439	Hs.592192	GO:0007165: signal transduction, GO:0007585: respiratory gaseous exchange, GO:0019221: cytokine and chemokine mediated signaling pathway, GO:0016020: membrane, GO:0030526: granulocyte macrophage colony-stimulating factor receptor complex, GO:0004872: receptor activity, GO:0004912: interleukin-3 receptor activity, GO:0004914: interleukin-5 receptor activity	04060: Cytokine-cytokine receptor interaction, 04210: Apoptosis, 04630: Jak-STAT signaling pathway	0.509	0.1638	0.0224	−1.2108	7.75	9.09	9.6	9.25	9.11	7.88	4
211668 _s_at	PLAU	plasminogen activator, urokinase	K03226	5328	Hs.77274	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0006935: chemotaxis, GO:0007165: signal transduction, GO:0007596: blood coagulation, GO:0042730: fibrinolysis, GO:0005615: extracellular space, GO:0004252: serine-type endopeptidase activity, GO:0008233: peptidase activity, GO:0008243: plasminogen activator activity, GO:0016301: kinase activity	04610: Complement and coagulation cascades	−0.1182	−0.5022	−0.28	−1.5473	4.41	5.92	5.81	5.42	5.64	4.38	4
213470 _s_at	HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	BF983406	3187	Hs.604001	GO:0006397: mRNA processing, GO:0008380: RNA splicing, GO:0005634: nucleus, GO:0005681: spliceosome, GO:0030530: heterogeneous nuclear ribonucleoprotein complex, GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0008266: poly(U) binding		−0.2436	−0.3945	−0.2397	−1.0207	7.21	7.98	7.73	7.58	7.74	6.96	4
205401 _at	AGPS	alkylglycerone phosphate synthase	NM_003659	8540	Hs.591631	GO:0006118: electron transport, GO:0006629: lipid metabolic process, GO:0008610: lipid biosynthetic process, GO:0005777: peroxisome, GO:0016020: membrane, GO:0008609: alkylglycerone-phosphate synthase activity, GO:0016740: transferase activity	00565: Ether lipid metabolism	0.037	−0.4804	−0.2928	−1.5684	5.74	6.88	6.91	6.4	6.58	5.31	4
210154 _at	ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	M55905	4200	Hs.233119	GO:0006108: malate metabolic process, GO:0005739: mitochondrion, GO:0004470: malic enzyme activity, GO:0004471: malate dehydrogenase (decarboxylating) activity, GO:0009055: electron carrier activity, GO:0016491: oxidoreductase activity, GO:0016616: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, GO:0016619: malate dehydrogenase (oxaloacetate-decarboxylating) activity, GO:0046872: metal ion binding, GO:0051287: NAD binding	00620: Pyruvate metabolism	−0.1807	−0.4599	−0.2824	−1.1002	6.24	6.52	6.34	6.06	6.24	5.42	4

(*Continued*)

TABLE E2. (*Continued*)

202654_x_at	7-Mar	membrane-associated ring finger (C3HC4) 7	NM_022826	64844	Hs.529272	GO:0006512: ubiquitin cycle, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016874: ligase activity, GO:0046872: metal ion binding		0.0576	0.0046	−0.1806	−1.1352	9.71	10.12	10.17	10.12	9.94	8.98	4
202479_s_at	TRIB2	tribbles homolog 2 (Drosophila)	BC002637	28951	Hs.467751	GO:0006468: protein amino acid phosphorylation, GO:0043405: regulation of MAPK activity, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0000166: nucleotide binding, GO:0004672: protein kinase activity, GO:0004860: protein kinase inhibitor activity, GO:0005515: protein binding, GO:0005524: ATP binding		0.1781	−0.0372	−0.1594	−1.3073	5.37	6.64	6.82	6.6	6.48	5.33	4
218465_at	TMEM33	transmembrane protein 33	NM_018126	55161	Hs.31082	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding		0.2629	−0.0125	−0.1244	−1.3572	7.33	7.87	8.13	7.86	7.74	6.51	4
219017_at	ETNK1	ethanolamine kinase 1	NM_018638	55500	Hs.29464	GO:0006646: phosphatidylethanolamine biosynthetic process, GO:0005737: cytoplasm, GO:0004305: ethanolamine kinase activity, GO:0016301: kinase activity, GO:0016740: transferase activity	00564: Glycerophospholipid metabolism	0.1858	−0.0114	−0.1504	−1.1399	6.79	7.52	7.71	7.51	7.37	6.38	4
203123_s_at	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	AU154469	4891	Hs.505545	GO:0006810: transport, GO:0006811: ion transport, GO:0006826: iron ion transport, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005215: transporter activity, GO:0005381: iron ion transmembrane transporter activity, GO:0005506: iron ion binding		0.247	−0.0824	−0.1952	−1.2027	8.6	9.35	9.59	9.26	9.15	8.14	4
205170_at	STAT2	signal transducer and activator of transcription 2, 113kDa	NM_005419	6773	Hs.530595	GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007242: intracellular signaling cascade, GO:0007259: JAK-STAT cascade, GO:0009615: response to virus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0004871: signal transducer activity, GO:0005062: hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity, GO:0005509: calcium ion binding, GO:0005515: protein binding	04630: Jak-STAT signaling pathway	0.3544	0.0541	−0.1963	−1.3625	6.37	7.55	7.91	7.61	7.36	6.19	4
202089_s_at	SLC39A6	solute carrier family 39 (zinc transporter), member 6	NM_012319	25800	Hs.79136	GO:0006811: ion transport, GO:0006829: zinc ion transport, GO:0030001: metal ion transport, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0008270: zinc ion binding, GO:0046873: metal ion transmembrane transporter activity		0.153	−0.0431	−0.223	−1.0873	11.06	11.85	12	11.81	11.63	10.76	4
213292_s_at	SNX13	sorting nexin 13	AA908770	23161	Hs.585343	GO:0007154: cell communication, GO:0007242: intracellular signaling cascade, GO:0009968: negative regulation of signal transduction, GO:0015031: protein transport, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0035091: phosphoinositide binding		0.221	0.0009	−0.2034	−1.1335	6.1	6.54	6.76	6.54	6.33	5.4	4

(*Continued*)

TABLE E2. (*Continued*)

209723_at	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	BC002538	5272	Hs.104879	GO:0006916: anti-apoptosis, GO:0007165: signal transduction, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding		0.2588	−0.0571	−0.3848	−1.5477	5.49	7.54	7.8	7.48	7.15	5.99	4
203535_at	S100A9	S100 calcium binding protein A9	NM_002965	6280	Hs.112405	GO:0006954: inflammatory response, GO:0007267: cell-cell signaling, GO:0030595: leukocyte chemotaxis, GO:0031532: actin cytoskeleton reorganization, GO:0045113: regulation of integrin biosynthetic process, GO:0005615: extracellular space, GO:0004871: signal transducer activity, GO:0005509: calcium ion binding		−0.0128	−0.1892	−1.1888	−3.5878	11.78	15.58	15.56	15.39	14.39	11.99	4
201571_s_at	DCTD	dCMP deaminase	AI656493	1635	Hs.183850	GO:0006220: pyrimidine nucleotide metabolic process, GO:0009165: nucleotide biosynthetic process, GO:0004132: dCMP deaminase activity, GO:0008270: zinc ion binding, GO:0016787: hydrolase activity, GO:0046872: metal ion binding	00240: Pyrimidine metabolism	0.0148	−0.0534	−0.3709	−1.2219	7.88	8.78	8.8	8.73	8.41	7.56	4
202918_s_at	MOBKL3	MOB1, Mps One Binder kinase activator-like 3 (yeast)	AF151853	25843	Hs.645458	GO:0006810: transport, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.0071	−0.0619	−0.3604	−1.0973	10.52	11.27	11.27	11.2	10.91	10.17	4
219850_s_at	EHF	ets homologous factor	AF203977	26298	Hs.502306	GO:0006350: transcription, GO:0007275: multicellular organismal development, GO:0008283: cell proliferation, GO:0030855: epithelial cell differentiation, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0043565: sequence-specific DNA binding		0.0322	−0.4067	−1.1961	−4.2465	7.44	10.62	10.65	10.21	9.42	6.37	4
201298_s_at	MOBKL1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	BC003398	55233	Hs.196437	GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0313	−0.1202	−0.4271	−1.4122	8.88	9.77	9.73	9.65	9.34	8.35	4
201504_s_at	TSN	translin	AI435302	7247	Hs.75066	GO:0006310: DNA recombination, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003723: RNA binding, GO:0005515: protein binding		0.0088	−0.1094	−0.3823	−1.3231	8.45	9.06	9.07	8.95	8.68	7.74	4
211801_x_at	MFN1	mitofusin 1	AF329637	55669	Hs.478383	GO:0008053: mitochondrial fusion, GO:0008150: biological_process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019867: outer membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding, GO:0016787: hydrolase activity		0.0074	−0.1766	−0.6596	−2.044	6.14	7.52	7.52	7.34	6.86	5.47	4

(*Continued*)

TABLE E2. (*Continued*)

205543_at	HSPA4L	heat shock 70kDa protein 4-like	NM_014278	22824	Hs.135554	GO:0006457: protein folding, GO:0006986: response to unfolded protein, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005524: ATP binding		0.0344	−0.24	−0.7248	−2.3519	7.07	8.54	8.57	8.3	7.82	6.19	4
206094_x_at	UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6	NM_001072	54578	Hs.654499	GO:0006805: xenobiotic metabolic process, GO:0008152: metabolic process, GO:0008152: metabolic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0015020: glucuronosyltransferase activity, GO:0016758: transferase activity, transferring hexosyl groups	00040: Pentose and glucuronate interconversions, 00150: Androgen and estrogen metabolism, 00500: Starch and sucrose metabolism, 00860: Porphyrin and chlorophyll metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	0.0274	−0.1273	−0.4316	−1.4074	7.85	8.72	8.75	8.59	8.29	7.31	4
218884_s_at	GUF1	GUF1 GTPase homolog (S. cerevisiae)	AK025248	60558	Hs.546419	GO:0006413: translational initiation, GO:0007264: small GTPase mediated signal transduction, GO:0005622: intracellular, GO:0000166: nucleotide binding, GO:0003743: translation initiation factor activity, GO:0003924: GTPase activity, GO:0005525: GTP binding		0.0105	0.0777	−0.487	−1.3282	6.22	6.95	6.96	7.03	6.46	5.62	4
213872_at	C6orf62	chromosome 6 open reading frame 62	BE465032	81688	Hs.519930	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0003674: molecular_function		−0.05	0.0391	−0.5373	−1.7245	10.2	11.19	11.14	11.23	10.65	9.47	4
217821_s_at	WBP11	WW domain binding protein 11	NM_016312	51729	Hs.655138	GO:0006364: rRNA processing, GO:0006397: mRNA processing, GO:0008380: RNA splicing, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003697: single-stranded DNA binding, GO:0005515: protein binding		−0.0844	0.0281	−0.3686	−1.0284	7.67	7.96	7.88	7.99	7.59	6.93	4
204941_s_at	ALDH3B2	aldehyde dehydrogenase 3 family, member B2	AA071510	222	Hs.87539	GO:0006066: alcohol metabolic process, GO:0006081: aldehyde metabolic process, GO:0006629: lipid metabolic process, GO:0008152: metabolic process, GO:0004028: 3-chloroallyl aldehyde dehydrogenase activity, GO:0004030: aldehyde dehydrogenase [NAD(P)+] activity, GO:0016491: oxidoreductase activity	00010: Glycolysis / Gluconeogenesis, 00340: Histidine metabolism, 00350: Tyrosine metabolism, 00360: Phenylalanine metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	0.1666	0.1366	−0.8137	−2.6849	7.2	9.02	9.18	9.15	8.2	6.33	4
209000_s_at	8-Sep	septin 8	BC001329	23176	Hs.533017	GO:0007049: cell cycle, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005525: GTP binding		−0.0364	0.0386	−0.3579	−1.097	7.85	8.34	8.3	8.38	7.98	7.24	4
203265_s_at	MAP2K4	mitogen-activated protein kinase kinase 4	NM_003010	6416	Hs.514681	GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007254: JNK cascade, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004713: protein-tyrosine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04012: ErbB signaling pathway, 04620: Toll-like receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 04912: GnRH signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection	0.1199	−0.0425	−0.3614	−1.6326	6.86	7.5	7.62	7.46	7.14	5.87	4

(*Continued*)

TABLE E2. (*Continued*)

210052_s_at	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	AF098158	22974	Hs.244580	GO:0007067: mitosis, GO:0008283: cell proliferation, GO:0000922: spindle pole, GO:0005634: nucleus, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005525: GTP binding		0.0478	−0.0621	−0.3118	−1.2144	6.69	7.86	7.9	7.79	7.54	6.64	4
201259_s_at	SYPL1	synaptophysin-like 1	AI768845	6856	Hs.80919	GO:0006810: transport, GO:0007268: synaptic transmission, GO:0005887: integral to plasma membrane, GO:0008021: synaptic vesicle, GO:0016020: membrane, GO:0031410: cytoplasmic vesicle, GO:0005215: transporter activity		0.0619	−0.037	−0.2656	−1.0632	10.82	11.36	11.42	11.32	11.09	10.29	4
202874_s_at	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	NM_001695	528	Hs.86905	GO:0006811: ion transport, GO:0015986: ATP synthesis coupled proton transport, GO:0015992: proton transport, GO:0016469: proton-transporting two-sector ATPase complex, GO:0005215: transporter activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008553: hydrogen-exporting ATPase activity, phosphorylative mechanism, GO:0016787: hydrolase activity, GO:0016820: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, GO:0046872: metal ion binding, GO:0046961: hydrogen ion transporting ATPase activity, rotational mechanism	00190: Oxidative phosphorylation, 05110: Cholera - Infection, 05120: Epithelial cell signaling in Helicobacter pylori infection	0.058	−0.0521	−0.3612	−1.2925	8.07	8.64	8.7	8.59	8.28	7.35	4
205916_at	S100A7	S100 calcium binding protein A7	NM_002963	6278	Hs.112408	GO:0000302: response to reactive oxygen species, GO:0001525: angiogenesis, GO:0008544: epidermis development, GO:0030216: keratinocyte differentiation, GO:0045087: innate immune response, GO:0050829: defense response to Gram-negative bacterium, GO:0051238: sequestering of metal ion, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0005829: cytosol, GO:0005925: focal adhesion, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0008270: zinc ion binding		0.0088	−0.0433	−0.4384	−1.5718	14.39	15.75	15.76	15.7	15.31	14.17	4

(*Continued*)

TABLE E2. (*Continued*)

208097_s_at	TXNDC1	thioredoxin domain containing 1	NM_030755	81542	Hs.125221, Hs.560285	GO:0006118: electron transport, GO:0006260: DNA replication, GO:0006810: transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0006916: anti-apoptosis, GO:0006950: response to stress, GO:0007165: signal transduction, GO:0008283: cell proliferation, GO:0045321: leukocyte activation, GO:0045454: cell redox homeostasis, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0045927: positive regulation of growth, GO:0005624: membrane fraction, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030508: thiol-disulfide exchange intermediate activity, GO:0030612: arsenate reductase (thioredoxin) activity		−0.0143	−0.0691	−0.6142	−2.2308	8.13	9.27	9.26	9.2	8.66	7.04	4
221497_x_at	EGLN1	egl nine homolog 1 (C. elegans)	BC005369	54583	Hs.444450	GO:0019538: protein metabolic process, GO:0005829: cytosol, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016491: oxidoreductase activity, GO:0016702: oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, GO:0016706: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors, GO:0031418: L-ascorbic acid binding, GO:0046872: metal ion binding	05211: Renal cell carcinoma	0.0075	0.0083	−0.3262	−1.1901	7.55	8.12	8.13	8.13	7.79	6.93	4
212763_at	CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	AW593213	23271	Hs.23585			0.0033	0.0018	−0.3524	−1.1448	4.58	5.51	5.51	5.51	5.16	4.36	4
215150_at	YOD1	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)	AF090896	55432	Hs.567533, Hs.689471	GO:0006512: ubiquitin cycle, GO:0006519: amino acid and derivative metabolic process, GO:0005622: intracellular, GO:0003676: nucleic acid binding, GO:0008234: cysteine-type peptidase activity, GO:0008270: zinc ion binding, GO:0016289: CoA hydrolase activity, GO:0046872: metal ion binding	00632: Benzoate degradation via CoA ligation, 00903: Limonene and pinene degradation	0.1517	0.0995	−0.8376	−3.2435	5.54	8.22	8.37	8.32	7.38	4.97	4
216652_s_at	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	AL137673	1810	Hs.348418	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003714: transcription corepressor activity, GO:0008134: transcription factor binding, GO:0043565: sequence-specific DNA binding		0.0972	0.0596	−0.3257	−1.2369	7.77	8.27	8.36	8.33	7.94	7.03	4

(*Continued*)

TABLE E2. (*Continued*)

221220 _s_at	SCYL2	SCY1-like 2 (S. cerevisiae)	NM_017988	55681	Hs.506481	GO:0006468: protein amino acid phosphorylation, GO:0005737: cytoplasm, GO:0005768: endosome, GO:0016020: membrane, GO:0031410: cytoplasmic vesicle, GO:0004672: protein kinase activity, GO:0005524: ATP binding		0.0596	0.0849	−0.3974	−1.5544	2.88	4.15	4.21	4.23	3.75	2.59	4
208596 _s_at	UGT1A3	UDP glucuronosyltransferase 1 family, polypeptide A3	NM_019093	54659	Hs.654499	GO:0008152: metabolic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0015020: glucuronosyltransferase activity	00040: Pentose and glucuronate interconversions, 00150: Androgen and estrogen metabolism, 00500: Starch and sucrose metabolism, 00860: Porphyrin and chlorophyll metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	−0.0738	−0.2369	−0.7772	−2.622	6.88	8.41	8.33	8.17	7.63	5.79	4
212194 _s_at	TM9SF4	transmembrane 9 superfamily protein member 4	AI418892	9777	Hs.654665	GO:0016020: membrane, GO:0016021: integral to membrane		0.0421	0.0202	−0.4006	−1.3964	7.98	8.77	8.81	8.79	8.37	7.37	4
220775 _s_at	UEVLD	UEV and lactate/malate dehyrogenase domains	NM_018314	55293	Hs.407991	GO:0006096: glycolysis, GO:0006100: tricarboxylic acid cycle intermediate metabolic process, GO:0006464: protein modification process, GO:0006512: ubiquitin cycle, GO:0015031: protein transport, GO:0016491: oxidoreductase activity, GO:0016616: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, GO:0019787: small conjugating protein ligase activity		−0.0245	0.0567	−0.3368	−1.393	8.91	9.27	9.24	9.32	8.93	7.87	4
202166 _s_at	PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2	NM_006241	5504	Hs.535731	GO:0005975: carbohydrate metabolic process, GO:0005977: glycogen metabolic process, GO:0006091: generation of precursor metabolites and energy, GO:0009966: regulation of signal transduction, GO:0043666: regulation of phosphoprotein phosphatase activity, GO:0004864: protein phosphatase inhibitor activity, GO:0004865: type 1 serine/threonine specific protein phosphatase inhibitor activity, GO:0005515: protein binding		−0.0056	0.0155	−0.2748	−1.2425	9.5	10.09	10.08	10.1	9.81	8.85	4
218340 _s_at	UBE1L2	ubiquitin-activating enzyme E1-like 2	NM_018227	55236	Hs.212774	GO:0006464: protein modification process, GO:0006512: ubiquitin cycle, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0008641: small protein activating enzyme activity, GO:0016874: ligase activity		−0.2661	−0.4135	−0.7029	−2.7123	5.93	7.76	7.49	7.34	7.05	5.04	4
210285 _x_at	WTAP	Wilms tumor 1 associated protein	BC000383	9589	Hs.446091	GO:0005634: nucleus, GO:0031965: nuclear membrane		−0.0447	−0.2034	−0.28	−1.1431	7.79	8.29	8.25	8.09	8.01	7.15	4
201130 _s_at	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	NM_004360	999	Hs.461086	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0007156: homophilic cell adhesion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0030054: cell junction, GO:0003674: molecular_function, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005515: protein binding	04514: Cell adhesion molecules (CAMs), 04520: Adherens junction, 05130: Pathogenic Escherichia coli infection - EHEC, 05131: Pathogenic Escherichia coli infection - EPEC, 05213: Endometrial cancer, 05216: Thyroid cancer, 05218: Melanoma, 05219: Bladder cancer	−0.1411	−0.5028	−0.5779	−2.3276	8.26	9.63	9.48	9.12	9.05	7.3	4

(*Continued*)

TABLE E2. (*Continued*)

208853_s_at	CANX	calnexin	L18887	821	Hs.567968	GO:0001525: angiogenesis, GO:0006457: protein folding, GO:0009306: protein secretion, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0005509: calcium ion binding, GO:0005529: sugar binding, GO:0051082: unfolded protein binding	04612: Antigen processing and presentation	−0.0917	−0.3054	−0.3442	−1.5132	9.49	10.3	10.2110	9.96	8.79	4
215236_s_at	PICALM	phosphatidylinositol binding clathrin assembly protein	AV721177	8301	Hs.163893	GO:0006461: protein complex assembly, GO:0006898: receptor-mediated endocytosis, GO:0048268: clathrin cage assembly, GO:0005905: coated pit, GO:0016020: membrane, GO:0030118: clathrin coat, GO:0031410: cytoplasmic vesicle, GO:0005543: phospholipid binding, GO:0005545: phosphatidylinositol binding, GO:0030276: clathrin binding		0.1151	−0.1503	−0.2711	−1.6428	8.57	9.29	9.4	9.14	9.02	7.65	4
217301_x_at	RBBP4	retinoblastoma binding protein 4	X71810	5928	Hs.647652	GO:0006260: DNA replication, GO:0006338: chromatin remodeling, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007049: cell cycle, GO:0008285: negative regulation of cell proliferation, GO:0005634: nucleus, GO:0005515: protein binding, GO:0008094: DNA-dependent ATPase activity		0.0378	−0.1829	−0.2395	−1.2619	9.2	9.76	9.8	9.58	9.52	8.5	4
216205_s_at	MFN2	mitofusin 2	AK021947	9927	Hs.376681	GO:0001825: blastocyst formation, GO:0006626: protein targeting to mitochondrion, GO:0007006: mitochondrial membrane organization and biogenesis, GO:0007050: cell cycle arrest, GO:0008053: mitochondrial fusion, GO:0046580: negative regulation of Ras protein signal transduction, GO:0048662: negative regulation of smooth muscle cell proliferation, GO:0051646: mitochondrion localization, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0005829: cytosol, GO:0015630: microtubule cytoskeleton, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019867: outer membrane, GO:0031306: intrinsic to mitochondrial outer membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0016787: hydrolase activity		0.0659	−0.0622	−0.2054	−1.1201	6.45	6.83	6.89	6.77	6.62	5.71	4

(*Continued*)

TABLE E2. (*Continued*)

216689_x_at	ARHGAP1	Rho GTPase activating protein 1	U62794	392	Hs.138860	GO:0007010: cytoskeleton organization and biogenesis, GO:0007165: signal transduction, GO:0007165: signal transduction, GO:0007264: small GTPase mediated signal transduction, GO:0007266: Rho protein signal transduction, GO:0043087: regulation of GTPase activity, GO:0001726: ruffle, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0005070: SH3/SH2 adaptor activity, GO:0005096: GTPase activator activity, GO:0005100: Rho GTPase activator activity, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0030675: Rac GTPase activator activity		0.05	−0.1646	−0.4117	−1.8301	6.36	7.13	7.18	6.97	6.72	5.3	4
206429_at	F2RL1	coagulation factor II (thrombin) receptor-like 1	NM_005242	2150	Hs.154299	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0007596: blood coagulation, GO:0005794: Golgi apparatus, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0005102: receptor binding, GO:0015057: thrombin receptor activity	04080: Neuroactive ligand-receptor interaction	0.1074	−0.2003	−0.4806	−1.9512	5.67	6.42	6.52	6.22	5.94	4.47	4
208351_s_at	MAPK1	mitogen-activated protein kinase 1	NM_002745	5594	Hs.431850	GO:0000165: MAPKKK cascade, GO:0006468: protein amino acid phosphorylation, GO:0006917: induction of apoptosis, GO:0006935: chemotaxis, GO:0006974: response to DNA damage stimulus, GO:0007049: cell cycle, GO:0007165: signal transduction, GO:0007268: synaptic transmission, GO:0009887: organ morphogenesis, GO:0019858: cytosine metabolic process, GO:0045596: negative regulation of cell differentiation, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0001784: phosphotyrosine binding, GO:0004674: protein serine/threonine kinase activity, GO:0004707: MAP kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04012: ErbB signaling pathway, 04150: mTOR signaling pathway, 04320: Dorso-ventral axis formation, 04350: TGF-beta signaling pathway, 04360: Axon guidance, 04370: VEGF signaling pathway, 04510: Focal adhesion, 04520: Adherens junction, 04540: Gap junction, 04620: Toll-like receptor signaling pathway, 04650: Natural killer cell mediated cytotoxicity, 04664: Fc epsilon RI signaling pathway, 04720: Long-term potentiation, 04730: Long-term depression, 04810: Regulation of actin cytoskeleton, 04910: Insulin signaling pathway, 04912: GnRH signaling pathway, 04916: Melanogenesis, 04930: Type II diabetes mellitus, 05210: Colorectal cancer, 05211: Renal cell carcinoma, 05212: Pancreatic cancer, 05213: Endometrial cancer, 05214: Glioma, 05215: Prostate cancer, 05216: Thyroid cancer, 05218: Melanoma, 05219: Bladder cancer, 05220: Chronic myeloid leukemia, 05221: Acute myeloid leukemia, 05223: Non-small cell lung cancer	−0.0805	−0.0279	−0.2907	−1.7159	6.71	7.4	7.31	7.37	7.1	5.68	4

(*Continued*)

TABLE E2. (*Continued*)

211194_s_at	TP63	tumor protein p63	AB010153	8626	Hs.137569	GO:0006350: transcription, GO:0006915: apoptosis, GO:0006917: induction of apoptosis, GO:0007219: Notch signaling pathway, GO:0007275: multicellular organismal development, GO:0045747: positive regulation of Notch signaling pathway, GO:0045892: negative regulation of transcription, DNA-dependent, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0051289: protein homotetramerization, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0016563: transcription activator activity, GO:0016563: transcription activator activity, GO:0016564: transcription repressor activity, GO:0042802: identical protein binding, GO:0046872: metal ion binding		0.1448	−0.1444	−0.4532	−2.193	10.06	11.1	11.24	10.95	10.64	8.9	4
211195_s_at	TP63	tumor protein p63	AF116771	8626	Hs.137569	GO:0006350: transcription, GO:0006915: apoptosis, GO:0006917: induction of apoptosis, GO:0007219: Notch signaling pathway, GO:0007275: multicellular organismal development, GO:0045747: positive regulation of Notch signaling pathway, GO:0045892: negative regulation of transcription, DNA-dependent, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0051289: protein homotetramerization, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0016563: transcription activator activity, GO:0016563: transcription activator activity, GO:0016564: transcription repressor activity, GO:0042802: identical protein binding, GO:0046872: metal ion binding		0.1443	−0.0387	−0.3234	−1.4609	4.93	6.15	6.3	6.11	5.83	4.69	4
212568_s_at	DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	BF978872	1737	Hs.335551	GO:0006085: acetyl-CoA biosynthetic process, GO:0006090: pyruvate metabolic process, GO:0006096: glycolysis, GO:0008152: metabolic process, GO:0005739: mitochondrion, GO:0005967: mitochondrial pyruvate dehydrogenase complex, GO:0045254: pyruvate dehydrogenase complex, GO:0004742: dihydrolipoyllysine-residue acetyltransferase activity, GO:0004742: dihydrolipoyllysine-residue acetyltransferase activity, GO:0005515: protein binding, GO:0008415: acyltransferase activity, GO:0016740: transferase activity, GO:0031405: lipoic acid binding	00010: Glycolysis / Gluconeogenesis, 00252: Alanine and aspartate metabolism, 00620: Pyruvate metabolism	−0.1657	−0.1189	−0.3516	−1.1231	8.85	9.18	9.02	9.07	8.83	8.06	4

(*Continued*)

TABLE E2. (*Continued*)

214553_s_at	ARPP-19	cyclic AMP phosphoprotein, 19 kD	NM_006628	10776	Hs.512908	GO:0045722: positive regulation of gluconeogenesis, GO:0046326: positive regulation of glucose import, GO:0005737: cytoplasm, GO:0005102: receptor binding, GO:0015459: potassium channel regulator activity		−0.1385	−0.0515	−0.3208	−1.1054	6.08	6.52	6.38	6.47	6.2	5.41	4
202816_s_at	SS18	synovial sarcoma translocation, chromosome 18	AW292882	6760	Hs.404263	GO:0005634: nucleus		0.1353	0.0402	−0.2388	−1.2543	9.3	9.75	9.88	9.79	9.51	8.49	4
211536_x_at	MAP3K7	mitogen-activated protein kinase kinase kinase 7	AB009358	6885	Hs.644143	GO:0002726: positive regulation of T cell cytokine production, GO:0006468: protein amino acid phosphorylation, GO:0007179: transforming growth factor beta receptor signaling pathway, GO:0007250: activation of NF-kappaB-inducing kinase, GO:0050852: T cell receptor signaling pathway, GO:0050870: positive regulation of T cell activation, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004674: protein serine/threonine kinase activity, GO:0004709: MAP kinase kinase kinase activity, GO:0004713: protein-tyrosine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04310: Wnt signaling pathway, 04520: Adherens junction, 04620: Toll-like receptor signaling pathway	−0.1153	−0.0642	−0.2552	−1.3168	8.2	8.48	8.36	8.42	8.22	7.16	4
202199_s_at	SRPK1	SFRS protein kinase 1	AW082913	6732	Hs.443861	GO:0000074: regulation of progression through cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0007059: chromosome segregation, GO:0007243: protein kinase cascade, GO:0008380: RNA splicing, GO:0030154: cell differentiation, GO:0050684: regulation of mRNA processing, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004674: protein serine/threonine kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0016740: transferase activity		0.1799	0.0391	−0.3046	−1.757	7.02	8.1	8.28	8.14	7.8	6.34	4
202543_s_at	GMFB	glia maturation factor, beta	BC005359	2764	Hs.151413	GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007399: nervous system development, GO:0005622: intracellular, GO:0003779: actin binding, GO:0004860: protein kinase inhibitor activity, GO:0004871: signal transducer activity, GO:0008047: enzyme activator activity, GO:0008083: growth factor activity		0.1226	0.0746	−0.4365	−2.1824	7.01	8.14	8.26	8.21	7.7	5.95	4
202917_s_at	S100A8	S100 calcium binding protein A8	NM_002964	6279	Hs.416073	GO:0006954: inflammatory response, GO:0005615: extracellular space, GO:0005509: calcium ion binding		−0.0399	−0.1209	−0.3883	−1.512	13.75	15.4	15.36	15.28	15.01	13.89	4

(*Continued*)

TABLE E2. (*Continued*)

204426_at	TMED2	transmembrane emp24 domain trafficking protein 2	NM_006815	10959	Hs.75914	GO:0006888: ER to Golgi vesicle-mediated transport, GO:0015031: protein transport, GO:0005792: microsome, GO:0005793: ER-Golgi intermediate compartment, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0031410: cytoplasmic vesicle, GO:0042589: zymogen granule membrane, GO:0005515: protein binding	−0.1171	−0.1579	−0.2962	−1.0513	10.51	11.16	11.05	11.01	10.87	10.11	4
201688_s_at	TPD52	tumor protein D52	BG389015	7163	Hs.368433	GO:0009653: anatomical structure morphogenesis, GO:0030183: B cell differentiation, GO:0046903: secretion, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0048471: perinuclear region of cytoplasm, GO:0005509: calcium ion binding, GO:0042803: protein homodimerization activity, GO:0046982: protein heterodimerization activity	−0.0639	−0.0873	−0.3038	−1.3749	10.01	10.38	10.32	10.3	10.08	9.01	4
201992_s_at	KIF5B	kinesin family member 5B	NM_004521	3799	Hs.644646	GO:0047496: vesicle transport along microtubule, GO:0005871: kinesin complex, GO:0005874: microtubule, GO:0048471: perinuclear region of cytoplasm, GO:0000166: nucleotide binding, GO:0003777: microtubule motor activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008017: microtubule binding	−0.1647	−0.2481	−0.3633	−1.657	6.11	6.97	6.8	6.72	6.61	5.31	4
201211_s_at	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	NM_001356	1654	Hs.380774	GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003723: RNA binding, GO:0004004: ATP-dependent RNA helicase activity, GO:0005524: ATP binding, GO:0016787: hydrolase activity	−0.2055	−0.1335	−0.4125	−2.3998	7.9	9.25	9.05	9.12	8.84	6.85	4
201485_s_at	RCN2	reticulocalbin 2, EF-hand calcium binding domain	BC004892	5955	Hs.79088	GO:0005783: endoplasmic reticulum, GO:0005509: calcium ion binding, GO:0005515: protein binding	−0.1097	−0.0525	−0.271	−1.048	9.23	9.74	9.63	9.69	9.47	8.69	4
200890_s_at	SSR1	signal sequence receptor, alpha (translocon-associated protein alpha)	NM_003144	6745	Hs.114033	GO:0006613: cotranslational protein targeting to membrane, GO:0008284: positive regulation of cell proliferation, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005048: signal sequence binding, GO:0005509: calcium ion binding	−0.0141	−0.1081	−0.287	−1.6995	8.91	9.73	9.72	9.63	9.45	8.04	4
200892_s_at	SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	BC000451	6434	Hs.533122	GO:0000398: nuclear mRNA splicing, via spliceosome, GO:0008380: RNA splicing, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0005515: protein binding, GO:0031202: RNA splicing factor activity, transesterification mechanism	−0.1172	−0.1617	−0.3193	−1.101	10.74	11.19	11.08	11.03	10.87	10.09	4
220800_s_at	TMOD3	tropomodulin 3 (ubiquitous)	NM_014547	29766	Hs.4998	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0008290: F-actin capping protein complex, GO:0003779: actin binding, GO:0005523: tropomyosin binding	0.0011	−0.136	−0.5237	−2.1787	7.37	8.63	8.63	8.49	8.1	6.45	4

(*Continued*)

TABLE E2. (*Continued*)

200607 _s_at	RAD21	RAD21 homolog (S. pombe)	BG289967	5885	Hs.81848	GO:0006302: double-strand break repair, GO:0006915: apoptosis, GO:0007001: chromosome organization and biogenesis (sensu Eukaryota), GO:0007049: cell cycle, GO:0007059: chromosome segregation, GO:0007067: mitosis, GO:0007131: meiotic recombination, GO:0051301: cell division, GO:0000228: nuclear chromosome, GO:0005515: protein binding		−0.1385	−0.1568	−0.3097	−1.1236	8.89	9.38	9.24	9.22	9.07	8.25	4
200641 _s_at	YWHAZ	tyrosine 3-monooxygenase/ tryptophan 5-monooxygenase activation protein, zeta polypeptide	BC003623	7534	Hs.492407	GO:0006605: protein targeting, GO:0006916: anti-apoptosis, GO:0007165: signal transduction, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0004497: monooxygenase activity, GO:0008134: transcription factor binding, GO:0019904: protein domain specific binding	04110: Cell cycle, 05130: Pathogenic Escherichia coli infection - EHEC, 05131: Pathogenic Escherichia coli infection - EPEC	−0.1944	−0.2327	−0.5526	−1.8978	11.76	12.65	12.45	12.41	12.09	10.75	4
218036 _x_at	NMD3	NMD3 homolog (S. cerevisiae)	AL520719	51068	Hs.656143			−0.0754	−0.1245	−0.2184	−1.1243	8.05	8.42	8.35	8.3	8.2	7.3	4
218474 _s_at	KCTD5	potassium channel tetramerisation domain containing 5	NM_018992	54442	Hs.61960	GO:0006813: potassium ion transport, GO:0008076: voltage-gated potassium channel complex, GO:0016020: membrane, GO:0005249: voltage-gated potassium channel activity, GO:0005515: protein binding		−0.103	−0.1082	−0.2711	−1.0779	8.39	9.14	9.04	9.04	8.87	8.07	4
213548 _s_at	CDV3	CDV3 homolog (mouse)	BG257762	55573	Hs.518265	GO:0008283: cell proliferation, GO:0005575: cellular_component, GO:0003674: molecular_function		−0.2239	−0.2873	−0.5872	−2.0866	6.05	7.33	7.1	7.04	6.74	5.24	4
215125 _s_at	UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6	AV691323	54578	Hs.654499	GO:0006805: xenobiotic metabolic process, GO:0008152: metabolic process, GO:0008152: metabolic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0015020: glucuronosyltransferase activity, GO:0016758: transferase activity, transferring hexosyl groups	00040: Pentose and glucuronate interconversions, 00150: Androgen and estrogen metabolism, 00500: Starch and sucrose metabolism, 00860: Porphyrin and chlorophyll metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	0.1116	−0.0153	−0.4807	−2.4149	7.53	8.76	8.87	8.74	8.28	6.34	4
212514 _x_at	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	R60068	1654	Hs.380774	GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003723: RNA binding, GO:0004004: ATP-dependent RNA helicase activity, GO:0005524: ATP binding, GO:0016787: hydrolase activity		−0.1015	−0.1963	−0.4006	−2.0439	9.59	10.59	10.49	10.4	10.19	8.55	4
212800 _at	STX6	syntaxin 6	AI740832	10228	Hs.518417	GO:0006886: intracellular protein transport, GO:0006906: vesicle fusion, GO:0007032: endosome organization and biogenesis, GO:0048193: Golgi vesicle transport, GO:0005769: early endosome, GO:0005794: Golgi apparatus, GO:0005802: trans-Golgi network, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0030136: clathrin-coated vesicle, GO:0048471: perinuclear region of cytoplasm, GO:0005515: protein binding, GO:0008565: protein transporter activity	04130: SNARE interactions in vesicular transport	−0.0695	−0.0682	−0.263	−1.1162	5.37	6.21	6.14	6.14	5.95	5.09	4

(*Continued*)

TABLE E2. (*Continued*)

210716_s_at	CLIP1	CAP-GLY domain containing linker protein 1	M97501	6249	Hs.524809	GO:0007067: mitosis, GO:0000776: kinetochore, GO:0005737: cytoplasm, GO:0005768: endosome, GO:0005874: microtubule, GO:0005882: intermediate filament, GO:0003676: nucleic acid binding, GO:0005515: protein binding, GO:0008017: microtubule binding, GO:0008270: zinc ion binding, GO:0042803: protein homodimerization activity, GO:0046872: metal ion binding		−0.184	−0.132	−0.3997	−1.5276	9.69	9.9	9.72	9.77	9.5	8.37	4
212107_s_at	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	BE561014	1660	Hs.191518	GO:0005622: intracellular, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003725: double-stranded RNA binding, GO:0004003: ATP-dependent DNA helicase activity, GO:0004004: ATP-dependent RNA helicase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016787: hydrolase activity		−0.1672	−0.1893	−0.5586	−1.7387	6.97	7.85	7.68	7.66	7.29	6.11	4
208750_s_at	ARF1	ADP-ribosylation factor 1	AF052179	375	Hs.286221	GO:0006888: ER to Golgi vesicle-mediated transport, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0016192: vesicle-mediated transport, GO:0005622: intracellular, GO:0005829: cytosol, GO:0005886: plasma membrane, GO:0012505: endomembrane system, GO:0030017: sarcomere, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005057: receptor signaling protein activity, GO:0005515: protein binding, GO:0005525: GTP binding	05110: Cholera - Infection	−0.1308	−0.1865	−0.3308	−1.1688	9.64	10.09	9.96	9.9	9.76	8.92	4
208867_s_at	CSNK1A1	casein kinase 1, alpha 1	AF119911	1452	Hs.529862, Hs.654547	GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0016055: Wnt receptor signaling pathway, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004681: casein kinase I activity, GO:0005524: ATP binding, GO:0016740: transferase activity	04310: Wnt signaling pathway, 04340: Hedgehog signaling pathway	−0.1007	−0.1357	−0.4342	−1.435	10.54	11.35	11.25	11.22	10.92	9.92	4
201768_s_at	CLINT1	clathrin interactor 1	BC004467	9685	Hs.644000	GO:0006897: endocytosis, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0031410: cytoplasmic vesicle, GO:0005515: protein binding, GO:0008289: lipid binding		−0.0148	−0.2075	−0.3852	−1.6027	8.65	9.49	9.48	9.28	9.11	7.89	4
202129_s_at	RIOK3	RIO kinase 3 (yeast)	AW006290	8780	Hs.445511	GO:0006468: protein amino acid phosphorylation, GO:0007059: chromosome segregation, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity		0.129	0.0515	−0.2825	−1.4456	8.82	9.57	9.69	9.62	9.28	8.12	4

(*Continued*)

TABLE E2. (*Continued*)

200722_s_at	CAPRIN1	cell cycle associated protein 1	BG258784	4076	Hs.471818	GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005515: protein binding, GO:0048503: GPI anchor binding		−0.029	−0.1344	−0.2534	−1.1667	8.66	9.32	9.29	9.19	9.07	8.15	4
201742_x_at	SFRS1	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	M69040	6426	Hs.68714	GO:0006376: mRNA splice site selection, GO:0006397: mRNA processing, GO:0008380: RNA splicing, GO:0005681: spliceosome, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005515: protein binding		−0.0056	−0.1147	−0.2645	−1.4632	10.63	11.18	11.17	11.06	10.91	9.71	4
214007_s_at	TWF1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	AW665024	5756	Hs.189075			−0.2256	−0.3955	−0.9266	−3.1629	8.29	9.98	9.75	9.58	9.05	6.81	4
215707_s_at	PRNP	prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)	AV725328	5621	Hs.472010, Hs.610285, Hs.657376	GO:0006878: cellular copper ion homeostasis, GO:0006979: response to oxidative stress, GO:0008152: metabolic process, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0005794: Golgi apparatus, GO:0005886: plasma membrane, GO:0016020: membrane, GO:0019898: extrinsic to membrane, GO:0045121: lipid raft, GO:0005507: copper ion binding, GO:0005515: protein binding, GO:0008017: microtubule binding, GO:0048503: GPI anchor binding	01510: Neurodegenerative Disorders, 05060: Prion disease	−0.0505	−0.0463	−0.3628	−1.6008	8.62	9.2	9.15	9.15	8.83	7.6	4
204427_s_at	TMED2	transmembrane emp24 domain trafficking protein 2	NM_006815	10959	Hs.75914	GO:0006888: ER to Golgi vesicle-mediated transport, GO:0015031: protein transport, GO:0005792: microsome, GO:0005793: ER-Golgi intermediate compartment, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0031410: cytoplasmic vesicle, GO:0042589: zymogen granule membrane, GO:0005515: protein binding		0.0171	−0.0803	−0.2002	−1.2403	10.4	10.9811	10.9	10.78	9.74	4
206383_s_at	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	NM_012297	9908	Hs.303676	GO:0006810: transport, GO:0007253: cytoplasmic sequestering of NF-kappaB, GO:0007265: Ras protein signal transduction, GO:0051028: mRNA transport, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0030159: receptor signaling complex scaffold activity		−0.1211	−0.1807	−0.2513	−1.0647	4.84	5.53	5.41	5.35	5.28	4.47	4
202270_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	NM_002053	2633	Hs.62661	GO:0006955: immune response, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding, GO:0005525: GTP binding		−0.0558	−0.1516	−0.4224	−1.5279	9.43	10.94	10.89	10.79	10.52	9.42	4
202583_s_at	RANBP9	RAN binding protein 9	NM_005493	10048	Hs.306242	GO:0006461: protein complex assembly, GO:0007020: microtubule nucleation, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005875: microtubule associated complex, GO:0005515: protein binding, GO:0008536: Ran GTPase binding		0.0076	−0.0558	−0.2885	−1.3032	8.98	9.72	9.72	9.66	9.43	8.41	4

(*Continued*)

TABLE E2. (*Continued*)

219399_at	LIN7C	lin-7 homolog C (C. elegans)	NM_018362	55327	Hs.91393	GO:0006887: exocytosis, GO:0007269: neurotransmitter secretion, GO:0015031: protein transport, GO:0005923: tight junction, GO:0016020: membrane, GO:0019717: synaptosome, GO:0030054: cell junction, GO:0045202: synapse, GO:0005515: protein binding		−0.1449	−0.2124	−0.329	−1.547	8.13	9.04	8.9	8.83	8.72	7.5	4
221770_at	RPE	ribulose-5-phosphate-3-epimerase	BE964473	6120	Hs.282260	GO:0005975: carbohydrate metabolic process, GO:0008152: metabolic process, GO:0004750: ribulose-phosphate 3-epimerase activity, GO:0005515: protein binding, GO:0016853: isomerase activity	00030: Pentose phosphate pathway, 00040: Pentose and glucuronate interconversions, 00710: Carbon fixation	−0.039	−0.0993	−0.2635	−1.1471	8.39	8.78	8.74	8.68	8.52	7.64	4
208840_s_at	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	AB014560	9908	Hs.303676	GO:0006810: transport, GO:0007253: cytoplasmic sequestering of NF-kappaB, GO:0007265: Ras protein signal transduction, GO:0051028: mRNA transport, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0030159: receptor signaling complex scaffold activity		−0.1258	−0.165	−0.1875	−1.0589	8.35	8.7	8.57	8.53	8.51	7.64	4
209895_at	PTPN11	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	AF119855	5781	Hs.506852, Hs.646231	GO:0006470: protein amino acid dephosphorylation, GO:0007242: intracellular signaling cascade, GO:0007605: sensory perception of sound, GO:0005737: cytoplasm, GO:0004726: non-membrane spanning protein tyrosine phosphatase activity, GO:0005515: protein binding, GO:0016787: hydrolase activity	04630: Jak-STAT signaling pathway, 04650: Natural killer cell mediated cytotoxicity, 04670: Leukocyte transendothelial migration, 04920: Adipocytokine signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection, 05211: Renal cell carcinoma, 05220: Chronic myeloid leukemia	−0.1054	−0.1387	−0.1733	−1.2662	8.28	8.67	8.56	8.53	8.49	7.4	4
213461_at	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	AI800983	11051	Hs.528834	GO:0006397: mRNA processing, GO:0005813: centrosome, GO:0042382: paraspeckles, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0016787: hydrolase activity		−0.1216	−0.1117	−0.1896	−1.4498	6.43	7.02	6.9	6.91	6.83	5.57	4
214975_s_at	MTMR1	myotubularin related protein 1	AK001816	8776	Hs.347187	GO:0046839: phospholipid dephosphorylation, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0004438: phosphatidylinositol-3-phosphatase activity, GO:0004721: phosphoprotein phosphatase activity, GO:0016787: hydrolase activity	00051: Fructose and mannose metabolism, 00530: Aminosugars metabolism, 00730: Thiamine metabolism, 00740: Riboflavin metabolism, 00760: Nicotinate and nicotinamide metabolism	0.2873	0.1081	−0.3645	−2.2841	5.59	7.09	7.37	7.2	6.72	4.8	4
215177_s_at	ITGA6	integrin, alpha 6	AV733308	3655	Hs.133397	GO:0007044: cell-substrate junction assembly, GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0008305: integrin complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0005509: calcium ion binding, GO:0005515: protein binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 04514: Cell adhesion molecules (CAMs), 04640: Hematopoietic cell lineage, 04810: Regulation of actin cytoskeleton, 05222: Small cell lung cancer	−0.1726	−0.2428	−0.1296	−1.2122	9.74	9.9	9.72	9.65	9.77	8.68	4

(*Continued*)

TABLE E2. (*Continued*)

204533_at	CXCL10	chemokine (C-X-C motif) ligand 10	NM_001565	3627	Hs.632586	GO:0006928: cell motility, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007166: cell surface receptor linked signal transduction, GO:0007267: cell-cell signaling, GO:0007517: muscle development, GO:0008015: circulation, GO:0008284: positive regulation of cell proliferation, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0008009: chemokine activity, GO:0008603: cAMP-dependent protein kinase regulator activity	04060: Cytokine-cytokine receptor interaction, 04620: Toll-like receptor signaling pathway	−0.5086	−0.7881	−0.6776	−2.3964	4.51	6.6	6.09	5.81	5.93	4.21	4
205763_s_at	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	NM_006773	8886	Hs.363492	GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003723: RNA binding, GO:0004004: ATP-dependent RNA helicase activity, GO:0004386: helicase activity, GO:0005524: ATP binding, GO:0016787: hydrolase activity	00500: Starch and sucrose metabolism, 00790: Folate biosynthesis	−0.2195	−0.2687	−0.3474	−1.2153	8.45	8.86	8.64	8.59	8.51	7.64	4
200769_s_at	MAT2A	methionine adenosyltransferase II, alpha	BC001686	4144	Hs.516157	GO:0006556: S-adenosylmethionine biosynthetic process, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004478: methionine adenosyltransferase activity, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0030955: potassium ion binding, GO:0050897: cobalt ion binding		−0.2727	−0.3982	−0.3271	−1.4449	5.64	6.26	5.98	5.86	5.93	4.81	4
201169_s_at	BHLHB2	basic helix-loop-helix domain containing, class B, 2	BG326045	8553	Hs.171825	GO:0045892: negative regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0016564: transcription repressor activity	04710: Circadian rhythm	−0.5403	−0.7042	−0.8668	−2.6662	6.24	7.95	7.41	7.24	7.08	5.28	4

Fold change >2 for any time point; FDR <0.05.

TABLE E3. Genes up-regulated by etanercept in responders

R_1vs0	Log2 Fold change between Wk1 vs Wk0 in Responders
R_2vs0	Log2 Fold change between Wk2 vs Wk0 in Responders
R_4vs0	Log2 Fold change between Wk4 vs Wk0 in Responders
R_12vs0	Log2 Fold change between Wk12 vs Wk0 in Responders
R_NL	Mean expression value estimate (Log2) for Responders in NL skin
R_0	Mean expression value estimate (Log2) for Responders in LS skin
R_1	Mean expression value estimate (Log2) for Responders in LS at Wk 1
R_2	Mean expression value estimate (Log2) for Responders in LS at Wk 2
R_4	Mean expression value estimate (Log2) for Responders in LS at Wk 4
R_12	Mean expression value estimate (Log2) for Responders in LS at Wk 12
Cluster	Final cluster membership

Probe	Symbol	Description	GenBank	Gene	UniGene	Gene Ontology	Pathway	R_1vs0	R_2vs0	R_4vs0	R_12vs0	R_0	R_1	R_2	R_4	R_12	R_NL	Cluster
205969_at	AADAC	arylacetamide deacetylase (esterase)	NM_001086	13	Hs.506908	GO:0008152: metabolic process, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016298: lipase activity, GO:0019213: deacetylase activity	00623: 2,4-Dichlorobenzoate degradation, 00650: Butanoate metabolism, 00960: Alkaloid biosynthesis II	0.6946	2.3491	2.3105	1.5177	4.93	5.62	7.28	7.24	6.44	6.75	1
209686_at	S100B	S100 calcium binding protein B	BC001766	6285	Hs.422181	GO:0007409: axonogenesis, GO:0007417: central nervous system development, GO:0007613: memory, GO:0008283: cell proliferation, GO:0048168: regulation of neuronal synaptic plasticity, GO:0001726: ruffle, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005737: cytoplasm, GO:0043025: cell soma, GO:0005509: calcium ion binding, GO:0008270: zinc ion binding, GO:0042803: protein homodimerization activity, GO:0042803: protein homodimerization activity, GO:0048154: S100 beta binding, GO:0048156: tau protein binding, GO:0048306: calcium-dependent protein binding		0.9129	1.4494	1.1334	1.0801	5.83	6.74	7.28	6.96	6.91	6.86	1
221019_s_at	COLEC12	collectin sub-family member 12	NM_030781	81035	Hs.464422	GO:0006817: phosphate transport, GO:0006910: phagocytosis, recognition, GO:0009756: carbohydrate mediated signaling, GO:0045087: innate immune response, GO:0045194: oxidized low-density lipoprotein catabolic process, GO:0051260: protein homooligomerization, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0005044: scavenger receptor activity, GO:0005529: sugar binding, GO:0005534: galactose binding, GO:0008329: pattern recognition receptor activity, GO:0030169: low-density lipoprotein binding		0.8762	1.0981	1.6087	0.8905	7.03	7.9	8.12	8.64	7.92	8.61	1
218858_at	DEPDC6	DEP domain containing 6	NM_022783	64798	Hs.112981	GO:0007242: intracellular signaling cascade, GO:0005622: intracellular, GO:0005515: protein binding		0.7396	0.8726	1.1246	0.6956	6.3	7.04	7.17	7.42	6.99	7.37	1
205987_at	CD1C	CD1c molecule	NM_001765	911	Hs.132448	GO:0006955: immune response, GO:0019882: antigen processing and presentation, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane	04640: Hematopoietic cell lineage	1.6996	1.6476	1.9783	1.4909	5.8	7.5	7.45	7.78	7.29	6.5	1
201417_at	SOX4	SRY (sex determining region Y)-box 4	AL136179	6659	Hs.643910	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0031017: exocrine pancreas development, GO:0005634: nucleus, GO:0003700: transcription factor activity		0.9705	1.0279	1.1597	0.8633	9.7	10.67	10.73	10.86	10.57	10.64	1
203910_at	ARHGAP29	Rho GTPase activating protein 29	NM_004815	9411	Hs.483238	GO:0007242: intracellular signaling cascade, GO:0007266: Rho protein signal transduction, GO:0005622: intracellular, GO:0005100: Rho GTPase activator activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.7578	0.8674	1.0246	0.6889	10.01	10.76	10.87	11.03	10.69	10.74	1
204112_s_at	HNMT	histamine N-methyltransferase	NM_006895	3176	Hs.42151	GO:0007585: respiratory gaseous exchange, GO:0005737: cytoplasm, GO:0008168: methyltransferase activity, GO:0016740: transferase activity, GO:0046539: histamine N-methyltransferase activity	00340: Histidine metabolism	0.7168	0.7092	1.0217	0.6092	8.41	9.12	9.11	9.43	9.01	9.53	1

(Continued)

TABLE E3. (*Continued*)

213566_at	RNASE6	ribonuclease, RNase A family, k6	NM_005615	6039	Hs.23262, Hs.694217	GO:0006401: RNA catabolic process, GO:0006952: defense response, GO:0005576: extracellular region, GO:0003676: nucleic acid binding, GO:0004519: endonuclease activity, GO:0004522: pancreatic ribonuclease activity, GO:0004540: ribonuclease activity, GO:0016787: hydrolase activity		1.129	0.8721	1.0274	0.0021	4.89	6.02	5.76	5.92	4.89	4.74	1
211712_s_at	ANXA9	annexin A9	BC005830	8416	Hs.653223	GO:0016337: cell-cell adhesion, GO:0005829: cytosol, GO:0009986: cell surface, GO:0001786: phosphatidylserine binding, GO:0005509: calcium ion binding, GO:0005544: calcium-dependent phospholipid binding, GO:0015464: acetylcholine receptor activity, GO:0042803: protein homodimerization activity		0.9369	1.021	0.8568	0.2528	8.65	9.58	9.67	9.5	8.9	8.66	1
213456_at	SOSTDC1	sclerostin domain containing 1	AI927000	25928	Hs.648106	GO:0007389: pattern specification process, GO:0016055: Wnt receptor signaling pathway, GO:0030514: negative regulation of BMP signaling pathway, GO:0042475: odontogenesis (sensu Vertebrata), GO:0005615: extracellular space, GO:0005515: protein binding		1.0746	1.5664	1.2368	0.7369	9	10.08	10.57	10.24	9.74	9.27	1
211548_s_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	J05594	3248	Hs.655491	GO:0006629: lipid metabolic process, GO:0006631: fatty acid metabolic process, GO:0006693: prostaglandin metabolic process, GO:0007179: transforming growth factor beta receptor signaling pathway, GO:0007565: female pregnancy, GO:0007567: parturition, GO:0008152: metabolic process, GO:0019372: lipoxygenase pathway, GO:0045786: negative regulation of progression through cell cycle, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0004957: prostaglandin E receptor activity, GO:0016404: 15-hydroxyprostaglandin dehydrogenase (NAD+) activity, GO:0016404: 15-hydroxyprostaglandin dehydrogenase (NAD+) activity, GO:0016491: oxidoreductase activity, GO:0042803: protein homodimerization activity, GO:0051287: NAD binding		0.808	1.0461	1.0983	0.1871	9.42	10.23	10.47	10.52	9.61	9.91	1
215784_at	CD1E	CD1e molecule	AA309511	913	Hs.249217	GO:0006955: immune response, GO:0006955: immune response, GO:0019882: antigen processing and presentation, GO:0005887: integral to plasma membrane, GO:0016020: membrane	04640: Hematopoietic cell lineage		1.3982	1.5256	1.9083	0.6174	5.27	6.67	6.8	7.18	5.89	5.29	1
203914_x_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	NM_000860	3248	Hs.655491	GO:0006629: lipid metabolic process, GO:0006631: fatty acid metabolic process, GO:0006693: prostaglandin metabolic process, GO:0007179: transforming growth factor beta receptor signaling pathway, GO:0007565: female pregnancy, GO:0007567: parturition, GO:0008152: metabolic process, GO:0019372: lipoxygenase pathway, GO:0045786: negative regulation of progression through cell cycle, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0004957: prostaglandin E receptor activity, GO:0016404: 15-hydroxyprostaglandin dehydrogenase (NAD+) activity, GO:0016404: 15-hydroxyprostaglandin dehydrogenase (NAD+) activity, GO:0016491: oxidoreductase activity, GO:0042803: protein homodimerization activity, GO:0051287: NAD binding		0.7698	1.0051	1.0689	0.3592	9.74	10.51	10.74	10.81	10.1	10.32	1
217889_s_at	CYBRD1	cytochrome b reductase 1	AL136693	79901	Hs.221941	GO:0006118: electron transport, GO:0016021: integral to membrane, GO:0000293: ferric-chelate reductase activity			0.7975	1.3357	1.4983	0.6172	6.29	7.09	7.63	7.79	6.91	7.86	1

(*Continued*)

TABLE E3. (*Continued*)

203300_x_at	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	NM_003916	8905	Hs.656471	GO:0006461: protein complex assembly, GO:0006886: intracellular protein transport, GO:0006897: endocytosis, GO:0016192: vesicle-mediated transport, GO:0005794: Golgi apparatus, GO:0005886: plasma membrane, GO:0030117: membrane coat, GO:0030130: clathrin coat of trans-Golgi network vesicle, GO:0030131: clathrin adaptor complex, GO:0031410: cytoplasmic vesicle, GO:0005515: protein binding, GO:0008565: protein transporter activity	0.8001	0.7533	1.3327	0.4195	6.75	7.55	7.51	8.09	7.17	7.38	1
207173_x_at	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	D21254	1009	Hs.116471	GO:0001503: ossification, GO:0007156: homophilic cell adhesion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding	0.504	0.7234	1.3174	0.4973	8.6	9.11	9.33	9.92	9.1	9.17	1
212385_at	TCF4	transcription factor 4	AU118026	6925	Hs.644653	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0005667: transcription factor complex, GO:0003700: transcription factor activity, GO:0003714: transcription corepressor activity, GO:0008013: beta-catenin binding, GO:0046982: protein heterodimerization activity	0.3986	0.5682	1.0272	0.3707	7.54	7.94	8.11	8.57	7.91	8	1
214830_at	SLC38A6	solute carrier family 38, member 6	AI537540	145389	Hs.200738		0.7012	0.5981	1.1843	0.2745	4.87	5.57	5.47	6.05	5.14	5.5	1
207172_s_at	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	D21254	1009	Hs.116471	GO:0001503: ossification, GO:0007156: homophilic cell adhesion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding	0.4064	0.8099	1.233	0.1582	5.47	5.88	6.28	6.71	5.63	5.84	1
210875_s_at	ZEB1	zinc finger E-box binding homeobox 1	U12170	6935	Hs.124503	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006955: immune response, GO:0007417: central nervous system development, GO:0008283: cell proliferation, GO:0048598: embryonic morphogenesis, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0003713: transcription coactivator activity, GO:0003714: transcription corepressor activity, GO:0008270: zinc ion binding, GO:0008270: zinc ion binding, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding	0.5415	0.9803	1.4628	0.5595	6.01	6.55	6.99	7.47	6.57	7.03	1
212956_at	TBC1D9	TBC1 domain family, member 9 (with GRAM domain)	AI348094	23158	Hs480819, Hs.694161	GO:0032313: regulation of Rab GTPase activity, GO:0005622: intracellular, GO:0005096: GTPase activator activity, GO:0005097: Rab GTPase activator activity, GO:0005509: calcium ion binding	0.7524	0.7398	1.0599	0.4836	7.86	8.61	8.6	8.92	8.35	8.71	1
213415_at	CLIC2	chloride intracellular channel 2	AI768628	1193	Hs.655445	GO:0006811: ion transport, GO:0006821: chloride transport, GO:0007165: signal transduction, GO:0005622: intracellular, GO:0005624: membrane fraction, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0005244: voltage-gated ion channel activity, GO:0005247: voltage-gated chloride channel activity, GO:0031404: chloride ion binding	0.7773	0.7059	1.1724	0.4646	6.25	7.03	6.95	7.42	6.71	6.86	1

(*Continued*)

TABLE E3. (*Continued*)

207265_s_at	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	NM_016657	11015	Hs.693805	GO:0006621: protein retention in ER, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0015031: protein transport, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0046923: ER retention sequence binding		0.0646	0.3951	1.0348	0.6386	6.13	6.19	6.52	7.16	6.76	6.27	2
210261_at	KCNK2	potassium channel, subfamily K, member 2	AF004711	3776	Hs.497745	GO:0006811: ion transport, GO:0006813: potassium ion transport, GO:0006813: potassium ion transport, GO:0016020: membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005216: ion channel activity, GO:0005244: voltage-gated ion channel activity, GO:0005267: potassium channel activity, GO:0015271: outward rectifier potassium channel activity, GO:0030955: potassium ion binding		0.0241	0.3756	1.0445	0.5487	2.39	2.42	2.77	3.44	2.94	2.75	2
202311_s_at	COL1A1	collagen, type I, alpha 1	AI743621	1277	Hs.172928	GO:0001501: skeletal development, GO:0006817: phosphate transport, GO:0007605: sensory perception of sound, GO:0008544: epidermis development, GO:0005581: collagen, GO:0005584: collagen type I, GO:0005737: cytoplasm, GO:0005201: extracellular matrix structural constituent, GO:0005515: protein binding, GO:0008147: structural constituent of bone	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.1464	0.689	1.5289	0.7797	12.51	12.66	13.2	14.04	13.29	12.09	2
203325_s_at	COL5A1	collagen, type V, alpha 1	AI130969	1289	Hs.210283	GO:0006817: phosphate transport, GO:0007155: cell adhesion, GO:0005581: collagen, GO:0005588: collagen type V, GO:0005737: cytoplasm, GO:0005201: extracellular matrix structural constituent, GO:0008201: heparin binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.2656	0.7499	1.5682	0.9564	9.78	10.04	10.53	11.34	10.73	10.06	2
214163_at	C1orf41	chromosome 1 open reading frame 41	AV700696	51668	Hs.525462, Hs.624686	GO:0007155: cell adhesion		0.1566	0.3959	1.1648	0.5198	3.37	3.53	3.77	4.54	3.89	4.29	2
207496_at	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)	NM_000139	2206	Hs.386748	GO:0006959: humoral immune response, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0008283: cell proliferation, GO:0005887: integral to plasma membrane, GO:0009897: external side of plasma membrane, GO:0016020: membrane, GO:0004872: receptor activity, GO:0005262: calcium channel activity, GO:0019863: IgE binding	04664: Fc epsilon RI signaling pathway	0.3362	0.5066	1.66	0.9094	3.57	3.91	4.08	5.23	4.48	5.05	2
213959_s_at	RPGRIP1L	RPGRIP1-like	BF515597	23322	Hs.298382			0.0335	0.3772	1.0996	0.4938	2.89	2.92	3.26	3.98	3.38	3.45	2
202319_at	SENP6	SUMO1/sentrin specific peptidase 6	NM_015571	26054	Hs.485784	GO:0006508: proteolysis, GO:0006512: ubiquitin cycle, GO:0008234: cysteine-type peptidase activity		0.0859	0.3071	1.1235	0.2905	3.81	3.9	4.12	4.94	4.1	4.87	2
209012_at	TRIO	triple functional domain (PTPRF interacting)	AV718192	7204	Hs.130031	GO:0006468: protein amino acid phosphorylation, GO:0007185: transmembrane receptor protein tyrosine phosphatase signaling pathway, GO:0035023: regulation of Rho protein signal transduction, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0005524: ATP binding, GO:0016740: transferase activity		0.2049	0.4886	1.0956	0.4639	6.67	6.88	7.16	7.77	7.13	7.56	2
221730_at	COL5A2	collagen, type V, alpha 2	AL575735	1290	Hs.445827	GO:0006817: phosphate transport, GO:0030199: collagen fibril organization, GO:0043588: skin development, GO:0005581: collagen, GO:0005588: collagen type V, GO:0005737: cytoplasm, GO:0005201: extracellular matrix structural constituent	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.3095	0.6073	1.2926	0.7929	9.82	10.13	10.43	11.11	10.61	9.67	2

(*Continued*)

TABLE E3. (*Continued*)

202664_at	WIPF1	WAS/WASL interacting protein family, member 1	AW058622	7456	Hs.654521	GO:0006461: protein complex assembly, GO:0008154: actin polymerization and/or depolymerization, GO:0030048: actin filament-based movement, GO:0005737: cytoplasm, GO:0015629: actin cytoskeleton, GO:0031410: cytoplasmic vesicle, GO:0003779: actin binding, GO:0005522: profilin binding		0.4397	0.4124	1.035	0.6953	9.03	9.47	9.45	10.07	9.73	9.48	2
204114_at	NID2	nidogen 2 (osteonidogen)	NM_007361	22795	Hs.369840	GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0008218: bioluminescence, GO:0018298: protein-chromophore linkage, GO:0005604: basement membrane, GO:0016020: membrane, GO:0005509: calcium ion binding, GO:0005518: collagen binding		0.5552	0.4639	1.2036	0.8644	6.77	7.33	7.24	7.98	7.64	7.05	2
212489_at	COL5A1	collagen, type V, alpha 1	AI983428	1289	Hs.210283	GO:0006817: phosphate transport, GO:0007155: cell adhesion, GO:0005581: collagen, GO:0005588: collagen type V, GO:0005737: cytoplasm, GO:0005201: extracellular matrix structural constituent, GO:0008201: heparin binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.2519	0.6482	1.4412	0.8988	9.73	9.98	10.38	11.17	10.63	9.8	2
221729_at	COL5A2	collagen, type V, alpha 2	AL575735	1290	Hs.445827	GO:0006817: phosphate transport, GO:0030199: collagen fibril organization, GO:0043588: skin development, GO:0005581: collagen, GO:0005588: collagen type V, GO:0005737: cytoplasm, GO:0005201: extracellular matrix structural constituent	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.2568	0.5386	1.2408	0.7385	11.36	11.61	11.9	12.6	12.1	11.24	2
215446_s_at	LOX	lysyl oxidase	L16895	4015	Hs.102267	GO:0001568: blood vessel development, GO:0006464: protein modification process, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0030199: collagen fibril organization, GO:0030324: lung development, GO:0048251: elastic fiber assembly, GO:0005581: collagen, GO:0004720: protein-lysine 6-oxidase activity, GO:0005507: copper ion binding, GO:0005515: protein binding, GO:0016491: oxidoreductase activity, GO:0046872: metal ion binding		0.8052	1.2781	2.0344	1.2243	8.74	9.55	10.02	10.78	9.97	9.98	2
218006_s_at	ZNF22	zinc finger protein 22 (KOX 15)	AA744771	7570	Hs.462693, Hs.655124	GO:0006355: regulation of transcription, DNA-dependent, GO:0042476: odontogenesis, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.4093	0.7462	1.2312	0.7572	3.87	4.28	4.61	5.1	4.63	4.93	2
203988_s_at	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	NM_004480	2530	Hs.654961	GO:0001701: in utero embryonic development, GO:0006491: N-glycan processing, GO:0009312: oligosaccharide biosynthetic process, GO:0042355: L-fucose catabolic process, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0008424: glycoprotein 6-alpha-L-fucosyltransferase activity, GO:0016757: transferase activity, transferring glycosyl groups	00510: N-Glycan biosynthesis, 00533: Keratan sulfate biosynthesis, 01030: Glycan structures - biosynthesis 1	0.3706	0.4839	1.1287	0.7419	5.24	5.61	5.72	6.37	5.98	5.66	2
213304_at	KIAA0423	KIAA0423	AI823592	23116	Hs.371078	GO:0005488: binding		0.4479	0.6031	1.0662	0.7402	7.26	7.7	7.86	8.32	8	8.31	2
209568_s_at	RGL1	ral guanine nucleotide dissociation stimulator-like 1	AF186779	23179	Hs.497148	GO:0007165: signal transduction, GO:0051056: regulation of small GTPase mediated signal transduction, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005515: protein binding, GO:0008321: Ral guanyl-nucleotide exchange factor activity		0.834	0.7897	1.0629	0.9591	7.39	8.23	8.18	8.46	8.35	7.92	2
211734_s_at	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	BC005912	2205	Hs.897	GO:0006955: immune response, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0004872: receptor activity, GO:0005057: receptor signaling protein activity, GO:0019863: IgE binding	04664: Fc epsilon RI signaling pathway	1.0189	1.4043	1.5905	1.1614	8.75	9.77	10.16	10.34	9.91	9.65	2

(*Continued*)

TABLE E3. (*Continued*)

215536_at	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	X87344	3120	Hs.409934	GO:0002504: antigen processing and presentation of peptide or polysaccharide antigen via MHC class II, GO:0006955: immune response, GO:0006955: immune response, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0042613: MHC class II protein complex, GO:0042613: MHC class II protein complex, GO:0032395: MHC class II receptor activity	04514: Cell adhesion molecules (CAMs), 04612: Antigen processing and presentation, 04940: Type I diabetes mellitus	1.3182	1.9016	1.88	1.7926	7.94	9.26	9.85	9.82	9.74	9.62	2
203485_at	RTN1	reticulon 1	NM_021136	6252	Hs.368626	GO:0007165: signal transduction, GO:0030182: neuron differentiation, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030176: integral to endoplasmic reticulum membrane, GO:0004871: signal transducer activity		1.1126	1.423	1.8453	1.5017	4.9	6.01	6.32	6.75	6.4	6.1	2
210325_at	CD1A	CD1a molecule	M28825	909	Hs.1309	GO:0006955: immune response, GO:0019882: antigen processing and presentation, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0042612: MHC class I protein complex	04640: Hematopoietic cell lineage	2.0744	2.8715	3.0835	2.7522	5.68	7.76	8.55	8.77	8.43	8.52	2
218633_x_at	ABHD10	abhydrolase domain containing 10	NM_018394	55347	Hs.477115	GO:0006725: aromatic compound metabolic process, GO:0005739: mitochondrion, GO:0004252: serine-type endopeptidase activity, GO:0008233: peptidase activity		0.7579	0.9052	1.1016	0.9535	5.86	6.62	6.77	6.96	6.81	7.1	2
220124_at	GAN	giant axonal neuropathy (gigaxonin)	NM_022041	8139	Hs.112569	GO:0008150: biological_process, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005883: neurofilament, GO:0003674: molecular_function, GO:0005515: protein binding		0.5309	0.7288	1.0105	0.7727	5.67	6.2	6.4	6.68	6.45	6.56	2
209485_s_at	OSBPL1A	oxysterol binding protein-like 1A	AF274714	114876	Hs.370725	GO:0006869: lipid transport, GO:0008202: steroid metabolic process, GO:0008203: cholesterol metabolic process, GO:0016192: vesicle-mediated transport, GO:0005622: intracellular, GO:0005543: phospholipid binding		0.6427	0.9957	1.1548	0.9989	7.11	7.75	8.1	8.26	8.11	8.29	2
213186_at	DZIP3	zinc finger DAZ interacting protein 3	BG502305	9666	Hs.409210	GO:0000209: protein polyubiquitination, GO:0006512: ubiquitin cycle, GO:0005737: cytoplasm, GO:0003723: RNA binding, GO:0004842: ubiquitin-protein ligase activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016874: ligase activity, GO:0031593: polyubiquitin binding, GO:0046872: metal ion binding	00380: Tryptophan metabolism	0.6158	0.7003	1.001	0.7215	5.47	6.08	6.17	6.47	6.19	6.36	2
218901_at	PLSCR4	phospholipid scramblase 4	NM_020353	57088	Hs.477869	GO:0007596: blood coagulation, GO:0017121: phospholipid scrambling, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0017128: phospholipid scramblase activity		0.8013	0.9826	1.3608	1.0329	9.18	9.98	10.16	10.54	10.21	10.38	2
201990_s_at	CREBL2	cAMP responsive element binding protein-like 2	NM_001310	1389	Hs.591156	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity		0.7174	0.7508	1.0391	0.8167	8.42	9.14	9.17	9.46	9.24	9.58	2
206637_at	P2RY14	purinergic receptor P2Y, G-protein coupled, 14	NM_014879	9934	Hs.2465	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0045028: purinergic nucleotide receptor activity, G-protein coupled, GO:0045029: UDP-activated nucleotide receptor activity	04080: Neuroactive ligand-receptor interaction	0.7026	0.9866	1.3276	1.0676	7.45	8.15	8.43	8.78	8.52	8.67	2

(*Continued*)

TABLE E3. (*Continued*)

218005_at	ZNF22	zinc finger protein 22 (KOX 15)	AA744771	7570	Hs.462693, Hs.655124	GO:0006355: regulation of transcription, DNA-dependent, GO:0042476: odontogenesis, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.6915	0.984	1.345	1.0043	6.24	6.93	7.22	7.58	7.24	7.46	2
210198_s_at	PLP1	proteolipid protein 1 (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated)	BC002665	5354	Hs.1787	GO:0007268: synaptic transmission, GO:0008366: axon ensheathment, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005198: structural molecule activity		0.9892	1.3763	1.789	1.525	7.04	8.03	8.42	8.83	8.57	8.92	2
212798_s_at	ANKMY2	ankyrin repeat and MYND domain containing 2	AK001389	57037	Hs.157378	GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.8808	1.0926	1.2456	1.2136	7.89	8.77	8.99	9.14	9.11	9.02	2
203680_at	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	NM_002736	5577	Hs.433068	GO:0006468: protein amino acid phosphorylation, GO:0006631: fatty acid metabolic process, GO:0007242: intracellular signaling cascade, GO:0007612: learning, GO:0005952: cAMP-dependent protein kinase complex, GO:0000166: nucleotide binding, GO:0008603: cAMP-dependent protein kinase regulator activity, GO:0030552: cAMP binding	04210: Apoptosis, 04910: Insulin signaling pathway	0.8778	1.4115	1.5411	1.597	6.7	7.58	8.11	8.24	8.29	8.81	2
204290_s_at	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	NM_005589	4329	Hs.293970	GO:0006220: pyrimidine nucleotide metabolic process, GO:0006573: valine metabolic process, GO:0006573: valine metabolic process, GO:0008152: metabolic process, GO:0019859: thymine metabolic process, GO:0005739: mitochondrion, GO:0000062: acyl-CoA binding, GO:0004491: methylmalonate-semialdehyde dehydrogenase (acylating) activity, GO:0004491: methylmalonate-semialdehyde dehydrogenase (acylating) activity, GO:0016491: oxidoreductase activity, GO:0018478: malonate-semialdehyde dehydrogenase (acetylating) activity	00031: Inositol metabolism, 00280: Valine, leucine and isoleucine degradation, 00640: Propanoate metabolism	0.6863	1.1643	1.1311	1.2279	5.36	6.04	6.52	6.49	6.58	7.03	2
220428_at	CD207	CD207 molecule, langerin	NM_015717	50489	Hs.199731	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030139: endocytic vesicle, GO:0005529: sugar binding, GO:0005537: mannose binding		2.2658	3.3608	3.5053	3.2504	5.6	7.86	8.96	9.1	8.85	9.06	2
201116_s_at	CPE	carboxypeptidase E	NM_001873	1363	Hs.75360	GO:0006464: protein modification process, GO:0006508: proteolysis, GO:0007218: neuropeptide signaling pathway, GO:0008152: metabolic process, GO:0030070: insulin processing, GO:0005886: plasma membrane, GO:0004180: carboxypeptidase activity, GO:0004182: carboxypeptidase A activity, GO:0004183: carboxypeptidase E activity, GO:0008237: metallopeptidase activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	04940: Type I diabetes mellitus	0.8564	1.4083	1.763	1.4815	7.59	8.44	8.99	9.35	9.07	9.33	2
203575_at	CSNK2A2	casein kinase 2, alpha prime polypeptide	NM_001896	1459	Hs.82201	GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007286: spermatid development, GO:0016055: Wnt receptor signaling pathway, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004682: protein kinase CK2 activity, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0047485: protein N-terminus binding	04310: Wnt signaling pathway, 04520: Adherens junction, 04530: Tight junction	0.4628	1.0103	0.9241	0.9057	9.26	9.72	10.27	10.18	10.16	9.87	2
203758_at	CTSO	cathepsin O	AV729484	1519	Hs.75262	GO:0006508: proteolysis, GO:0004197: cysteine-type endopeptidase activity		0.6371	0.774	1.0123	0.7365	7.01	7.65	7.79	8.03	7.75	7.84	2
203185_at	RASSF2	Ras association (RalGDS/AF-6) domain family 2	NM_014737	9770	Hs.631504	GO:0007049: cell cycle, GO:0007165: signal transduction, GO:0045786: negative regulation of progression through cell cycle, GO:0005515: protein binding		0.5735	0.6349	1.0397	0.684	6.66	7.23	7.29	7.7	7.34	6.76	2

(*Continued*)

TABLE E3. (*Continued*)

210757_x_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	AF188298	1601	Hs.481980	GO:0000904: cellular morphogenesis during differentiation, GO:0001701: in utero embryonic development, GO:0006898: receptor-mediated endocytosis, GO:0006907: pinocytosis, GO:0007588: excretion, GO:0008283: cell proliferation, GO:0005905: coated pit, GO:0016020: membrane, GO:0031410: cytoplasmic vesicle, GO:0008022: protein C-terminus binding		0.7399	0.9603	1.4725	0.9535	7.76	8.5	8.72	9.23	8.71	8.77	2
207719_x_at	CEP170	centrosomal protein 170kDa	NM_014812	9859	Hs.408293, Hs.533635	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005874: microtubule		0.4389	0.5156	1.0354	0.6145	7.99	8.43	8.51	9.03	8.61	8.72	2
210658_s_at	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	BC000284	23062	Hs.460336	GO:0006461: protein complex assembly, GO:0006886: intracellular protein transport, GO:0016192: vesicle-mediated transport, GO:0005622: intracellular, GO:0005768: endosome, GO:0005802: trans-Golgi network, GO:0016020: membrane, GO:0030131: clathrin adaptor complex, GO:0005515: protein binding, GO:0008565: protein transporter activity, GO:0030306: ADP-ribosylation factor binding		0.6562	0.658	1.2448	0.6641	5.09	5.75	5.75	6.33	5.75	6.02	2
36829_at	PER1	period homolog 1 (Drosophila)	AF022991	5187	Hs.445534	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0009649: entrainment of circadian clock, GO:0016481: negative regulation of transcription, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0004871: signal transducer activity, GO:0005515: protein binding	04710: Circadian rhythm	0.4261	0.0779	0.372	1.1174	5.36	5.78	5.43	5.73	6.47	6.67	3
215294_s_at	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	AK026426	6594	Hs.152292	GO:0006338: chromatin remodeling, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007420: brain development, GO:0030182: neuron differentiation, GO:0043193: positive regulation of gene-specific transcription, GO:0005634: nucleus, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0004386: helicase activity, GO:0004386: helicase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008094: DNA-dependent ATPase activity, GO:0016787: hydrolase activity, GO:0030528: transcription regulator activity		0.2341	0.6626	1.0965	0.7333	4.8	5.04	5.46	5.9	5.54	5.75	3
204749_at	NAP1L3	nucleosome assembly protein 1-like 3	NM_004538	4675	Hs.21365	GO:0006334: nucleosome assembly, GO:0005634: nucleus, GO:0005678: chromatin assembly complex		0.22	1.1196	2.0008	1.3811	3.64	3.86	4.76	5.64	5.02	5.16	3
205139_s_at	UST	uronyl-2-sulfotransferase	NM_005715	10090	Hs.657370	GO:0006477: protein amino acid sulfation, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0008146: sulfotransferase activity, GO:0016740: transferase activity	00532: Chondroitin sulfate biosynthesis, 01030: Glycan structures - biosynthesis 1	0.8323	1.3361	2.6277	2.62	3.99	4.82	5.33	6.62	6.61	6.9	3
212667_at	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	AL575922	6678	Hs.111779	GO:0001503: ossification, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0005576: extracellular region, GO:0005604: basement membrane, GO:0005507: copper ion binding, GO:0005509: calcium ion binding, GO:0005518: collagen binding		0.1715	0.7829	1.2978	1.135	12.68	12.85	13.46	13.97	13.81	13.38	3
212713_at	MFAP4	microfibrillar-associated protein 4	R72286	4239	Hs.296049	GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0001527: microfibril, GO:0005578: proteinaceous extracellular matrix, GO:0003674: molecular_function, GO:0005102: receptor binding, GO:0005509: calcium ion binding		0.3586	1.0435	1.4759	1.6539	9.51	9.86	10.55	10.98	11.16	10.65	3
212327_at	LIMCH1	LIM and calponin homology domains 1	AK026815	22998	Hs.335163	GO:0031032: actomyosin structure organization and biogenesis, GO:0003779: actin binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.3607	0.6985	1.0714	1.0165	8.56	8.92	9.26	9.63	9.58	9.65	3

(*Continued*)

TABLE E3. (*Continued*)

212387_at	TCF4	transcription factor 4	BG495771	6925	Hs.644653	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0005667: transcription factor complex, GO:0003700: transcription factor activity, GO:0003714: transcription corepressor activity, GO:0008013: beta-catenin binding, GO:0046982: protein heterodimerization activity		0.305	0.5897	1.0885	1.1219	8.79	9.09	9.38	9.88	9.91	9.71	3
221249_s_at	FAM117A	family with sequence similarity 117, member A	NM_030802	81558	Hs.514308			0.5071	0.8337	0.9811	1.5445	6.83	7.33	7.66	7.81	8.37	8.3	3
221272_s_at	C1orf21	chromosome 1 open reading frame 21	NM_030806	81563	Hs.497159, Hs.571795			0.1378	0.6919	0.9965	1.4067	5.43	5.57	6.13	6.43	6.84	6.94	3
203146_s_at	GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	NM_001470	2550	Hs.167017	GO:0006464: protein modification process, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007194: negative regulation of adenylate cyclase activity, GO:0007214: gamma-aminobutyric acid signaling pathway, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030054: cell junction, GO:0045202: synapse, GO:0004872: receptor activity, GO:0004965: GABA-B receptor activity, GO:0004965: GABA-B receptor activity	04080: Neuroactive ligand-receptor interaction	0.8133	1.0256	1.5338	1.4682	5.35	6.16	6.38	6.89	6.82	6.98	3
203498_at	RCAN2	regulator of calcineurin 2	NM_005822	10231	Hs.440168	GO:0007417: central nervous system development, GO:0019722: calcium-mediated signaling, GO:0005575: cellular_component, GO:0030346: protein phosphatase 2B binding		0.8682	1.3289	1.7385	2.3426	7.54	8.4	8.87	9.27	9.88	9.96	3
210495_x_at	FN1	fibronectin 1	AF130095	2335	Hs.203717	GO:0006953: acute-phase response, GO:0007155: cell adhesion, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0009611: response to wounding, GO:0016477: cell migration, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005793: ER-Golgi intermediate compartment, GO:0005201: extracellular matrix structural constituent, GO:0005518: collagen binding, GO:0008201: heparin binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 04810: Regulation of actin cytoskeleton, 05222: Small cell lung cancer	0.1745	0.4846	1.0766	1.2055	11.12	11.3	11.61	12.2	12.33	11.87	3
210517_s_at	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	AB003476	9590	Hs.371240	GO:0006605: protein targeting, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005515: protein binding, GO:0051018: protein kinase A binding		0.6711	0.9563	1.6343	1.4911	6.71	7.38	7.66	8.34	8.2	8.2	3

(*Continued*)

TABLE E3. (*Continued*)

209897_s_at	SLIT2	slit homolog 2 (Drosophila)	AF055585	9353	Hs.29802	GO:0001657: ureteric bud development, GO:0006935: chemotaxis, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0007509: mesoderm migration, GO:0007608: sensory perception of smell, GO:0008038: neuron recognition, GO:0008045: motor axon guidance, GO:0008347: glial cell migration, GO:0030154: cell differentiation, GO:0050772: positive regulation of axonogenesis, GO:0050929: induction of negative chemotaxis, GO:0050929: induction of negative chemotaxis, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0016021: integral to membrane, GO:0004963: follicle-stimulating hormone receptor activity, GO:0005102: receptor binding, GO:0005509: calcium ion binding, GO:0005515: protein binding	04360: Axon guidance	0.3539	0.8062	1.6816	2.0716	4.7	5.05	5.5	6.38	6.77	6.49	3
210135_s_at	SHOX2	short stature homeobox 2	AF022654	6474	Hs.55967	GO:0001501: skeletal development, GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0007507: heart development, GO:0048557: embryonic digestive tract morphogenesis, GO:0048598: embryonic morphogenesis, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding		0.4917	0.6764	1.811	1.5072	4.35	4.84	5.02	6.16	5.86	5.33	3
208609_s_at	TNXB	tenascin XB	NM_019105	7148	Hs.42853, Hs.485104	GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0032963: collagen metabolic process, GO:0048251: elastic fiber assembly, GO:0005578: proteinaceous extracellular matrix, GO:0005583: fibrillar collagen, GO:0005622: intracellular, GO:0005102: receptor binding, GO:0005178: integrin binding, GO:0008201: heparin binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.1345	0.6335	1.2711	1.9157	9	9.14	9.64	10.27	10.92	10.47	3
208741_at	SAP18	Sin3A-associated protein, 18kDa	AW274856	10284	Hs.524899	GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0000118: histone deacetylase complex, GO:0003714: transcription corepressor activity, GO:0005515: protein binding		0.2411	0.5838	1.058	1.3288	6.25	6.49	6.84	7.31	7.58	7.86	3
206030_at	ASPA	aspartoacylase (Canavan disease)	NM_000049	443	Hs.171142	GO:0006533: aspartate catabolic process, GO:0008152: metabolic process, GO:0004046: aminoacylase activity, GO:0016788: hydrolase activity, acting on ester bonds, GO:0019807: aspartoacylase activity	00252: Alanine and aspartate metabolism, 00340: Histidine metabolism	0.694	0.9579	1.4735	1.465	2.76	3.45	3.72	4.23	4.22	4.66	3
207996_s_at	C18orf1	chromosome 18 open reading frame 1	NM_004338	753	Hs.149363	GO:0008150: biological_process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003674: molecular_function		0.5101	0.771	1.3674	1.3078	5.13	5.64	5.9	6.49	6.43	6.76	3

(*Continued*)

TABLE E3. (*Continued*)

205399_at	DCLK1	doublecortin-like kinase 1	NM_004734	9201	Hs.507755	GO:0006468: protein amino acid phosphorylation, GO:0007242: intracellular signaling cascade, GO:0007275: multicellular organismal development, GO:0007417: central nervous system development, GO:0016197: endosome transport, GO:0030154: cell differentiation, GO:0005887: integral to plasma membrane, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005057: receptor signaling protein activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity		0.5704	0.8812	1.6183	1.4346	7.82	8.39	8.7	9.44	9.26	9.36	3
205529_s_at	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	NM_004349	862	Hs.368431	GO:0006091: generation of precursor metabolites and energy, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0045444: fat cell differentiation, GO:0051101: regulation of DNA binding, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016564: transcription repressor activity, GO:0042803: protein homodimerization activity, GO:0046872: metal ion binding	05221: Acute myeloid leukemia	0.4472	0.8542	1.624	2.4483	6.34	6.78	7.19	7.96	8.78	8.1	3
204719_at	ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	NM_007168	10351	Hs.58351	GO:0006810: transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0016887: ATPase activity, GO:0042626: ATPase activity, coupled to transmembrane movement of substances	02010: ABC transporters - General	0.5724	0.9985	1.6243	1.4394	8.2	8.77	9.19	9.82	9.63	9.91	3
204834_at	FGL2	fibrinogen-like 2	NM_006682	10875	Hs.520989	GO:0007165: signal transduction, GO:0005577: fibrinogen complex, GO:0005102: receptor binding		0.4449	0.7141	1.1773	1.0624	8.46	8.91	9.18	9.64	9.52	9	3
203404_at	ARMCX2	armadillo repeat containing, X-linked 2	NM_014782	9823	Hs.48924	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005488: binding		0.4974	0.7127	1.272	1.2134	6.39	6.89	7.1	7.66	7.6	7.67	3
203417_at	MFAP2	microfibrillar-associated protein 2	NM_017459	4237	Hs.389137	GO:0001527: microfibril, GO:0005578: proteinaceous extracellular matrix, GO:0005201: extracellular matrix structural constituent		0.5758	0.9459	1.4829	1.2612	8.27	8.85	9.22	9.76	9.53	8.87	3
203296_s_at	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	NM_000702	477	Hs.34114	GO:0006813: potassium ion transport, GO:0006814: sodium ion transport, GO:0006942: regulation of striated muscle contraction, GO:0008152: metabolic process, GO:0015672: monovalent inorganic cation transport, GO:0030317: sperm motility, GO:0030641: cellular hydrogen ion homeostasis, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0005890: sodium:potassium-exchanging ATPase complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0005391: sodium:potassium-exchanging ATPase activity, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0015077: monovalent inorganic cation transmembrane transporter activity, GO:0015662: ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, GO:0016787: hydrolase activity, GO:0016820: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, GO:0030955: potassium ion binding, GO:0031402: sodium ion binding		0.1837	0.8454	1.0852	1.9758	4.52	4.7	5.36	5.6	6.49	6.45	3

(*Continued*)

TABLE E3. (*Continued*)

203329_at	PTPRM	protein tyrosine phosphatase, receptor type, M	NM_002845	5797	Hs.49774	GO:0006470: protein amino acid dephosphorylation, GO:0006470: protein amino acid dephosphorylation, GO:0007155: cell adhesion, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004725: protein tyrosine phosphatase activity, GO:0004872: receptor activity, GO:0005001: transmembrane receptor protein tyrosine phosphatase activity, GO:0005515: protein binding, GO:0016787: hydrolase activity, GO:0016791: phosphoric monoester hydrolase activity	04514: Cell adhesion molecules (CAMs), 04520: Adherens junction	0.4494	0.6532	1.2588	1.4481	7.02	7.47	7.67	8.27	8.46	8.17	3
202202_s_at	LAMA4	laminin, alpha 4	NM_002290	3910	Hs.654572	GO:0030155: regulation of cell adhesion, GO:0030334: regulation of cell migration, GO:0045995: regulation of embryonic development, GO:0005605: basal lamina, GO:0005606: laminin-1 complex, GO:0005102: receptor binding, GO:0005201: extracellular matrix structural constituent	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 05222: Small cell lung cancer	0.4025	0.6417	1.1629	1.4986	9.2	9.6	9.84	10.36	10.7	10.11	3
202242_at	TSPAN7	tetraspanin 7	NM_004615	7102	Hs.441664	GO:0006487: protein amino acid N-linked glycosylation, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane		0.3006	0.5742	1.1401	1.4146	7.63	7.93	8.2	8.77	9.04	9.03	3
218918_at	MAN1C1	mannosidase, alpha, class 1C, member 1	NM_020379	57134	Hs.197043	GO:0006487: protein amino acid N-linked glycosylation, GO:0008152: metabolic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030173: integral to Golgi membrane, GO:0004571: mannosyl-oligosaccharide 1,2-alpha-mannosidase activity, GO:0004571: mannosyl-oligosaccharide 1,2-alpha-mannosidase activity, GO:0005509: calcium ion binding, GO:0005509: calcium ion binding, GO:0016798: hydrolase activity, acting on glycosyl bonds	00510: N-Glycan biosynthesis, 01030: Glycan structures - biosynthesis 1	0.7677	1.1246	1.7323	1.4889	5.43	6.2	6.56	7.16	6.92	6.75	3
43427_at	ACACB	acetyl-Coenzyme A carboxylase beta	AI970898	32	Hs.234898	GO:0006633: fatty acid biosynthetic process, GO:0008152: metabolic process, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0003989: acetyl-CoA carboxylase activity, GO:0004075: biotin carboxylase activity, GO:0005524: ATP binding, GO:0009374: biotin binding, GO:0016874: ligase activity, GO:0030145: manganese ion binding, GO:0046872: metal ion binding	00061: Fatty acid biosynthesis, 00620: Pyruvate metabolism, 00640: Propanoate metabolism, 04910: Insulin signaling pathway, 04920: Adipocytokine signaling pathway	0.8967	1.3204	1.5799	2.772	5.97	6.87	7.29	7.55	8.74	8.25	3
205381_at	LRRC17	leucine rich repeat containing 17	NM_005824	10234	Hs.567412	GO:0005515: protein binding		0.8879	1.2033	2.1809	2.0082	4.56	5.45	5.76	6.74	6.57	5.76	3
205518_s_at	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase)	NM_003570	8418	Hs.484918	GO:0008150: biological_process, GO:0005737: cytoplasm, GO:0030338: CMP-N-acetylneuraminate monooxygenase activity		0.4896	1.3707	2.2537	2.6514	5	5.49	6.37	7.25	7.65	8.73	3
205226_at	PDGFRL	platelet-derived growth factor receptor-like	NM_006207	5157	Hs.458573	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0004992: platelet activating factor receptor activity, GO:0005019: platelet-derived growth factor beta-receptor activity		1.0806	1.4789	2.3926	2.2892	6.61	7.69	8.09	9	8.9	8.43	3
205908_s_at	OMD	osteomodulin	NM_005014	4958	Hs.94070	GO:0007155: cell adhesion, GO:0005578: proteinaceous extracellular matrix, GO:0005515: protein binding		1.0714	1.6768	2.6083	2.2531	4.74	5.81	6.41	7.35	6.99	6.88	3

(*Continued*)

TABLE E3. (*Continued*)

207092_at	LEP	leptin (obesity homolog, mouse)	NM_000230	3952	Hs.194236	GO:0006006: glucose metabolic process, GO:0006112: energy reserve metabolic process, GO:0006629: lipid metabolic process, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0008206: bile acid metabolic process, GO:0008343: adult feeding behavior, GO:0030300: regulation of cholesterol absorption, GO:0032099: negative regulation of appetite, GO:0042755: eating behavior, GO:0045639: positive regulation of myeloid cell differentiation, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005179: hormone activity, GO:0005515: protein binding, GO:0008083: growth factor activity	04060: Cytokine-cytokine receptor interaction, 04080: Neuroactive ligand-receptor interaction, 04630: Jak-STAT signaling pathway, 04920: Adipocytokine signaling pathway	0.3168	1.2289	0.7474	2.8488	4.66	4.98	5.89	5.41	7.51	7.23	3
207233_s_at	MITF	microphthalmia-associated transcription factor	NM_000248	4286	Hs.166017, Hs.618266	GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0007605: sensory perception of sound, GO:0030318: melanocyte differentiation, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0016563: transcription activator activity, GO:0016563: transcription activator activity	04916: Melanogenesis, 05218: Melanoma	0.2399	0.5877	0.8457	1.1368	8.58	8.82	9.17	9.43	9.72	9.83	3
203494_s_at	CEP57	centrosomal protein 57kDa	NM_014679	9702	Hs.101014	GO:0000060: protein import into nucleus, translocation, GO:0007286: spermatid development, GO:0008543: fibroblast growth factor receptor signaling pathway, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0005813: centrosome, GO:0005874: microtubule, GO:0017134: fibroblast growth factor binding, GO:0042803: protein homodimerization activity		0.6816	0.7569	0.8851	1.0794	8.1	8.78	8.86	8.99	9.18	9.09	3
203571_s_at	C10orf116	chromosome 10 open reading frame 116	BC004471	10974	Hs.642660, Hs.663834	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0003674: molecular_function		0.2054	0.5846	0.7682	1.8096	10.11	10.32	10.7	10.88	11.92	11.59	3
200795_at	SPARCL1	SPARC-like 1 (mast9, hevin)	NM_004684	8404	Hs.62886	GO:0005578: proteinaceous extracellular matrix, GO:0005509: calcium ion binding		0.259	0.4441	0.8252	1.0942	11.45	11.71	11.9	12.28	12.55	12.42	3
200885_at	PPM1J	protein phosphatase 1J (PP2C domain containing)	NM_005167	333926	Hs.655231	GO:0004721: phosphoprotein phosphatase activity, GO:0015071: protein phosphatase type 2C activity, GO:0016787: hydrolase activity	04530: Tight junction	0.1866	0.3887	0.8356	1.0627	8.33	8.52	8.72	9.17	9.4	9.36	3
203817_at	GUCY1B3	guanylate cyclase 1, soluble, beta 3	W93728	2983	Hs.77890	GO:0006182: cGMP biosynthetic process, GO:0007263: nitric oxide mediated signal transduction, GO:0008015: circulation, GO:0005737: cytoplasm, GO:0008074: guanylate cyclase complex, soluble, GO:0004383: guanylate cyclase activity, GO:0004872: receptor activity, GO:0005506: iron ion binding, GO:0020037: heme binding, GO:0046872: metal ion binding	00230: Purine metabolism, 04540: Gap junction, 04730: Long-term depression	0.4977	0.59	1.1962	0.965	6.42	6.92	7.01	7.62	7.38	7.41	3
209070_s_at	RGS5	regulator of G-protein signaling 5	AI183997	8490	Hs.24950	GO:0008277: regulation of G-protein coupled receptor protein signaling pathway, GO:0009968: negative regulation of signal transduction, GO:0004871: signal transducer activity, GO:0005096: GTPase activator activity		0.2039	0.6748	1.0092	0.8356	9.12	9.32	9.8	10.13	9.96	9.7	3
203088_at	FBLN5	fibulin 5	NM_006329	10516	Hs.332708	GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007596: blood coagulation, GO:0005578: proteinaceous extracellular matrix, GO:0005625: soluble fraction, GO:0016020: membrane, GO:0004888: transmembrane receptor activity, GO:0005178: integrin binding, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.3525	0.6466	1.1665	0.9952	8.23	8.59	8.88	9.4	9.23	9.58	3
203799_at	CD302	CD302 molecule	NM_014880	9936	Hs.130014	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005529: sugar binding		0.4119	0.6046	1.01	0.8939	8.94	9.35	9.55	9.95	9.84	9.93	3
221825_at	ANGEL2	angel homolog 2 (Drosophila)	BE671941	90806	Hs.157078			0.4557	0.7653	1.113	1.0275	7.83	8.29	8.6	8.94	8.86	8.93	3

(*Continued*)

TABLE E3. (*Continued*)

221834_at	LONP2	lon peptidase 2, peroxisomal	AV700132	83752	Hs.694785	GO:0006508: proteolysis, GO:0006510: ATP-dependent proteolysis, GO:0007031: peroxisome organization and biogenesis, GO:0005777: peroxisome, GO:0000166: nucleotide binding, GO:0004176: ATP-dependent peptidase activity, GO:0004252: serine-type endopeptidase activity, GO:0005524: ATP binding, GO:0017111: nucleoside-triphosphatase activity		0.2225	0.4678	1.0646	1.4318	8.32	8.54	8.79	9.38	9.75	9.73	3
218309_at	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	NM_018584	55450	Hs.197922	GO:0030425: dendrite, GO:0043025: cell soma, GO:0008427: calcium-dependent protein kinase inhibitor activity, GO:0016301: kinase activity, GO:0019901: protein kinase binding		0.3377	0.9198	1.4353	1.8873	6.91	7.25	7.83	8.35	8.8	9.28	3
218353_at	RGS5	regulator of G-protein signaling 5	NM_025226	8490	Hs.24950	GO:0008277: regulation of G-protein coupled receptor protein signaling pathway, GO:0009968: negative regulation of signal transduction, GO:0004871: signal transducer activity, GO:0005096: GTPase activator activity		0.2883	0.5877	1.0585	1.1416	10.24	10.53	10.83	11.3	11.38	10.97	3
213496_at	LPPR4	plasticity related gene 1	AW592563	9890	Hs.13245			0.4968	0.637	1.3962	1.2001	4.79	5.28	5.42	6.18	5.99	6	3
214012_at	ARTS-1	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	BE551138	51752	Hs.436186	GO:0001525: angiogenesis, GO:0006509: membrane protein ectodomain proteolysis, GO:0008217: blood pressure regulation, GO:0019885: antigen processing and presentation of endogenous peptide antigen via MHC class I, GO:0045088: regulation of innate immune response, GO:0045444: fat cell differentiation, GO:0045766: positive regulation of angiogenesis, GO:0005576: extracellular region, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0005788: endoplasmic reticulum lumen, GO:0005829: cytosol, GO:0016021: integral to membrane, GO:0004178: leucyl aminopeptidase activity, GO:0004179: membrane alanyl aminopeptidase activity, GO:0004239: methionyl aminopeptidase activity, GO:0005138: interleukin-6 receptor binding, GO:0005151: interleukin-1, Type II receptor binding, GO:0005515: protein binding, GO:0008237: metallopeptidase activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.3999	0.8105	1.0732	1.0021	6.4	6.8	7.21	7.47	7.4	7.63	3
213033_s_at	NFIB	nuclear factor I/B	AI186739	4781	Hs.370359	GO:0006260: DNA replication, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity		0.5918	0.5169	1.3439	1.3284	6.5	7.09	7.02	7.84	7.83	7.94	3
213050_at	COBL	cordon-bleu homolog (mouse)	AA594937	23242	Hs.99141			0.1259	0.8276	1.2066	2.5083	5.58	5.71	6.41	6.79	8.09	9	3
210664_s_at	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	AF021834	7035	Hs.516578	GO:0007596: blood coagulation, GO:0007596: blood coagulation, GO:0005576: extracellular region, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0030414: protease inhibitor activity	04610: Complement and coagulation cascades	0.5526	0.743	1.2623	1.1483	6.18	6.73	6.92	7.44	7.32	7.23	3
210986_s_at	TPM1	tropomyosin 1 (alpha)	Z24727	7168	Hs.133892	GO:0006928: cell motility, GO:0006937: regulation of muscle contraction, GO:0008016: regulation of heart contraction, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005862: muscle thin filament tropomyosin, GO:0003779: actin binding, GO:0005200: structural constituent of cytoskeleton, GO:0008307: structural constituent of muscle		0.3187	0.606	1.0266	1.302	11.14	11.46	11.74	12.16	12.44	12.36	3

(*Continued*)

TABLE E3. (*Continued*)

217757_at	A2M	alpha-2-macroglobulin	NM_000014	2	Hs.212838	GO:0006886: intracellular protein transport, GO:0051260: protein homooligomerization, GO:0005576: extracellular region, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0008320: protein carrier activity, GO:0017114: wide-spectrum protease inhibitor activity, GO:0019899: enzyme binding, GO:0019959: interleukin-8 binding, GO:0019966: interleukin-1 binding, GO:0043120: tumor necrosis factor binding	04610: Complement and coagulation cascades, 05010: Alzheimer's disease	0.3129	0.4218	0.8132	1.0878	11.35	11.66	11.77	12.16	12.43	12.1	3
217867_x_at	BACE2	beta-site APP-cleaving enzyme 2	AF178532	25825	Hs.529408	GO:0006464: protein modification process, GO:0006509: membrane protein ectodomain proteolysis, GO:0006509: membrane protein ectodomain proteolysis, GO:0009306: protein secretion, GO:0016486: peptide hormone processing, GO:0042985: negative regulation of amyloid precursor protein biosynthetic process, GO:0042985: negative regulation of amyloid precursor protein biosynthetic process, GO:0005624: membrane fraction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004194: pepsin A activity, GO:0008233: peptidase activity, GO:0009049: aspartic-type signal peptidase activity	05010: Alzheimer's disease	0.2015	0.473	0.8465	1.2186	6.4	6.6	6.88	7.25	7.62	7.3	3
214475_x_at	CAPN3	calpain 3, (p94)	AF127764	825	Hs.143261	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007517: muscle development, GO:0005622: intracellular, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0004198: calpain activity, GO:0004198: calpain activity, GO:0004871: signal transducer activity, GO:0005509: calcium ion binding		1.0412	0.9437	1.3284	1.5584	5.94	6.99	6.89	7.27	7.5	7.86	3
201539_s_at	FHL1	four and a half LIM domains 1	U29538	2273	Hs.435369	GO:0007275: multicellular organismal development, GO:0007517: muscle development, GO:0009887: organ morphogenesis, GO:0016049: cell growth, GO:0030154: cell differentiation, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0003674: molecular_function, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.4978	1.2191	1.6025	1.5627	8.07	8.57	9.29	9.68	9.64	10.38	3
37462_i_at	SF3A2	splicing factor 3a, subunit 2, 66kDa	L21990	8175	Hs.115232	GO:0000389: nuclear mRNA 3′-splice site recognition, GO:0000398: nuclear mRNA splicing, via spliceosome, GO:0008380: RNA splicing, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005681: spliceosome, GO:0030532: small nuclear ribonucleoprotein complex, GO:0003676: nucleic acid binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.3304	0.6424	0.235	1.5652	5.25	5.58	5.89	5.48	6.81	6.13	3

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TABLE E3. (*Continued*)

204894_s_at	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	AF067406	8639	Hs.198241	GO:0006118: electron transport, GO:0006954: inflammatory response, GO:0007155: cell adhesion, GO:0009308: amine metabolic process, GO:0009308: amine metabolic process, GO:0005886: plasma membrane, GO:0009986: cell surface, GO:0016021: integral to membrane, GO:0005507: copper ion binding, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0008131: amine oxidase activity, GO:0016491: oxidoreductase activity, GO:0042803: protein homodimerization activity, GO:0048038: quinone binding	00220: Urea cycle and metabolism of amino groups, 00260: Glycine, serine and threonine metabolism, 00340: Histidine metabolism, 00350: Tyrosine metabolism, 00360: Phenylalanine metabolism, 00380: Tryptophan metabolism, 00410: beta-Alanine metabolism, 00960: Alkaloid biosynthesis II	0.3539	0.8098	1.1026	1.8515	8.04	8.39	8.85	9.14	9.89	9.6	3
204940_at	PLN	phospholamban	NM_002667	5350	Hs.170839	GO:0002026: cardiac inotropy, GO:0006874: cellular calcium ion homeostasis, GO:0006936: muscle contraction, GO:0008015: circulation, GO:0045822: negative regulation of heart contraction, GO:0048738: cardiac muscle development, GO:0051924: regulation of calcium ion transport, GO:0005790: smooth endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016529: sarcoplasmic reticulum, GO:0005246: calcium channel regulator activity, GO:0005515: protein binding, GO:0042030: ATPase inhibitor activity	04020: Calcium signaling pathway	0.3445	0.8285	1.499	2.0402	4.95	5.3	5.78	6.45	6.99	6.81	3
212677_s_at	CEP68	centrosomal protein 68kDa	BG530481	23177	Hs.693614			0.2637	0.8128	0.984	1.8238	7.34	7.61	8.15	8.33	9.17	8.87	3
212695_at	CRY2	cryptochrome 2 (photolyase-like)	AB014558	1408	Hs.532491	GO:0006281: DNA repair, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006606: protein import into nucleus, GO:0007623: circadian rhythm, GO:0018298: protein-chromophore linkage, GO:0050896: response to stimulus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003913: DNA photolyase activity, GO:0004872: receptor activity, GO:0005515: protein binding		0.0454	0.131	0.3523	1.008	6.94	6.99	7.07	7.29	7.95	8	3
210230_at	LOC728965	hypothetical protein LOC728965	BC003629	728965	Hs.676605			−0.2217	−0.3039	0.0173	1.0384	6.49	6.27	6.19	6.51	7.53	7.04	3
210469_at	DLG5	discs, large homolog 5 (Drosophila)	BC002915	9231	Hs.654780	GO:0000074: regulation of progression through cell cycle, GO:0007242: intracellular signaling cascade, GO:0008285: negative regulation of cell proliferation, GO:0016337: cell-cell adhesion, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0030054: cell junction, GO:0005515: protein binding, GO:0030159: receptor signaling complex scaffold activity		−0.0835	0.0443	0.1354	1.008	4.03	3.95	4.08	4.17	5.04	4.71	3
204468_s_at	TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	NM_005424	7075	Hs.78824	GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007498: mesoderm development, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004713: protein-tyrosine kinase activity, GO:0004714: transmembrane receptor protein tyrosine kinase activity, GO:0004872: receptor activity, GO:0005524: ATP binding, GO:0016740: transferase activity		0.2902	0.1881	0.7962	1.1362	4.98	5.27	5.17	5.78	6.12	5.47	3

(*Continued*)

TABLE E3. (*Continued*)

204482_at	CLDN5	claudin 5 (transmembrane protein deleted in velocardiofacial syndrome)	NM_003277	7122	Hs.505337	GO:0016338: calcium-independent cell-cell adhesion, GO:0005923: tight junction, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030054: cell junction, GO:0005198: structural molecule activity, GO:0042802: identical protein binding	04514: Cell adhesion molecules (CAMs), 04530: Tight junction, 04670: Leukocyte transendothelial migration	0.3122	0.6322	0.7842	1.53	8.37	8.69	9.01	9.16	9.9	9.38	3
202861_at	PER1	period homolog 1 (Drosophila)	NM_002616	5187	Hs.445534	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0009649: entrainment of circadian clock, GO:0016481: negative regulation of transcription, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0004871: signal transducer activity, GO:0005515: protein binding	04710: Circadian rhythm	0.1671	−0.0575	0.3947	1.1683	5.93	6.1	5.87	6.33	7.1	7.47	3
202920_at	ANK2	ankyrin 2, neuronal	NM_001148	287	Hs.620557	GO:0007165: signal transduction, GO:0005737: cytoplasm, GO:0015629: actin cytoskeleton, GO:0016020: membrane, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding, GO:0005515: protein binding		0.2196	0.3107	0.8867	1.0369	8.9	9.12	9.21	9.78	9.93	9.78	3
209169_at	GPM6B	glycoprotein M6B	N63576	2824	Hs.495710	GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0030154: cell differentiation, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003674: molecular_function		−0.0327	0.2782	0.7362	1.0201	7	6.96	7.28	7.73	8.02	8.21	3
209184_s_at	IRS2	insulin receptor substrate 2	AF073310	8660	Hs.442344	GO:0006006: glucose metabolic process, GO:0007165: signal transduction, GO:0007420: brain development, GO:0008283: cell proliferation, GO:0008284: positive regulation of cell proliferation, GO:0008286: insulin receptor signaling pathway, GO:0004871: signal transducer activity, GO:0005158: insulin receptor binding, GO:0005515: protein binding, GO:0019901: protein kinase binding	04910: Insulin signaling pathway, 04920: Adipocytokine signaling pathway, 04930: Type II diabetes mellitus	0.3432	0.3884	0.5435	1.0384	7.57	7.91	7.95	8.11	8.6	8.76	3
209156_s_at	COL6A2	collagen, type VI, alpha 2	AY029208	1292	Hs.420269	GO:0006817: phosphate transport, GO:0016337: cell-cell adhesion, GO:0030198: extracellular matrix organization and biogenesis, GO:0005581: collagen, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0005201: extracellular matrix structural constituent, GO:0030674: protein binding, bridging	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.2409	0.5241	0.8835	1.0195	11.99	12.23	12.51	12.87	13.01	12.49	3
209167_at	GPM6B	glycoprotein M6B	AI419030	2824	Hs.495710	GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0030154: cell differentiation, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003674: molecular_function		0.1993	0.4297	0.8635	1.04	6.33	6.53	6.76	7.19	7.37	7.56	3
209071_s_at	RGS5	regulator of G-protein signaling 5	AF159570	8490	Hs.24950	GO:0008277: regulation of G-protein coupled receptor protein signaling pathway, GO:0009968: negative regulation of signal transduction, GO:0004871: signal transducer activity, GO:0005096: GTPase activator activity		0.1277	0.5287	0.8598	1.2019	10.86	10.99	11.39	11.72	12.06	11.55	3
209074_s_at	FAM107A	family with sequence similarity 107, member A	AF089853	11170	Hs.506357	GO:0001558: regulation of cell growth, GO:0005634: nucleus, GO:0003674: molecular_function, GO:0005515: protein binding		0.0781	0.3679	0.6051	1.551	6.47	6.55	6.84	7.08	8.02	8.02	3
209005_at	FBXL5	F-box and leucine-rich repeat protein 5	AF157323	26234	Hs.643433	GO:0016567: protein ubiquitination, GO:0000151: ubiquitin ligase complex, GO:0004842: ubiquitin-protein ligase activity, GO:0005515: protein binding		0.3389	0.6803	0.9367	1.2234	6.06	6.4	6.74	7	7.29	7.19	3

(*Continued*)

TABLE E3. (*Continued*)

209047_at	AQP1	aquaporin 1 (Colton blood group)	AL518391	358	Hs.76152	GO:0006810: transport, GO:0006833: water transport, GO:0007588: excretion, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019867: outer membrane, GO:0005215: transporter activity, GO:0005372: water transporter activity, GO:0015288: porin activity		0.064	0.4586	0.8749	1.2648	11.39	11.45	11.85	12.26	12.65	12.34	3
208981_at	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)	AA702701	5175	Hs.514412	GO:0006928: cell motility, GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0008037: cell recognition, GO:0005886: plasma membrane, GO:0005911: intercellular junction, GO:0016021: integral to membrane, GO:0005515: protein binding	04514: Cell adhesion molecules (CAMs), 04670: Leukocyte transendothelial migration	0.2787	0.3815	0.9128	1.2149	9.38	9.66	9.77	10.3	10.6	10.29	3
208982_at	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)	M37780	5175	Hs.514412	GO:0006928: cell motility, GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0008037: cell recognition, GO:0005886: plasma membrane, GO:0005911: intercellular junction, GO:0016021: integral to membrane, GO:0005515: protein binding	04514: Cell adhesion molecules (CAMs), 04670: Leukocyte transendothelial migration	0.2242	0.2529	0.7013	1.3179	10.02	10.24	10.27	10.72	11.33	10.69	3
208963 _x_at	FADS1	fatty acid desaturase 1	AL512760	3992	Hs.503546	GO:0006629: lipid metabolic process, GO:0006633: fatty acid biosynthetic process, GO:0016020: membrane, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0016491: oxidoreductase activity, GO:0016717: oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water, GO:0020037: heme binding	00591: Linoleic acid metabolism	0.1318	0.4871	0.8133	2.0478	5.87	6	6.35	6.68	7.91	8.36	3
208978_at	CRIP2	cysteine-rich protein 2	U36190	1397	Hs.534309	GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.4362	0.4125	0.3969	1.2194	8.94	8.51	9.36	9.34	10.16	10.41	3
208942 _s_at	TLOC1	translocation protein 1	U93239	7095	Hs.592561	GO:0006605: protein targeting, GO:0006613: cotranslational protein targeting to membrane, GO:0015031: protein transport, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0008565: protein transporter activity		0.086	0.4061	0.6398	1.0543	10.58	10.67	10.99	11.22	11.64	11.46	3
208962 _s_at	FADS1	fatty acid desaturase 1	BE540552	3992	Hs.503546	GO:0006629: lipid metabolic process, GO:0006633: fatty acid biosynthetic process, GO:0016020: membrane, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0016491: oxidoreductase activity, GO:0016717: oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water, GO:0020037: heme binding	00591: Linoleic acid metabolism	0.1773	0.4989	1.4281	2.1002	6.66	6.84	7.16	8.09	8.76	9.27	3
208806_at	CHD3	chromodomain helicase DNA binding protein 3	BE379542	1107	Hs.25601	GO:0006333: chromatin assembly or disassembly, GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007001: chromosome organization and biogenesis (sensu Eukaryota), GO:0016568: chromatin modification, GO:0000785: chromatin, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003682: chromatin binding, GO:0004003: ATP-dependent DNA helicase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008270: zinc ion binding, GO:0016787: hydrolase activity, GO:0046872: metal ion binding		0.2683	0.2218	0.3659	1.1254	2.78	3.04	3	3.14	3.9	3.14	3

(*Continued*)

TABLE E3. (*Continued*)

208913_at	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	AA868560	23062	Hs.460336	GO:0006461: protein complex assembly, GO:0006886: intracellular protein transport, GO:0016192: vesicle-mediated transport, GO:0005622: intracellular, GO:0005768: endosome, GO:0005802: trans-Golgi network, GO:0016020: membrane, GO:0030131: clathrin adaptor complex, GO:0005515: protein binding, GO:0008565: protein transporter activity, GO:0030306: ADP-ribosylation factor binding	0.4115	0.429	0.7871	1.0252	6.63	7.04	7.06	7.42	7.65	7.45	3
208791_at	CLU	clusterin	M25915	1191	Hs.436657	GO:0006629: lipid metabolic process, GO:0006915: apoptosis, GO:0006958: complement activation, classical pathway, GO:0008219: cell death, GO:0045087: innate immune response, GO:0005615: extracellular space	0.5855	0.6391	0.7628	1.0423	10.45	11.03	11.09	11.21	11.49	11.42	3
208792_s_at	CLU	clusterin	M25915	1191	Hs.436657	GO:0006629: lipid metabolic process, GO:0006915: apoptosis, GO:0006958: complement activation, classical pathway, GO:0008219: cell death, GO:0045087: innate immune response, GO:0005615: extracellular space	0.4356	0.5674	0.6575	1.0314	10.62	11.06	11.19	11.28	11.65	11.55	3
208789_at	PTRF	polymerase I and transcript release factor	BC004295	284119	Hs.437191	GO:0006350: transcription, GO:0006353: transcription termination, GO:0006355: regulation of transcription, DNA-dependent, GO:0006361: transcription initiation from RNA polymerase I promoter, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016599: caveolar membrane, GO:0003716: RNA polymerase I transcription termination factor activity, GO:0005515: protein binding, GO:0042134: rRNA primary transcript binding	0.1176	0.4122	0.8556	1.3791	11.26	11.38	11.67	12.11	12.64	12.46	3
208790_s_at	PTRF	polymerase I and transcript release factor	AF312393	284119	Hs.437191	GO:0006350: transcription, GO:0006353: transcription termination, GO:0006355: regulation of transcription, DNA-dependent, GO:0006361: transcription initiation from RNA polymerase I promoter, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016599: caveolar membrane, GO:0003716: RNA polymerase I transcription termination factor activity, GO:0005515: protein binding, GO:0042134: rRNA primary transcript binding	−0.1937	0.2793	0.7294	1.1284	7.75	7.56	8.03	8.48	8.88	8.83	3
208740_at	SAP18	Sin3A-associated protein, 18kDa	BF593650	10284	Hs.524899	GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0000118: histone deacetylase complex, GO:0003714: transcription corepressor activity, GO:0005515: protein binding	0.3258	0.5972	0.723	1.3329	7.77	8.1	8.37	8.49	9.1	8.96	3
208763_s_at	TSC22D3	TSC22 domain family, member 3	AL110191	1831	Hs.522074	GO:0006355: regulation of transcription, DNA-dependent, GO:0006355: regulation of transcription, DNA-dependent, GO:0006916: anti-apoptosis, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity	0.232	0.3124	0.8994	1.0417	9.6	9.83	9.91	10.5	10.64	10.99	3

(*Continued*)

TABLE E3. (*Continued*)

208712_at	CCND1	cyclin D1	M73554	595	Hs.523852	GO:0000082: G1/S transition of mitotic cell cycle, GO:0000320: re-entry into mitotic cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0007049: cell cycle, GO:0030968: unfolded protein response, GO:0045444: fat cell differentiation, GO:0051301: cell division, GO:0000307: cyclin-dependent protein kinase holoenzyme complex, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005829: cytosol, GO:0004672: protein kinase activity, GO:0005515: protein binding, GO:0016538: cyclin-dependent protein kinase regulator activity	04110: Cell cycle, 04115: p53 signaling pathway, 04310: Wnt signaling pathway, 04510: Focal adhesion, 04630: Jak-STAT signaling pathway, 05210: Colorectal cancer, 05212: Pancreatic cancer, 05213: Endometrial cancer, 05214: Glioma, 05215: Prostate cancer, 05216: Thyroid cancer, 05218: Melanoma, 05219: Bladder cancer, 05220: Chronic myeloid leukemia, 05221: Acute myeloid leukemia, 05222: Small cell lung cancer, 05223: Non-small cell lung cancer	0.0729	0.459	0.8278	1.2745	9.53	9.6	9.99	10.36	10.8	10.78	3
208723_at	USP11	ubiquitin specific peptidase 11	BC000350	8237	Hs.171501	GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0004197: cysteine-type endopeptidase activity, GO:0004221: ubiquitin thiolesterase activity		0.1481	0.3965	0.6393	1.1544	7.11	7.26	7.5	7.75	8.26	8.06	3
208158_s_at	OSBPL1A	oxysterol binding protein-like 1A	NM_018030	114876	Hs.370725	GO:0006869: lipid transport, GO:0008202: steroid metabolic process, GO:0008203: cholesterol metabolic process, GO:0016192: vesicle-mediated transport, GO:0005622: intracellular, GO:0005543: phospholipid binding		0.3147	0.6273	0.8592	1.1239	8.6	8.91	9.23	9.46	9.72	9.6	3
208711_s_at	CCND1	cyclin D1	BC000076	595	Hs.523852	GO:0000082: G1/S transition of mitotic cell cycle, GO:0000320: re-entry into mitotic cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0007049: cell cycle, GO:0030968: unfolded protein response, GO:0045444: fat cell differentiation, GO:0051301: cell division, GO:0000307: cyclin-dependent protein kinase holoenzyme complex, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005829: cytosol, GO:0004672: protein kinase activity, GO:0005515: protein binding, GO:0016538: cyclin-dependent protein kinase regulator activity	04110: Cell cycle, 04115: p53 signaling pathway, 04310: Wnt signaling pathway, 04510: Focal adhesion, 04630: Jak-STAT signaling pathway, 05210: Colorectal cancer, 05212: Pancreatic cancer, 05213: Endometrial cancer, 05214: Glioma, 05215: Prostate cancer, 05216: Thyroid cancer, 05218: Melanoma, 05219: Bladder cancer, 05220: Chronic myeloid leukemia, 05221: Acute myeloid leukemia, 05222: Small cell lung cancer, 05223: Non-small cell lung cancer	−0.2216	0.3028	0.6419	1.0372	4.96	4.73	5.26	5.6	5.99	5.84	3
207966_s_at	GLG1	golgi apparatus protein 1	NM_012201	2734	Hs.201712	GO:0000139: Golgi membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005102: receptor binding, GO:0017134: fibroblast growth factor binding	04514: Cell adhesion molecules (CAMs)	0.0105	0.2963	0.53	1.0184	7.71	7.72	8.01	8.24	8.73	8.37	3

(*Continued*)

TABLE E3. (*Continued*)

208131_s_at	PTGIS	prostaglandin I2 (prostacyclin) synthase	NM_000961	5740	Hs.302085	GO:0001516: prostaglandin biosynthetic process, GO:0006118: electron transport, GO:0006629: lipid metabolic process, GO:0006633: fatty acid biosynthetic process, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004497: monooxygenase activity, GO:0005506: iron ion binding, GO:0008116: prostaglandin-I synthase activity, GO:0016853: isomerase activity, GO:0020037: heme binding, GO:0046872: metal ion binding	00590: Arachidonic acid metabolism	0.0756	0.5074	0.8945	1.2799	8.78	8.86	9.29	9.68	10.06	10.22	3
207955_at	CCL27	chemokine (C-C motif) ligand 27	NM_006664	10850	Hs.459590, Hs.648124	GO:0006935: chemotaxis, GO:0006955: immune response, GO:0007267: cell-cell signaling, GO:0005615: extracellular space, GO:0008009: chemokine activity	04060: Cytokine-cytokine receptor interaction	−0.3202	0.586	0.8586	2.1361	7.65	7.33	8.24	8.51	9.79	10.8	3
207961_x_at	MYH11	myosin, heavy chain 11, smooth muscle	NM_022870	4629	Hs.460109	GO:0006939: smooth muscle contraction, GO:0006941: striated muscle contraction, GO:0030241: muscle thick filament assembly, GO:0048251: elastic fiber assembly, GO:0048746: smooth muscle fiber development, GO:0005863: striated muscle thick filament, GO:0016459: myosin complex, GO:0000166: nucleotide binding, GO:0003774: motor activity, GO:0003779: actin binding, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0008307: structural constituent of muscle		0.0855	0.5253	0.9174	1.42	8.99	9.08	9.52	9.91	10.41	10.2	3
207317_s_at	CASQ2	calsequestrin 2 (cardiac muscle)	NM_001232	845	Hs.57975	GO:0006941: striated muscle contraction, GO:0007507: heart development, GO:0005790: smooth endoplasmic reticulum, GO:0016529: sarcoplasmic reticulum, GO:0005509: calcium ion binding		−0.0356	0.4047	0.2318	1.0517	2.75	2.71	3.15	2.98	3.8	3.48	3
207760_s_at	NCOR2	nuclear receptor co-repressor 2	NM_006312	9612	Hs.137510	GO:0045892: negative regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0016604: nuclear body, GO:0003677: DNA binding, GO:0003714: transcription corepressor activity, GO:0004872: receptor activity, GO:0005112: Notch binding, GO:0005515: protein binding	04330: Notch signaling pathway	0.1399	0.2903	0.5714	1.0151	8.69	8.83	8.98	9.26	9.7	9.43	3
207283_at	RPL23AP13	ribosomal protein L23a pseudogene 13	NM_020217	56969	Hs.657366	GO:0030529: ribonucleoprotein complex, GO:0000166: nucleotide binding		0.0969	0.3064	0.9277	1.567	6.46	6.56	6.77	7.39	8.03	7.76	3
207302_at	SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	NM_000231	6445	Hs.37167	GO:0007010: cytoskeleton organization and biogenesis, GO:0007517: muscle development, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005886: plasma membrane, GO:0016012: sarcoglycan complex, GO:0016021: integral to membrane, GO:0005515: protein binding		0.107	0.4179	0.5727	1.19	3.5	3.61	3.92	4.08	4.69	4.88	3
206702_at	TEK	TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	NM_000459	7010	Hs.89640	GO:0006468: protein amino acid phosphorylation, GO:0007160: cell-matrix adhesion, GO:0007165: signal transduction, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007267: cell-cell signaling, GO:0016337: cell-cell adhesion, GO:0030334: regulation of cell migration, GO:0045765: regulation of angiogenesis, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004714: transmembrane receptor protein tyrosine kinase activity, GO:0004872: receptor activity, GO:0004872: receptor activity, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity		0.1308	0.4796	0.9952	1.1738	4.18	4.31	4.65	5.17	5.35	5.16	3

(*Continued*)

TABLE E3. (*Continued*)

206898_at	CDH19	cadherin 19, type 2	NM_021153	28513	Hs.42771	GO:0007156: homophilic cell adhesion, GO:0007156: homophilic cell adhesion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.084	0.4996	0.7194	1.2184	4.89	4.97	5.39	5.61	6.11	6.42	3
206548_at	hCG_1776259	hypothetical protein FLJ23556	NM_024880	79938	Hs.655463			−0.0721	0.2842	0.8288	1.5402	5.95	5.87	6.23	6.78	7.49	6.92	3
206595_at	CST6	cystatin E/M	NM_001323	1474	Hs.139389	GO:0008544: epidermis development, GO:0009653: anatomical structure morphogenesis, GO:0001533: cornified envelope, GO:0004869: cysteine protease inhibitor activity		0.1952	0.667	0.9412	1.1069	11.56	11.76	12.23	12.5	12.67	12.78	3
206194_at	HOXC6	homeobox C6	AW299598	3223	Hs.549040	GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007275: multicellular organismal development, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003714: transcription corepressor activity, GO:0043565: sequence-specific DNA binding		0.2537	0.2513	0.5811	1.003	5.37	5.62	5.62	5.95	6.37	5.95	3
206509_at	PIP	prolactin-induced protein	NM_002652	5304	Hs.99949	GO:0008150: biological_process, GO:0005576: extracellular region, GO:0003779: actin binding, GO:0005515: protein binding		−0.3159	0.8057	1.2662	2.0893	10.27	9.95	11.07	11.54	12.36	13.14	3
206059_at	ZNF91	zinc finger protein 91	NM_003430	7644	Hs.654471	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.173	0.4261	0.7032	1.1178	8.61	8.79	9.04	9.32	9.73	9.95	3
206170_at	ADRB2	adrenergic, beta-2-, receptor, surface	NM_000024	154	Hs.591251	GO:0000187: activation of MAPK activity, GO:0002024: diet induced thermogenesis, GO:0002025: norepinephrine-epinephrine vasodilation during regulation of blood pressure, GO:0002028: regulation of sodium ion transport, GO:0002032: arrestin mediated desensitization of G-protein coupled receptor protein signaling pathway, GO:0006898: receptor-mediated endocytosis, GO:0007171: transmembrane receptor protein tyrosine kinase activation (dimerization), GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007190: adenylate cyclase activation, GO:0007243: protein kinase cascade, GO:0008333: endosome to lysosome transport, GO:0009409: response to cold, GO:0030501: positive regulation of bone mineralization, GO:0031649: heat generation, GO:0040015: negative regulation of body size, GO:0043410: positive regulation of MAPKKK cascade, GO:0045453: bone resorption, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0045986: negative regulation of smooth muscle contraction, GO:0050873: brown fat cell differentiation, GO:0005624: membrane fraction, GO:0005634: nucleus, GO:0005764: lysosome, GO:0005768: endosome, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016324: apical plasma membrane, GO:0043235: receptor complex, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004941: beta2-adrenergic receptor activity, GO:0005515: protein binding, GO:0042803: protein homodimerization activity, GO:0051380: norepinephrine binding	04020: Calcium signaling pathway, 04080: Neuroactive ligand-receptor interaction	−0.0182	0.3072	0.7735	1.3798	2.66	2.64	2.97	3.43	4.04	4.91	3

(*Continued*)

TABLE E3. (*Continued*)

205883_at	ZBTB16	zinc finger and BTB domain containing 16	NM_006006	7704	Hs.591945, Hs.682144	GO:0001823: mesonephros development, GO:0006350: transcription, GO:0006915: apoptosis, GO:0007417: central nervous system development, GO:0030099: myeloid cell differentiation, GO:0045638: negative regulation of myeloid cell differentiation, GO:0045892: negative regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0016605: PML body, GO:0016607: nuclear speck, GO:0017053: transcriptional repressor complex, GO:0003677: DNA binding, GO:0008270: zinc ion binding, GO:0016566: specific transcriptional repressor activity, GO:0042803: protein homodimerization activity, GO:0046872: metal ion binding	05221: Acute myeloid leukemia	−0.321	−0.2643	0.9467	2.1186	5.23	4.9	4.96	6.17	7.34	8.22	3
205923_at	RELN	reelin	NM_005045	5649	Hs.655654	GO:0007155: cell adhesion, GO:0007275: multicellular organismal development, GO:0005578: proteinaceous extracellular matrix, GO:0005615: extracellular space, GO:0004252: serine-type endopeptidase activity, GO:0005515: protein binding, GO:0008233: peptidase activity	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.3003	0.4498	0.9286	1.0681	4.29	4.59	4.74	5.22	5.36	5.4	3
205765_at	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	NM_000777	1577	Hs.150276	GO:0006118: electron transport, GO:0008202: steroid metabolic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0004497: monooxygenase activity, GO:0005506: iron ion binding, GO:0019825: oxygen binding, GO:0020037: heme binding, GO:0046872: metal ion binding, GO:0050381: unspecific monooxygenase activity	00361: gamma-Hexachlorocyclohexane degradation, 00591: Linoleic acid metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	0.4106	0.6016	0.9294	1.3729	7.59	8	8.19	8.52	8.96	9.17	3
205878_at	POU6F1	POU class 6 homeobox 1	NM_002702	5463	Hs.594817, Hs.632482, Hs.646545	GO:0006355: regulation of transcription, DNA-dependent, GO:0007420: brain development, GO:0007507: heart development, GO:0007517: muscle development, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding		0.1369	0.1337	0.4836	1.1164	3.47	3.6	3.6	3.95	4.58	4.28	3
205726_at	DIAPH2	diaphanous homolog 2 (Drosophila)	NM_006729	1730	Hs.656813	GO:0000910: cytokinesis, GO:0007275: multicellular organismal development, GO:0016043: cellular component organization and biogenesis, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0030154: cell differentiation, GO:0048477: oogenesis, GO:0005737: cytoplasm, GO:0005768: endosome, GO:0003779: actin binding, GO:0005102: receptor binding, GO:0017048: Rho GTPase binding	04810: Regulation of actin cytoskeleton	0.5526	0.8054	0.9758	1.3858	7.14	7.69	7.94	8.11	8.52	8.22	3
205730_s_at	ABLIM3	actin binding LIM protein family, member 3	NM_014945	22885	Hs.49688	GO:0007010: cytoskeleton organization and biogenesis, GO:0005737: cytoplasm, GO:0003779: actin binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	04360: Axon guidance	0.2888	0.5456	0.793	1.7876	3.18	3.47	3.73	3.97	4.97	4.48	3
205613_at	SYT17	synaptotagmin XVII	NM_016524	51760	Hs.258326	GO:0006810: transport, GO:0008021: synaptic vesicle, GO:0016020: membrane, GO:0005215: transporter activity		0.0359	0.1609	0.4618	1.0493	2.5	2.53	2.66	2.96	3.55	3.14	3
205619_s_at	MEOX1	mesenchyme homeobox 1	NM_004527	4222	Hs.438	GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0008150: biological_process, GO:0005575: cellular_component, GO:0005634: nucleus, GO:0003674: molecular_function, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding		0.3832	0.6052	0.9429	1.6048	5.95	6.33	6.55	6.89	7.55	7.04	3
205547_s_at	TAGLN	transgelin	NM_003186	6876	Hs.632099	GO:0007517: muscle development, GO:0007517: muscle development, GO:0005737: cytoplasm, GO:0003779: actin binding, GO:0005515: protein binding		0.2294	0.6245	0.9999	1.4657	10.85	11.08	11.48	11.85	12.32	12.22	3

(*Continued*)

TABLE E3. (*Continued*)

205583_s_at	CXorf45	chromosome X open reading frame 45	NM_024810	79868	Hs.110853, Hs.443061			0.4446	0.5153	0.8971	1.0186	8.37	8.82	8.89	9.27	9.39	9.37	3
205471_s_at	DACH1	dachshund homolog 1 (Drosophila)	NM_004392	1602	Hs.129452	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0005515: protein binding		−0.2224	0.3592	0.1686	1.0492	4.98	4.76	5.34	5.15	6.03	5.51	3
205478_at	PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	NM_006741	5502	Hs.505662	GO:0005975: carbohydrate metabolic process, GO:0005977: glycogen metabolic process, GO:0007165: signal transduction, GO:0004864: protein phosphatase inhibitor activity, GO:0004865: type 1 serine/threonine specific protein phosphatase inhibitor activity, GO:0005515: protein binding	04720: Long-term potentiation	0.2333	0.521	0.5217	1.8206	4.22	4.45	4.74	4.74	6.04	5.9	3
205384_at	FXYD1	FXYD domain containing ion transport regulator 1 (phospholemman)	NM_005031	5348	Hs.442498	GO:0006811: ion transport, GO:0006821: chloride transport, GO:0006936: muscle contraction, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005216: ion channel activity, GO:0005254: chloride channel activity, GO:0031404: chloride ion binding		0.0863	0.3406	0.6911	1.2612	2.71	2.8	3.05	3.4	3.97	3.75	3
205463_s_at	PDGFA	platelet-derived growth factor alpha polypeptide	NM_002607	5154	Hs.645488	GO:0000074: regulation of progression through cell cycle, GO:0007166: cell surface receptor linked signal transduction, GO:0007267: cell-cell signaling, GO:0008283: cell proliferation, GO:0008283: cell proliferation, GO:0008284: positive regulation of cell proliferation, GO:0005615: extracellular space, GO:0016020: membrane, GO:0005161: platelet-derived growth factor receptor binding, GO:0008083: growth factor activity	04010: MAPK signaling pathway, 04510: Focal adhesion, 04540: Gap junction, 04810: Regulation of actin cytoskeleton, 05214: Glioma, 05215: Prostate cancer, 05218: Melanoma	−0.0043	0.3691	0.7758	1.1414	4.24	4.24	4.61	5.02	5.39	5.48	3
205330_at	MN1	meningioma (disrupted in balanced translocation) 1	NM_002430	4330	Hs.268515	GO:0007049: cell cycle, GO:0008150: biological_process, GO:0045786: negative regulation of progression through cell cycle, GO:0005575: cellular_component, GO:0003674: molecular_function		0.357	0.6458	0.8351	1.024	5.44	5.8	6.08	6.27	6.46	5.9	3
205383_s_at	ZBTB20	zinc finger and BTB domain containing 20	NM_015642	26137	Hs.655108, Hs.693802	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0003677: DNA binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.1374	0.4968	0.9882	1.4207	9.13	9.26	9.62	10.11	10.55	10.23	3
205277_at	PRDM2	PR domain containing 2, with ZNF domain	NM_012231	7799	Hs.371823	GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.3763	0.2971	0.76	1.35	2.78	3.16	3.08	3.54	4.13	4.17	3
205315_s_at	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	NM_006750	6645	Hs.461117	GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005874: microtubule, GO:0016010: dystrophin-associated glycoprotein complex, GO:0016020: membrane, GO:0031410: cytoplasmic vesicle, GO:0003779: actin binding, GO:0005509: calcium ion binding, GO:0005516: calmodulin binding		−0.0587	0.1459	0.2884	1.3935	7.03	6.97	7.18	7.32	8.43	7.87	3

(*Continued*)

TABLE E3. (*Continued*)

205236_x_at	SOD3	superoxide dismutase 3, extracellular	NM_003102	6649	Hs.2420	GO:0001666: response to hypoxia, GO:0006801: superoxide metabolic process, GO:0005578: proteinaceous extracellular matrix, GO:0005625: soluble fraction, GO:0005802: trans-Golgi network, GO:0004785: copper, zinc superoxide dismutase activity, GO:0005507: copper ion binding, GO:0005515: protein binding, GO:0008201: heparin binding, GO:0008270: zinc ion binding, GO:0016209: antioxidant activity, GO:0016491: oxidoreductase activity, GO:0046872: metal ion binding		0.317	0.6345	0.5971	1.0843	5.67	5.99	6.31	6.27	6.76	6.73	3
205258_at	INHBB	inhibin, beta B	NM_002193	3625	Hs.1735	GO:0001541: ovarian follicle development, GO:0006952: defense response, GO:0009605: response to external stimulus, GO:0030154: cell differentiation, GO:0040007: growth, GO:0046881: positive regulation of follicle-stimulating hormone secretion, GO:0046882: negative regulation of follicle-stimulating hormone secretion, GO:0048178: negative regulation of hepatocyte growth factor biosynthetic process, GO:0005576: extracellular region, GO:0005125: cytokine activity, GO:0005179: hormone activity, GO:0008083: growth factor activity, GO:0042803: protein homodimerization activity, GO:0046789: host cell surface receptor binding	04060: Cytokine-cytokine receptor interaction, 04350: TGF-beta signaling pathway	0.161	0.2811	0.4367	1.0208	2.99	3.16	3.28	3.43	4.02	4.43	3
205168_at	DDR2	discoidin domain receptor family, member 2	NM_006182	4921	Hs.591469, Hs.593833	GO:0006468: protein amino acid phosphorylation, GO:0007155: cell adhesion, GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0008284: positive regulation of cell proliferation, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004713: protein-tyrosine kinase activity, GO:0004714: transmembrane receptor protein tyrosine kinase activity, GO:0004714: transmembrane receptor protein tyrosine kinase activity, GO:0004872: receptor activity, GO:0005524: ATP binding, GO:0016740: transferase activity		0.0189	0.2032	0.5159	1.2478	3.17	3.19	3.38	3.69	4.42	3.99	3

(*Continued*)

TABLE E3. (*Continued*)

205198_s_at	ATP7A	ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)	NM_000052	538	Hs.496414	GO:0006810: transport, GO:0006811: ion transport, GO:0006825: copper ion transport, GO:0006825: copper ion transport, GO:0006878: cellular copper ion homeostasis, GO:0008152: metabolic process, GO:0015694: mercury ion transport, GO:0030001: metal ion transport, GO:0051353: positive regulation of oxidoreductase activity, GO:0005737: cytoplasm, GO:0005770: late endosome, GO:0005783: endoplasmic reticulum, GO:0005794: Golgi apparatus, GO:0005802: trans-Golgi network, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016323: basolateral plasma membrane, GO:0030140: trans-Golgi network transport vesicle, GO:0030173: integral to Golgi membrane, GO:0048471: perinuclear region of cytoplasm, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004008: copper-exporting ATPase activity, GO:0004008: copper-exporting ATPase activity, GO:0005375: copper ion transmembrane transporter activity, GO:0005507: copper ion binding, GO:0005507: copper ion binding, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0015097: mercury ion transmembrane transporter activity, GO:0015662: ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, GO:0016787: hydrolase activity, GO:0016820: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, GO:0032767: copper-dependent protein binding, GO:0046872: metal ion binding, GO:0046873: metal ion transmembrane transporter activity		0.4522	0.6455	0.8414	1.0169	7.22	7.67	7.87	8.06	8.24	8.41	3
205110_s_at	FGF13	fibroblast growth factor 13	NM_004114	2258	Hs.6540	GO:0000165: MAPKKK cascade, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0007399: nervous system development, GO:0005615: extracellular space, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0008083: growth factor activity, GO:0030295: protein kinase activator activity	04010: MAPK signaling pathway, 04810: Regulation of actin cytoskeleton, 05218: Melanoma	0.192	0.4707	0.8567	1.0747	5.09	5.28	5.56	5.95	6.17	6.16	3
205132_at	ACTC1	actin, alpha, cardiac muscle 1	NM_005159	70	Hs.118127	GO:0006936: muscle contraction, GO:0008016: regulation of heart contraction, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005884: actin filament, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008307: structural constituent of muscle		−0.0437	0.2403	0.4425	1.1093	7.66	7.62	7.9	8.11	8.77	8.26	3
205073_at	CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	NM_000775	1573	Hs.152096	GO:0006118: electron transport, GO:0006690: icosanoid metabolic process, GO:0008016: regulation of heart contraction, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0005506: iron ion binding, GO:0008392: arachidonic acid epoxygenase activity, GO:0020037: heme binding, GO:0046872: metal ion binding, GO:0050381: unspecific monooxygenase activity	00590: Arachidonic acid metabolism, 00591: Linoleic acid metabolism	0.075	0.5452	0.8544	1.393	2.79	2.87	3.34	3.65	4.19	4.47	3
205081_at	CRIP1	cysteine-rich protein 1 (intestinal)	NM_001311	1396	Hs.70327	GO:0008283: cell proliferation, GO:0005737: cytoplasm, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.1498	0.3283	0.7772	1.5558	10.56	10.41	10.89	11.34	12.12	12.38	3

(*Continued*)

TABLE E3. (*Continued*)

205006_s_at	NMT2	N-myristoyltransferase 2	NM_004808	9397	Hs.60339	GO:0006499: N-terminal protein myristoylation, GO:0009249: protein lipoylation, GO:0005737: cytoplasm, GO:0004379: glycylpeptide N-tetradecanoyltransferase activity, GO:0008415: acyltransferase activity, GO:0016740: transferase activity		0.0993	0.4827	0.5484	1.0135	6.62	6.72	7.1	7.17	7.63	7.79	3
205011_at	LOH11CR2A	loss of heterozygosity, 11, chromosomal region 2, gene A	NM_014622	4013	Hs.152944	GO:0007049: cell cycle, GO:0045786: negative regulation of progression through cell cycle		0.2286	0.4568	0.6822	1.0473	7.1	7.33	7.56	7.78	8.15	8.31	3
204964_s_at	SSPN	sarcospan (Kras oncogene-associated gene)	AL136756	8082	Hs.183428	GO:0006936: muscle contraction, GO:0007155: cell adhesion, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005887: integral to plasma membrane, GO:0016010: dystrophin-associated glycoprotein complex, GO:0016020: membrane, GO:0030133: transport vesicle		0.1107	0.3964	0.8831	1.4833	2.12	2.23	2.52	3.01	3.61	3.57	3
204985_s_at	TRAPPC6A	trafficking protein particle complex 6A	NM_024108	79090	Hs.466929	GO:0006810: transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0005783: endoplasmic reticulum		0.3534	0.6045	0.9796	1.2657	6	6.35	6.6	6.98	7.26	7.43	3
204838_s_at	MLH3	mutL homolog 3 (E. coli)	NM_014381	27030	Hs.436650	GO:0006298: mismatch repair, GO:0006298: mismatch repair, GO:0007131: meiotic recombination, GO:0005634: nucleus, GO:0003696: satellite DNA binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0030983: mismatched DNA binding		0.3912	0.4319	0.9993	1.006	4.69	5.08	5.12	5.69	5.69	5.66	3
204948_s_at	FST	follistatin	NM_013409	10468	Hs.9914	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0007276: gamete generation, GO:0007389: pattern specification process, GO:0008585: female gonad development, GO:0030509: BMP signaling pathway, GO:0042475: odontogenesis (sensu Vertebrata), GO:0045596: negative regulation of cell differentiation, GO:0046882: negative regulation of follicle-stimulating hormone secretion, GO:0051798: positive regulation of hair follicle development, GO:0005576: extracellular region, GO:0005515: protein binding, GO:0017106: activin inhibitor activity	04350: TGF-beta signaling pathway	0.4978	0.4777	0.6852	1.2315	6.68	7.17	7.15	7.36	7.91	8.38	3
204797_s_at	EML1	echinoderm microtubule associated protein like 1	NM_004434	2009	Hs.12451	GO:0007601: visual perception, GO:0005737: cytoplasm, GO:0005874: microtubule, GO:0005875: microtubule associated complex		0.3083	0.7107	0.9737	1.0751	7.4	7.71	8.11	8.38	8.48	8.59	3
204800_s_at	DHRS12	dehydrogenase/reductase (SDR family) member 12	NM_024705	79758	Hs.266728	GO:0008152: metabolic process, GO:0016491: oxidoreductase activity		0.6142	0.6429	0.8984	1.0539	3.23	3.84	3.87	4.13	4.28	4.73	3
204718_at	EPHB6	EPH receptor B6	NM_004445	2051	Hs.380089	GO:0006468: protein amino acid phosphorylation, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0004713: protein-tyrosine kinase activity, GO:0004872: receptor activity, GO:0005003: ephrin receptor activity, GO:0005524: ATP binding	04360: Axon guidance	0.3447	0.6194	0.6635	1.0097	9.45	9.8	10.07	10.12	10.46	10.35	3
204788_s_at	PPOX	protoporphyrinogen oxidase	NM_000309	5498	Hs.517373	GO:0006118: electron transport, GO:0006783: heme biosynthetic process, GO:0005739: mitochondrion, GO:0016020: membrane, GO:0031304: intrinsic to mitochondrial inner membrane, GO:0031966: mitochondrial membrane, GO:0004729: protoporphyrinogen oxidase activity, GO:0016491: oxidoreductase activity, GO:0050660: FAD binding	00860: Porphyrin and chlorophyll metabolism	0.1468	0.4477	0.7409	1.3453	6.94	7.08	7.38	7.68	8.28	8.25	3

(*Continued*)

TABLE E3. (*Continued*)

204497_at	ADCY9	adenylate cyclase 9	AB011092	115	Hs.391860, Hs.610484	GO:0006171: cAMP biosynthetic process, GO:0007242: intracellular signaling cascade, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0000287: magnesium ion binding, GO:0004016: adenylate cyclase activity	00230: Purine metabolism, 04020: Calcium signaling pathway, 04540: Gap junction, 04912: GnRH signaling pathway, 04916: Melanogenesis, 05110: Cholera - Infection	0.1977	0.4814	0.9038	1.1459	7.89	8.09	8.37	8.79	9.03	8.89	3
204610_s_at	CCDC85B	coiled-coil domain containing 85B	NM_006848	11007	Hs.66713	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0003674: molecular_function		0.0952	0.4293	0.5786	1.0369	7.81	7.9	8.24	8.39	8.84	8.55	3
204431_at	TLE2	transducin-like enhancer of split 2 (E(spl) homolog, Drosophila)	NM_003260	7089	Hs.332173	GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0009887: organ morphogenesis, GO:0016055: Wnt receptor signaling pathway, GO:0005634: nucleus, GO:0005515: protein binding		0.0486	0.1854	0.5456	1.0432	2.88	2.93	3.07	3.43	3.92	3.81	3
204442_x_at	LTBP4	latent transforming growth factor beta binding protein 4	NM_003573	8425	Hs.466766	GO:0001558: regulation of cell growth, GO:0006457: protein folding, GO:0007275: multicellular organismal development, GO:0008150: biological_process, GO:0016049: cell growth, GO:0016049: cell growth, GO:0017015: regulation of transforming growth factor beta receptor signaling pathway, GO:0030162: regulation of proteolysis, GO:0030162: regulation of proteolysis, GO:0030252: growth hormone secretion, GO:0045595: regulation of cell differentiation, GO:0005575: cellular_component, GO:0005578: proteinaceous extracellular matrix, GO:0005578: proteinaceous extracellular matrix, GO:0005578: proteinaceous extracellular matrix, GO:0005024: transforming growth factor beta receptor activity, GO:0005178: integrin binding, GO:0005509: calcium ion binding, GO:0005509: calcium ion binding, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005539: glycosaminoglycan binding, GO:0008083: growth factor activity, GO:0008083: growth factor activity, GO:0050431: transforming growth factor beta binding		0.0326	0.3395	0.5464	1.5753	7.12	7.16	7.46	7.67	8.7	8.32	3
204303_s_at	KIAA0427	KIAA0427	NM_014772	9811	Hs.145230	GO:0016070: RNA metabolic process, GO:0005515: protein binding		−0.0848	0.0686	0.1362	1.2012	3.53	3.45	3.6	3.67	4.73	4.03	3

(*Continued*)

TABLE E3. (*Continued*)

204422_s_at	FGF2	fibroblast growth factor 2 (basic)	NM_002006	2247	Hs.284244	GO:0000074: regulation of progression through cell cycle, GO:0000186: activation of MAPKK activity, GO:0000187: activation of MAPK activity, GO:0001525: angiogenesis, GO:0001759: induction of an organ, GO:0001934: positive regulation of protein amino acid phosphorylation, GO:0006935: chemotaxis, GO:0007165: signal transduction, GO:0007265: Ras protein signal transduction, GO:0007267: cell-cell signaling, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0007517: muscle development, GO:0008283: cell proliferation, GO:0008285: negative regulation of cell proliferation, GO:0009887: organ morphogenesis, GO:0010001: glial cell differentiation, GO:0021940: positive regulation of granule cell precursor proliferation, GO:0030324: lung development, GO:0045597: positive regulation of cell differentiation, GO:0046668: regulation of retinal programmed cell death, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005515: protein binding, GO:0008083: growth factor activity, GO:0008201: heparin binding	04010: MAPK signaling pathway, 04810: Regulation of actin cytoskeleton, 05218: Melanoma	0.0256	0.2751	0.6482	1.3245	2.89	2.91	3.16	3.53	4.21	4.63	3
204257_at	FADS3	fatty acid desaturase 3	NM_021727	3995	Hs.21765	GO:0006629: lipid metabolic process, GO:0006636: unsaturated fatty acid biosynthetic process, GO:0005624: membrane fraction, GO:0016020: membrane, GO:0003674: molecular_function, GO:0005506: iron ion binding, GO:0016491: oxidoreductase activity, GO:0016717: oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water, GO:0020037: heme binding, GO:0046914: transition metal ion binding	00591: Linoleic acid metabolism	0.1313	0.4992	0.5782	1.0391	7.02	7.15	7.52	7.6	8.06	7.75	3
204288_s_at	SORBS2	sorbin and SH3 domain containing 2	NM_021069	8470	Hs.655143	GO:0008150: biological_process, GO:0005634: nucleus, GO:0005634: nucleus, GO:0015629: actin cytoskeleton, GO:0030018: Z disc, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding, GO:0008093: cytoskeletal adaptor activity, GO:0008307: structural constituent of muscle		0.3635	0.7113	0.8953	1.742	6.34	6.71	7.06	7.24	8.09	7.96	3
204151_x_at	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	NM_001353	1645	Hs.460260	GO:0006118: electron transport, GO:0006805: xenobiotic metabolic process, GO:0007586: digestion, GO:0008206: bile acid metabolic process, GO:0015721: bile acid and bile salt transport, GO:0030299: cholesterol absorption, GO:0042632: cholesterol homeostasis, GO:0051260: protein homooligomerization, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0004033: aldo-keto reductase activity, GO:0016491: oxidoreductase activity, GO:0032052: bile acid binding, GO:0047006: 20-alpha-hydroxysteroid dehydrogenase activity, GO:0047042: 3-alpha-hydroxysteroid dehydrogenase (B-specific) activity, GO:0047115: trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	00980: Metabolism of xenobiotics by cytochrome P450	0.222	0.4522	0.6067	1.0318	10.86	11.08	11.31	11.46	11.89	11.74	3

(*Continued*)

TABLE E3. (*Continued*)

204248_at	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	NM_002067	2767	Hs.278432, Hs.654784, Hs.655202	GO:0001501: skeletal development, GO:0001508: regulation of action potential, GO:0006471: protein amino acid ADP-ribosylation, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007507: heart development, GO:0045634: regulation of melanocyte differentiation, GO:0048066: pigmentation during development, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0016459: myosin complex, GO:0000166: nucleotide binding, GO:0003774: motor activity, GO:0003924: GTPase activity, GO:0004871: signal transducer activity, GO:0005525: GTP binding	04020: Calcium signaling pathway, 04540: Gap junction, 04730: Long-term depression, 04912: GnRH signaling pathway	−0.1196	0.0982	0.4275	1.1665	6.96	6.84	7.05	7.38	8.12	7.9	3
204106_at	TESK1	testis-specific kinase 1	NM_006285	7016	Hs.653259	GO:0006468: protein amino acid phosphorylation, GO:0007283: spermatogenesis, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004674: protein serine/threonine kinase activity, GO:0004713: protein-tyrosine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0030145: manganese ion binding		−0.1353	0.1684	0.2575	1.0749	6.59	6.45	6.76	6.85	7.66	7.52	3
204134_at	PDE2A	phosphodiesterase 2A, cGMP-stimulated	NM_002599	5138	Hs.503163	GO:0007165: signal transduction, GO:0016020: membrane, GO:0004114: 3′,5′-cyclic-nucleotide phosphodiesterase activity, GO:0004118: cGMP-stimulated cyclic-nucleotide phosphodiesterase activity, GO:0016787: hydrolase activity	00230: Purine metabolism	0.2491	0.4724	0.7757	1.4004	4.19	4.44	4.66	4.96	5.59	5.12	3
204066_s_at	CENTG2	centaurin, gamma 2	NM_014914	116987	Hs.435039			0.1954	0.5644	0.9413	1.2544	6.46	6.66	7.02	7.4	7.71	7.65	3
204069_at	MEIS1	Meis homeobox 1	NM_002398	4211	Hs.526754, Hs.603755	GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0005634: nucleus, GO:0005667: transcription factor complex, GO:0003705: RNA polymerase II transcription factor activity, enhancer binding, GO:0005515: protein binding, GO:0043565: sequence-specific DNA binding		0.4517	0.5827	0.9104	1.0218	4.61	5.06	5.19	5.52	5.63	5.56	3
203929_s_at	MAPT	microtubule-associated protein tau	AI056359	4137	Hs.101174	GO:0000226: microtubule cytoskeleton organization and biogenesis, GO:0007026: negative regulation of microtubule depolymerization, GO:0031116: positive regulation of microtubule polymerization, GO:0045773: positive regulation of axon extension, GO:0048699: generation of neurons, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0005856: cytoskeleton, GO:0005875: microtubule associated complex, GO:0005886: plasma membrane, GO:0030424: axon, GO:0030426: growth cone, GO:0045298: tubulin complex, GO:0005200: structural constituent of cytoskeleton, GO:0008017: microtubule binding, GO:0008034: lipoprotein binding, GO:0017124: SH3 domain binding, GO:0019899: enzyme binding	01510: Neurodegenerative Disorders, 04010: MAPK signaling pathway, 05010: Alzheimer's disease	0.3437	0.564	0.9458	1.4093	8.22	8.57	8.79	9.17	9.63	9.53	3

(*Continued*)

TABLE E3. (*Continued*)

204021_s_at	PURA	purine-rich element binding protein A	NM_005859	5813	Hs.443121	GO:0006268: DNA unwinding during replication, GO:0006270: DNA replication initiation, GO:0006350: transcription, GO:0007399: nervous system development, GO:0008284: positive regulation of cell proliferation, GO:0045892: negative regulation of transcription, DNA-dependent, GO:0000784: nuclear chromosome, telomeric region, GO:0005634: nucleus, GO:0005662: DNA replication factor A complex, GO:0005737: cytoplasm, GO:0003691: double-stranded telomeric DNA binding, GO:0003697: single-stranded DNA binding, GO:0003705: RNA polymerase II transcription factor activity, enhancer binding, GO:0008134: transcription factor binding, GO:0046332: SMAD binding		−0.0743	0.0928	0.3814	1.2666	7.61	7.54	7.7	7.99	8.88	8.33	3
203872_at	ACTA1	actin, alpha 1, skeletal muscle	NM_001100	58	Hs.1288	GO:0006936: muscle contraction, GO:0030240: muscle thin filament assembly, GO:0048741: skeletal muscle fiber development, GO:0001725: stress fiber, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005865: striated muscle thin filament, GO:0005884: actin filament, GO:0000166: nucleotide binding, GO:0005198: structural molecule activity, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0017022: myosin binding, GO:0043531: ADP binding		0.3162	1.0276	0.9379	1.3143	5.45	5.76	6.48	6.39	6.76	6.62	3
203906_at	IQSEC1	IQ motif and Sec7 domain 1	AI652645	9922	Hs.475506	GO:0032012: regulation of ARF protein signal transduction, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005086: ARF guanyl-nucleotide exchange factor activity		0.2555	0.5892	0.6144	1.1401	6.22	6.48	6.81	6.83	7.36	6.98	3
203851_at	IGFBP6	insulin-like growth factor binding protein 6	NM_002178	3489	Hs.274313	GO:0001558: regulation of cell growth, GO:0007165: signal transduction, GO:0008285: negative regulation of cell proliferation, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005520: insulin-like growth factor binding		0.2709	0.4704	0.9445	1.8845	7.83	8.1	8.3	8.78	9.72	9.78	3
203865_s_at	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	NM_015833	104	Hs.474018	GO:0006397: mRNA processing, GO:0005622: intracellular, GO:0003725: double-stranded RNA binding, GO:0004000: adenosine deaminase activity, GO:0008270: zinc ion binding, GO:0016787: hydrolase activity, GO:0046872: metal ion binding		0.2219	0.5212	0.6872	1.0912	8.27	8.5	8.8	8.96	9.37	9.2	3
203813_s_at	SLIT3	slit homolog 3 (Drosophila)	AB011538	6586	Hs.604116	GO:0007275: multicellular organismal development, GO:0007417: central nervous system development, GO:0030154: cell differentiation, GO:0005615: extracellular space, GO:0005198: structural molecule activity, GO:0005509: calcium ion binding, GO:0005515: protein binding	04360: Axon guidance	0.1523	0.5126	0.9894	1.1743	8.12	8.28	8.64	9.11	9.3	9.03	3
203825_at	BRD3	bromodomain containing 3	NM_007371	8019	Hs.522472	GO:0008150: biological_process, GO:0005634: nucleus, GO:0003674: molecular_function		0.1797	0.4561	0.7306	1.2182	8.34	8.52	8.79	9.07	9.56	9.3	3
203729_at	EMP3	epithelial membrane protein 3	NM_001425	2014	Hs.9999	GO:0007275: multicellular organismal development, GO:0008219: cell death, GO:0008285: negative regulation of cell proliferation, GO:0016049: cell growth, GO:0005624: membrane fraction, GO:0016020: membrane, GO:0016021: integral to membrane		0.1115	0.3762	0.8935	1.1415	9.14	9.25	9.51	10.03	10.28	10.09	3
203756_at	ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17	NM_014786	9828	Hs.533719	GO:0030036: actin cytoskeleton organization and biogenesis, GO:0035023: regulation of Rho protein signal transduction, GO:0005622: intracellular, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity		0.2066	0.2809	0.5474	1.1891	4.05	4.26	4.33	4.6	5.24	4.7	3

(*Continued*)

TABLE E3. (*Continued*)

203706_s_at	FZD7	frizzled homolog 7 (Drosophila)	NM_003507	8324	Hs.173859	GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007275: multicellular organismal development, GO:0016055: Wnt receptor signaling pathway, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004926: non-G-protein coupled 7TM receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0042813: Wnt receptor activity	04310: Wnt signaling pathway, 04916: Melanogenesis, 05210: Colorectal cancer, 05217: Basal cell carcinoma	0.3391	0.6227	0.9912	1.2456	8.49	8.83	9.11	9.48	9.73	9.99	3
203723_at	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	NM_002221	3707	Hs.528087, Hs.659396	GO:0007165: signal transduction, GO:0000166: nucleotide binding, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0008440: inositol trisphosphate 3-kinase activity, GO:0016301: kinase activity, GO:0016740: transferase activity	00562: Inositol phosphate metabolism, 04020: Calcium signaling pathway, 04070: Phosphatidylinositol signaling system	0.1945	0.4247	0.8853	1.2356	7.53	7.72	7.95	8.41	8.76	8.75	3
203697_at	FRZB	frizzled-related protein	U91903	2487	Hs.128453	GO:0001501: skeletal development, GO:0007275: multicellular organismal development, GO:0016055: Wnt receptor signaling pathway, GO:0030154: cell differentiation, GO:0030178: negative regulation of Wnt receptor signaling pathway, GO:0005576: extracellular region, GO:0016020: membrane, GO:0017147: Wnt-protein binding		0.4004	0.7216	0.9957	1.5466	7.29	7.69	8.01	8.29	8.84	8.89	3
203698_s_at	FRZB	frizzled-related protein	U91903	2487	Hs.128453	GO:0001501: skeletal development, GO:0007275: multicelllular organismal development, GO:0016055: Wnt receptor signaling pathway, GO:0030154: cell differentiation, GO:0030178: negative regulation of Wnt receptor signaling pathway, GO:0005576: extracellular region, GO:0016020: membrane, GO:0017147: Wnt-protein binding		0.3914	0.6619	0.909	1.2359	4.42	4.81	5.08	5.33	5.66	5.91	3
203632_s_at	GPRC5B	G protein-coupled receptor, family C, group 5, member B	NM_016235	51704	Hs.148685	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007601: visual perception, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0031410: cytoplasmic vesicle, GO:0004872: receptor activity, GO:0005118: sevenless binding, GO:0008067: metabotropic glutamate, GABA-B-like receptor activity		0.2092	0.7301	0.8015	1.364	3.92	4.12	4.65	4.72	5.28	4.82	3

(*Continued*)

TABLE E3. (*Continued*)

203685_at	BCL2	B-cell CLL/lymphoma 2	NM_000633	596	Hs.150749	GO:0000074: regulation of progression through cell cycle, GO:0001836: release of cytochrome c from mitochondria, GO:0006916: anti-apoptosis, GO:0006959: humoral immune response, GO:0007565: female pregnancy, GO:0009314: response to radiation, GO:0009636: response to toxin, GO:0010039: response to iron ion, GO:0032848: negative regulation of cellular pH reduction, GO:0035094: response to nicotine, GO:0043496: regulation of protein homodimerization, GO:0043497: regulation of protein heterodimerization, GO:0043524: negative regulation of neuron apoptosis, GO:0046902: regulation of mitochondrial membrane permeability, GO:0051402: neuron apoptosis, GO:0051607: defense response to virus, GO:0051881: regulation of mitochondrial membrane potential, GO:0051902: negative regulation of mitochondrial depolarization, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0005741: mitochondrial outer membrane, GO:0005783: endoplasmic reticulum, GO:0005829: cytosol, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0031965: nuclear membrane, GO:0002020: protease binding, GO:0042803: protein homodimerization activity, GO:0046982: protein heterodimerization activity, GO:0051434: BH3 domain binding	01510: Neurodegenerative Disorders, 04210: Apoptosis, 04510: Focal adhesion, 05030: Amyotrophic lateral sclerosis (ALS), 05060: Prion disease, 05210: Colorectal cancer, 05215: Prostate cancer, 05222: Small cell lung cancer	0.3467	0.5542	0.9815	1.5175	6.51	6.86	7.07	7.49	8.03	8.24	3
203521_s_at	ZNF318	zinc finger protein 318	NM_014345	24149	Hs.509718	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.3506	0.5294	0.78	1.0815	4.28	4.63	4.81	5.06	5.36	5.35	3
203628_at	IGF1R	insulin-like growth factor 1 receptor	H05812	3480	Hs.643120, Hs.653608, Hs.695288	GO:0000074: regulation of progression through cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0006916: anti-apoptosis, GO:0007165: signal transduction, GO:0007420: brain development, GO:0008284: positive regulation of cell proliferation, GO:0008286: insulin receptor signaling pathway, GO:0009887: organ morphogenesis, GO:0030238: male sex determination, GO:0046777: protein amino acid autophosphorylation, GO:0048009: insulin-like growth factor receptor signaling pathway, GO:0051262: protein tetramerization, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004713: protein-tyrosine kinase activity, GO:0004872: receptor activity, GO:0005010: insulin-like growth factor receptor activity, GO:0005520: insulin-like growth factor binding, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0043548: phosphoinositide 3-kinase binding, GO:0043560: insulin receptor substrate binding	04510: Focal adhesion, 04520: Adherens junction, 04730: Long-term depression, 05210: Colorectal cancer, 05214: Glioma, 05215: Prostate cancer, 05218: Melanoma	−0.4535	0.4148	0.595	1.2242	6.05	5.6	6.47	6.65	7.28	7.43	3
203424_s_at	IGFBP5	insulin-like growth factor binding protein 5	AW157548	3488	Hs.635441	GO:0001558: regulation of cell growth, GO:0007165: signal transduction, GO:0005576: extracellular region, GO:0005783: endoplasmic reticulum, GO:0005520: insulin-like growth factor binding		0.1404	0.1056	0.4911	1.21	2.2	2.34	2.3	2.69	3.41	2.59	3

(*Continued*)

TABLE E3. (*Continued*)

203509_at	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	NM_003105	6653	Hs.368592	GO:0006629: lipid metabolic process, GO:0006869: lipid transport, GO:0006898: receptor-mediated endocytosis, GO:0008202: steroid metabolic process, GO:0008203: cholesterol metabolic process, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004888: transmembrane receptor activity, GO:0005319: lipid transporter activity		0.1546	0.2281	0.6288	1.0921	7.4	7.55	7.63	8.03	8.49	8.35	3
203355_s_at	PSD3	pleckstrin and Sec7 domain containing 3	NM_015310	23362	Hs.434255	GO:0032012: regulation of ARF protein signal transduction, GO:0005622: intracellular, GO:0005086: ARF guanyl-nucleotide exchange factor activity		0.3227	0.412	0.9842	1.3475	8.13	8.45	8.54	9.11	9.48	9.04	3
203382_s_at	APOE	apolipoprotein E	NM_000041	348	Hs.654439	GO:0000302: response to reactive oxygen species, GO:0006707: cholesterol catabolic process, GO:0006869: lipid transport, GO:0006874: cellular calcium ion homeostasis, GO:0006917: induction of apoptosis, GO:0007010: cytoskeleton organization and biogenesis, GO:0007271: synaptic transmission, cholinergic, GO:0007611: learning and/or memory, GO:0008015: circulation, GO:0030516: regulation of axon extension, GO:0042157: lipoprotein metabolic process, GO:0042311: vasodilation, GO:0042632: cholesterol homeostasis, GO:0046907: intracellular transport, GO:0048168: regulation of neuronal synaptic plasticity, GO:0051262: protein tetramerization, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005737: cytoplasm, GO:0042627: chylomicron, GO:0001540: beta-amyloid binding, GO:0005319: lipid transporter activity, GO:0005543: phospholipid binding, GO:0008034: lipoprotein binding, GO:0008201: heparin binding, GO:0016209: antioxidant activity, GO:0048156: tau protein binding, GO:0050749: apolipoprotein E receptor binding	01510: Neurodegenerative Disorders, 05010: Alzheimer's disease	0.2889	0.4652	0.8277	1.1437	9.15	9.44	9.62	9.98	10.3	10.48	3
203249_at	EZH1	enhancer of zeste homolog 1 (Drosophila)	AB002386	2145	Hs.194669	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0009653: anatomical structure morphogenesis, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003682: chromatin binding, GO:0005515: protein binding		0.5492	0.7083	0.9098	1.4439	7.15	7.7	7.86	8.06	8.6	8.47	3
203304_at	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	NM_012342	25805	Hs.533336	GO:0005737: cytoplasm, GO:0016020: membrane, GO:0016021: integral to membrane		−0.0253	0.0608	0.192	1.0069	3.91	3.89	3.97	4.1	4.92	5.4	3
203151_at	MAP1A	microtubule-associated protein 1A	NM_002373	4130	Hs.194301, Hs.619338, Hs.655300	GO:0007605: sensory perception of sound, GO:0005829: cytosol, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0005198: structural molecule activity, GO:0005515: protein binding		0.1954	0.297	0.7703	1.8852	5.62	5.82	5.92	6.39	7.51	6.9	3
203188_at	B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	NM_006876	11041	Hs.8526	GO:0030311: poly-N-acetyllactosamine biosynthetic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030173: integral to Golgi membrane, GO:0008532: N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase activity, GO:0016757: transferase activity, transferring glycosyl groups	00533: Keratan sulfate biosynthesis, 00602: Glycosphingolipid biosynthesis - neo-lactoseries, 01030: Glycan structures - biosynthesis 1, 01031: Glycan structures - biosynthesis 2	0.3705	0.5459	0.7565	1.0837	6.92	7.29	7.47	7.68	8.01	8.12	3

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TABLE E3. (*Continued*)

203071_at	SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	NM_004636	7869	Hs.82222	GO:0007267: cell-cell signaling, GO:0007275: multicellular organismal development, GO:0007411: axon guidance, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0004872: receptor activity	04360: Axon guidance	−0.009	0.2194	0.7082	1.5339	2.32	2.31	2.54	3.03	3.86	2.8	3
203081_at	CTNNBIP1	catenin, beta interacting protein 1	NM_020248	56998	Hs.463759	GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0007275: multicellular organismal development, GO:0008283: cell proliferation, GO:0016055: Wnt receptor signaling pathway, GO:0005737: cytoplasm, GO:0008013: beta-catenin binding	04310: Wnt signaling pathway	0.0415	0.4585	0.7006	1.0814	9.4	9.44	9.86	10.1	10.48	10.62	3
203020_at	RABGAP1L	RAB GTPase activating protein 1-like	NM_014857	9910	Hs.585378	GO:0032313: regulation of Rab GTPase activity, GO:0005622: intracellular, GO:0005097: Rab GTPase activator activity		0.5381	0.7701	0.9945	1.0591	8.39	8.93	9.16	9.38	9.45	9.64	3
203065_s_at	CAV1	caveolin 1, caveolae protein, 22kDa	NM_001753	857	Hs.74034	GO:0000188: inactivation of MAPK activity, GO:0001937: negative regulation of endothelial cell proliferation, GO:0006641: triacylglycerol metabolic process, GO:0009968: negative regulation of signal transduction, GO:0019217: regulation of fatty acid metabolic process, GO:0019915: sequestering of lipid, GO:0030301: cholesterol transport, GO:0042632: cholesterol homeostasis, GO:0045019: negative regulation of nitric oxide biosynthetic process, GO:0045907: positive regulation of vasoconstriction, GO:0045908: negative regulation of vasodilation, GO:0051260: protein homooligomerization, GO:0000139: Golgi membrane, GO:0000299: integral to membrane of membrane fraction, GO:0005783: endoplasmic reticulum, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016599: caveolar membrane, GO:0016599: caveolar membrane, GO:0045121: lipid raft, GO:0048471: perinuclear region of cytoplasm, GO:0005198: structural molecule activity, GO:0005515: protein binding, GO:0015485: cholesterol binding	04510: Focal adhesion	0.1694	0.4656	0.9033	1.1987	10.56	10.73	11.02	11.46	11.76	11.63	3
202982_s_at	ACOT2	acyl-CoA thioesterase 2	NM_006821	10965	Hs.446685, Hs.666961	GO:0000038: very-long-chain fatty acid metabolic process, GO:0001676: long-chain fatty acid metabolic process, GO:0006629: lipid metabolic process, GO:0006637: acyl-CoA metabolic process, GO:0005739: mitochondrion, GO:0005515: protein binding, GO:0016290: palmitoyl-CoA hydrolase activity, GO:0016787: hydrolase activity		0.206	0.2937	0.8557	1.3924	6.2	6.4	6.49	7.05	7.59	8.01	3
203006_at	INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	NM_005539	3632	Hs.523360, Hs.694734	GO:0007154: cell communication, GO:0016020: membrane, GO:0004437: inositol or phosphatidylinositol phosphatase activity, GO:0004445: inositol-polyphosphate 5-phosphatase activity, GO:0016787: hydrolase activity	00562: Inositol phosphate metabolism, 04070: Phosphatidylinositol signaling system	0.1278	0.5772	0.854	1.2156	8.69	8.82	9.27	9.55	9.91	10.04	3
202908_at	WFS1	Wolfram syndrome 1 (wolframin)	NM_006005	7466	Hs.518602	GO:0006091: generation of precursor metabolites and energy, GO:0007399: nervous system development, GO:0007601: visual perception, GO:0007605: sensory perception of sound, GO:0005624: membrane fraction, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane		0.0637	0.4672	0.7422	1.8439	5.23	5.3	5.7	5.97	7.08	6.96	3
202975_s_at	RHOBTB3	Rho-related BTB domain containing 3	N21138	22836	Hs.445030	GO:0008150: biological_process, GO:0003924: GTPase activity, GO:0005515: protein binding		0.1168	0.6472	0.9984	1.6647	3.67	3.79	4.32	4.67	5.34	5.71	3
202759_s_at	PALM2-AKAP2	PALM2-AKAP2 protein	BE879367	445815	Hs.591908			0.3352	0.5086	0.9429	1.0228	8.85	9.18	9.36	9.79	9.87	10	3

(*Continued*)

TABLE E3. (*Continued*)

202796_at	SYNPO	synaptopodin	NM_007286	11346	Hs.435228, Hs.654723	GO:0005737: cytoplasm, GO:0005923: tight junction, GO:0015629: actin cytoskeleton, GO:0016020: membrane, GO:0030054: cell junction, GO:0042995: cell projection, GO:0043197: dendritic spine, GO:0045202: synapse, GO:0003779: actin binding		0.0236	0.2304	0.2962	1.1446	7.33	7.35	7.56	7.62	8.47	7.92	3
202724_s_at	FOXO1	forkhead box O1	NM_002015	2308	Hs.370666	GO:0001568: blood vessel development, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006916: anti-apoptosis, GO:0008286: insulin receptor signaling pathway, GO:0042127: regulation of cell proliferation, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0016563: transcription activator activity, GO:0043565: sequence-specific DNA binding	04910: Insulin signaling pathway, 05215: Prostate cancer	0.1231	0.4004	0.7467	1.1156	8.4	8.52	8.8	9.15	9.52	9.7	3
202732_at	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	NM_007066	11142	Hs.651213	GO:0006469: negative regulation of protein kinase activity, GO:0004862: cAMP-dependent protein kinase inhibitor activity, GO:0005515: protein binding		0.1586	0.5597	0.8657	1.2571	8.09	8.25	8.65	8.96	9.35	9.12	3
202669_s_at	EFNB2	ephrin-B2	U16797	1948	Hs.149239	GO:0007267: cell-cell signaling, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0009653: anatomical structure morphogenesis, GO:0030154: cell differentiation, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0046875: ephrin receptor binding	04360: Axon guidance	−0.2544	0.1501	0.6348	1.346	2.63	2.37	2.78	3.26	3.98	3.73	3
202723_s_at	FOXO1	forkhead box O1	AW117498	2308	Hs.370666	GO:0001568: blood vessel development, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006916: anti-apoptosis, GO:0008286: insulin receptor signaling pathway, GO:0042127: regulation of cell proliferation, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0016563: transcription activator activity, GO:0043565: sequence-specific DNA binding	04910: Insulin signaling pathway, 05215: Prostate cancer	0.4702	0.4523	0.7746	1.4942	7.01	7.48	7.46	7.79	8.51	8.12	3
202519_at	MLXIP	MLX interacting protein	NM_014938	22877	Hs.437153	GO:0045449: regulation of transcription, GO:0005634: nucleus, GO:0030528: transcription regulator activity		0.2357	0.3756	0.8368	1.2994	8.07	8.31	8.45	8.91	9.37	9.34	3
202548_s_at	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	NM_003899	8874	Hs.508738	GO:0007165: signal transduction, GO:0035023: regulation of Rho protein signal transduction, GO:0005622: intracellular, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity	04810: Regulation of actin cytoskeleton	0.4034	0.5717	0.8952	1.2972	7.49	7.9	8.07	8.39	8.79	8.81	3
202500_at	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2	NM_006736	3300	Hs.77768	GO:0006457: protein folding, GO:0006986: response to unfolded protein, GO:0031072: heat shock protein binding, GO:0051082: unfolded protein binding		0.1877	0.5121	0.7796	1.2516	7.68	7.86	8.19	8.46	8.93	9.08	3
202512_s_at	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	AK001899	9474	Hs.486063	GO:0006914: autophagy, GO:0006915: apoptosis, GO:0005737: cytoplasm, GO:0005776: autophagic vacuole, GO:0005515: protein binding	04140: Regulation of autophagy	0.4103	0.6127	0.9701	1.2343	4.49	4.9	5.11	5.46	5.73	5.89	3
202468_s_at	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	NM_003798	8727	Hs.58488	GO:0006915: apoptosis, GO:0007155: cell adhesion, GO:0005737: cytoplasm, GO:0015629: actin cytoskeleton, GO:0016020: membrane, GO:0005198: structural molecule activity, GO:0045296: cadherin binding		0.1709	0.6297	0.8472	1.135	8.24	8.41	8.87	9.09	9.37	9.62	3

(*Continued*)

TABLE E3. (*Continued*)

202481_at	DHRS3	dehydrogenase/reductase (SDR family) member 3	NM_004753	9249	Hs.289347	GO:0007601: visual perception, GO:0008152: metabolic process, GO:0042572: retinol metabolic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0009055: electron carrier activity, GO:0016491: oxidoreductase activity	00361: gamma-Hexachlorocyclohexane degradation, 00363: Bisphenol A degradation, 00624: 1- and 2-Methylnaphthalene degradation, 00626: Naphthalene and anthracene degradation, 00632: Benzoate degradation via CoA ligation, 00642: Ethylbenzene degradation, 00903: Limonene and pinene degradation	0.3915	0.5585	0.6722	1.0071	8.15	8.54	8.71	8.82	9.16	9.12	3
202328_s_at	PKD1	polycystic kidney disease 1 (autosomal dominant)	NM_000296	5310	Hs.75813	GO:0007156: homophilic cell adhesion, GO:0007161: calcium-independent cell-matrix adhesion, GO:0007218: neuropeptide signaling pathway, GO:0008150: biological_process, GO:0009653: anatomical structure morphogenesis, GO:0005575: cellular_component, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003674: molecular_function, GO:0005515: protein binding, GO:0005529: sugar binding		0.0676	0.3205	0.7893	1.2998	6.23	6.29	6.55	7.02	7.53	7.31	3
202368_s_at	TRAM2	translocation associated membrane protein 2	NM_012288	9697	Hs.520182	GO:0006605: protein targeting, GO:0015031: protein transport, GO:0016020: membrane, GO:0016021: integral to membrane		−0.2608	0.1796	0.8199	1.6336	3.69	3.43	3.87	4.51	5.33	4.38	3
202273_at	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	NM_002609	5159	Hs.509067	GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0050730: regulation of peptidyl-tyrosine phosphorylation, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0004872: receptor activity, GO:0004992: platelet activating factor receptor activity, GO:0005017: platelet-derived growth factor receptor activity, GO:0005021: vascular endothelial growth factor receptor activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04020: Calcium signaling pathway, 04060: Cytokine-cytokine receptor interaction, 04510: Focal adhesion, 04540: Gap junction, 04810: Regulation of actin cytoskeleton, 05210: Colorectal cancer, 05214: Glioma, 05215: Prostate cancer, 05218: Melanoma	0.245	0.4949	0.9726	1.1867	9.52	9.76	10.01	10.49	10.7	10.22	3
202289_s_at	TACC2	transforming, acidic coiled-coil containing protein 2	NM_006997	10579	Hs.501252, Hs.695119	GO:0005737: cytoplasm, GO:0005515: protein binding		0.1256	0.3649	0.6447	1.0095	10.41	10.54	10.78	11.06	11.42	11.56	3
202250_s_at	WDR42A	WD repeat domain 42A	NM_015726	50717	Hs.632447			0.2409	0.4397	0.5474	1.051	7.53	7.77	7.97	8.08	8.58	8.38	3
202262_x_at	DDAH2	dimethylarginine dimethylaminohydrolase 2	NM_013974	23564	Hs.247362	GO:0006527: arginine catabolic process, GO:0006809: nitric oxide biosynthetic process, GO:0006916: anti-apoptosis, GO:0007263: nitric oxide mediated signal transduction, GO:0016403: dimethylargininase activity, GO:0016787: hydrolase activity		−0.0108	0.3139	0.8441	1.3876	7.52	7.51	7.84	8.37	8.91	8.66	3
202196_s_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	NM_013253	27122	Hs.292156	GO:0007275: multicellular organismal development, GO:0009653: anatomical structure morphogenesis, GO:0016055: Wnt receptor signaling pathway, GO:0030178: negative regulation of Wnt receptor signaling pathway, GO:0005576: extracellular region, GO:0005615: extracellular space		−0.1433	0.4234	0.6769	1.0143	7.55	7.41	7.97	8.23	8.56	8.48	3

(*Continued*)

TABLE E3. (*Continued*)

202222_s_at	DES	desmin	NM_001927	1674	Hs.594952	GO:0006936: muscle contraction, GO:0007010: cytoskeleton organization and biogenesis, GO:0008016: regulation of heart contraction, GO:0005626: insoluble fraction, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005882: intermediate filament, GO:0030018: Z disc, GO:0042383: sarcolemma, GO:0043292: contractile fiber, GO:0045202: synapse, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding	01430: Cell Communication	0.0726	0.8078	1.0228	1.5113	7.35	7.43	8.16	8.38	8.87	8.73	3
202177_at	GAS6	growth arrest-specific 6	NM_000820	2621	Hs.646346	GO:0001558: regulation of cell growth, GO:0007165: signal transduction, GO:0008283: cell proliferation, GO:0005576: extracellular region, GO:0005102: receptor binding, GO:0005509: calcium ion binding		0.1953	0.4246	0.8029	1.122	8.73	8.92	9.15	9.53	9.85	9.64	3
202191_s_at	GAS7	growth arrest-specific 7	BE439987	8522	Hs.462214	GO:0007050: cell cycle arrest, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0008360: regulation of cell shape, GO:0030041: actin filament polymerization, GO:0030154: cell differentiation, GO:0051017: actin filament bundle formation, GO:0001726: ruffle, GO:0005737: cytoplasm, GO:0005884: actin filament, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0051015: actin filament binding		−0.0481	0.342	0.4364	1.2035	8.43	8.38	8.77	8.87	9.64	9.26	3
202054_s_at	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_000382	224	Hs.499886	GO:0006081: aldehyde metabolic process, GO:0006629: lipid metabolic process, GO:0007417: central nervous system development, GO:0007422: peripheral nervous system development, GO:0008152: metabolic process, GO:0008544: epidermis development, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004028: 3-chloroallyl aldehyde dehydrogenase activity, GO:0004029: aldehyde dehydrogenase (NAD) activity, GO:0004030: aldehyde dehydrogenase [NAD(P)+] activity, GO:0016491: oxidoreductase activity	00010: Glycolysis / Gluconeogenesis, 00053: Ascorbate and aldarate metabolism, 00071: Fatty acid metabolism, 00120: Bile acid biosynthesis, 00220: Urea cycle and metabolism of amino groups, 00280: Valine, leucine and isoleucine degradation, 00310: Lysine degradation, 00340: Histidine metabolism, 00380: Tryptophan metabolism, 00410: beta-Alanine metabolism, 00561: Glycerolipid metabolism, 00620: Pyruvate metabolism, 00640: Propanoate metabolism, 00650: Butanoate metabolism, 00903: Limonene and pinene degradation	0.3177	0.581	0.8669	1.0707	9.9	10.21	10.48	10.76	10.97	11.24	3

(*Continued*)

TABLE E3. (*Continued*)

202112_at	VWF	von Willebrand factor	NM_000552	7450	Hs.440848	GO:0009611: response to wounding, GO:0030168: platelet activation, GO:0030168: platelet activation, GO:0031589: cell-substrate adhesion, GO:0051260: protein homooligomerization, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005783: endoplasmic reticulum, GO:0031091: platelet alpha granule, GO:0001948: glycoprotein binding, GO:0002020: protease binding, GO:0005178: integrin binding, GO:0005518: collagen binding, GO:0019865: immunoglobulin binding, GO:0042803: protein homodimerization activity, GO:0047485: protein N-terminus binding, GO:0051087: chaperone binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 04610: Complement and coagulation cascades	0.204	0.1968	0.3886	1.0053	10.12	10.33	10.32	10.51	11.13	10.58	3
202017_at	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	NM_000120	2052	Hs.89649	GO:0006805: xenobiotic metabolic process, GO:0009636: response to toxin, GO:0019439: aromatic compound catabolic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004301: epoxide hydrolase activity, GO:0004301: epoxide hydrolase activity, GO:0016787: hydrolase activity	00980: Metabolism of xenobiotics by cytochrome P450	0.1169	0.5314	0.3468	1.0303	8.05	8.17	8.58	8.4	9.08	9.08	3
202022_at	ALDOC	aldolase C, fructose-bisphosphate	NM_005165	230	Hs.155247	GO:0006000: fructose metabolic process, GO:0006096: glycolysis, GO:0008152: metabolic process, GO:0004332: fructose-bisphosphate aldolase activity, GO:0016829: lyase activity	00010: Glycolysis / Gluconeogenesis, 00030: Pentose phosphate pathway, 00051: Fructose and mannose metabolism, 00710: Carbon fixation	−0.0051	0.4569	0.4868	1.0445	7.75	7.74	8.21	8.23	8.79	8.79	3
201917_s_at	SLC25A36	solute carrier family 25, member 36	NM_018155	55186	Hs.144130	GO:0006810: transport, GO:0006839: mitochondrial transport, GO:0005739: mitochondrion, GO:0005743: mitochondrial inner membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005215: transporter activity, GO:0005488: binding		0.0331	0.9883	1.0971	1.3016	5.74	5.77	6.73	6.83	7.04	6.87	3
201952_at	ALCAM	activated leukocyte cell adhesion molecule	AA156721	214	Hs.591293	GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0008045: motor axon guidance, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0009897: external side of plasma membrane, GO:0016020: membrane, GO:0030424: axon, GO:0043025: cell soma, GO:0005102: receptor binding	04514: Cell adhesion molecules (CAMs)	0.2521	0.5059	0.7822	1.2076	8.6	8.85	9.1	9.38	9.81	10.09	3
201810_s_at	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	AL562152	9467	Hs.257761, Hs.654642	GO:0007242: intracellular signaling cascade, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0004860: protein kinase inhibitor activity, GO:0005070: SH3/SH2 adaptor activity, GO:0005515: protein binding		0.1472	0.5024	0.8598	1.3064	7.35	7.49	7.85	8.21	8.65	8.53	3

(*Continued*)

TABLE E3. (*Continued*)

201911_s_at	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	NM_005766	10160	Hs.403917	GO:0035023: regulation of Rho protein signal transduction, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0019898: extrinsic to membrane, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0005488: binding, GO:0008092: cytoskeletal protein binding		0.1319	0.6033	0.9628	1.1795	6.66	6.79	7.26	7.62	7.84	7.79	3
201802_at	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	NM_004955	2030	Hs.25450	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006810: transport, GO:0015858: nucleoside transport, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005337: nucleoside transmembrane transporter activity, GO:0005515: protein binding		0.3431	0.4066	0.8554	1.0821	2.56	2.9	2.96	3.41	3.64	3.61	3
201809_s_at	ENG	endoglin (Osler-Rendu-Weber syndrome 1)	NM_000118	2022	Hs.76753	GO:0006810: transport, GO:0007155: cell adhesion, GO:0008015: circulation, GO:0009887: organ morphogenesis, GO:0017015: regulation of transforming growth factor beta receptor signaling pathway, GO:0045449: regulation of transcription, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding		0.352	0.4174	0.5732	1.2636	6.61	6.96	7.03	7.18	7.87	7.27	3
201660_at	ACSL3	acyl-CoA synthetase long-chain family member 3	AL525798	2181	Hs.655772	GO:0006629: lipid metabolic process, GO:0006631: fatty acid metabolic process, GO:0008152: metabolic process, GO:0005739: mitochondrion, GO:0005777: peroxisome, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000287: magnesium ion binding, GO:0004321: fatty-acyl-CoA synthase activity, GO:0004467: long-chain-fatty-acid-CoA ligase activity, GO:0005515: protein binding, GO:0016874: ligase activity	00071: Fatty acid metabolism, 03320: PPAR signaling pathway, 04920: Adipocytokine signaling pathway	0.6826	0.7703	0.9865	1.1843	6.78	7.47	7.55	7.77	7.97	8.43	3
201737_s_at	6-Mar	membrane-associated ring finger (C3HC4) 6	NM_005885	10299	Hs.432862	GO:0006512: ubiquitin cycle, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016874: ligase activity, GO:0046872: metal ion binding		−0.0192	0.3849	0.6954	1.3982	8.52	8.5	8.9	9.21	9.91	9.9	3
201602_s_at	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	NM_002480	4659	Hs.49582	GO:0006937: regulation of muscle contraction, GO:0005737: cytoplasm, GO:0015629: actin cytoskeleton, GO:0004871: signal transducer activity, GO:0005515: protein binding	04510: Focal adhesion, 04720: Long-term potentiation, 04810: Regulation of actin cytoskeleton	−0.3017	0.0828	0.2788	1.0077	6.13	5.83	6.21	6.41	7.14	7	3
201655_s_at	HSPG2	heparan sulfate proteoglycan 2	AI991033	3339	Hs.651231	GO:0007155: cell adhesion, GO:0005604: basement membrane, GO:0005615: extracellular space, GO:0005515: protein binding	04512: ECM-receptor interaction	0.2133	0.3994	0.7162	1.3017	9.14	9.35	9.54	9.85	10.44	9.7	3
201525_at	APOD	apolipoprotein D	NM_001647	347	Hs.522555	GO:0006629: lipid metabolic process, GO:0006810: transport, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005215: transporter activity, GO:0005319: lipid transporter activity, GO:0005501: retinoid binding, GO:0005515: protein binding, GO:0008035: high-density lipoprotein binding, GO:0008289: lipid binding		0.4072	0.5813	0.8446	1.2353	10.21	10.61	10.79	11.05	11.44	11.81	3
201578_at	PODXL	podocalyxin-like	NM_005397	5420	Hs.16426	GO:0005887: integral to plasma membrane, GO:0016020: membrane		0.0294	0.3825	0.7676	1.2021	8.22	8.25	8.61	8.99	9.43	9.16	3

(*Continued*)

TABLE E3. (*Continued*)

201389_at	ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	NM_002205	3678	Hs.505654	GO:0007044: cell-substrate junction assembly, GO:0007155: cell adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0007613: memory, GO:0001726: ruffle, GO:0008305: integrin complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019717: synaptosome, GO:0004872: receptor activity, GO:0005178: integrin binding, GO:0005509: calcium ion binding, GO:0005515: protein binding	04510: Focal adhesion, 04512: ECM-receptor interaction, 04640: Hematopoietic cell lineage, 04810: Regulation of actin cytoskeleton	−0.1731	0.0042	0.2416	1.0732	7.26	7.09	7.26	7.5	8.33	7.8	3
201416_at	SOX4	SRY (sex determining region Y)-box 4	NM_003107	6659	Hs.643910	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0031017: exocrine pancreas development, GO:0005634: nucleus, GO:0003700: transcription factor activity		0.893	0.9106	0.996	1.5017	5.57	6.46	6.48	6.56	7.07	6.18	3
201261_x_at	BGN	biglycan	BC002416	633	Hs.821	GO:0008150: biological_process, GO:0005578: proteinaceous extracellular matrix, GO:0030133: transport vesicle, GO:0005201: extracellular matrix structural constituent, GO:0005515: protein binding		−0.0224	0.4885	0.8231	1.5692	8.56	8.54	9.05	9.38	10.13	9.15	3
201313_at	ENO2	enolase 2 (gamma, neuronal)	NM_001975	2026	Hs.511915	GO:0006096: glycolysis, GO:0000015: phosphopyruvate hydratase complex, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0000287: magnesium ion binding, GO:0004634: phosphopyruvate hydratase activity, GO:0016829: lyase activity	00010: Glycolysis / Gluconeogenesis	0.003	0.089	0.4365	1.3929	2.13	2.13	2.21	2.56	3.52	3.75	3
200974_at	ACTA2	actin, alpha 2, smooth muscle, aorta	NM_001613	59	Hs.500483	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0000166: nucleotide binding, GO:0005198: structural molecule activity, GO:0005515: protein binding, GO:0005524: ATP binding		0.1412	0.4811	0.772	1.1332	12.09	12.23	12.57	12.86	13.22	13.15	3
201058_s_at	MYL9	myosin, light chain 9, regulatory	NM_006097	10398	Hs.504687	GO:0006937: regulation of muscle contraction, GO:0005859: muscle myosin complex, GO:0016459: myosin complex, GO:0003774: motor activity, GO:0005509: calcium ion binding, GO:0008307: structural constituent of muscle		0.1682	0.7475	1.0251	1.5967	9.2	9.37	9.95	10.23	10.8	10.67	3
200676_s_at	UBE2L3	ubiquitin-conjugating enzyme E2L 3	NM_003347	7332	Hs.108104, Hs.693707	GO:0006464: protein modification process, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0000151: ubiquitin ligase complex, GO:0004842: ubiquitin-protein ligase activity, GO:0016874: ligase activity, GO:0019899: enzyme binding	05020: Parkinson's disease	0.2967	0.4914	0.5109	1.0335	4.18	4.47	4.67	4.69	5.21	5	3
200747_s_at	NUMA1	nuclear mitotic apparatus protein 1	NM_006185	4926	Hs.325978	GO:0000090: mitotic anaphase, GO:0006997: nuclear organization and biogenesis, GO:0000922: spindle pole, GO:0005634: nucleus, GO:0005876: spindle microtubule, GO:0005198: structural molecule activity, GO:0005515: protein binding		0.2526	0.4591	0.5874	1.1976	8.95	9.2	9.41	9.53	10.14	9.86	3
1598_g_at	GAS6	growth arrest-specific 6	L13720	2621	Hs.646346	GO:0001558: regulation of cell growth, GO:0007165: signal transduction, GO:0008283: cell proliferation, GO:0005576: extracellular region, GO:0005102: receptor binding, GO:0005509: calcium ion binding		0.3547	0.5929	0.9173	1.4271	9.11	9.47	9.71	10.03	10.54	10.16	3
200621_at	CSRP1	cysteine and glycine-rich protein 1	NM_004078	1465	Hs.108080	GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0269	0.2877	0.41	1.0213	10.18	10.16	10.47	10.59	11.2	10.89	3
58780_s_at	FLJ10357	hypothetical protein FLJ10357	R42449	55701	Hs.35125	GO:0035023: regulation of Rho protein signal transduction, GO:0005622: intracellular, GO:0005089: Rho guanyl-nucleotide exchange factor activity		0.3516	0.8967	1.3399	1.8698	6.66	7.01	7.55	8	8.53	8.36	3
208109_s_at	C15orf5	chromosome 15 open reading frame 5	NM_030944	81698	Hs.656938			0.28	0.2342	1.0013	0.9828	6.19	6.47	6.42	7.19	7.17	7.01	3

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TABLE E3. (*Continued*)

222357_at	ZBTB20	zinc finger and BTB domain containing 20	AW974823	26137	Hs.655108, Hs.693802	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0003677: DNA binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.1245	0.6043	1.4645	2.2004	3.82	3.94	4.42	5.28	6.02	5.47	3
37408_at	MRC2	mannose receptor, C type 2	AB014609	9902	Hs.7835	GO:0006897: endocytosis, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0005509: calcium ion binding, GO:0005529: sugar binding		0.2062	0.5944	1.0443	1.2351	9.01	9.22	9.61	10.06	10.25	9.63	3
221988_at	MED26	mediator complex subunit 26	AA463853	9441	Hs.356467	GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006367: transcription initiation from RNA polymerase II promoter, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003713: transcription coactivator activity, GO:0004872: receptor activity, GO:0005515: protein binding, GO:0030528: transcription regulator activity		0.375	0.7159	1.1998	1.8062	4.62	4.99	5.33	5.82	6.42	6.46	3
222101_s_at	DCHS1	dachsous 1 (Drosophila)	BF222893	8642	Hs.199850	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0016339: calcium-dependent cell-cell adhesion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.2936	0.8039	1.3002	1.775	5.64	5.93	6.44	6.94	7.41	6.97	3
221796_at	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	AA707199	4915	Hs.494312	GO:0006468: protein amino acid phosphorylation, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0030154: cell differentiation, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0004714: transmembrane receptor protein tyrosine kinase activity, GO:0004872: receptor activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0043121: neurotrophin binding	04010: MAPK signaling pathway	0.4389	0.9833	1.4894	1.5148	8.3	8.74	9.29	9.79	9.82	9.88	3
221814_at	GPR124	G protein-coupled receptor 124	BF511315	25960	Hs.274136	GO:0007165: signal transduction, GO:0007218: neuropeptide signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0005515: protein binding		0.1476	0.6489	1.1857	1.3718	8.29	8.44	8.94	9.47	9.66	9.11	3
221589_s_at	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	AW612403	4329	Hs.293970	GO:0006220: pyrimidine nucleotide metabolic process, GO:0006573: valine metabolic process, GO:0006573: valine metabolic process, GO:0008152: metabolic process, GO:0019859: thymine metabolic process, GO:0005739: mitochondrion, GO:0000062: acyl-CoA binding, GO:0004491: methylmalonate-semialdehyde dehydrogenase (acylating) activity, GO:0004491: methylmalonate-semialdehyde dehydrogenase (acylating) activity, GO:0016491: oxidoreductase activity, GO:0018478: malonate-semialdehyde dehydrogenase (acetylating) activity	00031: Inositol metabolism, 00280: Valine, leucine and isoleucine degradation, 00640: Propanoate metabolism	0.707	0.7715	1.2303	1.3538	7.38	8.09	8.15	8.61	8.73	8.98	3

(*Continued*)

TABLE E3. (*Continued*)

221645_s_at	ZNF83	zinc finger protein 83	M27877	55769	Hs.467210, Hs.499453, Hs.657492, Hs.665751	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	0.4395	0.7461	1.2516	1.3857	7.65	8.09	8.4	8.9	9.04	9.19	3
221127_s_at	RIG	regulated in glioma	NM_006394	10530	Hs.292156		0.0663	0.6317	1.0215	1.6525	6.28	6.34	6.91	7.3	7.93	7.61	3
221276_s_at	SYNC1	syncoilin, intermediate filament 1	NM_030786	81493	Hs.655938	GO:0005198: structural molecule activity	−0.2363	0.5915	1.0708	1.5306	4.24	4	4.83	5.31	5.77	5.9	3
220917_s_at	WDR19	WD repeat domain 19	NM_025132	57728	Hs.438482	GO:0006886: intracellular protein transport, GO:0016192: vesicle-mediated transport, GO:0005515: protein binding	0.6752	0.5955	1.131	1.464	4.18	4.85	4.77	5.31	5.64	5.32	3
221011_s_at	LBH	limb bud and heart development homolog (mouse)	NM_030915	81606	Hs.567598, Hs.593113		0.2496	0.4956	1.0536	1.029	7.52	7.77	8.01	8.57	8.55	8.22	3
220170_at	FHL5	four and a half LIM domains 5	NM_020482	9457	Hs.632608	GO:0003713: transcription coactivator activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	0.1661	0.6995	1.0289	1.2495	2.59	2.76	3.29	3.62	3.84	3.87	3
220692_at	POLR2J2	DNA directed RNA polymerase II polypeptide J-related	NM_014147	246721	Hs.654726, Hs.693633	GO:0006350: transcription, GO:0003677: DNA binding, GO:0003899: DNA-directed RNA polymerase activity, GO:0046983: protein dimerization activity	0.4037	0.6478	1.093	1.4889	5.68	6.08	6.33	6.77	7.17	6.87	3
219777_at	GIMAP6	GTPase, IMAP family member 6	NM_024711	474344	Hs.647105	GO:0005525: GTP binding	0.2837	0.6078	1.0781	1.4494	8.25	8.54	8.86	9.33	9.7	9.34	3
219778_at	ZFPM2	zinc finger protein, multitype 2	NM_012082	23414	Hs.431009	GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0005622: intracellular, GO:0003677: DNA binding, GO:0003702: RNA polymerase II transcription factor activity, GO:0003714: transcription corepressor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	0.0141	0.4433	1.095	1.3294	2.52	2.53	2.96	3.62	3.85	3.54	3
219440_at	RAI2	retinoic acid induced 2	NM_021785	10742	Hs.446680, Hs.654683	GO:0009790: embryonic development, GO:0005575: cellular_component, GO:0003674: molecular_function	0.4286	0.7488	1.3166	1.6238	6.27	6.7	7.02	7.59	7.9	7.89	3
219518_s_at	ELL3	elongation factor RNA polymerase II-like 3	NM_025165	80237	Hs.694861	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006368: RNA elongation from RNA polymerase II promoter, GO:0007283: spermatogenesis, GO:0045817: positive regulation of global transcription from RNA polymerase II promoter, GO:0005634: nucleus, GO:0008023: transcription elongation factor complex, GO:0005515: protein binding, GO:0008159: positive transcription elongation factor activity, GO:0016944: RNA polymerase II transcription elongation factor activity	0.2524	0.6225	1.2236	1.4418	6.9	7.15	7.52	8.12	8.34	8.88	3
219368_at	NAP1L2	nucleosome assembly protein 1-like 2	NM_021963	4674	Hs.66180	GO:0006334: nucleosome assembly, GO:0005634: nucleus, GO:0005678: chromatin assembly complex	0.1638	0.6499	1.2474	1.3487	4.2	4.37	4.85	5.45	5.55	5.92	3
219432_at	EVC	Ellis van Creveld syndrome	NM_014556	2121	Hs.646899, Hs.648745	GO:0001501: skeletal development, GO:0007517: muscle development, GO:0016020: membrane, GO:0016021: integral to membrane	0.3363	0.7055	1.0866	1.433	4.97	5.3	5.67	6.05	6.4	5.94	3
219134_at	ELTD1	EGF, latrophilin and seven transmembrane domain containing 1	NM_022159	64123	Hs.132314	GO:0007165: signal transduction, GO:0007218: neuropeptide signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0005509: calcium ion binding	0.2541	0.6542	1.1633	1.5929	8.1	8.35	8.75	9.26	9.69	9.32	3

(*Continued*)

TABLE E3. (*Continued*)

219213_at	JAM2	junctional adhesion molecule 2	NM_021219	58494	Hs.517227	GO:0016337: cell-cell adhesion, GO:0005887: integral to plasma membrane, GO:0005923: tight junction, GO:0016020: membrane, GO:0030054: cell junction	04514: Cell adhesion molecules (CAMs), 04530: Tight junction, 04670: Leukocyte transendothelial migration, 05120: Epithelial cell signaling in Helicobacter pylori infection	0.4349	0.6506	1.4152	1.6573	6.69	7.12	7.34	8.1	8.34	7.8	3
219025_at	CD248	CD248 molecule, endosialin	NM_020404	57124	Hs.195727	GO:0008150: biological_process, GO:0005578: proteinaceous extracellular matrix, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003674: molecular_function, GO:0005509: calcium ion binding, GO:0005529: sugar binding		−0.0834	0.4532	1.0207	1.54	8.11	8.03	8.56	9.13	9.65	9.02	3
219093_at	PID1	phosphotyrosine interaction domain containing 1	NM_017933	55022	Hs.409352	GO:0005737: cytoplasm		0.3443	0.7988	1.0243	1.1055	7.01	7.35	7.81	8.03	8.12	8.25	3
218718_at	PDGFC	platelet derived growth factor C	NM_016205	56034	Hs.570855	GO:0000074: regulation of progression through cell cycle, GO:0007417: central nervous system development, GO:0008283: cell proliferation, GO:0005576: extracellular region, GO:0016020: membrane, GO:0008083: growth factor activity	04060: Cytokine-cytokine receptor interaction, 04510: Focal adhesion, 04540: Gap junction, 05218: Melanoma	0.4449	0.8456	1.2336	1.4564	7.94	8.39	8.79	9.18	9.4	9.76	3
218966_at	MYO5C	myosin VC	NM_018728	55930	Hs.487036	GO:0016459: myosin complex, GO:0000166: nucleotide binding, GO:0003774: motor activity, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0051015: actin filament binding		0.4566	0.7839	1.5383	1.6124	3.98	4.43	4.76	5.51	5.59	6.13	3
218656_s_at	LHFP	lipoma HMGIC fusion partner	NM_005780	10186	Hs.507798, Hs.648603	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003677: DNA binding		0.4301	0.7318	1.1905	1.173	9.93	10.36	10.66	11.12	11.1	11.04	3
218692_at	GOLSYN	Golgi-localized protein	NM_017786	55638	Hs.390738	GO:0016020: membrane, GO:0016021: integral to membrane		0.4419	0.6769	1.3221	1.4062	5	5.45	5.68	6.33	6.41	6.83	3
218573_at	MAGEH1	melanoma antigen family H, 1	NM_014061	28986	Hs.279819	GO:0006915: apoptosis		0.5329	0.7437	1.1436	1.0525	6.57	7.11	7.32	7.72	7.63	7.64	3
218638_s_at	SPON2	spondin 2, extracellular matrix protein	NM_012445	10417	Hs.302963	GO:0006955: immune response, GO:0007155: cell adhesion, GO:0007275: multicellular organismal development, GO:0007411: axon guidance, GO:0005578: proteinaceous extracellular matrix, GO:0005615: extracellular space, GO:0005515: protein binding		0.4037	0.6724	1.1826	1.4538	7.95	8.35	8.62	9.13	9.4	9.19	3
218490_s_at	ZNF302	zinc finger protein 302	NM_018443	55900	Hs.436350	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0003677: DNA binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.6642	0.7614	1.2458	1.339	7.71	8.37	8.47	8.95	9.05	9.11	3
218532_s_at	FAM134B	family with sequence similarity 134, member B	NM_019000	54463	Hs.481704	GO:0016020: membrane, GO:0016021: integral to membrane		0.3178	0.4963	1.1269	1.4904	7.08	7.39	7.57	8.2	8.57	8.9	3
217858_s_at	ARMCX3	armadillo repeat containing, X-linked 3	NM_016607	51566	Hs.592225	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005488: binding		0.3236	0.6499	1.1438	1.2854	7.92	8.25	8.57	9.07	9.21	9.16	3
218211_s_at	MLPH	melanophilin	NM_024101	79083	Hs.102406	GO:0006605: protein targeting, GO:0030318: melanocyte differentiation, GO:0032400: melanosome localization, GO:0043473: pigmentation, GO:0005737: cytoplasm, GO:0015629: actin cytoskeleton, GO:0003779: actin binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0017137: Rab GTPase binding, GO:0031489: myosin V binding, GO:0046872: metal ion binding, GO:0051010: microtubule plus-end binding		0.572	0.7836	1.0977	1.42	4.08	4.65	4.86	5.18	5.5	5.69	3
217771_at	GOLM1	golgi membrane protein 1	NM_016548	51280	Hs.494337	GO:0005794: Golgi apparatus, GO:0005887: integral to plasma membrane, GO:0016020: membrane		0.6029	0.791	1.5362	1.3312	4.64	5.24	5.43	6.17	5.97	5.95	3

(*Continued*)

TABLE E3. (*Continued*)

217853_at	TNS3	tensin 3	NM_022748	64759	Hs.520814	GO:0007242: intracellular signaling cascade, GO:0030054: cell junction		0.7179	0.8223	1.1167	1.299	8.35	9.07	9.17	9.47	9.65	9.49	3
217025_s_at	DBN1	drebrin 1	AL110225	1627	Hs.130316	GO:0007015: actin filament organization, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0030154: cell differentiation, GO:0048168: regulation of neuronal synaptic plasticity, GO:0050773: regulation of dendrite development, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0015629: actin cytoskeleton, GO:0030425: dendrite, GO:0042641: actomyosin, GO:0003779: actin binding, GO:0003779: actin binding, GO:0005522: profilin binding		0.3872	0.8306	1.3589	1.8249	5.83	6.22	6.66	7.19	7.65	7.56	3
217504_at	ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	AA099357	23460	Hs.647403	GO:0006810: transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0016887: ATPase activity	02010: ABC transporters - General	0.6871	0.6201	1.0781	1.0569	4.19	4.88	4.81	5.27	5.25	5.49	3
216442_x_at	FN1	fibronectin 1	AK026737	2335	Hs.203717	GO:0006953: acute-phase response, GO:0007155: cell adhesion, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0009611: response to wounding, GO:0016477: cell migration, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005793: ER-Golgi intermediate compartment, GO:0005201: extracellular matrix structural constituent, GO:0005518: collagen binding, GO:0008201: heparin binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 04810: Regulation of actin cytoskeleton, 05222: Small cell lung cancer	0.2549	0.6076	1.1763	1.2728	10.86	11.11	11.47	12.04	12.13	11.69	3
216620_s_at	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	AF009205	9639	Hs.98594	GO:0035023: regulation of Rho protein signal transduction, GO:0005622: intracellular, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity		0.1682	0.7289	1.3385	1.6935	7.04	7.21	7.77	8.38	8.74	8.84	3
216320_x_at	MST1	macrophage stimulating 1 (hepatocyte growth factor-like)	U37055	4485	Hs.349110, Hs.512587	GO:0006508: proteolysis, GO:0007596: blood coagulation, GO:0008150: biological_process, GO:0005575: cellular_component, GO:0003674: molecular_function, GO:0004252: serine-type endopeptidase activity, GO:0005509: calcium ion binding		0.5485	0.9157	1.2084	1.9702	3.89	4.44	4.81	5.1	5.86	5.56	3
216333_x_at	TNXB	tenascin XB	M25813	7148	Hs.42853, Hs.485104	GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0032963: collagen metabolic process, GO:0048251: elastic fiber assembly, GO:0005578: proteinaceous extracellular matrix, GO:0005583: fibrillar collagen, GO:0005622: intracellular, GO:0005102: receptor binding, GO:0005178: integrin binding, GO:0008201: heparin binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.1353	0.5717	1.0996	1.8724	10.25	10.39	10.82	11.35	12.12	11.66	3
215322_at	LONRF1	LON peptidase N-terminal domain and ring finger 1	AL080190	91694	Hs.180178	GO:0006510: ATP-dependent proteolysis, GO:0004176: ATP-dependent peptidase activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.1667	1.124	1.4442	2.198	6.04	5.88	7.17	7.49	8.24	8.82	3
215516_at	LAMB4	laminin, beta 4	AC005048	22798	Hs.62022	GO:0005578: proteinaceous extracellular matrix	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 05222: Small cell lung cancer	0.0176	0.6178	1.2504	2.1017	5.89	5.91	6.51	7.14	8	8.82	3

(*Continued*)

TABLE E3. (*Continued*)

215073_s_at	NR2F2	nuclear receptor subfamily 2, group F, member 2	AL554245	7026	Hs.347991	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006629: lipid metabolic process, GO:0007165: signal transduction, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003706: ligand-regulated transcription factor activity, GO:0003707: steroid hormone receptor activity, GO:0003714: transcription corepressor activity, GO:0008270: zinc ion binding, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding		0.1861	0.5264	1.291	1.3095	7.51	7.7	8.04	8.8	8.82	8.92	3
215116_s_at	DNM1	dynamin 1	AF035321	1759	Hs.522413	GO:0006898: receptor-mediated endocytosis, GO:0007268: synaptic transmission, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005874: microtubule, GO:0005905: coated pit, GO:0000166: nucleotide binding, GO:0003774: motor activity, GO:0003924: GTPase activity, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0016787: hydrolase activity		0.2437	0.7881	1.1285	1.7867	7.25	7.49	8.04	8.38	9.03	8.68	3
214823_at	ZNF204	zinc finger protein 204	AF033199	7754	Hs.8198	GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.8031	0.8512	1.3295	1.5982	4.67	5.47	5.52	6	6.27	6.63	3
214850_at	GUSBP1	glucuronidase, beta pseudogene 1	X75940	153561	Hs.654588			0.1092	0.3182	1.2433	1.4115	5.12	5.23	5.44	6.36	6.53	6.44	3
214724_at	DIXDC1	DIX domain containing 1	AF070621	85458	Hs.655626	GO:0007275: multicellular organismal development, GO:0016055: Wnt receptor signaling pathway, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0030054: cell junction, GO:0003779: actin binding, GO:0004871: signal transducer activity		0.0974	0.7076	1.2126	1.7134	7.37	7.46	8.07	8.58	9.08	9.1	3
214761_at	ZNF423	zinc finger protein 423	AW149417	23090	Hs.530930	GO:0005622: intracellular, GO:0003676: nucleic acid binding, GO:0008270: zinc ion binding		0.404	0.9557	1.4703	1.6414	4.15	4.55	5.1	5.62	5.79	5.6	3
214439_x_at	BIN1	bridging integrator 1	AF043899	274	Hs.193163	GO:0007049: cell cycle, GO:0007275: multicellular organismal development, GO:0008283: cell proliferation, GO:0030100: regulation of endocytosis, GO:0030154: cell differentiation, GO:0045786: negative regulation of progression through cell cycle, GO:0005737: cytoplasm, GO:0015629: actin cytoskeleton, GO:0005515: protein binding		0.1994	0.4119	1.0569	1.1085	5.59	5.79	6	6.65	6.7	6.28	3
214451_at	TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	NM_003221	7021	Hs.33102	GO:0001822: kidney development, GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007399: nervous system development, GO:0045817: positive regulation of global transcription from RNA polymerase II promoter, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003713: transcription coactivator activity, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity		0.3756	0.8435	1.2835	1.6416	5.01	5.38	5.85	6.29	6.65	7.07	3
214180_at	MAN1C1	mannosidase, alpha, class 1C, member 1	AW340588	57134	Hs.197043	GO:0006487: protein amino acid N-linked glycosylation, GO:0008152: metabolic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030173: integral to Golgi membrane, GO:0004571: mannosyl-oligosaccharide 1,2-alpha-mannosidase activity, GO:0004571: mannosyl-oligosaccharide 1,2-alpha-mannosidase activity, GO:0005509: calcium ion binding, GO:0005509: calcium ion binding, GO:0016798: hydrolase activity, acting on glycosyl bonds	00510: N-Glycan biosynthesis, 01030: Glycan structures - biosynthesis 1	0.2367	0.7667	1.2301	1.2988	5.43	5.67	6.2	6.66	6.73	6.25	3

(*Continued*)

TABLE E3. (*Continued*)

214433_s_at	SELENBP1	selenium binding protein 1	NM_003944	8991	Hs.632460	GO:0015031: protein transport, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0008430: selenium binding, GO:0008430: selenium binding		0.4684	0.9249	1.2695	2.0564	6.84	7.31	7.76	8.11	8.9	8.87	3
214102_at	CENTD1	centaurin, delta 1	AK023737	116984	Hs.479451	GO:0007165: signal transduction, GO:0043087: regulation of GTPase activity, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005096: GTPase activator activity, GO:0005547: phosphatidylinositol-3,4,5-triphosphate binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.2755	0.6093	1.0071	1.3947	5.73	6.01	6.34	6.74	7.13	7.27	3
214152_at	CCPG1	cell cycle progression 1	AU144243	9236	Hs.612814			0.404	0.789	1.1599	1.1638	4.39	4.79	5.18	5.55	5.55	5.6	3
213939_s_at	RUFY3	RUN and FYVE domain containing 3	AI871641	22902	Hs.7972	GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0030154: cell differentiation, GO:0042995: cell projection		0.3949	0.7072	1.0812	1.3982	8.74	9.14	9.45	9.82	10.14	10.16	3
214027_x_at	DES	desmin	AA889653	1674	Hs.594952	GO:0006936: muscle contraction, GO:0007010: cytoskeleton organization and biogenesis, GO:0008016: regulation of heart contraction, GO:0005626: insoluble fraction, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005882: intermediate filament, GO:0030018: Z disc, GO:0042383: sarcolemma, GO:0043292: contractile fiber, GO:0045202: synapse, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding	01430: Cell Communication	−0.0034	0.7049	1.3309	2.1805	5.53	5.52	6.23	6.86	7.71	7.16	3
213675_at			W61005					0.2375	0.5442	1.0202	1.9128	6.21	6.44	6.75	7.23	8.12	7.8	3
213764_s_at	MFAP5	microfibrillar associated protein 5	AW665892	8076	Hs.512842	GO:0001527: microfibril, GO:0005578: proteinaceous extracellular matrix, GO:0005615: extracellular space, GO:0005201: extracellular matrix structural constituent		0.1286	0.8325	1.5418	1.6653	9.18	9.31	10.01	10.72	10.85	11.08	3
213568_at	OSR2	odd-skipped related 2 (Drosophila)	AI811298	116039	Hs.253247	GO:0008284: positive regulation of cell proliferation, GO:0048704: embryonic skeletal morphogenesis, GO:0005622: intracellular, GO:0003676: nucleic acid binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.41	0.7592	1.3415	1.6012	9.17	9.58	9.93	10.51	10.77	10.63	3
213620_s_at	ICAM2	intercellular adhesion molecule 2	AA126728	3384	Hs.431460	GO:0016337: cell-cell adhesion, GO:0001931: uropod, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005178: integrin binding, GO:0005515: protein binding	04514: Cell adhesion molecules (CAMs), 04650: Natural killer cell mediated cytotoxicity	0.2975	0.6032	1.178	1.7515	5.89	6.19	6.5	7.07	7.65	6.86	3
213451_x_at	TNXB	tenascin XB	BE044614	7148	Hs.42853, Hs.485104	GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0032963: collagen metabolic process, GO:0048251: elastic fiber assembly, GO:0005578: proteinaceous extracellular matrix, GO:0005583: fibrillar collagen, GO:0005622: intracellular, GO:0005102: receptor binding, GO:0005178: integrin binding, GO:0008201: heparin binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.0883	0.4981	1.0071	1.7806	10.32	10.41	10.82	11.33	12.1	11.68	3
213541_s_at	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	AI351043	2078	Hs.473819	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007275: multicellular organismal development, GO:0008283: cell proliferation, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0043565: sequence-specific DNA binding		−0.0129	0.3538	1.101	1.2876	4.15	4.13	4.5	5.25	5.43	4.94	3
213413_at	STON1	stonin 1	BG434174	11037	Hs.44385		03022: Basal transcription factors	0.1405	0.5212	1.2773	1.7607	4.32	4.46	4.84	5.6	6.08	6.16	3

(*Continued*)

TABLE E3. (*Continued*)

213422_s_at	MXRA8	matrix-remodelling associated 8	AW888223	54587	Hs.558570			0.3805	0.7064	1.0459	1.3829	8.41	8.79	9.12	9.46	9.79	9.45	3
213369_at	PCDH21	protocadherin 21	AI825832	92211	Hs.137556	GO:0007156: homophilic cell adhesion, GO:0016020: membrane, GO:0005509: calcium ion binding		0.0752	0.5861	1.1803	2.3514	8.13	8.21	8.72	9.31	10.49	10.85	3
213380_x_at	MSTP9	macrophage stimulating, pseudogene 9	AA911235	11223	Hs.655432	GO:0006508: proteolysis, GO:0004252: serine-type endopeptidase activity		0.6342	0.8991	1.1937	1.5493	2.93	3.56	3.83	4.12	4.48	4.31	3
213348_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	N33167	1028	Hs.106070	GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0000080: G1 phase of mitotic cell cycle, GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0007049: cell cycle, GO:0007050: cell cycle arrest, GO:0008285: negative regulation of cell proliferation, GO:0042551: neuron maturation, GO:0005634: nucleus, GO:0004861: cyclin-dependent protein kinase inhibitor activity, GO:0005515: protein binding	04110: Cell cycle	0.6131	0.8029	1.0643	1.5194	6.61	7.22	7.41	7.67	8.13	7.94	3
213364_s_at	SNX1	sorting nexin 1	AI052536	6642	Hs.188634	GO:0006886: intracellular protein transport, GO:0006897: endocytosis, GO:0007154: cell communication, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0005515: protein binding, GO:0008565: protein transporter activity, GO:0035091: phosphoinositide binding		0.3655	0.6368	1.1037	1.3761	9.05	9.41	9.68	10.15	10.42	10.64	3
213222_at	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	AL049593	23236	Hs.431173	GO:0000074: regulation of progression through cell cycle, GO:0007242: intracellular signaling cascade, GO:0016042: lipid catabolic process, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0004435: phosphoinositide phospholipase C activity, GO:0004871: signal transducer activity, GO:0005509: calcium ion binding, GO:0016787: hydrolase activity	00562: Inositol phosphate metabolism, 04020: Calcium signaling pathway, 04070: Phosphatidylinositol signaling system, 04310: Wnt signaling pathway, 04540: Gap junction, 04720: Long-term potentiation, 04730: Long-term depression, 04912: GnRH signaling pathway, 04916: Melanogenesis	0.3695	0.6225	1.3055	1.2818	4.7	5.07	5.32	6	5.98	6.58	3
213290_at	COL6A2	collagen, type VI, alpha 2	AL531750	1292	Hs.420269	GO:0006817: phosphate transport, GO:0016337: cell-cell adhesion, GO:0030198: extracellular matrix organization and biogenesis, GO:0005581: collagen, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0005201: extracellular matrix structural constituent, GO:0030674: protein binding, bridging	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.4764	0.7073	1.0895	1.4729	8.48	8.96	9.19	9.57	9.96	9.64	3
213169_at	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	BG109855	9037	Hs.27621	GO:0001569: patterning of blood vessels, GO:0007155: cell adhesion, GO:0007267: cell-cell signaling, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0007411: axon guidance, GO:0030154: cell differentiation, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0008046: axon guidance receptor activity	04360: Axon guidance	0.6362	0.6074	1.1491	1.1948	5.7	6.34	6.31	6.85	6.9	6.74	3
213217_at	ADCY2	adenylate cyclase 2 (brain)	AU149572	108	Hs.481545	GO:0006171: cAMP biosynthetic process, GO:0007242: intracellular signaling cascade, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000287: magnesium ion binding, GO:0004016: adenylate cyclase activity	00230: Purine metabolism, 04020: Calcium signaling pathway, 04540: Gap junction, 04912: GnRH signaling pathway, 04916: Melanogenesis	0.2485	0.9744	1.471	1.9286	4.68	4.93	5.65	6.15	6.61	7.03	3

(*Continued*)

TABLE E3. (*Continued*)

213106_at	ATP8A1	ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1	AI769688	10396	Hs.435052	GO:0006810: transport, GO:0008152: metabolic process, GO:0015914: phospholipid transport, GO:0015917: aminophospholipid transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0031410: cytoplasmic vesicle, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004012: phospholipid-translocating ATPase activity, GO:0005524: ATP binding, GO:0015662: ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, GO:0016787: hydrolase activity, GO:0016820: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, GO:0019829: cation-transporting ATPase activity		0.9437	0.9686	1.8433	1.851	5.81	6.75	6.78	7.65	7.66	7.75	3
213122_at	TSPYL5	TSPY-like 5	AI096375	85453	Hs.173094	GO:0006334: nucleosome assembly, GO:0005634: nucleus		0.3958	0.6314	1.2132	1.3302	7.15	7.54	7.78	8.36	8.48	8.76	3
213075_at	OLFML2A	olfactomedin-like 2A	AL050002	169611	Hs.357004	GO:0016020: membrane, GO:0016524: latrotoxin receptor activity		0.3484	0.7672	1.3069	1.8019	7.8	8.15	8.57	9.11	9.6	9.57	3
213093_at	PRKCA	protein kinase C, alpha	AI471375	5578	Hs.531704, Hs.680598	GO:0000074: regulation of progression through cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0007166: cell surface receptor linked signal transduction, GO:0007242: intracellular signaling cascade, GO:0008624: induction of apoptosis by extracellular signals, GO:0005624: membrane fraction, GO:0000166: nucleotide binding, GO:0004697: protein kinase C activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008270: zinc ion binding, GO:0016740: transferase activity, GO:0019992: diacylglycerol binding	04010: MAPK signaling pathway, 04012: ErbB signaling pathway, 04020: Calcium signaling pathway, 04070: Phosphatidylinositol signaling system, 04310: Wnt signaling pathway, 04370: VEGF signaling pathway, 04510: Focal adhesion, 04530: Tight junction, 04540: Gap junction, 04650: Natural killer cell mediated cytotoxicity, 04664: Fc epsilon RI signaling pathway, 04670: Leukocyte transendothelial migration, 04720: Long-term potentiation, 04730: Long-term depression, 04912: GnRH signaling pathway, 04916: Melanogenesis, 05110: Cholera - Infection, 05130: Pathogenic Escherichia coli infection - EHEC, 05131: Pathogenic Escherichia coli infection - EPEC, 05214: Glioma, 05223: Non-small cell lung cancer	0.4968	0.6671	1.0207	1.15	4.63	5.13	5.3	5.65	5.78	5.97	3
213058_at	TTC28	tetratricopeptide repeat domain 28	AL033538	23331	Hs.387856	GO:0005488: binding		0.5983	0.9943	1.4146	1.6888	5.96	6.56	6.96	7.38	7.65	7.43	3
213059_at	CREB3L1	cAMP responsive element binding protein 3-like 1	AF055009	90993	Hs.405961	GO:0006355: regulation of transcription, DNA-dependent, GO:0006986: response to unfolded protein, GO:0005634: nucleus, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity	04916: Melanogenesis, 05215: Prostate cancer	0.3538	0.6506	1.3475	1.2798	5.28	5.63	5.93	6.63	6.56	5.96	3
213018_at	GATAD1	GATA zinc finger domain containing 1	AI337901	57798	Hs.21145	GO:0006355: regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding		0.5588	0.6555	1.0758	1.253	5.17	5.73	5.83	6.25	6.43	6.38	3

(*Continued*)

TABLE E3. (*Continued*)

213032_at	NFIB	nuclear factor I/B	AI186739	4781	Hs.370359	GO:0006260: DNA replication, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity		0.488	0.5513	1.0997	1.4454	8.97	9.46	9.52	10.07	10.42	10.4	3
212980_at	USP34	ubiquitin specific peptidase 34	AL050376	9736	Hs.654807	GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0004221: ubiquitin thiolesterase activity, GO:0008234: cysteine-type peptidase activity		0.528	0.8417	1.3949	1.6862	6.68	7.21	7.52	8.08	8.37	8.51	3
212985_at			BF115739					0.3451	0.6309	1.0506	1.0556	7.57	7.91	8.2	8.62	8.62	8.65	3
212950_at	GPR116	G protein-coupled receptor 116	BF941499	221395	Hs.362806	GO:0007165: signal transduction, GO:0007218: neuropeptide signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0004930: G-protein coupled receptor activity		0.6267	0.8276	1.4994	1.6396	6.96	7.59	7.79	8.46	8.6	8.27	3
212951_at	GPR116	G protein-coupled receptor 116	N95226	221395	Hs.362806	GO:0007165: signal transduction, GO:0007218: neuropeptide signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0004930: G-protein coupled receptor activity		0.4029	0.4473	1.0948	1.3153	6.04	6.44	6.49	7.13	7.35	7.01	3
212845_at	SAMD4A	sterile alpha motif domain containing 4A	AB028976	23034	Hs.98259	GO:0045727: positive regulation of protein biosynthetic process, GO:0005737: cytoplasm, GO:0000900: translation repressor activity, nucleic acid binding, GO:0003730: mRNA 3′-UTR binding, GO:0005515: protein binding, GO:0030371: translation repressor activity		0.4563	0.8783	1.6201	1.6931	6.14	6.6	7.02	7.76	7.84	8.19	3
212914_at	CBX7	chromobox homolog 7	AV648364	23492	Hs.356416	GO:0006333: chromatin assembly or disassembly, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0016568: chromatin modification, GO:0000785: chromatin, GO:0005634: nucleus, GO:0003682: chromatin binding		0.5233	0.749	1.0817	1.3623	8.24	8.76	8.98	9.32	9.6	9.63	3
212793_at	DAAM2	dishevelled associated activator of morphogenesis 2	BF513244	23500	Hs.652207	GO:0016043: cellular component organization and biogenesis, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0003779: actin binding, GO:0017048: Rho GTPase binding	04310: Wnt signaling pathway	0.4055	0.8536	1.8267	2.2614	6.36	6.77	7.22	8.19	8.63	8.07	3
212805_at			AL138349	23273				0.3204	0.9377	1.5262	1.8868	6.68	7	7.62	8.21	8.57	8.39	3
212764_at	ZEB1	zinc finger E-box binding homeobox 1	AI373166	6935	Hs.124503	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006955: immune response, GO:0007417: central nervous system development, GO:0008283: cell proliferation, GO:0048598: embryonic morphogenesis, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0003713: transcription coactivator activity, GO:0003714: transcription corepressor activity, GO:0008270: zinc ion binding, GO:0008270: zinc ion binding, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding		0.5927	0.9566	1.5616	1.6313	8.08	8.67	9.03	9.64	9.71	9.48	3
212771_at	C10orf38	chromosome 10 open reading frame 38	AU150943	221061	Hs.66762	GO:0016020: membrane, GO:0016021: integral to membrane		0.3145	0.829	1.3025	1.5089	5.84	6.15	6.67	7.14	7.35	7.07	3

(*Continued*)

TABLE E3. (*Continued*)

212761_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	AI703074	6934	Hs.593995	GO:0000074: regulation of progression through cell cycle, GO:0006325: establishment and/or maintenance of chromatin architecture, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007165: signal transduction, GO:0030111: regulation of Wnt receptor signaling pathway, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0005515: protein binding	04310: Wnt signaling pathway, 04520: Adherens junction, 04916: Melanogenesis, 05210: Colorectal cancer, 05213: Endometrial cancer, 05215: Prostate cancer, 05216: Thyroid cancer, 05217: Basal cell carcinoma, 05221: Acute myeloid leukemia	0.5602	0.7769	1.148	1.3882	9.73	10.29	10.51	10.88	11.12	11.08	3
212762_s_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	AI375916	6934	Hs.593995	GO:0000074: regulation of progression through cell cycle, GO:0006325: establishment and/or maintenance of chromatin architecture, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007165: signal transduction, GO:0030111: regulation of Wnt receptor signaling pathway, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0005515: protein binding	04310: Wnt signaling pathway, 04520: Adherens junction, 04916: Melanogenesis, 05210: Colorectal cancer, 05213: Endometrial cancer, 05215: Prostate cancer, 05216: Thyroid cancer, 05217: Basal cell carcinoma, 05221: Acute myeloid leukemia	0.2779	0.8981	1.1729	1.3581	7.62	7.9	8.52	8.8	8.98	9.24	3
212675_s_at	CEP68	centrosomal protein 68kDa	AB011154	23177	Hs.693614			0.6917	0.885	1.406	1.5063	8.38	9.07	9.27	9.79	9.89	9.86	3
212690_at	DDHD2	DDHD domain containing 2	AB018268	23259	Hs.434966	GO:0046872: metal ion binding		0.6334	0.8654	1.2346	1.3075	7.73	8.36	8.59	8.96	9.04	9.1	3
212609_s_at	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	U79271	10000	Hs.498292	GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04012: ErbB signaling pathway, 04150: mTOR signaling pathway, 04210: Apoptosis, 04370: VEGF signaling pathway, 04510: Focal adhesion, 04530: Tight junction, 04620: Toll-like receptor signaling pathway, 04630: Jak-STAT signaling pathway, 04660: T cell receptor signaling pathway, 04662: B cell receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 04910: Insulin signaling pathway, 04920: Adipocytokine signaling pathway, 05210: Colorectal cancer, 05211: Renal cell carcinoma, 05212: Pancreatic cancer, 05213: Endometrial cancer, 05214: Glioma, 05215: Prostate cancer, 05218: Melanoma, 05220: Chronic myeloid leukemia, 05221: Acute myeloid leukemia, 05222: Small cell lung cancer, 05223: Non-small cell lung cancer	0.1765	0.4399	1.047	1.5588	7.93	8.11	8.37	8.98	9.49	9.04	3
212660_at	PHF15	PHD finger protein 15	AI735639	23338	Hs.483419	GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.4146	0.8085	1.1231	1.5283	5.19	5.61	6	6.31	6.72	6.87	3
212504_at	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	N31807	22982	Hs.432397	GO:0008152: metabolic process, GO:0005634: nucleus, GO:0003824: catalytic activity, GO:0008134: transcription factor binding		0.3361	0.6126	1.0962	1.7155	6.04	6.37	6.65	7.13	7.75	7.47	3

(*Continued*)

TABLE E3. (*Continued*)

212560_at	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	AV728268	6653	Hs.368592	GO:0006629: lipid metabolic process, GO:0006869: lipid transport, GO:0006898: receptor-mediated endocytosis, GO:0008202: steroid metabolic process, GO:0008203: cholesterol metabolic process, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004888: transmembrane receptor activity, GO:0005319: lipid transporter activity		0.5059	0.5632	1.083	1.2126	7.16	7.66	7.72	8.24	8.37	8.63	3
212488_at	COL5A1	collagen, type V, alpha 1	N30339	1289	Hs.210283	GO:0006817: phosphate transport, GO:0007155: cell adhesion, GO:0005581: collagen, GO:0005588: collagen type V, GO:0005737: cytoplasm, GO:0005201: extracellular matrix structural constituent, GO:0008201: heparin binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.275	0.8414	1.585	1.3889	9.4	9.67	10.24	10.98	10.79	9.63	3
212503_s_at	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	N22859	22982	Hs.432397	GO:0008152: metabolic process, GO:0005634: nucleus, GO:0003824: catalytic activity, GO:0008134: transcription factor binding		0.5049	0.9137	1.503	1.6228	6.59	7.09	7.5	8.09	8.21	8.16	3
212423_at	C10orf56	chromosome 10 open reading frame 56	AK024784	219654	Hs.523080	GO:0003676: nucleic acid binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.0525	0.6871	1.1449	1.543	8.75	8.8	9.43	9.89	10.29	9.91	3
212464_s_at	FN1	fibronectin 1	X02761	2335	Hs.203717	GO:0006953: acute-phase response, GO:0007155: cell adhesion, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0009611: response to wounding, GO:0016477: cell migration, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005793: ER-Golgi intermediate compartment, GO:0005201: extracellular matrix structural constituent, GO:0005518: collagen binding, GO:0008201: heparin binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 04810: Regulation of actin cytoskeleton, 05222: Small cell lung cancer	0.2048	0.5648	1.2167	1.2802	10.88	11.09	11.45	12.1	12.16	11.7	3
212343_at	YIPF6	Yip1 domain family, member 6	AL117461	286451	Hs.82719, Hs.694797	GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane		0.4211	0.6486	1.0051	1.1619	7.09	7.51	7.74	8.09	8.25	8.43	3
212419_at	C10orf56	chromosome 10 open reading frame 56	AA131324	219654	Hs.523080	GO:0003676: nucleic acid binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.3494	0.7089	1.1069	1.393	8.63	8.98	9.34	9.74	10.02	9.68	3
212158_at	SDC2	syndecan 2	AL577322	6383	Hs.1501, Hs.598247	GO:0008150: biological_process, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003674: molecular_function, GO:0008092: cytoskeletal protein binding	04512: ECM-receptor interaction, 04514: Cell adhesion molecules (CAMs)	0.4128	0.8817	1.2963	1.5061	8.96	9.37	9.84	10.26	10.47	10.55	3
212233_at			AL523076					0.2684	0.7204	1.3555	1.5816	8.41	8.68	9.13	9.76	9.99	9.87	3
211719_x_at	FN1	fibronectin 1	BC005858	2335	Hs.203717	GO:0006953: acute-phase response, GO:0007155: cell adhesion, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0009611: response to wounding, GO:0016477: cell migration, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005793: ER-Golgi intermediate compartment, GO:0005201: extracellular matrix structural constituent, GO:0005518: collagen binding, GO:0008201: heparin binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 04810: Regulation of actin cytoskeleton, 05222: Small cell lung cancer	0.1942	0.5347	1.1177	1.2328	11.58	11.77	12.11	12.69	12.81	12.33	3
212157_at	SDC2	syndecan 2	AI380298	6383	Hs.1501, Hs.598247	GO:0008150: biological_process, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003674: molecular_function, GO:0008092: cytoskeletal protein binding	04512: ECM-receptor interaction, 04514: Cell adhesion molecules (CAMs)	0.3122	0.8544	1.4494	1.8437	4.73	5.04	5.59	6.18	6.58	6.57	3
210944_s_at	CAPN3	calpain 3, (p94)	BC003169	825	Hs.143261	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007517: muscle development, GO:0005622: intracellular, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0004198: calpain activity, GO:0004198: calpain activity, GO:0004871: signal transducer activity, GO:0005509: calcium ion binding		0.5735	0.7513	1.0755	1.4952	8.95	9.53	9.7	10.03	10.45	10.33	3

(*Continued*)

TABLE E3. (*Continued*)

211105_s_at	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	U80918	4772	Hs.534074, Hs.655457	GO:0000082: G1/S transition of mitotic cell cycle, GO:0001837: epithelial to mesenchymal transition, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0006816: calcium ion transport, GO:0007242: intracellular signaling cascade, GO:0007507: heart development, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0005528: FK506 binding, GO:0016563: transcription activator activity	04310: Wnt signaling pathway, 04360: Axon guidance, 04370: VEGF signaling pathway, 04650: Natural killer cell mediated cytotoxicity, 04660: T cell receptor signaling pathway, 04662: B cell receptor signaling pathway	0.274	0.5915	1.0832	1.881	4.52	4.79	5.11	5.6	6.4	6.23	3
210297_s_at	MSMB	microseminoprotein, beta-	U22178	4477	Hs.255462	GO:0008150: biological_process, GO:0005615: extracellular space, GO:0005634: nucleus, GO:0003674: molecular_function		−0.0802	0.6679	2.0046	2.5899	4.4	4.32	5.06	6.4	6.99	7.23	3
210299_s_at	FHL1	four and a half LIM domains 1	AF063002	2273	Hs.435369	GO:0007275: multicellular organismal development, GO:0007517: muscle development, GO:0009887: organ morphogenesis, GO:0016049: cell growth, GO:0030154: cell differentiation, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0003674: molecular_function, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.2527	0.94	1.2098	1.4998	9.92	10.17	10.86	11.13	11.42	11.78	3
209763_at	CHRDL1	chordin-like 1	AL049176	91851	Hs.496587	GO:0001503: ossification, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0030154: cell differentiation		0.6905	0.8394	1.3479	1.6337	9.07	9.76	9.91	10.42	10.7	10.79	3
209815_at	PTCH1	patched homolog 1 (Drosophila)	BG054916	5727	Hs.494538	GO:0007049: cell cycle, GO:0007165: signal transduction, GO:0007224: smoothened signaling pathway, GO:0008283: cell proliferation, GO:0009887: organ morphogenesis, GO:0009953: dorsal/ventral pattern formation, GO:0016485: protein processing, GO:0030326: embryonic limb morphogenesis, GO:0040015: negative regulation of body size, GO:0043109: regulation of smoothened activity, GO:0045786: negative regulation of progression through cell cycle, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0005515: protein binding, GO:0008158: hedgehog receptor activity	04340: Hedgehog signaling pathway, 05217: Basal cell carcinoma	0.4776	0.8993	1.3174	1.7546	6.43	6.91	7.33	7.75	8.18	8.21	3
209655_s_at	TMEM47	transmembrane protein 47	AL136550	83604	Hs.8769	GO:0005886: plasma membrane, GO:0016021: integral to membrane		−0.0411	0.7297	1.14	1.0804	4.48	4.44	5.21	5.62	5.56	5.96	3

(*Continued*)

TABLE E3. (*Continued*)

209685_s_at	PRKCB1	protein kinase C, beta 1	M13975	5579	Hs.460355	GO:0006468: protein amino acid phosphorylation, GO:0006816: calcium ion transport, GO:0006874: cellular calcium ion homeostasis, GO:0007242: intracellular signaling cascade, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0000166: nucleotide binding, GO:0004697: protein kinase C activity, GO:0005246: calcium channel regulator activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008270: zinc ion binding, GO:0016740: transferase activity, GO:0019992: diacylglycerol binding	04010: MAPK signaling pathway, 04012: ErbB signaling pathway, 04020: Calcium signaling pathway, 04070: Phosphatidylinositol signaling system, 04310: Wnt signaling pathway, 04370: VEGF signaling pathway, 04510: Focal adhesion, 04530: Tight junction, 04540: Gap junction, 04650: Natural killer cell mediated cytotoxicity, 04662: B cell receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 04670: Leukocyte transendothelial migration, 04720: Long-term potentiation, 04730: Long-term depression, 04912: GnRH signaling pathway, 04916: Melanogenesis, 05214: Glioma, 05223: Non-small cell lung cancer	0.77	0.6892	1.4423	1.4861	4.1	4.87	4.79	5.54	5.58	6.05	3
209550_at	NDN	necdin homolog (mouse)	U35139	4692	Hs.50130	GO:0000074: regulation of progression through cell cycle, GO:0001558: regulation of cell growth, GO:0001764: neuron migration, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007413: axonal fasciculation, GO:0007417: central nervous system development, GO:0007585: respiratory gaseous exchange, GO:0008285: negative regulation of cell proliferation, GO:0008347: glial cell migration, GO:0019233: sensory perception of pain, GO:0048011: nerve growth factor receptor signaling pathway, GO:0048666: neuron development, GO:0048676: axon extension involved in development, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005813: centrosome, GO:0003677: DNA binding, GO:0005515: protein binding, GO:0043015: gamma-tubulin binding		0.5031	0.8056	1.2126	1.5128	7.47	7.97	8.28	8.68	8.98	8.51	3
209651_at	TGFB1I1	transforming growth factor beta 1 induced transcript 1	BC001830	7041	Hs.513530	GO:0006366: transcription from RNA polymerase II promoter, GO:0007155: cell adhesion, GO:0008285: negative regulation of cell proliferation, GO:0016055: Wnt receptor signaling pathway, GO:0030154: cell differentiation, GO:0045941: positive regulation of transcription, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0030054: cell junction, GO:0003713: transcription coactivator activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding, GO:0050681: androgen receptor binding		0.223	0.702	1.0748	1.6828	7.74	7.97	8.45	8.82	9.43	9.14	3

(*Continued*)

TABLE E3. (*Continued*)

209443_at	SERPINA5	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	J02639	5104	Hs.510334	GO:0007283: spermatogenesis, GO:0007342: fusion of sperm to egg plasma membrane, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0016020: membrane, GO:0043234: protein complex, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding, GO:0008201: heparin binding, GO:0032190: acrosin binding	04610: Complement and coagulation cascades	−0.2836	0.6712	1.3633	1.5265	3.01	2.72	3.68	4.37	4.53	3.9	3
209447_at	SYNE1	spectrin repeat containing, nuclear envelope 1	AF043290	23345	Hs.12967	GO:0006997: nuclear organization and biogenesis, GO:0007030: Golgi organization and biogenesis, GO:0042692: muscle cell differentiation, GO:0005635: nuclear envelope, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0005856: cytoskeleton, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0045211: postsynaptic membrane, GO:0003779: actin binding, GO:0003779: actin binding, GO:0005198: structural molecule activity, GO:0005521: lamin binding		0.307	0.6475	1.1756	1.3868	6.67	6.97	7.31	7.84	8.05	8.27	3
209335_at	DCN	decorin	BC005322	1634	Hs.694789	GO:0009887: organ morphogenesis, GO:0005578: proteinaceous extracellular matrix, GO:0005515: protein binding	04350: TGF-beta signaling pathway	0.593	0.8057	1.2555	1.1667	11.66	12.26	12.47	12.92	12.83	12.93	3
209343_at	EFHD1	EF-hand domain family, member D1	BC002449	80303	Hs.516769, Hs.653499	GO:0031175: neurite development, GO:0005743: mitochondrial inner membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.3941	0.6367	1.1915	2.1755	4.52	4.92	5.16	5.72	6.7	6.42	3
209292_at	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	AL022726	3400	Hs.519601	GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0008284: positive regulation of cell proliferation, GO:0016481: negative regulation of transcription, GO:0043350: neuroblast proliferation (sensu Vertebrata), GO:0045665: negative regulation of neuron differentiation, GO:0048712: negative regulation of astrocyte differentiation, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003714: transcription corepressor activity	04350: TGF-beta signaling pathway	0.1325	0.926	1.3644	1.9965	8.84	8.98	9.77	10.21	10.84	11.25	3
209298_s_at	ITSN1	intersectin 1 (SH3 domain protein)	AF114488	6453	Hs.160324	GO:0007242: intracellular signaling cascade, GO:0035023: regulation of Rho protein signal transduction, GO:0048488: synaptic vesicle endocytosis, GO:0005622: intracellular, GO:0016020: membrane, GO:0019717: synaptosome, GO:0030054: cell junction, GO:0045202: synapse, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0005509: calcium ion binding, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.4318	0.8702	1.5483	1.5258	6.03	6.46	6.9	7.58	7.56	7.67	3
209242_at	PEG3	paternally expressed 3	AL042588	5178	Hs.201776	GO:0006355: regulation of transcription, DNA-dependent, GO:0006915: apoptosis, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.4295	0.6154	1.3956	1.5747	3.63	4.06	4.24	5.02	5.2	5.29	3

(*Continued*)

TABLE E3. (*Continued*)

209291_at	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	AW157094	3400	Hs.519601	GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0008284: positive regulation of cell proliferation, GO:0016481: negative regulation of transcription, GO:0043350: neuroblast proliferation (sensu Vertebrata), GO:0045665: negative regulation of neuron differentiation, GO:0048712: negative regulation of astrocyte differentiation, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003714: transcription corepressor activity	04350: TGF-beta signaling pathway	0.3261	0.7942	1.1427	1.5537	10.37	10.69	11.16	11.51	11.92	12.25	3
209200_at	MEF2C	myocyte enhancer factor 2C	AL536517	4208	Hs.654474	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0007399: nervous system development, GO:0007517: muscle development, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0003713: transcription coactivator activity, GO:0043565: sequence-specific DNA binding	04010: MAPK signaling pathway	0.6044	0.8242	1.3432	1.5626	5.36	5.96	6.18	6.7	6.92	6.58	3
209210_s_at	PLEKHC1	pleckstrin homology domain containing, family C (with FERM domain) member 1	Z24725	10979	Hs.509343	GO:0007155: cell adhesion, GO:0008360: regulation of cell shape, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0001725: stress fiber, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005515: protein binding		0.1699	0.6038	1.298	1.43	8.86	9.03	9.47	10.16	10.29	10.25	3
209160_at	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	AB018580	8644	Hs.78183	GO:0006118: electron transport, GO:0006693: prostaglandin metabolic process, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0004033: aldo-keto reductase activity, GO:0004303: estradiol 17-beta-dehydrogenase activity, GO:0016491: oxidoreductase activity, GO:0047017: prostaglandin-F synthase activity, GO:0047026: 3-alpha-hydroxysteroid dehydrogenase (A-specific) activity, GO:0047115: trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	00590: Arachidonic acid metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	0.2597	0.7115	1.1651	1.3572	8.79	9.05	9.5	9.95	10.14	9.88	3
209183_s_at	C10orf10	chromosome 10 open reading frame 10	AL136653	11067	Hs.93675	GO:0005739: mitochondrion		0.7424	0.9121	1.4805	2.2714	7	7.74	7.91	8.48	9.27	8.6	3
209120_at	NR2F2	nuclear receptor subfamily 2, group F, member 2	AL037401	7026	Hs.347991	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006629: lipid metabolic process, GO:0007165: signal transduction, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003706: ligand-regulated transcription factor activity, GO:0003707: steroid hormone receptor activity, GO:0003714: transcription corepressor activity, GO:0008270: zinc ion binding, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding		0.5335	0.8509	1.3778	1.5067	10.02	10.55	10.87	11.4	11.53	11.37	3

(*Continued*)

TABLE E3. (*Continued*)

209121_x_at	NR2F2	nuclear receptor subfamily 2, group F, member 2	M64497	7026	Hs.347991	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006629: lipid metabolic process, GO:0007165: signal transduction, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003706: ligand-regulated transcription factor activity, GO:0003707: steroid hormone receptor activity, GO:0003714: transcription corepressor activity, GO:0008270: zinc ion binding, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding		0.4257	0.7593	1.1441	1.782	7.51	7.93	8.27	8.65	9.29	8.86	3
209094_at	DDAH1	dimethylarginine dimethylaminohydrolase 1	AL078459	23576	Hs.379858	GO:0006527: arginine catabolic process, GO:0007263: nitric oxide mediated signal transduction, GO:0008270: zinc ion binding, GO:0016403: dimethylargininase activity, GO:0016787: hydrolase activity, GO:0046872: metal ion binding		−0.0975	0.4772	1.4418	2.0019	5.75	5.65	6.23	7.19	7.75	8.27	3
209101_at	CTGF	connective tissue growth factor	M92934	1490	Hs.591346	GO:0001502: cartilage condensation, GO:0001503: ossification, GO:0001525: angiogenesis, GO:0001558: regulation of cell growth, GO:0006260: DNA replication, GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0008543: fibroblast growth factor receptor signaling pathway, GO:0008544: epidermis development, GO:0009611: response to wounding, GO:0016477: cell migration, GO:0030154: cell differentiation, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0005886: plasma membrane, GO:0005178: integrin binding, GO:0005515: protein binding, GO:0005520: insulin-like growth factor binding, GO:0008201: heparin binding		0.0009	0.3929	1.0518	1.1175	9.3	9.3	9.69	10.35	10.41	10.5	3
208964_s_at	FADS1	fatty acid desaturase 1	AL512760	3992	Hs.503546	GO:0006629: lipid metabolic process, GO:0006633: fatty acid biosynthetic process, GO:0016020: membrane, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0016491: oxidoreductase activity, GO:0016717: oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water, GO:0020037: heme binding	00591: Linoleic acid metabolism	0.1316	0.2906	1.1224	1.5524	6.55	6.69	6.84	7.68	8.11	8.69	3
208983_s_at	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)	M37780	5175	Hs.514412	GO:0006928: cell motility, GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0008037: cell recognition, GO:0005886: plasma membrane, GO:0005911: intercellular junction, GO:0016021: integral to membrane, GO:0005515: protein binding	04514: Cell adhesion molecules (CAMs), 04670: Leukocyte transendothelial migration	0.3954	0.4495	1.0184	1.0944	8	8.39	8.45	9.01	9.09	8.86	3
208760_at	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	AL031714	7329	Hs.302903	GO:0006464: protein modification process, GO:0006464: protein modification process, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0007049: cell cycle, GO:0007059: chromosome segregation, GO:0007067: mitosis, GO:0051301: cell division, GO:0000795: synaptonemal complex, GO:0016605: PML body, GO:0005515: protein binding, GO:0016874: ligase activity, GO:0019787: small conjugating protein ligase activity		0.4991	0.9691	1.2979	1.6781	5.53	6.03	6.5	6.83	7.21	7.17	3

(*Continued*)

TABLE E3. (*Continued*)

208869_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1	BF125756	23710	Hs.524250	GO:0005622: intracellular, GO:0005776: autophagic vacuole, GO:0005874: microtubule, GO:0005515: protein binding, GO:0005515: protein binding, GO:0048487: beta-tubulin binding, GO:0050811: GABA receptor binding	04140: Regulation of autophagy	0.7606	0.7987	1.3155	1.6631	6.45	7.21	7.25	7.77	8.11	8.14	3
208335_s_at	DARC	Duffy blood group, chemokine receptor	NM_002036	2532	Hs.153381	GO:0006952: defense response, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004950: chemokine receptor activity		0.397	0.5613	1.1116	1.5832	8.74	9.14	9.3	9.85	10.32	10.08	3
208498_s_at	AMY1A	amylase, alpha 1A (salivary)	NM_004038	276	Hs.655232	GO:0005975: carbohydrate metabolic process, GO:0007586: digestion, GO:0008152: metabolic process, GO:0005615: extracellular space, GO:0004556: alpha-amylase activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0016798: hydrolase activity, acting on glycosyl bonds, GO:0031404: chloride ion binding	00500: Starch and sucrose metabolism	0.5441	0.8713	1.3696	1.7591	5.73	6.28	6.6	7.1	7.49	7.74	3
208015_at	SMAD1	SMAD family member 1	NM_015583	4086	Hs.656534	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0007179: transforming growth factor beta receptor signaling pathway, GO:0009880: embryonic pattern specification, GO:0030509: BMP signaling pathway, GO:0005622: intracellular, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0016021: integral to membrane, GO:0005057: receptor signaling protein activity, GO:0005515: protein binding, GO:0016563: transcription activator activity	04350: TGF-beta signaling pathway	0.2096	0.5182	1.2178	1.6245	5.67	5.88	6.18	6.88	7.29	6.82	3
208096_s_at	COL21A1	collagen, type XXI, alpha 1	NM_030820	81578	Hs.47629	GO:0006817: phosphate transport, GO:0007155: cell adhesion, GO:0005737: cytoplasm, GO:0005198: structural molecule activity		0.5552	0.7738	1.6669	1.8319	6.52	7.08	7.29	8.19	8.35	8.42	3
207430_s_at	MSMB	microseminoprotein, beta-	NM_002443	4477	Hs.255462	GO:0008150: biological_process, GO:0005615: extracellular space, GO:0005634: nucleus, GO:0003674: molecular_function		−0.1724	0.4191	1.3098	2.2567	3.55	3.38	3.97	4.86	5.81	5.5	3
207522_s_at	ATP2A3	ATPase, Ca++ transporting, ubiquitous	NM_005173	489	Hs.513870	GO:0006810: transport, GO:0006812: cation transport, GO:0006816: calcium ion transport, GO:0008152: metabolic process, GO:0015992: proton transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016529: sarcoplasmic reticulum, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0005388: calcium-transporting ATPase activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0015662: ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, GO:0016787: hydrolase activity, GO:0016820: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	04020: Calcium signaling pathway	0.2282	0.3429	1.0325	1.3476	3.26	3.49	3.6	4.29	4.61	5.22	3

(*Continued*)

TABLE E3. (*Continued*)

207177_at	PTGFR	prostaglandin F receptor (FP)	NM_000959	5737	Hs.654365	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007567: parturition, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004958: prostaglandin F receptor activity, GO:0004958: prostaglandin F receptor activity, GO:0004960: thromboxane receptor activity	04020: Calcium signaling pathway, 04080: Neuroactive ligand-receptor interaction	0.0769	0.5762	1.1141	1.2615	5.97	6.04	6.54	7.08	7.23	7.23	3
207191_s_at	ISLR	immunoglobulin superfamily containing leucine-rich repeat	NM_005545	3671	Hs.513022, Hs.664723	GO:0007155: cell adhesion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding		0.7259	0.966	1.3969	1.9456	6.37	7.09	7.33	7.76	8.31	8.11	3
206873_at	CA6	carbonic anhydrase VI	NM_001215	765	Hs.100322	GO:0006730: one-carbon compound metabolic process, GO:0004089: carbonate dehydratase activity, GO:0004089: carbonate dehydratase activity, GO:0008270: zinc ion binding, GO:0016829: lyase activity, GO:0046872: metal ion binding	00910: Nitrogen metabolism	0.1681	0.9225	1.3288	1.7291	6.91	7.08	7.83	8.24	8.64	9.26	3
207123_s_at	MATN4	matrilin 4	NM_003833	8785	Hs.278489	GO:0030198: extracellular matrix organization and biogenesis, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005201: extracellular matrix structural constituent, GO:0005518: collagen binding		−0.0111	0.6431	1.1015	1.3193	5.88	5.87	6.53	6.98	7.2	6.38	3
206580_s_at	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	NM_016938	30008	Hs.647231	GO:0007596: blood coagulation, GO:0005604: basement membrane, GO:0016020: membrane, GO:0004888: transmembrane receptor activity, GO:0005201: extracellular matrix structural constituent, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.7306	0.9521	1.42	1.6955	7.82	8.55	8.77	9.24	9.51	8.93	3
206858_s_at	HOXC6	homeobox C6	NM_004503	3223	Hs.549040	GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007275: multicellular organismal development, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003714: transcription corepressor activity, GO:0043565: sequence-specific DNA binding		0.4684	0.7526	1.271	1.628	8.71	9.18	9.46	9.98	10.34	10.21	3
206373_at	ZIC1	Zic family member 1 (odd-paired homolog, Drosophila)	NM_003412	7545	Hs.598590, Hs.647962	GO:0007389: pattern specification process, GO:0007420: brain development, GO:0007610: behavior, GO:0008589: regulation of smoothened signaling pathway, GO:0030154: cell differentiation, GO:0042472: inner ear morphogenesis, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.5427	0.9624	1.3674	1.5211	2.59	3.13	3.55	3.96	4.11	3.35	3
206481_s_at	LDB2	LIM domain binding 2	NM_001290	9079	Hs.23748	GO:0007275: multicellular organismal development, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003712: transcription cofactor activity, GO:0003712: transcription cofactor activity, GO:0030274: LIM domain binding		0.5234	0.7287	1.42	1.4527	8.17	8.69	8.9	9.59	9.62	9.09	3
206159_at	GDF10	growth differentiation factor 10	NM_004962	2662	Hs.2171	GO:0001501: skeletal development, GO:0007179: transforming growth factor beta receptor signaling pathway, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005125: cytokine activity, GO:0008083: growth factor activity, GO:0008083: growth factor activity		0.2442	0.8241	1.2916	1.8703	2.75	2.99	3.57	4.04	4.62	3.93	3

(*Continued*)

TABLE E3. (*Continued*)

206201_s_at	MEOX2	mesenchyme homeobox 2	NM_005924	4223	Hs.170355	GO:0001757: somite specification, GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0008015: circulation, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding		0.3465	0.988	1.8489	1.9956	7.17	7.52	8.16	9.02	9.17	8.97	3
206070_s_at	EPHA3	EPH receptor A3	AF213459	2042	Hs.123642	GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0004713: protein-tyrosine kinase activity, GO:0004872: receptor activity, GO:0005003: ephrin receptor activity, GO:0005524: ATP binding, GO:0016740: transferase activity	04360: Axon guidance	0.0907	0.5143	1.1304	1.26	3.99	4.08	4.5	5.12	5.25	4.7	3
206093_x_at	TNXB	tenascin XB	NM_007116	7148	Hs.42853, Hs.485104	GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0032963: collagen metabolic process, GO:0048251: elastic fiber assembly, GO:0005578: proteinaceous extracellular matrix, GO:0005583: fibrillar collagen, GO:0005622: intracellular, GO:0005102: receptor binding, GO:0005178: integrin binding, GO:0008201: heparin binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.1578	0.5286	1.0697	1.78	10.29	10.44	10.82	11.36	12.07	11.55	3
205932_s_at	MSX1	msh homeobox 1	NM_002448	4487	Hs.424414, Hs.621772	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0001501: skeletal development, GO:0007275: multicellular organismal development, GO:0007517: muscle development, GO:0009887: organ morphogenesis, GO:0030326: embryonic limb morphogenesis, GO:0030900: forebrain development, GO:0030901: midbrain development, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0016564: transcription repressor activity, GO:0043565: sequence-specific DNA binding		0.1337	0.853	1.5004	2.1076	5.43	5.57	6.29	6.93	7.54	7.05	3
205933_at	SETBP1	SET binding protein 1	NM_015559	26040	Hs.435458	GO:0005634: nucleus, GO:0003677: DNA binding, GO:0005515: protein binding		0.6055	0.8514	1.0863	1.7134	5.83	6.43	6.68	6.91	7.54	7.08	3
205794_s_at	NOVA1	neuro-oncological ventral antigen 1	NM_002515	4857	Hs.31588	GO:0007268: synaptic transmission, GO:0007626: locomotory behavior, GO:0008380: RNA splicing, GO:0003723: RNA binding		0.3094	0.958	1.4779	1.5808	5.69	6	6.65	7.17	7.28	7.63	3
205802_at	TRPC1	transient receptor potential cation channel, subfamily C, member 1	NM_003304	7220	Hs.250687	GO:0006811: ion transport, GO:0006816: calcium ion transport, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005216: ion channel activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0015279: store-operated calcium channel activity	04020: Calcium signaling pathway	0.5516	0.5057	1.1758	1.1756	3.93	4.48	4.44	5.11	5.11	5.04	3
205620_at	F10	coagulation factor X	NM_000504	2159	Hs.361463	GO:0006508: proteolysis, GO:0007596: blood coagulation, GO:0005576: extracellular region, GO:0003804: coagulation factor Xa activity, GO:0005509: calcium ion binding, GO:0008233: peptidase activity	04610: Complement and coagulation cascades	0.3913	0.8158	1.062	1.3291	5.19	5.58	6	6.25	6.51	6.28	3
205752_s_at	GSTM5	glutathione S-transferase M5	NM_000851	2949	Hs.75652	GO:0008152: metabolic process, GO:0005737: cytoplasm, GO:0004364: glutathione transferase activity, GO:0004364: glutathione transferase activity, GO:0016740: transferase activity	00480: Glutathione metabolism, 00980: Metabolism of xenobiotics by cytochrome P450	0.4714	0.8485	1.0658	1.3259	3.34	3.81	4.19	4.41	4.67	4.52	3

(*Continued*)

TABLE E3. (*Continued*)

205609_at	ANGPT1	angiopoietin 1	NM_001146	284	Hs.369675	GO:0001525: angiogenesis, GO:0007165: signal transduction, GO:0007165: signal transduction, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007275: multicellular organismal development, GO:0030154: cell differentiation, GO:0005102: receptor binding, GO:0005102: receptor binding		0.4222	0.962	1.7609	2.4536	3.29	3.71	4.25	5.05	5.74	5.26	3
205614_x_at	MST1	macrophage stimulating 1 (hepatocyte growth factor-like)	NM_020998	4485	Hs.349110, Hs.512587	GO:0006508: proteolysis, GO:0007596: blood coagulation, GO:0008150: biological_process, GO:0005575: cellular_component, GO:0003674: molecular_function, GO:0004252: serine-type endopeptidase activity, GO:0005509: calcium ion binding		0.9702	0.8943	1.2026	1.7725	3.14	4.12	4.04	4.35	4.92	4.72	3
205528_s_at	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	X79990	862	Hs.368431	GO:0006091: generation of precursor metabolites and energy, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0045444: fat cell differentiation, GO:0051101: regulation of DNA binding, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016564: transcription repressor activity, GO:0042803: protein homodimerization activity, GO:0046872: metal ion binding	05221: Acute myeloid leukemia	0.0377	0.5592	1.3142	1.659	3.93	3.96	4.48	5.24	5.58	4.98	3
205594_at	ZNF652	zinc finger protein 652	NM_014897	22834	Hs.463375	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0003677: DNA binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.5826	0.8572	1.3865	1.7699	6.14	6.72	7	7.53	7.91	8.16	3
205440_s_at	NPY1R	neuropeptide Y receptor Y1	NM_000909	4886	Hs.519057	GO:0006006: glucose metabolic process, GO:0007165: signal transduction, GO:0007187: G-protein signaling, coupled to cyclic nucleotide second messenger, GO:0007193: G-protein signaling, adenylate cyclase inhibiting pathway, GO:0007218: neuropeptide signaling pathway, GO:0007626: locomotory behavior, GO:0007631: feeding behavior, GO:0008217: blood pressure regulation, GO:0019233: sensory perception of pain, GO:0040014: regulation of body size, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0001584: rhodopsin-like receptor activity, GO:0001601: peptide YY receptor activity, GO:0001602: pancreatic polypeptide receptor activity, GO:0004872: receptor activity, GO:0004983: neuropeptide Y receptor activity, GO:0005515: protein binding	04080: Neuroactive ligand-receptor interaction	0.5179	0.7958	1.1435	1.5326	6.93	7.45	7.72	8.07	8.46	8.93	3
205525_at	CALD1	caldesmon 1	NM_018495	800	Hs.490203	GO:0006928: cell motility, GO:0006936: muscle contraction, GO:0005856: cytoskeleton, GO:0003779: actin binding, GO:0003779: actin binding, GO:0005516: calmodulin binding, GO:0005516: calmodulin binding, GO:0005523: tropomyosin binding, GO:0017022: myosin binding		0.2005	0.4955	1.2391	1.9822	5.77	5.97	6.27	7.01	7.75	7.02	3
205392_s_at	CCL14	chemokine (C-C motif) ligand 14	NM_004166	6358	Hs.272493, Hs.656286	GO:0006874: cellular calcium ion homeostasis, GO:0006955: immune response, GO:0008284: positive regulation of cell proliferation, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0008009: chemokine activity	04060: Cytokine-cytokine receptor interaction	0.5112	0.7786	1.281	1.8679	7.33	7.85	8.11	8.62	9.2	8.88	3

(*Continued*)

TABLE E3. (*Continued*)

205404_at	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	NM_005525	3290	Hs.195040	GO:0006629: lipid metabolic process, GO:0008152: metabolic process, GO:0008202: steroid metabolic process, GO:0030324: lung development, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016491: oxidoreductase activity, GO:0033237: 11-beta-hydroxysteroid dehydrogenase (NADP+) activity	00140: C21-Steroid hormone metabolism, 00150: Androgen and estrogen metabolism	0.4993	0.9659	1.8127	1.751	5.59	6.09	6.56	7.4	7.34	8.9	3
205259_at	NR3C2	nuclear receptor subfamily 3, group C, member 2	NM_000901	4306	Hs.163924	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006883: cellular sodium ion homeostasis, GO:0007165: signal transduction, GO:0007588: excretion, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0003700: transcription factor activity, GO:0003707: steroid hormone receptor activity, GO:0004872: receptor activity, GO:0005496: steroid binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0008289: lipid binding, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding		0.2396	0.7482	1.2742	1.4503	4.54	4.78	5.29	5.81	5.99	6.45	3
205304_s_at	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	BF514158	3764	Hs.102308, Hs.619408	GO:0006811: ion transport, GO:0006813: potassium ion transport, GO:0005624: membrane fraction, GO:0008076: voltage-gated potassium channel complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030016: myofibril, GO:0005244: voltage-gated ion channel activity, GO:0015272: ATP-activated inward rectifier potassium channel activity, GO:0030955: potassium ion binding		0.3093	0.7616	1.1182	1.5284	3.89	4.2	4.65	5.01	5.42	4.79	3
205141_at	ANG	angiogenin, ribonuclease, RNase A family, 5	NM_001145	283	Hs.283749, Hs.695245	GO:0001525: angiogenesis, GO:0001525: angiogenesis, GO:0001541: ovarian follicle development, GO:0001666: response to hypoxia, GO:0001666: response to hypoxia, GO:0001890: placenta development, GO:0001938: positive regulation of endothelial cell proliferation, GO:0006651: diacylglycerol biosynthetic process, GO:0007154: cell communication, GO:0007202: phospholipase C activation, GO:0007275: multicellular organismal development, GO:0009303: rRNA transcription, GO:0016477: cell migration, GO:0017148: negative regulation of protein biosynthetic process, GO:0030041: actin filament polymerization, GO:0030154: cell differentiation, GO:0032148: activation of protein kinase B, GO:0032431: activation of phospholipase A2, GO:0042327: positive regulation of phosphorylation, GO:0042592: homeostatic process, GO:0048662: negative regulation of smooth muscle cell proliferation, GO:0050714: positive regulation of protein secretion, GO:0050714: positive regulation of protein secretion, GO:0005605: basal lamina, GO:0005615: extracellular space, GO:0005634: nucleus, GO:0005730: nucleolus, GO:0032311: angiogenin-PRI complex, GO:0003677: DNA binding, GO:0003779: actin binding, GO:0004519: endonuclease activity, GO:0004522: pancreatic ribonuclease activity, GO:0004540: ribonuclease activity, GO:0005102: receptor binding, GO:0005507: copper ion binding, GO:0008201: heparin binding, GO:0016787: hydrolase activity, GO:0019843: rRNA binding		0.5772	0.7929	1.085	1.5444	4.3	4.87	5.09	5.38	5.84	6.07	3

(*Continued*)

TABLE E3. (*Continued*)

205200_at	CLEC3B	C-type lectin domain family 3, member B	NM_003278	7123	Hs.476092	GO:0001501: skeletal development, GO:0005576: extracellular region, GO:0005529: sugar binding		0.2691	0.6806	1.2872	1.5025	11.16	11.43	11.84	12.45	12.67	12.58	3
205076 _s_at	MTMR11	myotubularin related protein 11	NM_006697	10903	Hs.425144	GO:0046839: phospholipid dephosphorylation, GO:0004437: inositol or phosphatidylinositol phosphatase activity		0.5166	0.6595	1.0216	1.1491	5.78	6.3	6.44	6.8	6.93	7.13	3
205116_at	LAMA2	laminin, alpha 2 (merosin, congenital muscular dystrophy)	NM_000426	3908	Hs.200841	GO:0007517: muscle development, GO:0030155: regulation of cell adhesion, GO:0030334: regulation of cell migration, GO:0045995: regulation of embryonic development, GO:0005604: basement membrane, GO:0005606: laminin-1 complex, GO:0005102: receptor binding, GO:0005198: structural molecule activity	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 05222: Small cell lung cancer	0.5858	0.5412	1.0333	1.1748	6.83	7.42	7.37	7.86	8	7.88	3
204992 _s_at	PFN2	profilin 2	NM_002628	5217	Hs.91747	GO:0007010: cytoskeleton organization and biogenesis, GO:0008064: regulation of actin polymerization and/or depolymerization, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0005737: cytoplasm, GO:0015629: actin cytoskeleton, GO:0003779: actin binding, GO:0005515: protein binding, GO:0005546: phosphatidylinositol-4,5-bisphosphate binding	04810: Regulation of actin cytoskeleton	0.4762	0.7234	1.0887	1.2608	8.15	8.62	8.87	9.24	9.41	9.5	3
205044_at	GABRP	gamma-aminobutyric acid (GABA) A receptor, pi	NM_014211	2568	Hs.26225	GO:0006811: ion transport, GO:0016021: integral to membrane, GO:0030054: cell junction, GO:0045202: synapse, GO:0045211: postsynaptic membrane, GO:0004890: GABA-A receptor activity, GO:0005216: ion channel activity, GO:0005230: extracellular ligand-gated ion channel activity, GO:0005254: chloride channel activity, GO:0030594: neurotransmitter receptor activity, GO:0031404: chloride ion binding	04080: Neuroactive ligand-receptor interaction	0.8393	0.9842	1.3276	1.7847	4.29	5.12	5.27	5.61	6.07	7.42	3
204754_at	HLF	hepatic leukemia factor	W60800	3131	Hs.196952	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0007275: multicellular organismal development, GO:0048511: rhythmic process, GO:0005634: nucleus, GO:0003690: double-stranded DNA binding, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity		0.5397	0.9809	1.285	1.6195	6.92	7.46	7.9	8.2	8.54	8.67	3
204773_at	IL11RA	interleukin 11 receptor, alpha	NM_004512	3590	Hs.591088	GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004896: hematopoietin/interferon-class (D200-domain) cytokine receptor activity	04060: Cytokine-cytokine receptor interaction, 04630: Jak-STAT signaling pathway, 04640: Hematopoietic cell lineage	0.4517	0.9231	1.3719	1.4866	7.58	8.03	8.5	8.95	9.06	8.59	3
204731_at	TGFBR3	transforming growth factor, beta receptor III	NM_003243	7049	Hs.482390	GO:0007165: signal transduction, GO:0007179: transforming growth factor beta receptor signaling pathway, GO:0007275: multicellular organismal development, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0005539: glycosaminoglycan binding		0.2455	0.6004	1.0663	1.4311	9.4	9.64	10	10.47	10.83	10.87	3
204734_at	KRT15	keratin 15	NM_002275	3866	Hs.654570	GO:0008544: epidermis development, GO:0005882: intermediate filament, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding	01430: Cell Communication	0.6765	0.8403	1.3804	1.4388	11.71	12.39	12.55	13.09	13.15	12.97	3

(*Continued*)

TABLE E3. (*Continued*)

204686_at	IRS1	insulin receptor substrate 1	NM_005544	3667	Hs.471508	GO:0007165: signal transduction, GO:0008286: insulin receptor signaling pathway, GO:0048009: insulin-like growth factor receptor signaling pathway, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005792: microsome, GO:0004871: signal transducer activity, GO:0005069: transmembrane receptor protein tyrosine kinase docking protein activity, GO:0005158: insulin receptor binding, GO:0005159: insulin-like growth factor receptor binding, GO:0005515: protein binding, GO:0019901: protein kinase binding, GO:0042169: SH2 domain binding, GO:0043548: phosphoinositide 3-kinase binding, GO:0043548: phosphoinositide 3-kinase binding	04910: Insulin signaling pathway, 04920: Adipocytokine signaling pathway, 04930: Type II diabetes mellitus	0.1312	0.6721	1.0714	1.4375	7.06	7.19	7.73	8.13	8.5	8.73	3
204688_at	SGCE	sarcoglycan, epsilon	NM_003919	8910	Hs.371199	GO:0007160: cell-matrix adhesion, GO:0007517: muscle development, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005887: integral to plasma membrane, GO:0016012: sarcoglycan complex, GO:0016012: sarcoglycan complex, GO:0016020: membrane, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.8422	0.9322	1.3358	1.5078	5.18	6.02	6.11	6.52	6.69	6.95	3
204671_s_at	ANKRD6	ankyrin repeat domain 6	BE677131	22881	Hs.656539			0.0919	0.5943	1.3603	1.7091	3.77	3.86	4.36	5.13	5.48	5.11	3
204677_at	CDH5	cadherin 5, type 2, VE-cadherin (vascular epithelium)	NM_001795	1003	Hs.76206	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0007156: homophilic cell adhesion, GO:0005624: membrane fraction, GO:0005886: plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030054: cell junction, GO:0005509: calcium ion binding, GO:0005515: protein binding	04514: Cell adhesion molecules (CAMs), 04670: Leukocyte transendothelial migration	0.3288	0.4799	1.0666	1.1837	7.09	7.42	7.57	8.15	8.27	7.88	3
204570_at	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	NM_001864	1346	Hs.421621	GO:0006118: electron transport, GO:0005739: mitochondrion, GO:0005746: mitochondrial respiratory chain, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004129: cytochrome-c oxidase activity, GO:0009055: electron carrier activity	00190: Oxidative phosphorylation	0.4764	0.89	1.284	1.721	8.39	8.87	9.28	9.68	10.12	9.99	3
204604_at	PFTK1	PFTAIRE protein kinase 1	NM_012395	5218	Hs.430742	GO:0006468: protein amino acid phosphorylation, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity		0.4526	0.7357	1.3885	1.6437	5.38	5.83	6.11	6.76	7.02	6.76	3
204352_at	TRAF5	TNF receptor-associated factor 5	NM_004619	7188	Hs.523930	GO:0007165: signal transduction, GO:0042981: regulation of apoptosis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005737: cytoplasm, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	05222: Small cell lung cancer	0.5142	0.5617	1.4006	1.5382	6.69	7.2	7.25	8.09	8.23	7.82	3
204363_at	F3	coagulation factor III (thromboplastin, tissue factor)	NM_001993	2152	Hs.62192	GO:0006955: immune response, GO:0007596: blood coagulation, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0004888: transmembrane receptor activity	04610: Complement and coagulation cascades	0.1655	0.6493	1.1943	1.49	9.01	9.17	9.66	10.2	10.5	11.2	3
204284_at	PPP1R3C	protein phosphatase 1, regulatory (inhibitor) subunit 3C	N26005	5507	Hs.303090	GO:0005975: carbohydrate metabolic process, GO:0005977: glycogen metabolic process	04910: Insulin signaling pathway	0.282	0.8248	1.293	1.5583	7.7	7.99	8.53	9	9.26	9.42	3

(*Continued*)

TABLE E3. (*Continued*)

204345_at	COL16A1	collagen, type XVI, alpha 1	NM_001856	1307	Hs.368921	GO:0006817: phosphate transport, GO:0007155: cell adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0007565: female pregnancy, GO:0005578: proteinaceous extracellular matrix, GO:0005597: collagen type XVI, GO:0005737: cytoplasm, GO:0005178: integrin binding, GO:0005198: structural molecule activity, GO:0005515: protein binding		0.2228	0.5346	1.015	1.2786	8.56	8.79	9.1	9.58	9.84	9.48	3
204223_at	PRELP	proline/arginine-rich end leucine-rich repeat protein	NM_002725	5549	Hs.632481	GO:0001501: skeletal development, GO:0005578: proteinaceous extracellular matrix, GO:0005201: extracellular matrix structural constituent, GO:0005515: protein binding		0.4033	0.7535	1.0022	1.5053	6.98	7.38	7.73	7.98	8.48	8.39	3
204276_at	TK2	thymidine kinase 2, mitochondrial	BE895437	7084	Hs.512619	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006260: DNA replication, GO:0005739: mitochondrion, GO:0005743: mitochondrial inner membrane, GO:0000166: nucleotide binding, GO:0004797: thymidine kinase activity, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0016773: phosphotransferase activity, alcohol group as acceptor	00240: Pyrimidine metabolism	0.3873	0.8016	1.2578	1.2996	6.34	6.73	7.14	7.6	7.64	7.65	3
204083_s_at	TPM2	tropomyosin 2 (beta)	NM_003289	7169	Hs.300772	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005862: muscle thin filament tropomyosin, GO:0003779: actin binding, GO:0008307: structural constituent of muscle		0.1724	0.7708	1.1163	1.8099	9.68	9.85	10.45	10.8	11.49	11.14	3
204115_at	GNG11	guanine nucleotide binding protein (G protein), gamma 11	NM_004126	2791	Hs.83381	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0005834: heterotrimeric G-protein complex, GO:0016020: membrane, GO:0003924: GTPase activity, GO:0004871: signal transducer activity		0.2879	0.6751	1.082	1.1505	9.87	10.16	10.54	10.95	11.02	10.84	3
204036_at	EDG2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	AW269335	1902	Hs.126667	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007202: phospholipase C activation, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016021: integral to membrane, GO:0001619: lysosphingolipid and lysophosphatidic acid receptor activity, GO:0004872: receptor activity	04080: Neuroactive ligand-receptor interaction, 04540: Gap junction	0.1907	0.5549	1.0224	1.2434	8.77	8.96	9.33	9.8	10.02	9.81	3
204037_at	EDG2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	BF055366	1902	Hs.126667	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007202: phospholipase C activation, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016021: integral to membrane, GO:0001619: lysosphingolipid and lysophosphatidic acid receptor activity, GO:0004872: receptor activity	04080: Neuroactive ligand-receptor interaction, 04540: Gap junction	0.1769	0.5478	1.0242	1.4802	7.65	7.83	8.2	8.68	9.13	8.71	3
203951_at	CNN1	calponin 1, basic, smooth muscle	NM_001299	1264	Hs.465929	GO:0006940: regulation of smooth muscle contraction, GO:0031032: actomyosin structure organization and biogenesis, GO:0003779: actin binding, GO:0005516: calmodulin binding		0.3324	0.8913	1.3328	1.9688	7.47	7.81	8.37	8.81	9.44	9.15	3
204030_s_at	SCHIP1	schwannomin interacting protein 1	NM_014575	29970	Hs.134665	GO:0005737: cytoplasm		0.0669	0.4	1.035	1.2461	5.56	5.63	5.96	6.6	6.81	6.37	3

(*Continued*)

TABLE E3. (*Continued*)

203903_s_at	HEPH	hephaestin	NM_014799	9843	Hs.31720	GO:0006811: ion transport, GO:0006825: copper ion transport, GO:0006826: iron ion transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005375: copper ion transmembrane transporter activity, GO:0005506: iron ion binding, GO:0005507: copper ion binding, GO:0016491: oxidoreductase activity, GO:0046872: metal ion binding		0.7092	0.8482	1.3445	1.6743	6.51	7.22	7.36	7.86	8.19	8.01	3
203919_at	TCEA2	transcription elongation factor A (SII), 2	NM_003195	6919	Hs.505004	GO:0006350: transcription, GO:0006354: RNA elongation, GO:0006354: RNA elongation, GO:0006355: regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0008023: transcription elongation factor complex, GO:0003677: DNA binding, GO:0003702: RNA polymerase II transcription factor activity, GO:0003711: transcription elongation regulator activity, GO:0003746: translation elongation factor activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0030528: transcription regulator activity, GO:0046872: metal ion binding		0.4954	0.9039	1.4316	2.111	3.44	3.93	4.34	4.87	5.55	4.94	3
203812_at	SLIT3	slit homolog 3 (Drosophila)	AB011538	6586	Hs.604116	GO:0007275: multicellular organismal development, GO:0007417: central nervous system development, GO:0030154: cell differentiation, GO:0005615: extracellular space, GO:0005198: structural molecule activity, GO:0005509: calcium ion binding, GO:0005515: protein binding	04360: Axon guidance	0.1787	0.5872	1.0965	1.6305	8.22	8.4	8.81	9.32	9.85	9.49	3
203881_s_at	DMD	dystrophin (muscular dystrophy, Duchenne and Becker types)	NM_004010	1756	Hs.495912	GO:0006936: muscle contraction, GO:0007016: cytoskeletal anchoring, GO:0007016: cytoskeletal anchoring, GO:0007517: muscle development, GO:0043043: peptide biosynthetic process, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0016010: dystrophin-associated glycoprotein complex, GO:0016010: dystrophin-associated glycoprotein complex, GO:0016010: dystrophin-associated glycoprotein complex, GO:0043034: costamere, GO:0003779: actin binding, GO:0003779: actin binding, GO:0003779: actin binding, GO:0005200: structural constituent of cytoskeleton, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0008307: structural constituent of muscle, GO:0008307: structural constituent of muscle		0.3439	0.8721	1.1531	1.3759	8.45	8.79	9.32	9.6	9.83	10.25	3
203766_s_at	LMOD1	leiomodin 1 (smooth muscle)	NM_012134	25802	Hs.519075	GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005523: tropomyosin binding		0.6139	1.0022	1.7834	2.8004	5.04	5.65	6.04	6.82	7.84	7.34	3
203794_at	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	NM_014826	8476	Hs.35433	GO:0006468: protein amino acid phosphorylation, GO:0007242: intracellular signaling cascade, GO:0031532: actin cytoskeleton reorganization, GO:0051056: regulation of small GTPase mediated signal transduction, GO:0005737: cytoplasm, GO:0005911: intercellular junction, GO:0031252: leading edge, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004674: protein serine/threonine kinase activity, GO:0005083: small GTPase regulator activity, GO:0005524: ATP binding, GO:0008270: zinc ion binding, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0019992: diacylglycerol binding, GO:0042802: identical protein binding		0.333	0.6855	1.1011	1.6468	4.42	4.75	5.11	5.52	6.07	5.64	3

(*Continued*)

TABLE E3. (*Continued*)

203657_s_at	CTSF	cathepsin F	NM_003793	8722	Hs.11590	GO:0006508: proteolysis, GO:0005764: lysosome, GO:0016946: cathepsin F activity		0.7806	0.8633	1.2657	1.5335	7.53	8.31	8.4	8.8	9.07	8.78	3
203666_at	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	NM_000609	6387	Hs.522891	GO:0006874: cellular calcium ion homeostasis, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0006955: immune response, GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007267: cell-cell signaling, GO:0008015: circulation, GO:0008064: regulation of actin polymerization and/or depolymerization, GO:0009615: response to virus, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0004871: signal transducer activity, GO:0008009: chemokine activity, GO:0008009: chemokine activity, GO:0008083: growth factor activity	04060: Cytokine-cytokine receptor interaction, 04360: Axon guidance, 04670: Leukocyte transendothelial migration	0.6928	0.7731	1.4134	1.3675	8.35	9.05	9.13	9.77	9.72	8.85	3
203335_at	PHYH	phytanoyl-CoA 2-hydroxylase	NM_006214	5264	Hs.498732	GO:0006629: lipid metabolic process, GO:0007399: nervous system development, GO:0007601: visual perception, GO:0007605: sensory perception of sound, GO:0050896: response to stimulus, GO:0005777: peroxisome, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0009055: electron carrier activity, GO:0031418: L-ascorbic acid binding, GO:0048244: phytanoyl-CoA dioxygenase activity		0.4703	0.9954	1.3906	1.587	7.78	8.25	8.78	9.17	9.37	9.69	3
203562_at	FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	NM_005103	9638	Hs.224008	GO:0007155: cell adhesion, GO:0007399: nervous system development, GO:0007411: axon guidance, GO:0005737: cytoplasm, GO:0005813: centrosome, GO:0016020: membrane, GO:0005515: protein binding, GO:0043015: gamma-tubulin binding		0.6519	0.8366	1.2276	1.3063	6.7	7.35	7.54	7.93	8.01	7.75	3
203001_s_at	STMN2	stathmin-like 2	NM_007029	11075	Hs.521651	GO:0007242: intracellular signaling cascade, GO:0030182: neuron differentiation, GO:0005624: membrane fraction, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0030426: growth cone, GO:0042995: cell projection, GO:0005515: protein binding		0.4706	0.391	1.3982	1.7985	4.72	5.19	5.11	6.12	6.52	5.32	3
203167_at	TIMP2	TIMP metallopeptidase inhibitor 2	NM_003255	7077	Hs.633514	GO:0008285: negative regulation of cell proliferation, GO:0030814: regulation of cAMP metabolic process, GO:0043408: regulation of MAPKKK cascade, GO:0045664: regulation of neuron differentiation, GO:0005604: basement membrane, GO:0009986: cell surface, GO:0004857: enzyme inhibitor activity, GO:0005178: integrin binding, GO:0005515: protein binding, GO:0008047: enzyme activator activity, GO:0008191: metalloendopeptidase inhibitor activity		0.596	0.956	1.084	1.3851	5.55	6.15	6.51	6.63	6.93	6.7	3
202994_s_at	FBLN1	fibulin 1	Z95331	2192	Hs.24601	GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0005201: extracellular matrix structural constituent, GO:0005509: calcium ion binding		0.3977	0.8111	1.3365	1.71	10.86	11.25	11.67	12.19	12.57	12.23	3
202995_s_at	FBLN1	fibulin 1	NM_006486	2192	Hs.24601	GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0005201: extracellular matrix structural constituent, GO:0005509: calcium ion binding		0.4402	0.8009	1.4126	1.3606	10.29	10.73	11.09	11.7	11.65	11.59	3

(*Continued*)

TABLE E3. (*Continued*)

202806_at	DBN1	drebrin 1	NM_004395	1627	Hs.130316	GO:0007015: actin filament organization, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0030154: cell differentiation, GO:0048168: regulation of neuronal synaptic plasticity, GO:0050773: regulation of dendrite development, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0015629: actin cytoskeleton, GO:0030425: dendrite, GO:0042641: actomyosin, GO:0003779: actin binding, GO:0003779: actin binding, GO:0005522: profilin binding		0.3401	0.9631	1.5906	2.0835	6.63	6.98	7.6	8.23	8.72	8.46	3
202976_s_at	RHOBTB3	Rho-related BTB domain containing 3	NM_014899	22836	Hs.445030	GO:0008150: biological_process, GO:0003924: GTPase activity, GO:0005515: protein binding		0.6658	0.9506	1.6411	1.9645	6.72	7.39	7.67	8.36	8.68	8.98	3
202747_s_at	ITM2A	integral membrane protein 2A	NM_004867	9452	Hs.17109	GO:0016020: membrane, GO:0016021: integral to membrane		0.3324	0.7399	1.2239	1.6073	7.93	8.27	8.67	9.16	9.54	9.58	3
202760_s_at	PALM2-AKAP2	PALM2-AKAP2 protein	NM_007203	445815	Hs.591908			0.2709	0.7379	1.2438	1.5553	6.61	6.88	7.35	7.85	8.16	8.17	3
202686_s_at	AXL	AXL receptor tyrosine kinase	NM_021913	558	Hs.590970	GO:0000074: regulation of progression through cell cycle, GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004714: transmembrane receptor protein tyrosine kinase activity, GO:0004872: receptor activity, GO:0005524: ATP binding, GO:0016740: transferase activity		0.4022	0.6341	1.0265	1.3705	8.89	9.29	9.53	9.92	10.26	10.16	3
202746_at	ITM2A	integral membrane protein 2A	AL021786	9452	Hs.17109	GO:0016020: membrane, GO:0016021: integral to membrane		0.5226	0.9649	1.5074	1.5699	8.72	9.25	9.69	10.23	10.29	10.69	3
202561_at	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	AF070613	8658	Hs.370267	GO:0006471: protein amino acid ADP-ribosylation, GO:0006605: protein targeting, GO:0007004: telomere maintenance via telomerase, GO:0015031: protein transport, GO:0051028: mRNA transport, GO:0000781: chromosome, telomeric region, GO:0005634: nucleus, GO:0005643: nuclear pore, GO:0005694: chromosome, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0003950: NAD+ ADP-ribosyltransferase activity, GO:0005515: protein binding, GO:0016757: transferase activity, transferring glycosyl groups		0.5554	0.7639	1.0079	1.2164	7.8	8.35	8.56	8.8	9.01	9.05	3
202609_at	EPS8	epidermal growth factor receptor pathway substrate 8	NM_004447	2059	Hs.591160	GO:0007165: signal transduction, GO:0007173: epidermal growth factor receptor signaling pathway, GO:0008283: cell proliferation, GO:0005070: SH3/SH2 adaptor activity, GO:0005515: protein binding		0.2854	0.5716	1.1531	1.3072	9.34	9.63	9.91	10.49	10.65	10.64	3
202465_at	PCOLCE	procollagen C-endopeptidase enhancer	NM_002593	5118	Hs.202097	GO:0007275: multicellular organismal development, GO:0005518: collagen binding		0.3611	0.6879	1.2581	1.1691	9.95	10.31	10.63	11.2	11.12	10.27	3
202555_s_at	MYLK	myosin, light chain kinase	NM_005965	4638	Hs.556600	GO:0006468: protein amino acid phosphorylation, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004687: myosin light chain kinase activity, GO:0004871: signal transducer activity, GO:0005509: calcium ion binding, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity	04020: Calcium signaling pathway, 04510: Focal adhesion, 04810: Regulation of actin cytoskeleton	0.1577	0.6397	1.2303	1.8605	9.59	9.75	10.23	10.83	11.46	11.19	3

(*Continued*)

TABLE E3. (*Continued*)

202291_s_at	MGP	matrix Gla protein	NM_000900	4256	Hs.365706	GO:0001502: cartilage condensation, GO:0001503: ossification, GO:0007275: multicellular organismal development, GO:0007605: sensory perception of sound, GO:0030154: cell differentiation, GO:0030500: regulation of bone mineralization, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005201: extracellular matrix structural constituent, GO:0005509: calcium ion binding, GO:0008147: structural constituent of bone		0.5336	0.8109	1.3496	1.4992	11.04	11.57	11.85	12.39	12.54	12.41	3
202350_s_at	MATN2	matrilin 2	NM_002380	4147	Hs.189445, Hs.660622	GO:0008150: biological_process, GO:0005578: proteinaceous extracellular matrix, GO:0003674: molecular_function, GO:0005509: calcium ion binding		0.392	0.8018	1.1416	1.3955	9.21	9.6	10.01	10.35	10.6	10.63	3
202156_s_at	CUGBP2	CUG triplet repeat, RNA binding protein 2	N36839	10659	Hs.309288	GO:0006397: mRNA processing, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003723: RNA binding		0.405	0.5702	1.2417	1.388	6.05	6.46	6.62	7.29	7.44	7.18	3
202172_at	VEZF1	vascular endothelial zinc finger 1	BG035116	7716	Hs.694720	GO:0001525: angiogenesis, GO:0001885: endothelial cell development, GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006968: cellular defense response, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003704: specific RNA polymerase II transcription factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.3501	0.6483	1.0752	1.4096	7.61	7.96	8.26	8.68	9.02	8.96	3
202125_s_at	TRAK2	trafficking protein, kinesin binding 2	NM_015049	66008	Hs.152774	GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0050811: GABA receptor binding		0.6205	0.9245	1.2854	1.492	8.26	8.88	9.19	9.55	9.76	9.72	3
202149_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	AL136139	4739	Hs.37982	GO:0000074: regulation of progression through cell cycle, GO:0001558: regulation of cell growth, GO:0007010: cytoskeleton organization and biogenesis, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0007229: integrin-mediated signaling pathway, GO:0051017: actin filament bundle formation, GO:0051301: cell division, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005819: spindle, GO:0005856: cytoskeleton, GO:0030054: cell junction, GO:0042995: cell projection, GO:0005515: protein binding		0.355	0.6659	1.2018	1.282	5.55	5.91	6.22	6.76	6.84	6.76	3
201843_s_at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	NM_004105	2202	Hs.76224	GO:0007601: visual perception, GO:0005578: proteinaceous extracellular matrix, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.5822	0.8145	1.2166	1.3278	8.17	8.75	8.98	9.38	9.49	9.91	3
201957_at	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	AF324888	4660	Hs.444403	GO:0006937: regulation of muscle contraction, GO:0007165: signal transduction, GO:0005737: cytoplasm, GO:0008047: enzyme activator activity	04810: Regulation of actin cytoskeleton	0.6939	0.8343	1.2021	1.4835	6.36	7.06	7.2	7.57	7.85	7.59	3
201792_at	AEBP1	AE binding protein 1	NM_001129	165	Hs.439463	GO:0001501: skeletal development, GO:0006508: proteolysis, GO:0007155: cell adhesion, GO:0007517: muscle development, GO:0005737: cytoplasm, GO:0003700: transcription factor activity, GO:0004180: carboxypeptidase activity, GO:0004180: carboxypeptidase activity, GO:0004182: carboxypeptidase A activity, GO:0008270: zinc ion binding		0.2995	0.6687	1.1166	1.4123	9.89	10.19	10.56	11.01	11.31	10.66	3
201839_s_at	TACSTD1	tumor-associated calcium signal transducer 1	NM_002354	4072	Hs.645285	GO:0005886: plasma membrane, GO:0016021: integral to membrane		0.0789	0.4647	1.0636	1.4826	6.52	6.6	6.99	7.59	8.01	8.93	3

(*Continued*)

TABLE E3. (*Continued*)

201753_s_at	ADD3	adducin 3 (gamma)	NM_019903	120	Hs.501012	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0016020: membrane, GO:0005200: structural constituent of cytoskeleton, GO:0005516: calmodulin binding, GO:0046872: metal ion binding		0.4794	0.6909	1.024	1.0684	10.51	10.99	11.21	11.54	11.58	11.79	3
201787_at	FBLN1	fibulin 1	NM_001996	2192	Hs.24601	GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0005201: extracellular matrix structural constituent, GO:0005509: calcium ion binding		0.3324	0.5623	1.1836	1.6256	9.57	9.9	10.13	10.76	11.2	10.86	3
201650_at	KRT19	keratin 19	NM_002276	3880	Hs.654568	GO:0045214: sarcomere organization, GO:0005882: intermediate filament, GO:0043034: costamere, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding, GO:0008307: structural constituent of muscle	01430: Cell Communication	0.1244	0.884	1.4457	2.1993	5.36	5.49	6.25	6.81	7.56	8.27	3
201719_s_at	EPB41L2	erythrocyte membrane protein band 4.1-like 2	NM_001431	2037	Hs.486470	GO:0030866: cortical actin cytoskeleton organization and biogenesis, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005886: plasma membrane, GO:0008091: spectrin, GO:0019898: extrinsic to membrane, GO:0003779: actin binding, GO:0005198: structural molecule activity, GO:0005200: structural constituent of cytoskeleton, GO:0005488: binding	04530: Tight junction	0.3714	0.5541	1.1621	1.3596	7.59	7.96	8.14	8.75	8.95	8.59	3
201540_at	FHL1	four and a half LIM domains 1	NM_001449	2273	Hs.435369	GO:0007275: multicellular organismal development, GO:0007517: muscle development, GO:0009887: organ morphogenesis, GO:0016049: cell growth, GO:0030154: cell differentiation, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0003674: molecular_function, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.3352	0.7379	1.0974	1.4799	11.45	11.79	12.19	12.55	12.93	12.94	3
201596_x_at	KRT18	keratin 18	NM_000224	3875	Hs.406013	GO:0007049: cell cycle, GO:0009653: anatomical structure morphogenesis, GO:0043000: Golgi to plasma membrane CFTR protein transport, GO:0005737: cytoplasm, GO:0045095: keratin filament, GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding	01430: Cell Communication, 05130: Pathogenic Escherichia coli infection - EHEC, 05131: Pathogenic Escherichia coli infection - EPEC	0.0656	0.8234	1.1825	2.0111	5.43	5.5	6.26	6.62	7.45	7.83	3
201431_s_at	DPYSL3	dihydropyrimidinase-like 3	NM_001387	1809	Hs.519659	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0007165: signal transduction, GO:0007399: nervous system development, GO:0005737: cytoplasm, GO:0042995: cell projection, GO:0004157: dihydropyrimidinase activity, GO:0016787: hydrolase activity		0.237	0.8698	1.3547	1.8194	8.04	8.28	8.91	9.4	9.86	9.59	3
201497_x_at	MYH11	myosin, heavy chain 11, smooth muscle	NM_022844	4629	Hs.460109	GO:0006939: smooth muscle contraction, GO:0006941: striated muscle contraction, GO:0030241: muscle thick filament assembly, GO:0048251: elastic fiber assembly, GO:0048746: smooth muscle fiber development, GO:0005863: striated muscle thick filament, GO:0016459: myosin complex, GO:0000166: nucleotide binding, GO:0003774: motor activity, GO:0003779: actin binding, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0008307: structural constituent of muscle		0.2107	0.8865	1.3121	1.8498	9.85	10.06	10.73	11.16	11.7	11.54	3
201307_at	11-Sep	septin 11	AL534972	55752	Hs.128199	GO:0007049: cell cycle, GO:0051291: protein heterooligomerization, GO:0051301: cell division, GO:0001725: stress fiber, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005525: GTP binding		0.228	0.4433	1.0468	1.0479	8.58	8.81	9.02	9.63	9.63	9.58	3

(*Continued*)

TABLE E3. (*Continued*)

201430_s_at	DPYSL3	dihydropyrimidinase-like 3	W72516	1809	Hs.519659	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0007165: signal transduction, GO:0007399: nervous system development, GO:0005737: cytoplasm, GO:0042995: cell projection, GO:0004157: dihydropyrimidinase activity, GO:0016787: hydrolase activity		0.305	0.5962	1.3079	1.2465	4.61	4.92	5.21	5.92	5.86	5.67	3
201150_s_at	TIMP3	TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy, pseudoinflammatory)	NM_000362	7078	Hs.644633	GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007601: visual perception, GO:0008624: induction of apoptosis by extracellular signals, GO:0050896: response to stimulus, GO:0005578: proteinaceous extracellular matrix, GO:0005604: basement membrane, GO:0003674: molecular_function, GO:0004857: enzyme inhibitor activity, GO:0008191: metalloendopeptidase inhibitor activity		0.2107	0.5955	1.105	1.498	11.3	11.51	11.89	12.4	12.8	12.81	3
201280_s_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	NM_001343	1601	Hs.481980	GO:0000904: cellular morphogenesis during differentiation, GO:0001701: in utero embryonic development, GO:0006898: receptor-mediated endocytosis, GO:0006907: pinocytosis, GO:0007588: excretion, GO:0008283: cell proliferation, GO:0005905: coated pit, GO:0016020: membrane, GO:0031410: cytoplasmic vesicle, GO:0008022: protein C-terminus binding		0.3127	0.6035	1.156	1.1088	8.97	9.28	9.58	10.13	10.08	9.76	3
201147_s_at	TIMP3	TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy, pseudoinflammatory)	NM_000362	7078	Hs.644633	GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007601: visual perception, GO:0008624: induction of apoptosis by extracellular signals, GO:0050896: response to stimulus, GO:0005578: proteinaceous extracellular matrix, GO:0005604: basement membrane, GO:0003674: molecular_function, GO:0004857: enzyme inhibitor activity, GO:0008191: metalloendopeptidase inhibitor activity		0.3269	0.8121	1.2899	1.5416	8.43	8.76	9.24	9.72	9.97	10.23	3
201148_s_at	TIMP3	TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy, pseudoinflammatory)	AW338933	7078	Hs.644633	GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007601: visual perception, GO:0008624: induction of apoptosis by extracellular signals, GO:0050896: response to stimulus, GO:0005578: proteinaceous extracellular matrix, GO:0005604: basement membrane, GO:0003674: molecular_function, GO:0004857: enzyme inhibitor activity, GO:0008191: metalloendopeptidase inhibitor activity		0.255	0.6689	1.3209	1.7824	6.46	6.71	7.13	7.78	8.24	8.24	3
219398_at	CIDEC	cell death-inducing DFFA-like effector c	NM_022094	63924	Hs.567562, Hs.635072	GO:0006915: apoptosis, GO:0006917: induction of apoptosis, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0003674: molecular_function, GO:0005515: protein binding		0.9991	1.9592	1.703	3.0445	4.62	5.62	6.58	6.32	7.66	8.13	3
200962_at	RPL31	ribosomal protein L31	AI348010	6160	Hs.469473	GO:0006412: translation, GO:0005622: intracellular, GO:0005840: ribosome, GO:0005842: cytosolic large ribosomal subunit (sensu Eukaryota), GO:0003723: RNA binding, GO:0003735: structural constituent of ribosome	03010: Ribosome	0.708	0.8115	1.2796	1.3718	4.92	5.62	5.73	6.2	6.29	6.91	3
222288_at			AI004009					0.91	1.759	2.9264	3.0055	5.68	6.59	7.44	8.61	8.69	7.97	3
205913_at	PLIN	perilipin	NM_002666	5346	Hs.103253	GO:0016042: lipid catabolic process, GO:0005811: lipid particle, GO:0005515: protein binding, GO:0008289: lipid binding	03320: PPAR signaling pathway	1.0392	2.0918	1.4641	2.9789	5.45	6.49	7.54	6.92	8.43	8.89	3

(*Continued*)

TABLE E3. (*Continued*)

221795_at	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	AA707199	4915	Hs.494312	GO:0006468: protein amino acid phosphorylation, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0030154: cell differentiation, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0004714: transmembrane receptor protein tyrosine kinase activity, GO:0004872: receptor activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0043121: neurotrophin binding	04010: MAPK signaling pathway	0.2069	1.2685	1.7157	2.3464	4.6	4.8	5.87	6.31	6.94	7.07	3
221950_at	EMX2	empty spiracles homeobox 2	AI478455	2018	Hs.202095	GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0009952: anterior/posterior pattern formation, GO:0030182: neuron differentiation, GO:0030900: forebrain development, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0043565: sequence-specific DNA binding		0.5846	1.0023	1.4588	1.8349	6.63	7.21	7.63	8.09	8.46	8.48	3
221470_s_at	IL1F7	interleukin 1 family, member 7 (zeta)	NM_014439	27178	Hs.166371	GO:0006955: immune response, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005152: interleukin-1 receptor antagonist activity		0.8688	1.5588	2.2037	2.7059	6.87	7.74	8.43	9.08	9.58	10.24	3
221530_s_at	BHLHB3	basic helix-loop-helix domain containing, class B, 3	AB044088	79365	Hs.177841	GO:0006355: regulation of transcription, DNA-dependent, GO:0008283: cell proliferation, GO:0009887: organ morphogenesis, GO:0030154: cell differentiation, GO:0005634: nucleus, GO:0003700: transcription factor activity	04710: Circadian rhythm	0.4842	1.1285	1.6714	2.408	5.26	5.74	6.39	6.93	7.67	7.91	3
219833_s_at	EFHC1	EF-hand domain (C-terminal) containing 1	NM_018100	114327	Hs.403171	GO:0005930: axoneme, GO:0043025: cell soma, GO:0005509: calcium ion binding, GO:0008022: protein C-terminus binding		0.6026	1.018	1.5237	1.8542	5.43	6.03	6.44	6.95	7.28	7.16	3
220559_at	EN1	engrailed homeobox 1	NM_001426	2019	Hs.271977	GO:0001501: skeletal development, GO:0006355: regulation of transcription, DNA-dependent, GO:0006813: potassium ion transport, GO:0007275: multicellular organismal development, GO:0009653: anatomical structure morphogenesis, GO:0009953: dorsal/ventral pattern formation, GO:0009954: proximal/distal pattern formation, GO:0030901: midbrain development, GO:0030902: hindbrain development, GO:0030917: midbrain-hindbrain boundary development, GO:0035115: embryonic forelimb morphogenesis, GO:0043473: pigmentation, GO:0048666: neuron development, GO:0005634: nucleus, GO:0008076: voltage-gated potassium channel complex, GO:0003700: transcription factor activity, GO:0005249: voltage-gated potassium channel activity, GO:0043565: sequence-specific DNA binding		0.491	1.1042	1.0926	1.6807	5.1	5.59	6.2	6.19	6.78	7.14	3
219087_at	ASPN	asporin	NM_017680	54829	Hs.435655	GO:0016021: integral to membrane, GO:0019867: outer membrane, GO:0005515: protein binding, GO:0015288: porin activity		0.3527	1.6274	2.0231	2.2701	7.6	7.95	9.22	9.62	9.87	10.04	3
219304_s_at	PDGFD	platelet derived growth factor D	AB033832	80310	Hs.352298	GO:0000074: regulation of progression through cell cycle, GO:0008283: cell proliferation, GO:0050730: regulation of peptidyl-tyrosine phosphorylation, GO:0016020: membrane, GO:0008083: growth factor activity	04510: Focal adhesion, 04540: Gap junction, 05218: Melanoma	0.8618	1.4707	2.0926	2.1004	6.12	6.98	7.59	8.21	8.22	8.65	3

(*Continued*)

TABLE E3. (*Continued*)

218820_at	C14orf132	chromosome 14 open reading frame 132	NM_020215	56967	Hs.6434	GO:0016020: membrane, GO:0016021: integral to membrane		0.3584	1.027	1.6183	2.0902	6.22	6.58	7.24	7.84	8.31	8.6	3
219064_at	ITIH5	inter-alpha (globulin) inhibitor H5	NM_030569	80760	Hs.498586	GO:0030212: hyaluronan metabolic process, GO:0004867: serine-type endopeptidase inhibitor activity		0.5657	1.1165	1.8106	1.819	7.83	8.4	8.95	9.64	9.65	8.83	3
218625_at	NRN1	neuritin 1	NM_016588	51299	Hs.103291	GO:0016020: membrane, GO:0048503: GPI anchor binding		0.7998	1.1582	1.8792	2.1665	7.03	7.83	8.19	8.91	9.2	9.25	3
218730_s_at	OGN	osteoglycin	AF202167	4969	Hs.109439	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0005578: proteinaceous extracellular matrix, GO:0005783: endoplasmic reticulum, GO:0003674: molecular_function, GO:0005515: protein binding, GO:0008083: growth factor activity		0.761	1.0713	2.2277	1.8396	2.86	3.62	3.93	5.09	4.7	4.55	3
218418_s_at	ANKRD25	ankyrin repeat domain 25	NM_015493	25959	Hs.284208			0.5909	1.0031	1.5643	1.9871	7.38	7.97	8.39	8.95	9.37	9.02	3
218546_at	C1orf115	chromosome 1 open reading frame 115	NM_024709	79762	Hs.519839	GO:0016020: membrane, GO:0016021: integral to membrane		0.8246	1.1913	1.6225	2.2662	5.96	6.79	7.15	7.58	8.23	8.19	3
218087_s_at	SORBS1	sorbin and SH3 domain containing 1	N21458	10580	Hs.38621	GO:0006810: transport, GO:0008286: insulin receptor signaling pathway, GO:0015758: glucose transport, GO:0043149: stress fiber formation, GO:0048041: focal adhesion formation, GO:0001725: stress fiber, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005915: zonula adherens, GO:0005924: cell-substrate adherens junction, GO:0016020: membrane, GO:0030054: cell junction, GO:0045121: lipid raft, GO:0003779: actin binding, GO:0005158: insulin receptor binding	03320: PPAR signaling pathway, 04520: Adherens junction, 04910: Insulin signaling pathway	0.5744	1.4642	1.6617	2.18	8.62	9.19	10.08	10.28	10.8	10.99	3
218312_s_at	ZSCAN18	zinc finger and SCAN domain containing 18	NM_023926	65982	Hs.235390	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.8564	1.1493	1.7297	2.0358	6.18	7.04	7.33	7.91	8.22	8.91	3
215303_at			BE046461					0.7103	1.0078	1.8196	1.5179	3.78	4.49	4.79	5.6	5.3	5.43	3
217506_at	LOC400642	hypothetical gene supported by BC041875; BX648984	H49382	400642	Hs.647596			0.4106	1.174	1.3434	2.0416	5.79	6.2	6.96	7.13	7.83	8.11	3
214151_s_at	CCPG1	cell cycle progression 1	AU144243	9236	Hs.612814			0.6492	1.0144	1.3604	1.4853	6.45	7.1	7.46	7.81	7.93	7.9	3
214927_at	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	AL359052	9358	Hs.584836	GO:0007155: cell adhesion, GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0008305: integrin complex, GO:0004872: receptor activity, GO:0005488: binding		0.1829	1.0763	1.8272	2.5171	6.43	6.61	7.51	8.26	8.95	8.59	3

(*Continued*)

TABLE E3. (*Continued*)

213397_x_at	ANG	angiogenin, ribonuclease, RNase A family, 5	AI761728	283	Hs.283749, Hs.695245	GO:0001525: angiogenesis, GO:0001525: angiogenesis, GO:0001541: ovarian follicle development, GO:0001666: response to hypoxia, GO:0001666: response to hypoxia, GO:0001890: placenta development, GO:0001938: positive regulation of endothelial cell proliferation, GO:0006651: diacylglycerol biosynthetic process, GO:0007154: cell communication, GO:0007202: phospholipase C activation, GO:0007275: multicellular organismal development, GO:0009303: rRNA transcription, GO:0016477: cell migration, GO:0017148: negative regulation of protein biosynthetic process, GO:0030041: actin filament polymerization, GO:0030154: cell differentiation, GO:0032148: activation of protein kinase B, GO:0032431: activation of phospholipase A2, GO:0042327: positive regulation of phosphorylation, GO:0042592: homeostatic process, GO:0048662: negative regulation of smooth muscle cell proliferation, GO:0050714: positive regulation of protein secretion, GO:0050714: positive regulation of protein secretion, GO:0005605: basal lamina, GO:0005615: extracellular space, GO:0005634: nucleus, GO:0005730: nucleolus, GO:0032311: angiogenin-PRI complex, GO:0003677: DNA binding, GO:0003779: actin binding, GO:0004519: endonuclease activity, GO:0004522: pancreatic ribonuclease activity, GO:0004540: ribonuclease activity, GO:0005102: receptor binding, GO:0005507: copper ion binding, GO:0008201: heparin binding, GO:0016787: hydrolase activity, GO:0019843: rRNA binding		0.6567	1.1658	1.5764	1.7223	8.77	9.42	9.93	10.34	10.49	10.84	3
213800_at	CFH	complement factor H	X04697	3075	Hs.363396	GO:0006957: complement activation, alternative pathway, GO:0005615: extracellular space	04610: Complement and coagulation cascades	0.5558	1.3031	1.7627	2.4027	9.1	9.65	10.4	10.86	11.5	11.48	3
213071_at	DPT	dermatopontin	AL049798	1805	Hs.80552	GO:0007155: cell adhesion, GO:0005578: proteinaceous extracellular matrix, GO:0005515: protein binding		0.377	1.2156	1.7501	1.8848	7.32	7.69	8.53	9.07	9.2	8.78	3
213156_at			BG251521					0.8449	1.1612	1.9635	2.3074	7.5	8.34	8.66	9.46	9.8	9.31	3
212326_at	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	AB007922	55187	Hs.439381	GO:0008104: protein localization		0.474	1.0201	1.3569	1.8536	7.47	7.94	8.49	8.82	9.32	9.4	3
212850_s_at	LRP4	low density lipoprotein receptor-related protein 4	AA584297	4038	Hs.4930	GO:0006897: endocytosis, GO:0008150: biological_process, GO:0005575: cellular_component, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0005509: calcium ion binding, GO:0005509: calcium ion binding		0.5925	1.0207	1.3489	1.694	7.39	7.99	8.41	8.74	9.09	9.6	3
209894_at	LEPR	leptin receptor	U50748	3953	Hs.23581	GO:0006112: energy reserve metabolic process, GO:0007166: cell surface receptor linked signal transduction, GO:0007275: multicellular organismal development, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004896: hematopoietin/interferon-class (D200-domain) cytokine receptor activity, GO:0005515: protein binding	04060: Cytokine-cytokine receptor interaction, 04080: Neuroactive ligand-receptor interaction, 04630: Jak-STAT signaling pathway, 04920: Adipocytokine signaling pathway	0.803	1.1799	1.6038	1.9843	8.91	9.71	10.09	10.51	10.89	11.76	3
211685_s_at	NCALD	neurocalcin delta	AF251061	83988	Hs.492427, Hs.680132	GO:0016192: vesicle-mediated transport, GO:0005622: intracellular, GO:0005829: cytosol, GO:0030130: clathrin coat of trans-Golgi network vesicle, GO:0003779: actin binding, GO:0005509: calcium ion binding, GO:0015631: tubulin binding, GO:0030276: clathrin binding		0.4516	1.0315	1.6993	2.3003	4.96	5.41	5.99	6.66	7.26	7.99	3
209656_s_at	TMEM47	transmembrane protein 47	AL136550	83604	Hs.8769	GO:0005886: plasma membrane, GO:0016021: integral to membrane		0.6538	1.0946	1.7002	1.9785	8.38	9.03	9.47	10.08	10.36	10.48	3

(*Continued*)

TABLE E3. (*Continued*)

209869_at	ADRA2A	adrenergic, alpha-2A-, receptor	AF284095	150	Hs.249159	GO:0000187: activation of MAPK activity, GO:0006928: cell motility, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007194: negative regulation of adenylate cyclase activity, GO:0007266: Rho protein signal transduction, GO:0008284: positive regulation of cell proliferation, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0042596: fear response, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004935: adrenoceptor activity, GO:0004938: alpha2-adrenergic receptor activity, GO:0005515: protein binding, GO:0015459: potassium channel regulator activity	04080: Neuroactive ligand-receptor interaction	0.8775	1.4094	2.1296	2.4692	5.94	6.82	7.35	8.07	8.41	7.96	3
209543_s_at	CD34	CD34 molecule	M81104	947	Hs.374990	GO:0007155: cell adhesion, GO:0016337: cell-cell adhesion, GO:0050900: leukocyte migration, GO:0009897: external side of plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding, GO:0030246: carbohydrate binding	04514: Cell adhesion molecules (CAMs), 04640: Hematopoietic cell lineage	0.432	1.037	1.7135	2.0552	5.7	6.13	6.74	7.41	7.75	7.48	3
209581_at	HRASLS3	HRAS-like suppressor 3	BC001387	11145	Hs.502775	GO:0007049: cell cycle, GO:0008150: biological_process, GO:0045786: negative regulation of progression through cell cycle, GO:0005575: cellular_component, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003674: molecular_function, GO:0005515: protein binding		0.7936	1.3342	1.1438	1.8976	4.48	5.27	5.81	5.62	6.38	6.55	3
207175_at	ADIPOQ	adiponectin, C1Q and collagen domain containing	NM_004797	9370	Hs.80485	GO:0006006: glucose metabolic process, GO:0006091: generation of precursor metabolites and energy, GO:0006635: fatty acid beta-oxidation, GO:0006817: phosphate transport, GO:0009749: response to glucose stimulus, GO:0042593: glucose homeostasis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0045721: negative regulation of gluconeogenesis, GO:0045923: positive regulation of fatty acid metabolic process, GO:0046326: positive regulation of glucose import, GO:0051260: protein homooligomerization, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0005179: hormone activity	03320: PPAR signaling pathway, 04920: Adipocytokine signaling pathway, 04930: Type II diabetes mellitus	1.1731	2.5071	2.1683	3.3082	6.63	7.8	9.13	8.8	9.94	10.14	3
209356_x_at	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	AB030655	30008	Hs.647231	GO:0007596: blood coagulation, GO:0005604: basement membrane, GO:0016020: membrane, GO:0004888: transmembrane receptor activity, GO:0005201: extracellular matrix structural constituent, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.6552	1.0189	1.675	1.7256	6.59	7.25	7.61	8.27	8.32	7.69	3
206167_s_at	ARHGAP6	Rho GTPase activating protein 6	NM_001174	395	Hs.435291	GO:0007165: signal transduction, GO:0007266: Rho protein signal transduction, GO:0030041: actin filament polymerization, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005884: actin filament, GO:0005070: SH3/SH2 adaptor activity, GO:0005096: GTPase activator activity, GO:0005100: Rho GTPase activator activity		0.7769	1.3161	2.1152	2.3286	5.62	6.4	6.94	7.74	7.95	7.9	3

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TABLE E3. (*Continued*)

206227_at	CILP	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	NM_003613	8483	Hs.442180	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0004721: phosphoprotein phosphatase activity		0.8568	1.8327	2.2987	2.4511	7.16	8.02	9	9.46	9.62	9.55	3
205549_at	PCP4	Purkinje cell protein 4	NM_006198	5121	Hs.80296	GO:0007417: central nervous system development, GO:0005634: nucleus, GO:0005737: cytoplasm		−0.0944	1.0605	1.6709	1.888	6.27	6.18	7.33	7.94	8.16	8.12	3
206149_at	CHP2	calcineurin B homologous protein 2	NM_022097	63928	Hs.178589	GO:0005509: calcium ion binding		0.5145	1.2327	1.7673	2.3502	8.23	8.74	9.46	9.99	10.58	11.06	3
204963_at	SSPN	sarcospan (Kras oncogene-associated gene)	AL136756	8082	Hs.183428	GO:0006936: muscle contraction, GO:0007155: cell adhesion, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005887: integral to plasma membrane, GO:0016010: dystrophin-associated glycoprotein complex, GO:0016020: membrane, GO:0030133: transport vesicle		0.6936	1.0941	1.6179	2.1381	7.2	7.89	8.29	8.82	9.34	9.39	3
205003_at	DOCK4	dedicator of cytokinesis 4	NM_014705	9732	Hs.654652	GO:0016020: membrane, GO:0005085: guanyl-nucleotide exchange factor activity		0.8209	1.0074	1.7078	1.722	5.74	6.56	6.75	7.45	7.46	7.57	3
204591_at	CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	NM_006614	10752	Hs.148909	GO:0001764: neuron migration, GO:0007155: cell adhesion, GO:0007165: signal transduction, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0007411: axon guidance, GO:0007610: behavior, GO:0030154: cell differentiation, GO:0031175: neurite development, GO:0005578: proteinaceous extracellular matrix, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030425: dendrite, GO:0045177: apical part of cell, GO:0005515: protein binding		0.8092	1.2183	2.2442	2.3492	6.45	7.25	7.66	8.69	8.79	9.58	3
204939_s_at	PLN	phospholamban	NM_002667	5350	Hs.170839	GO:0002026: cardiac inotropy, GO:0006874: cellular calcium ion homeostasis, GO:0006936: muscle contraction, GO:0008015: circulation, GO:0045822: negative regulation of heart contraction, GO:0048738: cardiac muscle development, GO:0051924: regulation of calcium ion transport, GO:0005790: smooth endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016529: sarcoplasmic reticulum, GO:0005246: calcium channel regulator activity, GO:0005515: protein binding, GO:0042030: ATPase inhibitor activity	04020: Calcium signaling pathway	0.7967	1.8287	2.5147	2.8743	6.18	6.97	8	8.69	9.05	9.05	3
203980_at	FABP4	fatty acid binding protein 4, adipocyte	NM_001442	2167	Hs.391561	GO:0001816: cytokine production, GO:0006469: negative regulation of protein kinase activity, GO:0006810: transport, GO:0016481: negative regulation of transcription, GO:0042632: cholesterol homeostasis, GO:0050729: positive regulation of inflammatory response, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0005215: transporter activity, GO:0005504: fatty acid binding, GO:0005515: protein binding, GO:0016564: transcription repressor activity	03320: PPAR signaling pathway	0.9834	1.4809	1.5258	2.1759	10.18	11.17	11.67	11.71	12.36	12.57	3
204589_at	NUAK1	NUAK family, SNF1-like kinase, 1	NM_014840	9891	Hs.524692	GO:0006468: protein amino acid phosphorylation, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity		0.6626	1.0133	1.2471	1.6614	8.5	9.17	9.52	9.75	10.17	9.7	3
203824_at	TSPAN8	tetraspanin 8	NM_004616	7103	Hs.170563	GO:0006486: protein amino acid glycosylation, GO:0005764: lysosome, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004871: signal transducer activity		0.8983	1.6931	2.4613	2.6415	6.99	7.89	8.68	9.45	9.63	10.02	3

(*Continued*)

TABLE E3. (*Continued*)

203895_at	PLCB4	phospholipase C, beta 4	AL535113	5332	Hs.472101	GO:0006629: lipid metabolic process, GO:0007242: intracellular signaling cascade, GO:0016042: lipid catabolic process, GO:0004435: phosphoinositide phospholipase C activity, GO:0004871: signal transducer activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0016787: hydrolase activity	00562: Inositol phosphate metabolism, 04020: Calcium signaling pathway, 04070: Phosphatidylinositol signaling system, 04310: Wnt signaling pathway, 04540: Gap junction, 04720: Long-term potentiation, 04730: Long-term depression, 04912: GnRH signaling pathway, 04916: Melanogenesis	0.3155	1.0168	1.7984	2.5286	4.17	4.49	5.19	5.97	6.7	7	3
203548_s_at	LPL	lipoprotein lipase	BF672975	4023	Hs.180878	GO:0006631: fatty acid metabolic process, GO:0008015: circulation, GO:0016042: lipid catabolic process, GO:0005576: extracellular region, GO:0016020: membrane, GO:0042627: chylomicron, GO:0004465: lipoprotein lipase activity, GO:0005319: lipid transporter activity, GO:0008201: heparin binding, GO:0016787: hydrolase activity, GO:0048503: GPI anchor binding	00561: Glycerolipid metabolism, 03320: PPAR signaling pathway, 05010: Alzheimer's disease	1.0895	2.4215	1.9541	2.8224	4.76	5.85	7.18	6.72	7.59	7.95	3
203549_s_at	LPL	lipoprotein lipase	NM_000237	4023	Hs.180878	GO:0006631: fatty acid metabolic process, GO:0008015: circulation, GO:0016042: lipid catabolic process, GO:0005576: extracellular region, GO:0016020: membrane, GO:0042627: chylomicron, GO:0004465: lipoprotein lipase activity, GO:0005319: lipid transporter activity, GO:0008201: heparin binding, GO:0016787: hydrolase activity, GO:0048503: GPI anchor binding	00561: Glycerolipid metabolism, 03320: PPAR signaling pathway, 05010: Alzheimer's disease	0.9655	2.0385	2.2119	3.1894	5.5	6.47	7.54	7.72	8.69	8.83	3
202409_at	IGF2	insulin-like growth factor 2 (somatomedin A)	X07868	3481	Hs.272259, Hs.523414, Hs.645610	GO:0000074: regulation of progression through cell cycle, GO:0001501: skeletal development, GO:0006349: imprinting, GO:0007275: multicellular organismal development, GO:0008283: cell proliferation, GO:0008286: insulin receptor signaling pathway, GO:0005576: extracellular region, GO:0005159: insulin-like growth factor receptor binding, GO:0005179: hormone activity, GO:0008083: growth factor activity, GO:0018445: prothoracicotrophic hormone activity		0.6288	1.0927	1.8232	2.6663	5.97	6.6	7.06	7.79	8.63	8.08	3
202973_x_at	FAM13A1	family with sequence similarity 13, member A1	NM_014883	10144	Hs.97270	GO:0007165: signal transduction, GO:0005622: intracellular		0.8775	1.0133	1.4183	1.6043	7.73	8.6	8.74	9.14	9.33	9.67	3
202274_at	ACTG2	actin, gamma 2, smooth muscle, enteric	NM_001615	72	Hs.516105	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0000166: nucleotide binding, GO:0005198: structural molecule activity, GO:0005515: protein binding, GO:0005524: ATP binding	05110: Cholera - Infection	0.2916	1.0237	1.2768	1.8054	9.17	9.46	10.19	10.44	10.97	10.72	3
202363_at	SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	AF231124	6695	Hs.654695	GO:0006928: cell motility, GO:0007155: cell adhesion, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0008283: cell proliferation, GO:0005578: proteinaceous extracellular matrix, GO:0005615: extracellular space, GO:0005509: calcium ion binding		0.5096	1.0657	1.1601	1.4306	5.2	5.71	6.27	6.36	6.64	7.03	3
201496_x_at	MYH11	myosin, heavy chain 11, smooth muscle	NM_022844	4629	Hs.460109	GO:0006939: smooth muscle contraction, GO:0006941: striated muscle contraction, GO:0030241: muscle thick filament assembly, GO:0048251: elastic fiber assembly, GO:0048746: smooth muscle fiber development, GO:0005863: striated muscle thick filament, GO:0016459: myosin complex, GO:0000166: nucleotide binding, GO:0003774: motor activity, GO:0003779: actin binding, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0008307: structural constituent of muscle		0.2725	1.1127	1.5471	1.9819	6.96	7.24	8.08	8.51	8.95	8.75	3
202052_s_at	RAI14	retinoic acid induced 14	NM_015577	26064	Hs.431400	GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005856: cytoskeleton, GO:0005515: protein binding		0.7837	1.0431	1.6788	2.063	7.4	8.18	8.44	9.08	9.46	9.58	3
217525_at	OLFML1	olfactomedin-like 1	AW305097	283298	Hs.503500			1.04	1.429	1.9915	2.0587	7.28	8.32	8.7	9.27	9.33	9.07	3

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TABLE E3. (*Continued*)

201124_at	ITGB5	integrin, beta 5	AL048423	3693	Hs.536663	GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0007275: multicellular organismal development, GO:0008305: integrin complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0005178: integrin binding, GO:0005515: protein binding	04510: Focal adhesion, 04512: ECM-receptor interaction, 04810: Regulation of actin cytoskeleton	0.9597	1.4762	1.8038	2.3245	5.73	6.69	7.21	7.53	8.05	7.91	3
204294_at	AMT	aminomethyltransferase	NM_000481	275	Hs.102	GO:0006546: glycine catabolic process, GO:0006546: glycine catabolic process, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005960: glycine cleavage complex, GO:0004047: aminomethyltransferase activity, GO:0008483: transaminase activity, GO:0016740: transferase activity	00260: Glycine, serine and threonine metabolism, 00670: One carbon pool by folate, 00910: Nitrogen metabolism	1.0014	1.3614	1.8762	2.1771	4.84	5.84	6.2	6.72	7.02	6.92	3
204519_s_at	PLLP	plasma membrane proteolipid (plasmolipin)	NM_015993	51090	Hs.632215	GO:0006811: ion transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005216: ion channel activity		1.0152	1.2013	1.4461	2.0922	6.76	7.77	7.96	8.2	8.85	9.17	3
65472_at	USP39	ubiquitin specific peptidase 39	AI161338	10713	Hs.654745	GO:0000245: spliceosome assembly, GO:0006397: mRNA processing, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0008380: RNA splicing, GO:0005622: intracellular, GO:0004221: ubiquitin thiolesterase activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.1195	0.3794	0.7352	1.3434	4.45	4.57	4.83	5.19	5.8	5.46	3
65718_at	GPR124	G protein-coupled receptor 124	AI655903	25960	Hs.274136	GO:0007165: signal transduction, GO:0007218: neuropeptide signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0005515: protein binding		0.134	0.5298	0.8971	1.2067	6.69	6.83	7.22	7.59	7.9	7.41	3
564_at	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	M69013	2767	Hs.278432, Hs.654784, Hs.655202	GO:0001501: skeletal development, GO:0001508: regulation of action potential, GO:0006471: protein amino acid ADP-ribosylation, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007507: heart development, GO:0045634: regulation of melanocyte differentiation, GO:0048066: pigmentation during development, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0016459: myosin complex, GO:0000166: nucleotide binding, GO:0003774: motor activity, GO:0003924: GTPase activity, GO:0004871: signal transducer activity, GO:0005525: GTP binding	04020: Calcium signaling pathway, 04540: Gap junction, 04730: Long-term depression, 04912: GnRH signaling pathway	−0.168	0.2556	0.5474	1.1758	7.26	7.09	7.51	7.81	8.43	8.27	3
57715_at	FAM26B	family with sequence similarity 26, member B	W72694	51063	Hs.241545	GO:0016020: membrane, GO:0016021: integral to membrane		0.0813	0.3734	0.8242	1.083	7.15	7.23	7.52	7.97	8.23	7.89	3
46256_at	SPSB3	splA/ryanodine receptor domain and SOCS box containing 3	AA522670	90864	Hs.592080	GO:0007242: intracellular signaling cascade		0.3804	0.6074	0.7057	1.1635	8	8.38	8.61	8.71	9.16	8.9	3
48825_at	ING4	inhibitor of growth family, member 4	AA887083	51147	Hs.524210	GO:0006473: protein amino acid acetylation, GO:0006915: apoptosis, GO:0007049: cell cycle, GO:0007050: cell cycle arrest, GO:0008285: negative regulation of cell proliferation, GO:0045892: negative regulation of transcription, DNA-dependent, GO:0045926: negative regulation of growth, GO:0005634: nucleus, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.2851	0.4389	0.6273	1.055	6.18	6.46	6.62	6.8	7.23	7.23	3
41644_at	SASH1	SAM and SH3 domain containing 1	AB018333	23328	Hs.193133	GO:0007049: cell cycle, GO:0045786: negative regulation of progression through cell cycle		0.1735	0.5173	0.4564	1.0416	8.79	8.97	9.31	9.25	9.84	9.5	3

(*Continued*)

TABLE E3. (*Continued*)

45297_at	EHD2	EH-domain containing 2	AI417917	30846	Hs.631554	GO:0006897: endocytosis, GO:0030866: cortical actin cytoskeleton organization and biogenesis, GO:0005624: membrane fraction, GO:0005634: nucleus, GO:0005886: plasma membrane, GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003924: GTPase activity, GO:0005509: calcium ion binding, GO:0005524: ATP binding, GO:0005525: GTP binding, GO:0019904: protein domain specific binding		0.131	0.4907	0.8393	1.7153	7.07	7.2	7.56	7.91	8.79	8.14	3
40446_at	PHF1	PHD finger protein 1	AL021366	5252	Hs.166204	GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.4113	0.7	0.9	1.4796	6.31	6.72	7.01	7.21	7.79	7.42	3
40837_at	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	M99436	7089	Hs.332173	GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0009887: organ morphogenesis, GO:0016055: Wnt receptor signaling pathway, GO:0005634: nucleus, GO:0005515: protein binding		0.204	0.4832	0.817	1.5887	4.99	5.19	5.47	5.8	6.58	6.59	3
36554_at	ASMTL	acetylserotonin O-methyltransferase-like	Y15521	8623	Hs.533514	GO:0030187: melatonin biosynthetic process, GO:0005575: cellular_component, GO:0017096: acetylserotonin O-methyltransferase activity		0.4192	0.6437	0.915	1.1536	7.39	7.81	8.03	8.3	8.54	8.6	3
39313_at	WNK1	WNK lysine deficient protein kinase 1	AB002342	65125	Hs.356604	GO:0006468: protein amino acid phosphorylation, GO:0006811: ion transport, GO:0007243: protein kinase cascade, GO:0050794: regulation of cellular process, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004860: protein kinase inhibitor activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity		−0.1536	0.0817	0.4331	1.1031	2.74	2.59	2.83	3.18	3.85	3.43	3
36030_at	HOM-TES-103	hypothetical protein LOC25900	AL080214	25900	Hs.15243	GO:0005198: structural molecule activity		0.5913	0.5704	0.9665	1.1649	6.51	7.1	7.08	7.48	7.68	7.26	3
36553_at	ASMTL	acetylserotonin O-methyltransferase-like	AA669799	8623	Hs.533514	GO:0030187: melatonin biosynthetic process, GO:0005575: cellular_component, GO:0017096: acetylserotonin O-methyltransferase activity		0.2379	0.4851	0.6977	1.1113	9.2	9.43	9.68	9.89	10.31	10.17	3
222372_at	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	AW971248	9223	Hs.651939	GO:0006461: protein complex assembly, GO:0007155: cell adhesion, GO:0007166: cell surface receptor linked signal transduction, GO:0005886: plasma membrane, GO:0005923: tight junction, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0008022: protein C-terminus binding, GO:0016301: kinase activity, GO:0016740: transferase activity	04530: Tight junction, 05050: Dentatorubropallidoluysian atrophy (DRPLA)	−0.1488	0.0262	0.7474	1.3546	6.37	6.22	6.39	7.11	7.72	7.14	3
32625_at	NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	X15357	4881	Hs.490330	GO:0006182: cGMP biosynthetic process, GO:0006468: protein amino acid phosphorylation, GO:0007166: cell surface receptor linked signal transduction, GO:0007242: intracellular signaling cascade, GO:0007589: fluid secretion, GO:0008217: blood pressure regulation, GO:0016525: negative regulation of angiogenesis, GO:0030146: diuresis, GO:0030147: natriuresis, GO:0030308: negative regulation of cell growth, GO:0042312: regulation of vasodilation, GO:0043114: regulation of vascular permeability, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004383: guanylate cyclase activity, GO:0004713: protein-tyrosine kinase activity, GO:0004872: receptor activity, GO:0005524: ATP binding, GO:0008528: peptide receptor activity, G-protein coupled, GO:0031404: chloride ion binding, GO:0042562: hormone binding	00230: Purine metabolism, 04540: Gap junction, 04730: Long-term depression	−0.0189	0.0299	0.2598	1.1654	3.23	3.21	3.26	3.49	4.39	3.89	3

(*Continued*)

TABLE E3. (*Continued*)

222362_at	HRBL	HIV-1 Rev binding protein-like	H07885	3268	Hs.521083	GO:0008150: biological_process, GO:0043087: regulation of GTPase activity, GO:0005575: cellular_component, GO:0003674: molecular_function, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0858	0.0151	0.5728	1.1315	2.93	2.84	2.95	3.5	4.06	4.14	3
222368_at			AW972351					−0.0479	0.16	0.6918	1.2957	6.15	6.11	6.31	6.85	7.45	7.75	3
222266_at	C19orf2	chromosome 19 open reading frame 2	BF796940	8725	Hs.466391	GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006457: protein folding, GO:0009615: response to virus, GO:0005634: nucleus, GO:0005665: DNA-directed RNA polymerase II, core complex, GO:0005737: cytoplasm, GO:0016272: prefoldin complex, GO:0003714: transcription corepressor activity, GO:0051082: unfolded protein binding		−0.1419	0.4154	0.6441	1.0252	9.1	8.96	9.52	9.75	10.13	10.3	3
222282_at	PAPD4	PAP associated domain containing 4	AV761453	167153	Hs.418198			−0.0821	0.3974	0.7576	1.1733	6.78	6.69	7.17	7.53	7.95	7.79	3
222146_s_at	TCF4	transcription factor 4	AK026674	6925	Hs.644653	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0005667: transcription factor complex, GO:0003700: transcription factor activity, GO:0003714: transcription corepressor activity, GO:0008013: beta-catenin binding, GO:0046982: protein heterodimerization activity		−0.052	0.2447	0.5796	1.0547	9.62	9.57	9.87	10.2	10.68	10.24	3
222240_s_at	ISYNA1	myo-inositol 1-phosphate synthase A1	AL137749	51477	Hs.405873	GO:0006021: inositol biosynthetic process, GO:0008654: phospholipid biosynthetic process, GO:0004512: inositol-3-phosphate synthase activity	00521: Streptomycin biosynthesis, 00562: Inositol phosphate metabolism	0.2247	0.2187	0.5742	1.1277	3.45	3.67	3.66	4.02	4.57	4.2	3
222116_s_at	TBC1D16	TBC1 domain family, member 16	AL157485	125058	Hs.369819	GO:0032313: regulation of Rab GTPase activity, GO:0005622: intracellular, GO:0005096: GTPase activator activity, GO:0005097: Rab GTPase activator activity		0.3736	0.5554	0.827	1.3109	7.22	7.59	7.78	8.05	8.53	8.41	3
222125_s_at	PH-4	hypoxia-inducible factor prolyl 4-hydroxylase	BC000580	54681	Hs.654944	GO:0019538: protein metabolic process, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0005506: iron ion binding, GO:0005509: calcium ion binding, GO:0016491: oxidoreductase activity, GO:0016702: oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, GO:0016706: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors, GO:0031418: L-ascorbic acid binding		0.3109	0.4874	0.688	1.1783	6.61	6.92	7.1	7.3	7.79	7.66	3
222027_at	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	AW515443	64710	Hs.632458, Hs.643846			−0.051	0.4707	0.7771	1.5562	4.43	4.38	4.9	5.2	5.98	5.5	3
222108_at	AMIGO2	adhesion molecule with Ig-like domain 2	AC004010	347902	Hs.121520	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0007157: heterophilic cell adhesion, GO:0043069: negative regulation of programmed cell death, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding		−0.3036	0.2715	0.6597	1.1521	6.4	6.09	6.67	7.06	7.55	7.29	3
221974_at	PWCR1	Prader-Willi syndrome chromosome region 1	AW770748	63968	Hs.658578			0.274	0.3117	0.6498	1.0951	3.34	3.61	3.65	3.99	4.44	4.38	3

(*Continued*)

TABLE E3. (*Continued*)

222024_s_at	AKAP13	A kinase (PRKA) anchor protein 13	AK022014	11214	Hs.459211, Hs.667658	GO:0007242: intracellular signaling cascade, GO:0035023: regulation of Rho protein signal transduction, GO:0005622: intracellular, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0004871: signal transducer activity, GO:0004872: receptor activity, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0008270: zinc ion binding, GO:0019992: diacylglycerol binding, GO:0046872: metal ion binding		−0.1734	0.1255	0.3923	1.3013	8.34	8.17	8.47	8.73	9.64	9.05	3
221928_at	ACACB	acetyl-Coenzyme A carboxylase beta	AI057637	32	Hs.234898	GO:0006633: fatty acid biosynthetic process, GO:0008152: metabolic process, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0003989: acetyl-CoA carboxylase activity, GO:0004075: biotin carboxylase activity, GO:0005524: ATP binding, GO:0009374: biotin binding, GO:0016874: ligase activity, GO:0030145: manganese ion binding, GO:0046872: metal ion binding	00061: Fatty acid biosynthesis, 00620: Pyruvate metabolism, 00640: Propanoate metabolism, 04910: Insulin signaling pathway, 04920: Adipocytokine signaling pathway	0.0774	0.2215	0.3935	1.0478	5.57	5.64	5.79	5.96	6.61	6.24	3
221942_s_at	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	AI719730	2982	Hs.24258	GO:0006182: cGMP biosynthetic process, GO:0007263: nitric oxide mediated signal transduction, GO:0008015: circulation, GO:0005737: cytoplasm, GO:0008074: guanylate cyclase complex, soluble, GO:0004383: guanylate cyclase activity, GO:0004872: receptor activity	00230: Purine metabolism, 04540: Gap junction, 04730: Long-term depression	0.0238	0.651	0.7388	1.2701	6.27	6.3	6.92	7.01	7.54	6.69	3
221870_at	EHD2	EH-domain containing 2	AI417917	30846	Hs.631554	GO:0006897: endocytosis, GO:0030866: cortical actin cytoskeleton organization and biogenesis, GO:0005624: membrane fraction, GO:0005634: nucleus, GO:0005886: plasma membrane, GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003924: GTPase activity, GO:0005509: calcium ion binding, GO:0005524: ATP binding, GO:0005525: GTP binding, GO:0019904: protein domain specific binding		0.0419	0.3405	0.7235	1.426	6.53	6.57	6.87	7.25	7.95	7.55	3
221900_at	COL8A2	collagen, type VIII, alpha 2	AI806793	1296	Hs.353001	GO:0006817: phosphate transport, GO:0016337: cell-cell adhesion, GO:0030198: extracellular matrix organization and biogenesis, GO:0005604: basement membrane, GO:0005737: cytoplasm, GO:0005201: extracellular matrix structural constituent, GO:0030674: protein binding, bridging		0.0288	0.6217	0.7708	1.0828	5.81	5.84	6.43	6.58	6.89	6.64	3
221748_s_at	TNS1	tensin 1	AL046979	7145	Hs.471381	GO:0007242: intracellular signaling cascade, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0030054: cell junction, GO:0003779: actin binding		0.2794	0.749	0.9547	1.4719	10.87	11.15	11.62	11.82	12.34	12.18	3
221864_at	ORAI3	ORAI calcium release-activated calcium modulator 3	AW517464	93129	Hs.460617	GO:0016020: membrane, GO:0016021: integral to membrane		0.4247	0.6859	0.8372	1.2703	6.35	6.78	7.04	7.19	7.62	7.29	3
221718_s_at	AKAP13	A kinase (PRKA) anchor protein 13	M90360	11214	Hs.459211, Hs.667658	GO:0007242: intracellular signaling cascade, GO:0035023: regulation of Rho protein signal transduction, GO:0005622: intracellular, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0004871: signal transducer activity, GO:0004872: receptor activity, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0008270: zinc ion binding, GO:0019992: diacylglycerol binding, GO:0046872: metal ion binding		−0.1064	0.2404	0.4245	1.0059	8.69	8.58	8.93	9.11	9.69	9.52	3

(*Continued*)

TABLE E3. (*Continued*)

221747_at	TNS1	tensin 1	AL046979	7145	Hs.471381	GO:0007242: intracellular signaling cascade, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0030054: cell junction, GO:0003779: actin binding		0.2374	0.5941	0.9898	1.5086	8.32	8.56	8.92	9.31	9.83	9.82	3
221646_s_at	ZDHHC11	zinc finger, DHHC-type containing 11	AF267859	79844	Hs.659832	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0008270: zinc ion binding, GO:0008415: acyltransferase activity, GO:0016740: transferase activity, GO:0046872: metal ion binding		−0.1131	0.5029	0.9419	1.9112	7.97	7.85	8.47	8.91	9.88	10.04	3
221675_s_at	CHPT1	choline phosphotransferase 1	AF195624	56994	Hs.293077	GO:0006663: platelet activating factor biosynthetic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000287: magnesium ion binding, GO:0004142: diacylglycerol cholinephosphotransferase activity, GO:0016740: transferase activity, GO:0016780: phosphotransferase activity, for other substituted phosphate groups, GO:0030145: manganese ion binding	00440: Aminophosphonate metabolism, 00564: Glycerophospholipid metabolism, 00565: Ether lipid metabolism	0.1561	0.5955	0.8622	1.0658	8.26	8.42	8.86	9.13	9.33	9.59	3
221565_s_at	FAM26B	family with sequence similarity 26, member B	BC000039	51063	Hs.241545	GO:0016020: membrane, GO:0016021: integral to membrane		0.2061	0.3723	0.8775	1.0034	6.87	7.07	7.24	7.74	7.87	7.75	3
221599_at	C11orf67	chromosome 11 open reading frame 67	BC002752	28971	Hs.503357			0.1367	0.4275	0.5417	1.0497	8.16	8.29	8.58	8.7	9.2	9.3	3
221527_s_at	PARD3	par-3 partitioning defective 3 homolog (C. elegans)	AF196185	56288	Hs.131489	GO:0006461: protein complex assembly, GO:0007049: cell cycle, GO:0007163: establishment and/or maintenance of cell polarity, GO:0007205: protein kinase C activation, GO:0007409: axonogenesis, GO:0008356: asymmetric cell division, GO:0005923: tight junction, GO:0005923: tight junction, GO:0016020: membrane, GO:0030054: cell junction, GO:0005515: protein binding	04080: Neuroactive ligand-receptor interaction, 04520: Adherens junction, 04530: Tight junction	−0.0277	0.3997	0.8125	1.3267	6.61	6.59	7.01	7.43	7.94	8.18	3
221552_at	ABHD6	abhydrolase domain containing 6	BC001698	57406	Hs.476454	GO:0006725: aromatic compound metabolic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016787: hydrolase activity		−0.2045	0.1824	0.7003	1.0817	5.4	5.2	5.58	6.1	6.48	7.08	3
221496_s_at	TOB2	transducer of ERBB2, 2	AL008582	10766	Hs.474978	GO:0000074: regulation of progression through cell cycle, GO:0007292: female gamete generation, GO:0008285: negative regulation of cell proliferation, GO:0005634: nucleus, GO:0005737: cytoplasm		−0.0455	0.247	0.2349	1.0464	2.16	2.12	2.41	2.4	3.21	2.89	3
221523_s_at	RRAGD	Ras-related GTP binding D	AL138717	58528	Hs.485938	GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005525: GTP binding		0.1906	0.5123	0.872	1.0544	7.44	7.63	7.95	8.31	8.5	9.02	3
221016_s_at	TCF7L1	transcription factor 7-like 1 (T-cell specific, HMG-box)	NM_031283	83439	Hs.516297	GO:0006325: establishment and/or maintenance of chromatin architecture, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008595: determination of anterior/posterior axis, embryo, GO:0030111: regulation of Wnt receptor signaling pathway, GO:0046022: positive regulation of transcription from RNA polymerase II promoter, mitotic, GO:0048319: axial mesoderm morphogenesis, GO:0005634: nucleus, GO:0003700: transcription factor activity	04310: Wnt signaling pathway, 04520: Adherens junction, 04916: Melanogenesis, 05210: Colorectal cancer, 05213: Endometrial cancer, 05215: Prostate cancer, 05216: Thyroid cancer, 05217: Basal cell carcinoma, 05221: Acute myeloid leukemia	0.1101	0.5294	0.7182	1.2078	5.76	5.87	6.29	6.48	6.97	6.7	3
221123_x_at	ZNF395	zinc finger protein 395	NM_018660	55893	Hs.435535, Hs.684561	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003677: DNA binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.009	0.1021	0.5173	1.4153	6.1	6.1	6.2	6.61	7.51	7.36	3
220744_s_at	IFT122	intraflagellar transport 122 homolog (Chlamydomonas)	NM_018262	55764	Hs.655284	GO:0005737: cytoplasm, GO:0019861: flagellum		0.3931	0.6676	0.9958	2.0124	4.02	4.41	4.69	5.02	6.03	5.78	3
220940_at	KIAA1641	KIAA1641	NM_025190	57730	Hs.532921, Hs.541894			−0.2105	0.1829	0.8141	1.4832	5.73	5.52	5.92	6.55	7.22	6.71	3

(*Continued*)

TABLE E3. (*Continued*)

220512_at	DLC1	deleted in liver cancer 1	NM_024767	10395	Hs.134296	GO:0007010: cytoskeleton organization and biogenesis, GO:0007165: signal transduction, GO:0007165: signal transduction, GO:0030155: regulation of cell adhesion, GO:0030308: negative regulation of cell growth, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005096: GTPase activator activity, GO:0005100: Rho GTPase activator activity, GO:0005515: protein binding		−0.2329	−0.0092	0.6156	1.0577	3.77	3.53	3.76	4.38	4.82	4.56	3
220609_at	LOC202181	hypothetical protein LOC202181	NM_024651	202181	Hs.189914, Hs.661598			−0.0467	0.239	0.426	1.078	5.23	5.18	5.47	5.65	6.31	5.93	3
220349_s_at	FLJ21865	endo-beta-N-acetylglucosaminidase	NM_022759	64772	Hs.29288	GO:0008152: metabolic process, GO:0005622: intracellular, GO:0016798: hydrolase activity, acting on glycosyl bonds	00511: N-Glycan degradation, 01032: Glycan structures - degradation	0.5133	0.679	0.958	1.1058	5.63	6.14	6.31	6.59	6.73	6.65	3
220432_s_at	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	NM_016593	51302	Hs.387367	GO:0006118: electron transport, GO:0006629: lipid metabolic process, GO:0006699: bile acid biosynthetic process, GO:0006707: cholesterol catabolic process, GO:0007586: digestion, GO:0008202: steroid metabolic process, GO:0030573: bile acid catabolic process, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0016020: membrane, GO:0004497: monooxygenase activity, GO:0005506: iron ion binding, GO:0008387: steroid 7-alpha-hydroxylase activity, GO:0008396: oxysterol 7-alpha-hydroxylase activity, GO:0020037: heme binding, GO:0046872: metal ion binding		0.291	0.6088	0.9622	1.3142	7	7.29	7.6	7.96	8.31	8.65	3
220276_at	FLJ22655	hypothetical protein FLJ22655	NM_024730	79785	Hs.115497	GO:0007264: small GTPase mediated signal transduction, GO:0005622: intracellular, GO:0005525: GTP binding		0.1926	0.4567	0.8608	1.8314	3.98	4.17	4.44	4.84	5.81	5.8	3
220327_at	VGLL3	vestigial like 3 (Drosophila)	NM_016206	389136	Hs.435013, Hs.606507	GO:0045449: regulation of transcription, GO:0005634: nucleus, GO:0030528: transcription regulator activity		−0.0799	0.2558	0.7448	1.0508	3.72	3.64	3.98	4.47	4.77	4.86	3
220184_at	NANOG	Nanog homeobox	NM_024865	79923	Hs.661360	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008283: cell proliferation, GO:0009790: embryonic development, GO:0045595: regulation of cell differentiation, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding		0.0588	0.1786	0.0692	1.0185	3.15	3.21	3.33	3.22	4.17	3.49	3
220244_at	LOH3CR2A	loss of heterozygosity, 3, chromosomal region 2, gene A	NM_013343	29931	Hs.591661			0.123	0.432	0.9104	1.5456	6	6.13	6.44	6.91	7.55	7.05	3
220065_at	TNMD	tenomodulin	NM_022144	64102	Hs.132957	GO:0016020: membrane, GO:0016021: integral to membrane		−0.0041	0.5559	0.8962	1.6739	3.21	3.21	3.77	4.11	4.89	4.66	3
220076_at	ANKH	ankylosis, progressive homolog (mouse)	NM_019847	56172	Hs.156727	GO:0001501: skeletal development, GO:0006810: transport, GO:0006817: phosphate transport, GO:0007605: sensory perception of sound, GO:0007626: locomotory behavior, GO:0030500: regulation of bone mineralization, GO:0030500: regulation of bone mineralization, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0019867: outer membrane, GO:0019867: outer membrane, GO:0005315: inorganic phosphate transmembrane transporter activity, GO:0030504: inorganic diphosphate transmembrane transporter activity		0.3002	0.4241	0.8915	1.2856	4.02	4.32	4.44	4.91	5.31	5.21	3
219999_at	MAN2A2	mannosidase, alpha, class 2A, member 2	NM_018621	4122	Hs.116459	GO:0005975: carbohydrate metabolic process, GO:0006013: mannose metabolic process, GO:0008152: metabolic process, GO:0000139: Golgi membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004559: alpha-mannosidase activity, GO:0004572: mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity, GO:0016798: hydrolase activity, acting on glycosyl bonds		0.2069	0.2774	0.5113	1.0667	6.15	6.36	6.43	6.66	7.22	7.16	3

(*Continued*)

TABLE E3. (*Continued*)

220016_at	AHNAK	AHNAK nucleoprotein	NM_024060	79026	Hs.502756	GO:0007399: nervous system development, GO:0005634: nucleus, GO:0005515: protein binding		−0.2716	0.4256	0.4187	1.0704	9.46	9.19	9.88	9.88	10.53	10.53	3
219909_at	MMP28	matrix metallopeptidase 28	NM_024302	79148	Hs.380710	GO:0000270: peptidoglycan metabolic process, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0005578: proteinaceous extracellular matrix, GO:0005578: proteinaceous extracellular matrix, GO:0004222: metalloendopeptidase activity, GO:0004222: metalloendopeptidase activity, GO:0005509: calcium ion binding, GO:0008270: zinc ion binding		0.0553	0.1819	0.5882	1.8045	2.85	2.91	3.03	3.44	4.66	4.6	3
219957_at	RUFY2	RUN and FYVE domain containing 2	NM_017987	55680	Hs.653144	GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0079	−0.051	0.4789	1.2536	7.27	7.26	7.22	7.75	8.52	8.07	3
219765_at	ZNF329	zinc finger protein 329	NM_024620	79673	Hs.458377	GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.1577	0.2417	0.7905	1.1401	4.83	4.98	5.07	5.62	5.97	5.81	3
219848_s_at	ZNF432	zinc finger protein 432	NM_014650	9668	Hs.655934	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0003677: DNA binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.5928	0.6892	0.9287	1.3686	6.61	7.2	7.3	7.54	7.98	7.93	3
219561_at	COPZ2	coatomer protein complex, subunit zeta 2	NM_016429	51226	Hs.408434	GO:0006461: protein complex assembly, GO:0006886: intracellular protein transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0016192: vesicle-mediated transport, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0005801: cis-Golgi network, GO:0016020: membrane, GO:0030117: membrane coat, GO:0030126: COPI vesicle coat, GO:0005515: protein binding, GO:0008565: protein transporter activity		0.0791	0.4508	0.8647	1.1296	7.94	8.02	8.39	8.8	9.07	8.62	3
219563_at	C14orf139	chromosome 14 open reading frame 139	NM_024633	79686	Hs.41502			0.3333	0.4997	0.9382	1.2241	9.37	9.7	9.86	10.3	10.59	10.58	3
219517_at	ELL3	elongation factor RNA polymerase II-like 3	NM_025165	80237	Hs.694861	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006368: RNA elongation from RNA polymerase II promoter, GO:0007283: spermatogenesis, GO:0045817: positive regulation of global transcription from RNA polymerase II promoter, GO:0005634: nucleus, GO:0008023: transcription elongation factor complex, GO:0005515: protein binding, GO:0008159: positive transcription elongation factor activity, GO:0016944: RNA polymerase II transcription elongation factor activity		0.142	0.3552	0.7892	1.1757	8.47	8.61	8.82	9.26	9.64	9.87	3
219534_x_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	NM_000076	1028	Hs.106070	GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0000080: G1 phase of mitotic cell cycle, GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0007049: cell cycle, GO:0007050: cell cycle arrest, GO:0008285: negative regulation of cell proliferation, GO:0042551: neuron maturation, GO:0005634: nucleus, GO:0004861: cyclin-dependent protein kinase inhibitor activity, GO:0005515: protein binding	04110: Cell cycle	0.604	0.6234	0.9223	1.2751	4.43	5.03	5.05	5.35	5.7	5.55	3
219468_s_at	CUEDC1	CUE domain containing 1	NM_017949	404093	Hs.46679			0.1156	0.2872	0.386	1.199	2.69	2.81	2.98	3.08	3.89	3.06	3
219511_s_at	SNCAIP	synuclein, alpha interacting protein (synphilin)	NM_005460	9627	Hs.426463	GO:0042417: dopamine metabolic process, GO:0046928: regulation of neurotransmitter secretion, GO:0005737: cytoplasm, GO:0042734: presynaptic membrane, GO:0043025: cell soma, GO:0005515: protein binding	05020: Parkinson's disease	−0.0188	0.0813	0.5066	1.0899	4.07	4.05	4.15	4.58	5.16	5.22	3

(*Continued*)

TABLE E3. (*Continued*)

219407_s_at	LAMC3	laminin, gamma 3	NM_006059	10319	Hs.201805	GO:0007155: cell adhesion, GO:0005578: proteinaceous extracellular matrix, GO:0005604: basement membrane, GO:0016020: membrane, GO:0005198: structural molecule activity, GO:0005515: protein binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 05222: Small cell lung cancer	0.0924	0.2841	0.8726	2.1541	2.56	2.65	2.84	3.43	4.71	4.37	3
219429_at	FA2H	fatty acid 2-hydroxylase	NM_024306	79152	Hs.461329	GO:0005506: iron ion binding, GO:0020037: heme binding		0.1385	−0.0491	0.9462	1.5121	3.84	3.98	3.79	4.79	5.36	5.77	3
219295_s_at	PCOLCE2	procollagen C-endopeptidase enhancer 2	NM_013363	26577	Hs.8944	GO:0008201: heparin binding		−0.0258	0.9558	1.3437	2.026	7.32	7.3	8.28	8.67	9.35	9.75	3
219390_at	FKBP14	FK506 binding protein 14, 22 kDa	NM_017946	55033	Hs.571333	GO:0006457: protein folding, GO:0005783: endoplasmic reticulum, GO:0003755: peptidyl-prolyl cis-trans isomerase activity, GO:0005509: calcium ion binding, GO:0016853: isomerase activity		0.0177	0.5279	0.7661	1.0821	4.55	4.57	5.08	5.32	5.64	5.04	3
219229_at	SLCO3A1	solute carrier organic anion transporter family, member 3A1	NM_013272	28232	Hs.311187	GO:0006811: ion transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005215: transporter activity		0.094	0.4319	0.9961	1.7521	6.37	6.46	6.8	7.36	8.12	7.9	3
219274_at	TSPAN12	tetraspanin 12	NM_012338	23554	Hs.16529	GO:0005624: membrane fraction, GO:0016020: membrane, GO:0016021: integral to membrane		−0.1867	0.1861	0.6245	1.0146	4.22	4.04	4.41	4.85	5.24	4.79	3
219167_at	RASL12	RAS-like, family 12	NM_016563	51285	Hs.27018	GO:0007264: small GTPase mediated signal transduction, GO:0000166: nucleotide binding, GO:0005525: GTP binding		0.1867	0.3716	0.9392	1.7607	5.59	5.77	5.96	6.53	7.35	6.69	3
219195_at	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	NM_013261	10891	Hs.527078	GO:0001659: thermoregulation, GO:0001678: cell glucose homeostasis, GO:0006094: gluconeogenesis, GO:0006118: electron transport, GO:0006350: transcription, GO:0006367: transcription initiation from RNA polymerase II promoter, GO:0006397: mRNA processing, GO:0006461: protein complex assembly, GO:0007005: mitochondrion organization and biogenesis, GO:0007586: digestion, GO:0008380: RNA splicing, GO:0019395: fatty acid oxidation, GO:0030521: androgen receptor signaling pathway, GO:0035066: positive regulation of histone acetylation, GO:0042594: response to starvation, GO:0045333: cellular respiration, GO:0045722: positive regulation of gluconeogenesis, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0046321: positive regulation of fatty acid oxidation, GO:0050821: protein stabilization, GO:0050873: brown fat cell differentiation, GO:0005634: nucleus, GO:0005665: DNA-directed RNA polymerase II, core complex, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003723: RNA binding, GO:0008134: transcription factor binding, GO:0016455: RNA polymerase II transcription mediator activity, GO:0030374: ligand-dependent nuclear receptor transcription coactivator activity, GO:0050681: androgen receptor binding	04910: Insulin signaling pathway, 04920: Adipocytokine signaling pathway	0.1593	0.6481	0.9932	1.5293	4.06	4.22	4.7	5.05	5.59	6.79	3
219132_at	PELI2	pellino homolog 2 (Drosophila)	NM_021255	57161	Hs.657926	GO:0005829: cytosol, GO:0016020: membrane, GO:0043234: protein complex, GO:0005515: protein binding		0.2803	0.5155	0.902	1.3894	3.73	4.01	4.24	4.63	5.12	5.16	3
219140_s_at	RBP4	retinol binding protein 4, plasma	AF119868	5950	Hs.50223	GO:0006810: transport, GO:0007601: visual perception, GO:0050896: response to stimulus, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005215: transporter activity, GO:0005488: binding, GO:0016918: retinal binding, GO:0019841: retinol binding		0.8837	1.8351	1.5773	3.0685	4.51	5.39	6.34	6.09	7.58	8.02	3
218974_at	SOBP	sine oculis binding protein homolog (Drosophila)	NM_018013	55084	Hs.445244			0.2076	0.7253	0.8268	2.1801	2.4	2.61	3.12	3.23	4.58	4.17	3

(*Continued*)

TABLE E3. (*Continued*)

219062_s_at	ZCCHC2	zinc finger, CCHC domain containing 2	BE676543	54877	Hs.114191, Hs.656351, Hs.658391	GO:0005737: cytoplasm, GO:0003676: nucleic acid binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.3154	0.6619	0.7317	1.0435	7.71	8.03	8.37	8.44	8.75	8.89	3
218934_s_at	HSPB7	heat shock 27kDa protein family, member 7 (cardiovascular)	NM_014424	27129	Hs.502612	GO:0006457: protein folding, GO:0006986: response to unfolded protein, GO:0008016: regulation of heart contraction, GO:0008022: protein C-terminus binding		−0.0059	0.2584	0.4411	1.1906	3.94	3.93	4.2	4.38	5.13	5	3
218952_at	PCSK1N	proprotein convertase subtilisin/kexin type 1 inhibitor	NM_013271	27344	Hs.522640	GO:0007218: neuropeptide signaling pathway, GO:0005615: extracellular space, GO:0005625: soluble fraction, GO:0004866: endopeptidase inhibitor activity, GO:0005102: receptor binding		0.4199	0.5493	0.6881	1.2338	4.25	4.67	4.8	4.94	5.49	4.68	3
218665_at	FZD4	frizzled homolog 4 (Drosophila)	NM_012193	8322	Hs.591968	GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007275: multicellular organismal development, GO:0016055: Wnt receptor signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004926: non-G-protein coupled 7TM receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0005515: protein binding, GO:0042813: Wnt receptor activity	04310: Wnt signaling pathway, 04916: Melanogenesis, 05210: Colorectal cancer, 05217: Basal cell carcinoma	0.1734	0.3361	0.6384	1.1327	6.59	6.76	6.93	7.23	7.72	7.65	3
218847_at	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2	NM_006548	10644	Hs.35354	GO:0009386: translational attenuation, GO:0009653: anatomical structure morphogenesis, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0003723: RNA binding, GO:0005515: protein binding		0.0532	0.252	0.4166	1.0643	6.74	6.79	6.99	7.15	7.8	7.75	3
218641_at	MGC3032	hypothetical protein MGC3032	NM_023941	65998	Hs.568945			0.3424	0.455	0.8688	1.1153	4.22	4.56	4.67	5.08	5.33	5.16	3
218651_s_at	LARP6	La ribonucleoprotein domain family, member 6	NM_018357	55323	Hs.416755	GO:0006396: RNA processing, GO:0005634: nucleus, GO:0030529: ribonucleoprotein complex, GO:0003723: RNA binding		0.1104	0.2158	0.3803	1.2975	2.72	2.83	2.93	3.1	4.01	3.65	3
218574_s_at	LMCD1	LIM and cysteine-rich domains 1	NM_014583	29995	Hs.475353	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0008150: biological_process, GO:0005575: cellular_component, GO:0005634: nucleus, GO:0003674: molecular_function, GO:0003714: transcription corepressor activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.1639	0.3388	0.9391	1.3671	6.99	7.15	7.33	7.93	8.35	8.12	3
218624_s_at	MGC2752	hypothetical protein MGC2752	NM_023939	65996	Hs.541177			−0.1053	0.2038	0.3975	1.0828	4.8	4.7	5	5.2	5.88	5.32	3
218486_at	KLF11	Kruppel-like factor 11	AA149594	8462	Hs.12229	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006350: transcription, GO:0006366: transcription from RNA polymerase II promoter, GO:0008285: negative regulation of cell proliferation, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.2385	0.5302	0.7455	1.0042	7.71	7.95	8.24	8.46	8.72	8.75	3
218517_at	PHF17	PHD finger protein 17	NM_024900	79960	Hs.12420	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006915: apoptosis, GO:0006950: response to stress, GO:0030308: negative regulation of cell growth, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.2862	0.4923	0.9082	1.8228	5.63	5.91	6.12	6.53	7.45	7.41	3
218437_s_at	LZTFL1	leucine zipper transcription factor-like 1	AA843132	54585	Hs.30824			0.3178	0.6578	0.9532	1.0826	7.37	7.69	8.03	8.33	8.46	8.71	3

(*Continued*)

TABLE E3. (*Continued*)

218450_at	HEBP1	heme binding protein 1	NM_015987	50865	Hs.642618	GO:0007623: circadian rhythm, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005829: cytosol, GO:0005488: binding, GO:0020037: heme binding		0.332	0.5419	0.7824	1.0089	8.97	9.3	9.51	9.75	9.98	10.04	3
218164_at	SPATA20	spermatogenesis associated 20	NM_022827	64847	Hs.103147	GO:0007275: multicellular organismal development, GO:0007283: spermatogenesis, GO:0030154: cell differentiation, GO:0005515: protein binding		0.3897	0.5029	0.6975	1.1992	7.37	7.76	7.87	8.07	8.57	8.27	3
218168_s_at	CABC1	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	NM_020247	56997	Hs.118241	GO:0006457: protein folding, GO:0005739: mitochondrion, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0016301: kinase activity, GO:0016740: transferase activity		0.6066	0.6919	0.7905	1.1709	7.7	8.31	8.39	8.49	8.87	8.92	3
218086_at	NPDC1	neural proliferation, differentiation and control, 1	NM_015392	56654	Hs.105547	GO:0016020: membrane, GO:0016021: integral to membrane		0.1451	0.2892	0.4947	1.2703	6.63	6.77	6.92	7.12	7.9	7.21	3
218149_s_at	ZNF395	zinc finger protein 395	NM_017606	55893	Hs.435535, Hs.684561	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003677: DNA binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.1546	0.3433	0.6376	1.1637	8.76	8.92	9.11	9.4	9.93	9.87	3
217897_at	FXYD6	FXYD domain containing ion transport regulator 6	NM_022003	53826	Hs.635508	GO:0006811: ion transport, GO:0008150: biological_process, GO:0005615: extracellular space, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0003674: molecular_function, GO:0005216: ion channel activity		0.2255	0.4943	0.9436	1.7607	3	3.22	3.49	3.94	4.76	4.88	3
217974_at	TM7SF3	transmembrane 7 superfamily member 3	NM_016551	51768	Hs.438641	GO:0016020: membrane, GO:0016021: integral to membrane		−0.2625	0.0813	0.2624	1.0418	7.54	7.28	7.63	7.81	8.59	8.24	3
217667_at	LOC729799	similar to SEC14-like protein 1	AV761014	729799	Hs.657623			−0.0249	−0.0216	0.246	1.1511	4.15	4.13	4.13	4.4	5.31	4.26	3
217734_s_at	WDR6	WD repeat domain 6	NM_018031	11180	Hs.654815	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0003674: molecular_function		0.2896	0.1703	0.7727	1.1426	6	6.29	6.17	6.77	7.14	6.67	3
217437_s_at	TACC1	transforming, acidic coiled-coil containing protein 1	AB029026	6867	Hs.279245	GO:0007049: cell cycle, GO:0051301: cell division, GO:0005737: cytoplasm, GO:0005515: protein binding		0.0548	0.2384	0.5775	1.1015	9.47	9.52	9.71	10.05	10.57	10.27	3
217627_at	ZNF573	zinc finger protein 573	BE515346	126231	Hs.531262	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0003676: nucleic acid binding, GO:0003677: DNA binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.2307	0.4129	0.8931	1.6132	6.1	6.33	6.51	6.99	7.71	7.35	3
217226_s_at	SFXN3	sideroflexin 3	M95929	81855	Hs.283844			0.0227	0.3851	0.7141	1.1012	8.8	8.83	9.19	9.52	9.9	9.77	3
217257_at			L37198					−0.1328	0.5177	0.8763	1.2252	7.05	6.91	7.56	7.92	8.27	8.32	3
217087_at	C1orf68	chromosome 1 open reading frame 68	AF005081	553168	Hs.601077	GO:0008544: epidermis development, GO:0005575: cellular_component, GO:0003674: molecular_function		0.3841	0.6937	0.8417	1.0679	10.11	10.5	10.81	10.95	11.18	11.39	3
217164_at			AK024108					0.0988	0.4245	0.7097	1.1195	7.14	7.24	7.57	7.85	8.26	8.01	3
216331_at	ITGA7	integrin, alpha 7	AK022548	3679	Hs.524484, Hs.639559	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0007517: muscle development, GO:0008360: regulation of cell shape, GO:0008305: integrin complex, GO:0016020: membrane, GO:0004872: receptor activity, GO:0005509: calcium ion binding, GO:0005515: protein binding	04510: Focal adhesion, 04512: ECM-receptor interaction, 04810: Regulation of actin cytoskeleton	0.4345	0.5968	0.9513	1.7646	8.08	8.52	8.68	9.03	9.85	9.34	3

(*Continued*)

TABLE E3. (*Continued*)

216614_at	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	AL049988	3709	Hs.512235, Hs.659892	GO:0006811: ion transport, GO:0006816: calcium ion transport, GO:0007165: signal transduction, GO:0005783: endoplasmic reticulum, GO:0005886: plasma membrane, GO:0016021: integral to membrane, GO:0005216: ion channel activity, GO:0005220: inositol 1,4,5-triphosphate-sensitive calcium-release channel activity, GO:0005262: calcium channel activity, GO:0005509: calcium ion binding, GO:0008095: inositol-1,4,5-triphosphate receptor activity, GO:0015085: calcium ion transmembrane transporter activity	04020: Calcium signaling pathway, 04070: Phosphatidylinositol signaling system, 04540: Gap junction, 04720: Long-term potentiation, 04730: Long-term depression, 04912: GnRH signaling pathway	−0.1419	0.3465	0.2608	1.6219	4.95	4.8	5.29	5.21	6.57	6.96	3
216080_s_at	FADS3	fatty acid desaturase 3	AC004770	3995	Hs.21765	GO:0006629: lipid metabolic process, GO:0006636: unsaturated fatty acid biosynthetic process, GO:0005624: membrane fraction, GO:0016020: membrane, GO:0003674: molecular_function, GO:0005506: iron ion binding, GO:0016491: oxidoreductase activity, GO:0016717: oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water, GO:0020037: heme binding, GO:0046914: transition metal ion binding	00591: Linoleic acid metabolism	0.0455	0.4334	0.4468	1.3488	2.42	2.47	2.85	2.87	3.77	3.79	3
216264_s_at	LAMB2	laminin, beta 2 (laminin S)	X79683	3913	Hs.439726	GO:0007155: cell adhesion, GO:0007268: synaptic transmission, GO:0005605: basal lamina, GO:0005198: structural molecule activity, GO:0005515: protein binding	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 05222: Small cell lung cancer	0.2616	0.5128	0.9748	1.5613	7.83	8.09	8.34	8.8	9.39	8.76	3
215768_at	SOX5	SRY (sex determining region Y)-box 5	AL049337	6660	Hs.657542	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0003700: transcription factor activity		−0.4936	0.1613	0.6352	1.213	2.92	2.42	3.08	3.55	4.13	3.99	3
216000_at	KIAA0484	KIAA0484 protein	AA732995	57240				0.0479	0.105	0.5484	1.1462	2.95	3	3.05	3.5	4.09	3.71	3
215617_at			AU145711					−0.0898	0.503	0.6143	1.3666	3.66	3.57	4.16	4.28	5.03	4.46	3
215695_s_at	GYG2	glycogenin 2	U94357	8908	Hs.567381	GO:0005978: glycogen biosynthetic process, GO:0016051: carbohydrate biosynthetic process, GO:0005625: soluble fraction, GO:0008466: glycogenin glucosyltransferase activity, GO:0016740: transferase activity, GO:0016758: transferase activity, transferring hexosyl groups		0.4105	0.8808	0.6638	2.2419	3.69	4.1	4.57	4.35	5.93	5.53	3
215537_x_at	DDAH2	dimethylarginine dimethylaminohydrolase 2	AJ012008	23564	Hs.247362	GO:0006527: arginine catabolic process, GO:0006809: nitric oxide biosynthetic process, GO:0006916: anti-apoptosis, GO:0007263: nitric oxide mediated signal transduction, GO:0016403: dimethylargininase activity, GO:0016787: hydrolase activity		0.0098	0.4029	0.8665	1.4462	7.38	7.39	7.78	8.25	8.83	8.43	3
215567_at	FCF1	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	AU144919	51077	Hs.579828	GO:0006364: rRNA processing		−0.0477	0.5308	0.573	1.2316	4.82	4.77	5.35	5.39	6.05	5.91	3
215235_at	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	AL110273	6709	Hs.372331	GO:0051016: barbed-end actin filament capping, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0008091: spectrin, GO:0016020: membrane, GO:0003779: actin binding, GO:0005200: structural constituent of cytoskeleton, GO:0005509: calcium ion binding, GO:0005516: calmodulin binding	04530: Tight junction	0.0184	0.3191	0.5272	1.2246	8.88	8.9	9.2	9.41	10.11	10.03	3
215358_x_at	ZNF37B	zinc finger protein 37B	AK026980	256112	Hs.646695, Hs.684178			−0.0069	0.2554	0.7327	1.2853	3.34	3.34	3.6	4.08	4.63	4.58	3

(*Continued*)

TABLE E3. (*Continued*)

215139_at	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	AL137508	9639	Hs.98594	GO:0035023: regulation of Rho protein signal transduction, GO:0005622: intracellular, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity		−0.2702	−0.1949	−0.0137	1.0965	4.17	3.9	3.97	4.15	5.26	4.95	3
215146_s_at	TTC28	tetratricopeptide repeat domain 28	AB028966	23331	Hs.387856	GO:0005488: binding		0.289	0.5533	0.9693	1.2641	6.59	6.88	7.14	7.56	7.85	7.61	3
215066_at	PTPRF	protein tyrosine phosphatase, receptor type, F	AU158443	5792	Hs.272062	GO:0006470: protein amino acid dephosphorylation, GO:0007155: cell adhesion, GO:0007185: transmembrane receptor protein tyrosine phosphatase signaling pathway, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004725: protein tyrosine phosphatase activity, GO:0004872: receptor activity, GO:0005001: transmembrane receptor protein tyrosine phosphatase activity, GO:0005515: protein binding, GO:0016787: hydrolase activity, GO:0016791: phosphoric monoester hydrolase activity	04514: Cell adhesion molecules (CAMs), 04520: Adherens junction, 04910: Insulin signaling pathway	−0.1045	−0.0697	0.226	1.0743	3.76	3.65	3.69	3.98	4.83	4.18	3
215129_at	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	AJ000008	5288	Hs.22500	GO:0007154: cell communication, GO:0008150: biological_process, GO:0005942: phosphoinositide 3-kinase complex, GO:0016020: membrane, GO:0005515: protein binding, GO:0016303: 1-phosphatidylinositol-3-kinase activity, GO:0016740: transferase activity, GO:0035005: phosphatidylinositol-4-phosphate 3-kinase activity, GO:0035091: phosphoinositide binding	04070: Phosphatidylinositol signaling system	0.2659	0.3492	0.7986	1.0362	3.28	3.55	3.63	4.08	4.32	4.46	3
214967_at	SAMD4A	sterile alpha motif domain containing 4A	AU146983	23034	Hs.98259	GO:0045727: positive regulation of protein biosynthetic process, GO:0005737: cytoplasm, GO:0000900: translation repressor activity, nucleic acid binding, GO:0003730: mRNA 3′-UTR binding, GO:0005515: protein binding, GO:0030371: translation repressor activity		−0.0828	−0.0248	0.491	1.2175	2.99	2.91	2.96	3.48	4.21	3.59	3
215016_x_at	DST	dystonin	BC004912	667	Hs.631992, Hs.669931	GO:0007010: cytoskeleton organization and biogenesis, GO:0007050: cell cycle arrest, GO:0007155: cell adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0045104: intermediate filament cytoskeleton organization and biogenesis, GO:0045104: intermediate filament cytoskeleton organization and biogenesis, GO:0045104: intermediate filament cytoskeleton organization and biogenesis, GO:0005604: basement membrane, GO:0005615: extracellular space, GO:0005737: cytoplasm, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005911: intercellular junction, GO:0016023: cytoplasmic membrane-bound vesicle, GO:0030056: hemidesmosome, GO:0003779: actin binding, GO:0005178: integrin binding, GO:0005200: structural constituent of cytoskeleton, GO:0005200: structural constituent of cytoskeleton, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005515: protein binding, GO:0008022: protein C-terminus binding, GO:0051015: actin filament binding		0.258	0.4812	0.9581	1.1246	9.53	9.79	10.01	10.49	10.66	10.65	3
214920_at	THSD7A	thrombospondin, type I, domain containing 7A	R33964	221981	Hs.120855, Hs.648482	GO:0016020: membrane, GO:0016021: integral to membrane		0.0815	0.4546	0.9678	1.4782	4.45	4.53	4.9	5.41	5.92	5.75	3

(*Continued*)

TABLE E3. (*Continued*)

214925_s_at	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	AK026484	6709	Hs.372331	GO:0051016: barbed-end actin filament capping, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0008091: spectrin, GO:0016020: membrane, GO:0003779: actin binding, GO:0005200: structural constituent of cytoskeleton, GO:0005509: calcium ion binding, GO:0005516: calmodulin binding	04530: Tight junction	−0.2124	−0.0935	0.4266	1.1611	6.85	6.64	6.76	7.28	8.01	7.69	3
214890_s_at	DKFZP564J102	DKFZP564J102 protein	AL080065	25854	Hs.357025			−0.0393	0.0691	0.1788	1.1777	3.58	3.54	3.65	3.76	4.76	4.34	3
214909_s_at	DDAH2	dimethylarginine dimethylaminohydrolase 2	AK026191	23564	Hs.247362	GO:0006527: arginine catabolic process, GO:0006809: nitric oxide biosynthetic process, GO:0006916: anti-apoptosis, GO:0007263: nitric oxide mediated signal transduction, GO:0016403: dimethylargininase activity, GO:0016787: hydrolase activity		0.1002	0.3561	0.6871	1.2686	7.51	7.61	7.87	8.2	8.78	8.5	3
214783_s_at	ANXA11	annexin A11	BG177920	311	Hs.530291	GO:0006955: immune response, GO:0005634: nucleus, GO:0005635: nuclear envelope, GO:0005654: nucleoplasm, GO:0005737: cytoplasm, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005544: calcium-dependent phospholipid binding		0.1207	0.3566	0.7474	1.0677	6.34	6.46	6.69	7.09	7.41	7.45	3
214808_at			AU147851					0.066	0.4967	0.6737	1.0922	7.3	7.37	7.8	7.98	8.4	8.05	3
214734_at	EXPH5	exophilin 5	AB014524	23086	Hs.269591	GO:0006886: intracellular protein transport, GO:0005515: protein binding, GO:0017137: Rab GTPase binding		−0.2853	0.5873	0.7263	1.5746	6.98	6.7	7.57	7.71	8.56	9.07	3
214739_at	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	AI357539	84859	Hs.518414, Hs.659335	GO:0005515: protein binding		0.206	0.5039	0.8922	1.0821	6	6.21	6.51	6.9	7.09	7.05	3
214598_at	CLDN8	claudin 8	AL049977	9073	Hs.162209	GO:0016338: calcium-independent cell-cell adhesion, GO:0005783: endoplasmic reticulum, GO:0005886: plasma membrane, GO:0005923: tight junction, GO:0016021: integral to membrane, GO:0030054: cell junction, GO:0005198: structural molecule activity, GO:0042802: identical protein binding	04514: Cell adhesion molecules (CAMs), 04530: Tight junction, 04670: Leukocyte transendothelial migration	0.2095	0.3241	0.8308	1.5197	2.24	2.45	2.56	3.07	3.76	5.62	3
214682_at	LOC399491	LOC399491 protein	AK023376	399491	Hs.648395	GO:0007218: neuropeptide signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane		0.0926	0.2487	0.4594	1.5161	4.03	4.12	4.28	4.49	5.54	4.75	3
214454_at	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2	NM_014244	9509	Hs.591725	GO:0006508: proteolysis, GO:0030574: collagen catabolic process, GO:0005578: proteinaceous extracellular matrix, GO:0008133: collagenase activity, GO:0008270: zinc ion binding, GO:0017074: procollagen N-endopeptidase activity, GO:0046872: metal ion binding		0.212	0.3899	0.9996	1.1696	4.48	4.69	4.87	5.48	5.65	4.84	3
214464_at	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	NM_003607	8476	Hs.35433	GO:0006468: protein amino acid phosphorylation, GO:0007242: intracellular signaling cascade, GO:0031532: actin cytoskeleton reorganization, GO:0051056: regulation of small GTPase mediated signal transduction, GO:0005737: cytoplasm, GO:0005911: intercellular junction, GO:0031252: leading edge, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004674: protein serine/threonine kinase activity, GO:0005083: small GTPase regulator activity, GO:0005524: ATP binding, GO:0008270: zinc ion binding, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0019992: diacylglycerol binding, GO:0042802: identical protein binding		0.0867	0.1446	0.6715	1.7732	3.24	3.33	3.39	3.91	5.02	4.35	3
214415_at	PLGLB1	plasminogen-like B1	N58120	5343	Hs.652169, Hs.652174			−0.0724	0.1798	0.4981	1.3215	4.05	3.98	4.23	4.55	5.37	5	3
214434_at	HSPA12A	heat shock 70kDa protein 12A	AB007877	259217	Hs.654682	GO:0000166: nucleotide binding, GO:0005524: ATP binding		0.0361	0.6368	0.8755	2.0267	3.76	3.79	4.39	4.63	5.78	5.73	3

(*Continued*)

TABLE E3. (*Continued*)

214247_s_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	AU148057	27122	Hs.292156	GO:0007275: multicellular organismal development, GO:0009653: anatomical structure morphogenesis, GO:0016055: Wnt receptor signaling pathway, GO:0030178: negative regulation of Wnt receptor signaling pathway, GO:0005576: extracellular region, GO:0005615: extracellular space		−0.0662	0.3931	0.6063	1.0121	10.63	10.56	11.02	11.23	11.64	11.43	3
214395_x_at	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	AI613383	1936	Hs.333388	GO:0006414: translational elongation, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0005853: eukaryotic translation elongation factor 1 complex, GO:0005853: eukaryotic translation elongation factor 1 complex, GO:0003746: translation elongation factor activity, GO:0004871: signal transducer activity, GO:0004871: signal transducer activity, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005515: protein binding		0.3084	0.4456	0.9424	1.6594	6.68	6.99	7.12	7.62	8.34	7.81	3
214234_s_at	CYP3A5P2	cytochrome P450, family 3, subfamily A, polypeptide 5 pseudogene 2	X90579	79424	Hs.150276			0.6377	0.6719	0.9255	1.1624	7.14	7.77	7.81	8.06	8.3	8.58	3
214239_x_at	CISD3	CDGSH iron sulfur domain 3	AI560455	284106	Hs.462923			0.1666	0.3957	0.6492	1.1377	7.77	7.94	8.17	8.42	8.91	8.59	3
214188_at	HEXIM1	hexamethylene bis-acetamide inducible 1	AW665096	10614	Hs.15299, Hs.586945, Hs.634944	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0045736: negative regulation of cyclin-dependent protein kinase activity, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0004861: cyclin-dependent protein kinase inhibitor activity, GO:0005515: protein binding, GO:0016564: transcription repressor activity, GO:0017069: snRNA binding		0.3027	0.2013	0.3893	1.0313	3.13	3.43	3.33	3.52	4.16	3.66	3
214212_x_at	PLEKHC1	pleckstrin homology domain containing, family C (with FERM domain) member 1	AI928241	10979	Hs.509343	GO:0007155: cell adhesion, GO:0008360: regulation of cell shape, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0001725: stress fiber, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005515: protein binding		−0.2527	0.125	0.4453	1.2606	2.93	2.68	3.05	3.37	4.19	3.95	3
214156_at	MYRIP	myosin VIIA and Rab interacting protein	AL050090	25924	Hs.594535	GO:0006886: intracellular protein transport, GO:0001750: photoreceptor outer segment, GO:0005737: cytoplasm, GO:0015629: actin cytoskeleton, GO:0042470: melanosome, GO:0045202: synapse, GO:0003779: actin binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0017022: myosin binding, GO:0017137: Rab GTPase binding, GO:0046872: metal ion binding		0.0654	−0.0431	0.4811	1.0474	3.75	3.81	3.71	4.23	4.8	4.82	3
214175_x_at	PDLIM4	PDZ and LIM domain 4	AI254547	8572	Hs.424312	GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0188	0.286	0.4409	1.2454	7.9	7.89	8.19	8.34	9.15	9.2	3
214041_x_at	RPL37A	ribosomal protein L37a	BE857772	6168	Hs.433701	GO:0006412: translation, GO:0005622: intracellular, GO:0005840: ribosome, GO:0003735: structural constituent of ribosome, GO:0005515: protein binding	03010: Ribosome	−0.0869	−0.0031	0.3434	1.0978	10.51	10.42	10.5	10.85	11.6	11.05	3
214110_s_at	LOC654342	similar to lymphocyte-specific protein 1	BF195104	654342	Hs.656760	GO:0007165: signal transduction, GO:0004871: signal transducer activity		0.1148	0.3806	0.702	1.029	7.13	7.24	7.51	7.83	8.16	7.85	3
214021_x_at	ITGB5	integrin, beta 5	AI335208	3693	Hs.536663	GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0007275: multicellular organismal development, GO:0008305: integrin complex, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0005178: integrin binding, GO:0005515: protein binding	04510: Focal adhesion, 04512: ECM-receptor interaction, 04810: Regulation of actin cytoskeleton	0.0191	0.0449	0.2301	1.0572	2.86	2.88	2.9	3.09	3.92	3.53	3
214036_at			BE464799					0.3042	0.4383	0.7485	1.4319	6.02	6.33	6.46	6.77	7.45	7.52	3

(*Continued*)

TABLE E3. (*Continued*)

213982_s_at	RABGAP1L	RAB GTPase activating protein 1-like	BG107203	9910	Hs.585378	GO:0032313: regulation of Rab GTPase activity, GO:0005622: intracellular, GO:0005097: Rab GTPase activator activity		0.5607	0.6556	0.9582	1.2874	6.45	7.01	7.11	7.41	7.74	7.53	3
214001_x_at	RPS10	ribosomal protein S10	AW302047	6204	Hs.645317, Hs.652597	GO:0006412: translation, GO:0005737: cytoplasm, GO:0005843: cytosolic small ribosomal subunit (sensu Eukaryota), GO:0030529: ribonucleoprotein complex, GO:0003723: RNA binding, G O:0003735: structural constituent of ribosome	03010: Ribosome	0.3256	0.2029	0.6969	1.3569	7.66	7.98	7.86	8.35	9.01	8.37	3
213931_at	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	AI819238	3398	Hs.180919	GO:0007275: multicellular organismal development, GO:0007507: heart development, GO:0016481: negative regulation of transcription, GO:0043433: negative regulation of transcription factor activity, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005515: protein binding, GO:0016564: transcription repressor activity	04350: TGF-beta signaling pathway	0.4633	0.4397	0.534	1.0567	7.68	8.14	8.12	8.21	8.74	8.03	3
213942_at	MEGF6	multiple EGF-like-domains 6	AL134303	1953	Hs.593645	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0005509: calcium ion binding, GO:0005509: calcium ion binding		0.0325	0.2034	0.5754	1.0959	4.62	4.65	4.82	5.19	5.71	5.09	3
213924_at	MPPE1	metallophosphoesterase 1	BF476502	65258	Hs.514713	GO:0016787: hydrolase activity		0.2977	0.5523	0.6762	1.2634	8.04	8.33	8.59	8.71	9.3	9.41	3
213925_at	C1orf95	chromosome 1 open reading frame 95	AL134612	375057	Hs.116827, Hs.592751	GO:0016020: membrane, GO:0016021: integral to membrane		0.0578	0.1387	0.3245	1.074	2.45	2.51	2.59	2.78	3.53	3.22	3
213900_at	C9orf61	chromosome 9 open reading frame 61	AA524029	9413	Hs.118003	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0003674: molecular_function		−0.2122	0.4831	0.5587	1.5676	5.35	5.14	5.83	5.91	6.92	7.46	3
213905_x_at	BGN	biglycan	AA845258	633	Hs.821	GO:0008150: biological_process, GO:0005578: proteinaceous extracellular matrix, GO:0030133: transport vesicle, GO:0005201: extracellular matrix structural constituent, GO:0005515: protein binding		0.0087	0.4701	0.8603	1.7209	7.66	7.67	8.13	8.52	9.38	8.26	3
213792_s_at			AA485908					0.1291	0.4278	0.6713	1.3028	8.1	8.23	8.52	8.77	9.4	9.16	3
213891_s_at	TCF4	transcription factor 4	AI927067	6925	Hs.644653	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0005667: transcription factor complex, GO:0003700: transcription factor activity, GO:0003714: transcription corepressor activity, GO:0008013: beta-catenin binding, GO:0046982: protein heterodimerization activity		0.2978	0.479	0.9027	1.0365	10.44	10.74	10.92	11.34	11.48	11.16	3
213705_at			AW301861					−0.0732	0.119	0.6283	1.0573	7.8	7.73	7.92	8.43	8.86	8.69	3
213706_at	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	AI368018	2819	Hs.524418	GO:0005975: carbohydrate metabolic process, GO:0006094: gluconeogenesis, GO:0046168: glycerol-3-phosphate catabolic process, GO:0005737: cytoplasm, GO:0009331: glycerol-3-phosphate dehydrogenase complex, GO:0004367: glycerol-3-phosphate dehydrogenase (NAD+) activity, GO:0051287: NAD binding	00564: Glycerophospholipid metabolism	0.2716	1.1734	0.9927	1.7755	4.81	5.08	5.98	5.8	6.58	6.84	3
213686_at	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	AI186145	23230	Hs.459790, Hs.662256	GO:0006895: Golgi to endosome transport, GO:0008104: protein localization, GO:0015031: protein transport, GO:0005622: intracellular		0.407	0.4982	0.9682	1.1868	4.44	4.85	4.94	5.41	5.63	5.8	3
213693_s_at	MUC1	mucin 1, cell surface associated	AI610869	4582	Hs.89603	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0003779: actin binding		−0.194	−0.0992	0.4444	1.3029	3.24	3.04	3.14	3.68	4.54	4.96	3
213661_at	DKFZP586-H2123	regeneration associated muscle protease	AI671186	25891	Hs.55044	GO:0006508: proteolysis, GO:0004252: serine-type endopeptidase activity		0.3815	0.333	0.7192	1.9369	5.85	6.23	6.19	6.57	7.79	8.25	3

(*Continued*)

TABLE E3. (*Continued*)

213668_s_at	SOX4	SRY (sex determining region Y)-box 4	AI989477	6659	Hs.643910	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0031017: exocrine pancreas development, GO:0005634: nucleus, GO:0003700: transcription factor activity		0.0889	0.2955	0.2322	1.1719	2.79	2.87	3.08	3.02	3.96	2.91	3
213605_s_at	LOC728411	similar to Beta-glucuronidase precursor	AL049987	728411	Hs.654942			0.1916	0.2791	0.8147	1.206	9.63	9.82	9.91	10.45	10.84	10.51	3
213657_s_at	ZNF710	zinc finger protein 710	BE858194	374655	Hs.459311	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0003677: DNA binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.3258	0.4337	0.7552	1.0603	5.42	5.75	5.86	6.18	6.48	6.65	3
213587_s_at	ATP6V0E2	ATPase, H+ transporting V0 subunit e2	AI884867	155066	Hs.556998, Hs.694765	GO:0006811: ion transport, GO:0015986: ATP synthesis coupled proton transport, GO:0015992: proton transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016469: proton-transporting two-sector ATPase complex, GO:0016787: hydrolase activity, GO:0046933: hydrogen ion transporting ATP synthase activity, rotational mechanism, GO:0046961: hydrogen ion transporting ATPase activity, rotational mechanism		0.2571	0.5591	0.7683	1.2344	6.55	6.8	7.11	7.31	7.78	7.62	3
213592_at	AGTRL1	angiotensin II receptor-like 1	X89271	187	Hs.438311	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016021: integral to membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004872: receptor activity	04080: Neuroactive ligand-receptor interaction	0.3485	0.4186	0.8621	1.294	6.44	6.79	6.86	7.3	7.73	6.8	3
213489_at	MAPRE2	microtubule-associated protein, RP/EB family, member 2	BE671156	10982	Hs.532824	GO:0006968: cellular defense response, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007165: signal transduction, GO:0008283: cell proliferation, GO:0051301: cell division, GO:0005737: cytoplasm, GO:0005874: microtubule, GO:0008017: microtubule binding		0.2438	0.4866	0.9503	1.6405	5.11	5.35	5.6	6.06	6.75	6.47	3
213543_at			AA570453					0.4116	0.425	0.8466	1.0162	4.56	4.97	4.99	5.41	5.58	5.22	3
213388_at	LOC727942	similar to phosphodiesterase 4D interacting protein isoform 2	H15535	727942	Hs.647804			0.0957	0.2803	0.9162	1.1062	2.87	2.96	3.15	3.78	3.97	4.41	3
213455_at	FAM114A1	family with sequence similarity 114, member A1	W87466	92689	Hs.476517	GO:0005737: cytoplasm		0.3872	0.7126	0.984	1.1341	8.45	8.84	9.17	9.44	9.59	9.43	3
213351_s_at	TMCC1	transmembrane and coiled-coil domain family 1	AB018322	23023	Hs.477547	GO:0016020: membrane, GO:0016021: integral to membrane		0.4226	0.4509	0.6756	1.0203	6.77	7.19	7.22	7.45	7.79	7.58	3
213371_at	LDB3	LIM domain binding 3	AI803302	11155	Hs.657271	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0042995: cell projection, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.0288	0.0322	0.3174	1.4557	2.64	2.61	2.67	2.96	4.09	3.13	3
213329_at	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	AA742261	23380	Hs.497575	GO:0007165: signal transduction, GO:0005622: intracellular, GO:0005096: GTPase activator activity	04360: Axon guidance	0.1554	0.3459	0.7688	1.0573	4.62	4.78	4.97	5.39	5.68	5.87	3
213350_at	RPS11	ribosomal protein S11	BF680255	6205	Hs.433529	GO:0006412: translation, GO:0006412: translation, GO:0005622: intracellular, GO:0005840: ribosome, GO:0005842: cytosolic large ribosomal subunit (sensu Eukaryota), GO:0005843: cytosolic small ribosomal subunit (sensu Eukaryota), GO:0003735: structural constituent of ribosome, GO:0003735: structural constituent of ribosome, GO:0019843: rRNA binding	03010: Ribosome	0.0154	−0.0471	0.3041	1.0267	9.82	9.84	9.77	10.13	10.85	10.48	3

(*Continued*)

TABLE E3. (*Continued*)

213317_at	CLIC5	chloride intracellular channel 5	AL049313	53405	Hs.485489	GO:0006811: ion transport, GO:0006821: chloride transport, GO:0006821: chloride transport, GO:0007565: female pregnancy, GO:0005626: insoluble fraction, GO:0005902: microvillus, GO:0015629: actin cytoskeleton, GO:0016020: membrane, GO:0005244: voltage-gated ion channel activity, GO:0005247: voltage-gated chloride channel activity, GO:0005515: protein binding, GO:0031404: chloride ion binding		0.0061	0.3592	0.6944	1.232	2.77	2.78	3.13	3.47	4.01	3.77	3
213326_at	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)	AU150319	6843	Hs.20021	GO:0016192: vesicle-mediated transport, GO:0005739: mitochondrion, GO:0005887: integral to plasma membrane, GO:0008021: synaptic vesicle, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019717: synaptosome, GO:0030054: cell junction, GO:0031410: cytoplasmic vesicle, GO:0045202: synapse	04130: SNARE interactions in vesicular transport	0.5562	0.7328	0.9872	1.1118	5.05	5.61	5.79	6.04	6.17	5.98	3
213260_at			AU145890					0.2197	0.2623	0.481	1.1118	4.87	5.09	5.13	5.35	5.98	6.41	3
213316_at	KIAA1462	KIAA1462	AL050154	57608	Hs.533953			0.1843	0.3567	0.8349	1.2291	4.74	4.93	5.1	5.58	5.97	5.27	3
213183_s_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	N95363	1028	Hs.106070	GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0000080: G1 phase of mitotic cell cycle, GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0007049: cell cycle, GO:0007050: cell cycle arrest, GO:0008285: negative regulation of cell proliferation, GO:0042551: neuron maturation, GO:0005634: nucleus, GO:0004861: cyclin-dependent protein kinase inhibitor activity, GO:0005515: protein binding	04110: Cell cycle	0.349	0.3536	0.7815	1.2965	4.09	4.44	4.45	4.88	5.39	5.16	3
213249_at	FBXL7	F-box and leucine-rich repeat protein 7	AU145127	23194	Hs.433057	GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0000151: ubiquitin ligase complex, GO:0004842: ubiquitin-protein ligase activity, GO:0005515: protein binding		0.0258	0.4315	0.784	1.0226	6.3	6.32	6.73	7.08	7.32	6.9	3
213116_at	NEK3	NIMA (never in mitosis gene a)-related kinase 3	AI191920	4752	Hs.409989	GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0051301: cell division, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004672: protein kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0004713: protein-tyrosine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0016740: transferase activity		0.4154	0.5346	0.8587	1.3012	6.19	6.61	6.73	7.05	7.49	7.13	3
213182_x_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	R78668	1028	Hs.106070	GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0000080: G1 phase of mitotic cell cycle, GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0007049: cell cycle, GO:0007050: cell cycle arrest, GO:0008285: negative regulation of cell proliferation, GO:0042551: neuron maturation, GO:0005634: nucleus, GO:0004861: cyclin-dependent protein kinase inhibitor activity, GO:0005515: protein binding	04110: Cell cycle	0.4255	0.3585	0.619	1.2158	3.97	4.4	4.33	4.59	5.19	4.83	3
213030_s_at	PLXNA2	plexin A2	AI688418	5362	Hs.497626	GO:0007275: multicellular organismal development, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity	04360: Axon guidance	−0.0071	0.5583	0.7159	1.5314	4.9	4.9	5.46	5.62	6.43	6.26	3
213089_at	GUSBP1	glucuronidase, beta pseudogene 1	AU158490	153561	Hs.654588			−0.0302	0.1694	0.6562	1.3761	8.87	8.84	9.04	9.53	10.25	9.52	3
213010_at	PRKCDBP	protein kinase C, delta binding protein	AI088622	112464	Hs.434044	GO:0016301: kinase activity		0.156	0.4251	0.6755	1.3005	7.25	7.41	7.68	7.93	8.55	8.17	3

(*Continued*)

TABLE E3. (*Continued*)

213029_at	NFIB	nuclear factor I/B	BG478428	4781	Hs.370359	GO:0006260: DNA replication, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity		0.1567	0.3435	0.7405	1.0338	10.14	10.3	10.49	10.88	11.18	11.23	3
212991_at	FBXO9	F-box protein 9	AL031178	26268	Hs.216653	GO:0016567: protein ubiquitination, GO:0000151: ubiquitin ligase complex, GO:0004842: ubiquitin-protein ligase activity		0.043	0.3473	0.3676	1.1748	5.99	6.03	6.34	6.36	7.17	6.67	3
212993_at			AA114166					−0.2448	0.1141	0.7864	1.0281	6.6	6.36	6.71	7.39	7.63	7.74	3
212923_s_at	C6orf145	chromosome 6 open reading frame 145	AK024828	221749	Hs.484500			0.0231	0.4358	0.7852	1.1176	8.98	9	9.41	9.76	10.09	9.99	3
212970_at			AI694303					0.1755	0.4558	0.6907	1.0733	6.56	6.74	7.02	7.25	7.64	7.67	3
212913_at	C6orf26	chromosome 6 open reading frame 26	BE674960	401251	Hs.371225			−0.1091	0.221	0.8397	2.1726	5.1	5	5.33	5.94	7.28	7.76	3
212915_at	PDZRN3	PDZ domain containing RING finger 3	AL569804	23024	Hs.434900	GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.373	0.6262	0.9561	1.1355	8.23	8.6	8.86	9.19	9.37	9.2	3
212822_at	HEG1	HEG homolog 1 (zebrafish)	AA121502	57493	Hs.477420	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005509: calcium ion binding		0.0248	0.154	0.4445	1.0504	7.12	7.14	7.27	7.56	8.17	7.51	3
212875_s_at	C21orf25	chromosome 21 open reading frame 25	AP001745	25966	Hs.473894, Hs.675058	GO:0005634: nucleus, GO:0005737: cytoplasm		0.562	0.6888	0.9331	1.0664	7.69	8.25	8.38	8.62	8.75	8.71	3
212775_at	OBSL1	obscurin-like 1	AI978623	23363	Hs.526594	GO:0004687: myosin light chain kinase activity, GO:0016301: kinase activity		0.2538	0.4502	0.5892	1.0423	7.5	7.76	7.95	8.09	8.54	8.37	3
212813_at	JAM3	junctional adhesion molecule 3	AA149644	83700	Hs.150718	GO:0016020: membrane, GO:0016021: integral to membrane	04514: Cell adhesion molecules (CAMs), 04530: Tight junction, 04670: Leukocyte transendothelial migration, 05120: Epithelial cell signaling in Helicobacter pylori infection	0.3677	0.6121	0.983	1.3538	8.46	8.82	9.07	9.44	9.81	9.57	3
212647_at	RRAS	related RAS viral (r-ras) oncogene homolog	NM_006270	6237	Hs.515536	GO:0007265: Ras protein signal transduction, GO:0005622: intracellular, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding	04010: MAPK signaling pathway, 04530: Tight junction, 04810: Regulation of actin cytoskeleton	0.4911	0.5575	0.7806	1.1249	7.87	8.36	8.43	8.65	9	8.78	3
212651_at	RHOBTB1	Rho-related BTB domain containing 1	AB018283	9886	Hs.148670	GO:0007264: small GTPase mediated signal transduction, GO:0005622: intracellular, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005525: GTP binding		0.3862	0.5866	0.9736	1.4655	5.92	6.3	6.5	6.89	7.38	7.12	3
212567_s_at	MAP4	microtubule-associated protein 4	AL523310	4134	Hs.517949	GO:0007026: negative regulation of microtubule depolymerization, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0005198: structural molecule activity		0.0108	0.1595	0.5	1.2418	7.96	7.97	8.12	8.46	9.2	8.78	3
212594_at	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	AI185160	27250	Hs.232543	GO:0006915: apoptosis, GO:0007049: cell cycle, GO:0007569: cell aging, GO:0016481: negative regulation of transcription, GO:0016481: negative regulation of transcription, GO:0043508: negative regulation of JNK activity, GO:0045786: negative regulation of progression through cell cycle, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0003723: RNA binding, GO:0005515: protein binding		0.334	0.5485	0.7753	1.1493	8.86	9.19	9.41	9.63	10.01	10.26	3
212510_at	GPD1L	glycerol-3-phosphate dehydrogenase 1-like	AA135522	23171	Hs.82432	GO:0005975: carbohydrate metabolic process, GO:0046168: glycerol-3-phosphate catabolic process, GO:0005737: cytoplasm, GO:0009331: glycerol-3-phosphate dehydrogenase complex, GO:0004367: glycerol-3-phosphate dehydrogenase (NAD+) activity, GO:0051287: NAD binding		0.4727	0.5597	0.9813	1.2594	7.21	7.68	7.77	8.19	8.47	8.79	3
212518_at	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	AB011161	23396	Hs.282177	GO:0007409: axonogenesis, GO:0046488: phosphatidylinositol metabolic process, GO:0016020: membrane, GO:0016301: kinase activity, GO:0016308: 1-phosphatidylinositol-4-phosphate 5-kinase activity, GO:0016740: transferase activity	00562: Inositol phosphate metabolism, 04070: Phosphatidylinositol signaling system, 04510: Focal adhesion, 04810: Regulation of actin cytoskeleton	0.0868	0.3436	0.4437	1.3919	5.35	5.44	5.69	5.79	6.74	6.37	3
212498_at			AF056433					0.3905	0.5387	0.9027	1.0221	9.95	10.34	10.49	10.85	10.97	11.13	3

(*Continued*)

TABLE E3. (*Continued*)

212509_s_at	MXRA7	matrix-remodelling associated 7	BF968134	439921	Hs.250723	GO:0016020: membrane, GO:0016021: integral to membrane		0.184	0.5843	0.9556	1.2629	10.97	11.16	11.56	11.93	12.24	12.08	3
212483_at	NIPBL	Nipped-B homolog (Drosophila)	AB019494	25836	Hs.481927	GO:0007049: cell cycle		0.0775	0.3007	0.7078	1.052	6.75	6.83	7.05	7.46	7.8	7.85	3
212494_at	TENC1	tensin like C1 domain containing phosphatase (tensin 2)	AB028998	23371	Hs.6147, Hs.343334	GO:0007242: intracellular signaling cascade, GO:0030054: cell junction, GO:0004721: phosphoprotein phosphatase activity, GO:0008270: zinc ion binding, GO:0016787: hydrolase activity, GO:0019992: diacylglycerol binding, GO:0046872: metal ion binding		0.2657	0.4727	0.7934	1.401	6.85	7.11	7.32	7.64	8.25	8.2	3
212427_at	KIAA0368	KIAA0368	AB002366	23392	Hs.368255	GO:0030433: ER-associated protein catabolic process, GO:0000502: proteasome complex (sensu Eukaryota), GO:0005634: nucleus, GO:0005769: early endosome, GO:0005770: late endosome, GO:0005783: endoplasmic reticulum, GO:0005802: trans-Golgi network, GO:0005813: centrosome, GO:0005829: cytosol, GO:0016023: cytoplasmic membrane-bound vesicle, GO:0030134: ER to Golgi transport vesicle, GO:0005488: binding		−0.1201	0.1901	0.4801	1.1314	3.21	3.09	3.4	3.69	4.34	4.63	3
212468_at	SPAG9	sperm associated antigen 9	AK023512	9043	Hs.463439, Hs.593620	GO:0007283: spermatogenesis, GO:0005737: cytoplasm, GO:0016021: integral to membrane		−0.0432	0.3392	0.6328	1.1007	3.49	3.44	3.83	4.12	4.59	4.39	3
212346_s_at	MXD4	MAX dimerization protein 4	AK026392	10608	Hs.655020	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006355: regulation of transcription, DNA-dependent, GO:0008285: negative regulation of cell proliferation, GO:0045449: regulation of transcription, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003714: transcription corepressor activity, GO:0005515: protein binding, GO:0030528: transcription regulator activity		0.578	0.7921	0.9468	1.2308	4.64	5.22	5.43	5.59	5.87	5.34	3
212372_at	MYH10	myosin, heavy chain 10, non-muscle	AK026977	4628	Hs.16355	GO:0008150: biological_process, GO:0008360: regulation of cell shape, GO:0001725: stress fiber, GO:0005737: cytoplasm, GO:0005938: cell cortex, GO:0016459: myosin complex, GO:0016459: myosin complex, GO:0030496: midbody, GO:0032154: cleavage furrow, GO:0000166: nucleotide binding, GO:0003774: motor activity, GO:0003779: actin binding, GO:0005515: protein binding, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0051015: actin filament binding	04530: Tight junction, 04810: Regulation of actin cytoskeleton	0.2782	0.4379	0.9304	1.0674	8.54	8.82	8.98	9.47	9.61	9.41	3

(*Continued*)

TABLE E3. (*Continued*)

212254_s_at	DST	dystonin	AI798790	667	Hs.631992, Hs.669931	GO:0007010: cytoskeleton organization and biogenesis, GO:0007050: cell cycle arrest, GO:0007155: cell adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0045104: intermediate filament cytoskeleton organization and biogenesis, GO:0045104: intermediate filament cytoskeleton organization and biogenesis, GO:0045104: intermediate filament cytoskeleton organization and biogenesis, GO:0005604: basement membrane, GO:0005615: extracellular space, GO:0005737: cytoplasm, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005911: intercellular junction, GO:0016023: cytoplasmic membrane-bound vesicle, GO:0030056: hemidesmosome, GO:0003779: actin binding, GO:0005178: integrin binding, GO:0005200: structural constituent of cytoskeleton, GO:0005200: structural constituent of cytoskeleton, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005515: protein binding, GO:0008022: protein C-terminus binding, GO:0051015: actin filament binding		0.3076	0.4812	0.9424	1.061	9.19	9.5	9.68	10.14	10.26	10.31	3
212328_at	LIMCH1	LIM and calponin homology domains 1	AB029025	22998	Hs.335163	GO:0031032: actomyosin structure organization and biogenesis, GO:0003779: actin binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.2368	0.6956	0.9605	1.129	8.75	8.99	9.44	9.71	9.88	9.81	3
212226_s_at	PPAP2B	phosphatidic acid phosphatase type 2B	AA628586	8613	Hs.405156, Hs.638793, Hs.662450	GO:0001568: blood vessel development, GO:0006629: lipid metabolic process, GO:0006644: phospholipid metabolic process, GO:0008354: germ cell migration, GO:0010003: gastrulation (sensu Mammalia), GO:0030111: regulation of Wnt receptor signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004721: phosphoprotein phosphatase activity, GO:0008195: phosphatidate phosphatase activity, GO:0016787: hydrolase activity, GO:0042577: lipid phosphatase activity	00561: Glycerolipid metabolism, 00564: Glycerophospholipid metabolism, 00565: Ether lipid metabolism, 00600: Sphingolipid metabolism	−0.1302	0.4427	0.7808	1.1608	11.15	11.02	11.59	11.93	12.31	12.23	3

(*Continued*)

TABLE E3. (*Continued*)

212240_s_at	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	AI679268	5295	Hs.132225, Hs.604502	GO:0007242: intracellular signaling cascade, GO:0008286: insulin receptor signaling pathway, GO:0046854: phosphoinositide phosphorylation, GO:0048009: insulin-like growth factor receptor signaling pathway, GO:0005622: intracellular, GO:0035030: phosphoinositide 3-kinase complex, class IA, GO:0005158: insulin receptor binding, GO:0005159: insulin-like growth factor receptor binding, GO:0005545: phosphatidylinositol binding, GO:0019903: protein phosphatase binding, GO:0035014: phosphoinositide 3-kinase regulator activity, GO:0043125: ErbB-3 class receptor binding, GO:0043559: insulin binding, GO:0043560: insulin receptor substrate binding	04012: ErbB signaling pathway, 04070: Phosphatidylinositol signaling system, 04150: mTOR signaling pathway, 04210: Apoptosis, 04370: VEGF signaling pathway, 04510: Focal adhesion, 04620: Toll-like receptor signaling pathway, 04630: Jak-STAT signaling pathway, 04650: Natural killer cell mediated cytotoxicity, 04660: T cell receptor signaling pathway, 04662: B cell receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 04670: Leukocyte transendothelial migration, 04810: Regulation of actin cytoskeleton, 04910: Insulin signaling pathway, 04930: Type II diabetes mellitus, 05210: Colorectal cancer, 05211: Renal cell carcinoma, 05212: Pancreatic cancer, 05213: Endometrial cancer, 05214: Glioma, 05215: Prostate cancer, 05218: Melanoma, 05220: Chronic myeloid leukemia, 05222: Small cell lung cancer, 05223: Non-small cell lung cancer	0.0825	0.2018	0.7504	1.0771	6.65	6.73	6.85	7.4	7.72	7.6	3
212104_s_at	RBM9	RNA binding motif protein 9	N95026	23543	Hs.282998	GO:0016070: RNA metabolic process, GO:0016481: negative regulation of transcription, GO:0030520: estrogen receptor signaling pathway, GO:0042127: regulation of cell proliferation, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003714: transcription corepressor activity, GO:0003723: RNA binding, GO:0008134: transcription factor binding		−0.1049	0.4231	0.4018	1.3455	7.24	7.14	7.66	7.64	8.59	8.01	3
212151_at	PBX1	pre-B-cell leukemia homeobox 1	BF967998	5087	Hs.654412	GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0006700: C21-steroid hormone biosynthetic process, GO:0007548: sex differentiation, GO:0009790: embryonic development, GO:0030154: cell differentiation, GO:0030902: hindbrain development, GO:0045898: regulation of transcriptional preinitiation complex assembly, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0043565: sequence-specific DNA binding		0.3078	0.8094	0.9515	1.0678	6.9	7.21	7.71	7.85	7.97	7.9	3

(*Continued*)

TABLE E3. (*Continued*)

212080_at	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	AV714029	4297	Hs.258855, Hs.664477	GO:0006306: DNA methylation, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0006461: protein complex assembly, GO:0006468: protein amino acid phosphorylation, GO:0009952: anterior/ posterior pattern formation, GO:0035162: embryonic hemopoiesis, GO:0051569: regulation of histone H3-K4 methylation, GO:0044428: nuclear part, GO:0003677: DNA binding, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0004672: protein kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008270: zinc ion binding, GO:0042803: protein homodimerization activity, GO:0046872: metal ion binding		0.2922	0.3657	0.7601	1.2147	7.26	7.56	7.63	8.02	8.48	8.43	3
212097_at	CAV1	caveolin 1, caveolae protein, 22kDa	AU147399	857	Hs.74034	GO:0000188: inactivation of MAPK activity, GO:0001937: negative regulation of endothelial cell proliferation, GO:0006641: triacylglycerol metabolic process, GO:0009968: negative regulation of signal transduction, GO:0019217: regulation of fatty acid metabolic process, GO:0019915: sequestering of lipid, GO:0030301: cholesterol transport, GO:0042632: cholesterol homeostasis, GO:0045019: negative regulation of nitric oxide biosynthetic process, GO:0045907: positive regulation of vasoconstriction, GO:0045908: negative regulation of vasodilation, GO:0051260: protein homooligomerization, GO:0000139: Golgi membrane, GO:0000299: integral to membrane of membrane fraction, GO:0005783: endoplasmic reticulum, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016599: caveolar membrane, GO:0016599: caveolar membrane, GO:0045121: lipid raft, GO:0048471: perinuclear region of cytoplasm, GO:0005198: structural molecule activity, GO:0005515: protein binding, GO:0015485: cholesterol binding	04510: Focal adhesion	0.182	0.4723	0.8146	1.0324	12.05	12.23	12.52	12.86	13.08	13.05	3
211998_at	H3F3B	H3 histone, family 3B (H3.3B)	Z48950	3021	Hs.180877	GO:0006334: nucleosome assembly, GO:0007001: chromosome organization and biogenesis (sensu Eukaryota), GO:0000786: nucleosome, GO:0005634: nucleus, GO:0005694: chromosome, GO:0003677: DNA binding		0.0363	0.5021	0.5769	1.4064	9.12	9.15	9.62	9.69	10.52	10.42	3
212071_s_at	SPTBN1	spectrin, beta, non-erythrocytic 1	BE968833	6711	Hs.503178, Hs.659362	GO:0051016: barbed-end actin filament capping, GO:0005730: nucleolus, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0008091: spectrin, GO:0016020: membrane, GO:0003779: actin binding, GO:0005200: structural constituent of cytoskeleton, GO:0005516: calmodulin binding		0.2548	0.4672	0.8455	1.0712	11.49	11.75	11.96	12.34	12.56	12.51	3

(*Continued*)

TABLE E3. (*Continued*)

211841 _s_at	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	U94510	8718	Hs.462529	GO:0007166: cell surface receptor linked signal transduction, GO:0008624: induction of apoptosis by extracellular signals, GO:0042981: regulation of apoptosis, GO:0005829: cytosol, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0004872: receptor activity, GO:0005031: tumor necrosis factor receptor activity, GO:0005515: protein binding	04060: Cytokine-cytokine receptor interaction	−0.0792	0.1302	0.4953	1.1535	4.72	4.64	4.85	5.21	5.87	6.17	3
211959 _at	IGFBP5	insulin-like growth factor binding protein 5	AW007532	3488	Hs.635441	GO:0001558: regulation of cell growth, GO:0007165: signal transduction, GO:0005576: extracellular region, GO:0005783: endoplasmic reticulum, GO:0005520: insulin-like growth factor binding		0.2811	0.3414	0.9859	1.0546	11.75	12.03	12.09	12.73	12.8	12.6	3
211538 _s_at	HSPA2	heat shock 70kDa protein 2	U56725	3306	Hs.432648	GO:0006457: protein folding, GO:0006986: response to unfolded protein, GO:0007140: male meiosis, GO:0007286: spermatid development, GO:0005739: mitochondrion, GO:0009986: cell surface, GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0051082: unfolded protein binding		0.0162	0.5495	0.7385	1.0619	9.42	9.44	9.97	10.16	10.48	10.76	3
211564 _s_at	PDLIM4	PDZ and LIM domain 4	BC003096	8572	Hs.424312	GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.4235	0.3663	0.6047	1.4155	6.02	5.59	6.38	6.62	7.43	7.72	3
211458 _s_at	GABARAPL3	GABA(A) receptors associated protein like 3	AF180519	23766	Hs.592014	GO:0005874: microtubule		0.4316	0.5465	0.832	1.2174	9.05	9.48	9.59	9.88	10.27	10.25	3
211535 _s_at	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	M60485	2260	Hs.264887	GO:0000165: MAPKKK cascade, GO:0001501: skeletal development, GO:0006468: protein amino acid phosphorylation, GO:0008543: fibroblast growth factor receptor signaling pathway, GO:0016049: cell growth, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004713: protein-tyrosine kinase activity, GO:0004872: receptor activity, GO:0005007: fibroblast growth factor receptor activity, GO:0005007: fibroblast growth factor receptor activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008201: heparin binding, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04520: Adherens junction, 04810: Regulation of actin cytoskeleton, 05215: Prostate cancer, 05218: Melanoma	0.0976	0.484	0.8413	1.2559	9.58	9.68	10.06	10.42	10.84	10.6	3
210987 _x_at	TPM1	tropomyosin 1 (alpha)	M19267	7168	Hs.133892	GO:0006928: cell motility, GO:0006937: regulation of muscle contraction, GO:0008016: regulation of heart contraction, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005862: muscle thin filament tropomyosin, GO:0003779: actin binding, GO:0005200: structural constituent of cytoskeleton, GO:0008307: structural constituent of muscle		0.2464	0.399	0.9004	1.1298	10.16	10.41	10.56	11.06	11.29	11.21	3
211026 _s_at	MGLL	monoglyceride lipase	BC006230	11343	Hs.277035	GO:0006629: lipid metabolic process, GO:0006725: aromatic compound metabolic process, GO:0006954: inflammatory response, GO:0004622: lysophospholipase activity, GO:0016787: hydrolase activity, GO:0047372: acylglycerol lipase activity	00561: Glycerolipid metabolism	0.3274	0.5716	0.4729	1.041	9.53	9.85	10.1	10	10.57	10.12	3
210778 _s_at	MXD4	MAX dimerization protein 4	BC002713	10608	Hs.655020	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0006355: regulation of transcription, DNA-dependent, GO:0008285: negative regulation of cell proliferation, GO:0045449: regulation of transcription, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003714: transcription corepressor activity, GO:0005515: protein binding, GO:0030528: transcription regulator activity		−0.0811	0.1144	0.5754	1.3102	2.57	2.48	2.68	3.14	3.88	2.84	3

(*Continued*)

TABLE E3. (*Continued*)

210946_at	PPAP2A	phosphatidic acid phosphatase type 2A	AF014403	8611	Hs.435122	GO:0007205: protein kinase C activation, GO:0008285: negative regulation of cell proliferation, GO:0008354: germ cell migration, GO:0019216: regulation of lipid metabolic process, GO:0030521: androgen receptor signaling pathway, GO:0046839: phospholipid dephosphorylation, GO:0005624: membrane fraction, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0008195: phosphatidate phosphatase activity, GO:0008195: phosphatidate phosphatase activity, GO:0016787: hydrolase activity	00561: Glycerolipid metabolism, 00564: Glycerophospholipid metabolism, 00565: Ether lipid metabolism, 00600: Sphingolipid metabolism	0.2544	0.5444	0.8862	1.0198	10.11	10.36	10.65	11	11.13	10.96	3
210511_s_at	INHBA	inhibin, beta A	M13436	3624	Hs.583348	GO:0000082: G1/S transition of mitotic cell cycle, GO:0001501: skeletal development, GO:0001541: ovarian follicle development, GO:0006917: induction of apoptosis, GO:0006952: defense response, GO:0007050: cell cycle arrest, GO:0007166: cell surface receptor linked signal transduction, GO:0007267: cell-cell signaling, GO:0007399: nervous system development, GO:0009605: response to external stimulus, GO:0030154: cell differentiation, GO:0030218: erythrocyte differentiation, GO:0030308: negative regulation of cell growth, GO:0032925: regulation of activin receptor signaling pathway, GO:0040007: growth, GO:0042326: negative regulation of phosphorylation, GO:0042541: hemoglobin biosynthetic process, GO:0045077: negative regulation of interferon-gamma biosynthetic process, GO:0045578: negative regulation of B cell differentiation, GO:0045648: positive regulation of erythrocyte differentiation, GO:0045650: negative regulation of macrophage differentiation, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0046881: positive regulation of follicle-stimulating hormone secretion, GO:0046882: negative regulation of follicle-stimulating hormone secretion, GO:0005576: extracellular region, GO:0043509: activin A complex, GO:0043512: inhibin A complex, GO:0005125: cytokine activity, GO:0005160: transforming growth factor beta receptor binding, GO:0005179: hormone activity, GO:0008083: growth factor activity, GO:0017106: activin inhibitor activity, GO:0042802: identical protein binding, GO:0048184: follistatin binding	04060: Cytokine-cytokine receptor interaction, 04350: TGF-beta signaling pathway	0.0946	0.2264	0.4465	1.1334	3.5	3.6	3.73	3.95	4.64	4.22	3
210762_s_at	DLC1	deleted in liver cancer 1	AF026219	10395	Hs.134296	GO:0007010: cytoskeleton organization and biogenesis, GO:0007165: signal transduction, GO:0007165: signal transduction, GO:0030155: regulation of cell adhesion, GO:0030308: negative regulation of cell growth, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005096: GTPase activator activity, GO:0005100: Rho GTPase activator activity, GO:0005515: protein binding		−0.2153	0.4607	0.825	1.5201	7.57	7.35	8.03	8.39	9.09	8.9	3
210078_s_at	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	L39833	7881	Hs.654519, Hs.661750	GO:0006811: ion transport, GO:0006813: potassium ion transport, GO:0006813: potassium ion transport, GO:0005737: cytoplasm, GO:0016021: integral to membrane, GO:0005244: voltage-gated ion channel activity, GO:0005249: voltage-gated potassium channel activity, GO:0015459: potassium channel regulator activity, GO:0016491: oxidoreductase activity, GO:0030955: potassium ion binding		0.0205	0.6158	0.9688	1.8186	6.42	6.44	7.04	7.39	8.24	7.96	3

(*Continued*)

TABLE E3. (*Continued*)

210139_s_at	PMP22	peripheral myelin protein 22	L03203	5376	Hs.372031	GO:0007268: synaptic transmission, GO:0007422: peripheral nervous system development, GO:0007605: sensory perception of sound, GO:0007638: mechanosensory behavior, GO:0008285: negative regulation of cell proliferation, GO:0005887: integral to plasma membrane, GO:0016020: membrane		0.2541	0.4466	0.8598	1.0134	11.55	11.8	12	12.41	12.56	12.6	3
210051_at	RAPGEF3	Rap guanine nucleotide exchange factor (GEF) 3	U78168	10411	Hs.8578	GO:0006468: protein amino acid phosphorylation, GO:0008283: cell proliferation, GO:0051056: regulation of small GTPase mediated signal transduction, GO:0005622: intracellular, GO:0005624: membrane fraction, GO:0005952: cAMP-dependent protein kinase complex, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0008603: cAMP-dependent protein kinase regulator activity, GO:0030552: cAMP binding	04670: Leukocyte transendothelial migration, 04720: Long-term potentiation	0.0526	0.1553	0.3473	1.6046	2.64	2.69	2.79	2.98	4.24	3.38	3
210069_at	CPT1B	carnitine palmitoyltransferase 1B (muscle)	U62733	1375	Hs.439777, Hs.654827	GO:0006629: lipid metabolic process, GO:0006631: fatty acid metabolic process, GO:0006635: fatty acid beta-oxidation, GO:0006810: transport, GO:0005739: mitochondrion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019867: outer membrane, GO:0004095: carnitine O-palmitoyltransferase activity, GO:0008415: acyltransferase activity, GO:0016740: transferase activity	00071: Fatty acid metabolism, 03320: PPAR signaling pathway, 04920: Adipocytokine signaling pathway	0.2491	0.526	0.7522	1.3102	3.33	3.57	3.85	4.08	4.64	3.83	3
209866_s_at	LPHN3	latrophilin 3	AF307080	23284	Hs.28391, Hs.694758	GO:0007165: signal transduction, GO:0007218: neuropeptide signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0005529: sugar binding, GO:0016524: latrotoxin receptor activity		−0.0706	0.2084	0.4039	1.1819	2.51	2.44	2.72	2.92	3.7	3.37	3
210002_at	GATA6	GATA binding protein 6	D87811	2627	Hs.514746	GO:0001889: liver development, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007517: muscle development, GO:0045941: positive regulation of transcription, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0005634: nucleus, GO:0003682: chromatin binding, GO:0003705: RNA polymerase II transcription factor activity, enhancer binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016563: transcription activator activity, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding		−0.1046	0.2388	0.508	1.2285	3.18	3.07	3.42	3.68	4.4	4.03	3
209782_s_at	DBP	D site of albumin promoter (albumin D-box) binding protein	U79283	1628	Hs.414480, Hs.528006	GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0048511: rhythmic process, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity		0.3985	0.8379	0.9411	1.2689	6.22	6.61	7.05	7.16	7.48	7.31	3

(*Continued*)

TABLE E3. (*Continued*)

209842_at	SOX10	SRY (sex determining region Y)-box 10	AI367319	6663	Hs.376984	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007605: sensory perception of sound, GO:0009653: anatomical structure morphogenesis, GO:0030154: cell differentiation, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0048469: cell maturation, GO:0005737: cytoplasm, GO:0003677: DNA binding, GO:0003682: chromatin binding, GO:0003705: RNA polymerase II transcription factor activity, enhancer binding, GO:0003713: transcription coactivator activity, GO:0005515: protein binding		0.2114	0.3635	0.5319	1.1773	5.04	5.25	5.41	5.57	6.22	6.51	3
209621_s_at	PDLIM3	PDZ and LIM domain 3	AF002280	27295	Hs.85862	GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		−0.3267	0.5867	0.9053	1.143	4.1	3.77	4.69	5.01	5.24	5.52	3
209663_s_at	ITGA7	integrin, alpha 7	AF072132	3679	Hs.524484, Hs.639559	GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0007517: muscle development, GO:0008360: regulation of cell shape, GO:0008305: integrin complex, GO:0016020: membrane, GO:0004872: receptor activity, GO:0005509: calcium ion binding, GO:0005515: protein binding	04510: Focal adhesion, 04512: ECM-receptor interaction, 04810: Regulation of actin cytoskeleton	−0.2347	0.1173	0.674	1.1924	5.76	5.52	5.87	6.43	6.95	6.76	3
209604_s_at	GATA3	GATA binding protein 3	AI796169	2625	Hs.524134	GO:0001709: cell fate determination, GO:0006350: transcription, GO:0006366: transcription from RNA polymerase II promoter, GO:0006952: defense response, GO:0007605: sensory perception of sound, GO:0009653: anatomical structure morphogenesis, GO:0042035: regulation of cytokine biosynthetic process, GO:0042421: norepinephrine biosynthetic process, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0048485: sympathetic nervous system development, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016563: transcription activator activity, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding		0.0779	0.5313	0.5952	1.076	11.38	11.46	11.91	11.97	12.46	12.79	3
209616_s_at	CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	S73751	1066	Hs.558865	GO:0008152: metabolic process, GO:0009636: response to toxin, GO:0005615: extracellular space, GO:0005783: endoplasmic reticulum, GO:0004091: carboxylesterase activity, GO:0004091: carboxylesterase activity, GO:0016787: hydrolase activity	00960: Alkaloid biosynthesis II	0.3557	0.8677	0.7746	1.8248	5.71	6.07	6.58	6.49	7.54	7.57	3

(*Continued*)

TABLE E3. (*Continued*)

209602_s_at	GATA3	GATA binding protein 3	AI796169	2625	Hs.524134	GO:0001709: cell fate determination, GO:0006350: transcription, GO:0006366: transcription from RNA polymerase II promoter, GO:0006952: defense response, GO:0007605: sensory perception of sound, GO:0009653: anatomical structure morphogenesis, GO:0042035: regulation of cytokine biosynthetic process, GO:0042421: norepinephrine biosynthetic process, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0048485: sympathetic nervous system development, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016563: transcription activator activity, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding		0.0811	0.6806	0.744	1.164	8.43	8.51	9.11	9.18	9.6	10.31	3
209603_at	GATA3	GATA binding protein 3	AI796169	2625	Hs.524134	GO:0001709: cell fate determination, GO:0006350: transcription, GO:0006366: transcription from RNA polymerase II promoter, GO:0006952: defense response, GO:0007605: sensory perception of sound, GO:0009653: anatomical structure morphogenesis, GO:0042035: regulation of cytokine biosynthetic process, GO:0042421: norepinephrine biosynthetic process, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0048485: sympathetic nervous system development, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016563: transcription activator activity, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding		0.4453	0.8571	0.939	1.4589	6.54	6.98	7.39	7.47	7.99	8.38	3
209561_at	THBS3	thrombospondin 3	L38969	7059	Hs.169875, Hs.282997	GO:0006928: cell motility, GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005198: structural molecule activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0008201: heparin binding	01430: Cell Communication, 04350: TGF-beta signaling pathway, 04510: Focal adhesion, 04512: ECM-receptor interaction	0.1266	0.4367	0.7986	1.0175	7.4	7.52	7.83	8.2	8.42	8.16	3
209590_at	BMP7	bone morphogenetic protein 7 (osteogenic protein 1)	AL157414	655	Hs.473163	GO:0001503: ossification, GO:0001707: mesoderm formation, GO:0001822: kidney development, GO:0001837: epithelial to mesenchymal transition, GO:0007389: pattern specification process, GO:0007411: axon guidance, GO:0007435: salivary gland morphogenesis, GO:0009887: organ morphogenesis, GO:0030509: BMP signaling pathway, GO:0040007: growth, GO:0042475: odontogenesis (sensu Vertebrata), GO:0045597: positive regulation of cell differentiation, GO:0045786: negative regulation of progression through cell cycle, GO:0045941: positive regulation of transcription, GO:0048468: cell development, GO:0048754: branching morphogenesis of a tube, GO:0051216: cartilage development, GO:0005615: extracellular space, GO:0005125: cytokine activity, GO:0005515: protein binding, GO:0008083: growth factor activity	04060: Cytokine-cytokine receptor interaction, 04340: Hedgehog signaling pathway, 04350: TGF-beta signaling pathway	−0.182	0.3753	0.4733	1.1447	7.21	7.03	7.58	7.68	8.35	8.18	3

(*Continued*)

TABLE E3. (*Continued*)

209534_x_at	AKAP13	A kinase (PRKA) anchor protein 13	BF222823	11214	Hs.459211, Hs.667658	GO:0007242: intracellular signaling cascade, GO:0035023: regulation of Rho protein signal transduction, GO:0005622: intracellular, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0004871: signal transducer activity, GO:0004872: receptor activity, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0008270: zinc ion binding, GO:0019992: diacylglycerol binding, GO:0046872: metal ion binding		0.1832	0.2211	0.4462	1.0752	7.88	8.06	8.1	8.32	8.95	8.5	3
209539_at	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	D25304	9459	Hs.522795	GO:0006915: apoptosis, GO:0007254: JNK cascade, GO:0035023: regulation of Rho protein signal transduction, GO:0005622: intracellular, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0005096: GTPase activator activity	04810: Regulation of actin cytoskeleton, 05212: Pancreatic cancer	0.5361	0.5826	0.8968	1.1405	8.35	8.89	8.93	9.25	9.49	9.23	3
209496_at	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	BC000069	5919	Hs.647064	GO:0001523: retinoid metabolic process, GO:0005575: cellular_component, GO:0003674: molecular_function		0.5397	0.6006	0.8176	1.1418	7.97	8.51	8.57	8.79	9.11	8.83	3
209522_s_at	CRAT	carnitine acetyltransferase	BC000723	1384	Hs.12068	GO:0006629: lipid metabolic process, GO:0006637: acyl-CoA metabolic process, GO:0006810: transport, GO:0015980: energy derivation by oxidation of organic compounds, GO:0005739: mitochondrion, GO:0005777: peroxisome, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0004092: carnitine O-acetyltransferase activity, GO:0008415: acyltransferase activity, GO:0016740: transferase activity	00252: Alanine and aspartate metabolism	0.1156	0.1169	0.8436	1.2579	8.93	9.05	9.05	9.77	10.19	10.51	3
209431_s_at	PATZ1	POZ (BTB) and AT hook containing zinc finger 1	AF254083	23598	Hs.517557	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0016564: transcription repressor activity, GO:0046872: metal ion binding		0.1941	0.2998	0.8968	1.1366	3.34	3.53	3.64	4.24	4.48	4.32	3
209487_at	RBPMS	RNA binding protein with multiple splicing	D84109	11030	Hs.334587	GO:0006396: RNA processing, GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005515: protein binding		0.3631	0.6158	0.735	1.442	7.26	7.62	7.88	8	8.7	8.42	3
209355_s_at	PPAP2B	phosphatidic acid phosphatase type 2B	AB000889	8613	Hs.405156, Hs.638793, Hs.662450	GO:0001568: blood vessel development, GO:0006629: lipid metabolic process, GO:0006644: phospholipid metabolic process, GO:0008354: germ cell migration, GO:0010003: gastrulation (sensu Mammalia), GO:0030111: regulation of Wnt receptor signaling pathway, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004721: phosphoprotein phosphatase activity, GO:0008195: phosphatidate phosphatase activity, GO:0016787: hydrolase activity, GO:0042577: lipid phosphatase activity	00561: Glycerolipid metabolism, 00564: Glycerophospholipid metabolism, 00565: Ether lipid metabolism, 00600: Sphingolipid metabolism	−0.1326	0.4813	0.854	1.164	10.32	10.19	10.8	11.18	11.49	11.51	3
209375_at	XPC	xeroderma pigmentosum, complementation group C	D21089	7508	Hs.475538	GO:0006289: nucleotide-excision repair, GO:0005634: nucleus, GO:0003684: damaged DNA binding, GO:0003697: single-stranded DNA binding, GO:0005515: protein binding		0.5774	0.6476	0.9949	1.1434	7.56	8.14	8.21	8.56	8.71	8.87	3
209285_s_at	C3orf63	chromosome 3 open reading frame 63	N38985	23272	Hs.116877			0.2521	0.3833	0.9217	1.0507	9.24	9.49	9.62	10.16	10.29	10.22	3

(*Continued*)

TABLE E3. (*Continued*)

209289_at	NFIB	nuclear factor I/B	AI700518	4781	Hs.370359	GO:0006260: DNA replication, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity		0.1063	0.4564	0.7722	1.1464	11.29	11.39	11.74	12.06	12.43	12.47	3
209264_s_at	TSPAN4	tetraspanin 4	AF054841	7106	Hs.654836	GO:0006461: protein complex assembly, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005515: protein binding		0.4677	0.4448	0.9234	1.0419	8.21	8.68	8.66	9.14	9.25	9.08	3
209283_at	CRYAB	crystallin, alpha B	AF007162	1410	Hs.408767	GO:0006457: protein folding, GO:0006916: anti-apoptosis, GO:0006936: muscle contraction, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007517: muscle development, GO:0007601: visual perception, GO:0032387: negative regulation of intracellular transport, GO:0005625: soluble fraction, GO:0005626: insoluble fraction, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0030018: Z disc, GO:0043292: contractile fiber, GO:0005212: structural constituent of eye lens, GO:0051082: unfolded protein binding		0.3154	0.4418	0.5686	1.4012	10	10.31	10.44	10.57	11.4	11.52	3
209185_s_at	IRS2	insulin receptor substrate 2	AF073310	8660	Hs.442344	GO:0006006: glucose metabolic process, GO:0007165: signal transduction, GO:0007420: brain development, GO:0008283: cell proliferation, GO:0008284: positive regulation of cell proliferation, GO:0008286: insulin receptor signaling pathway, GO:0004871: signal transducer activity, GO:0005158: insulin receptor binding, GO:0005515: protein binding, GO:0019901: protein kinase binding	04910: Insulin signaling pathway, 04920: Adipocytokine signaling pathway, 04930: Type II diabetes mellitus	0.5262	0.5952	0.7563	1.0224	8.63	9.16	9.23	9.39	9.65	10.03	3
209263_x_at	TSPAN4	tetraspanin 4	BC000389	7106	Hs.654836	GO:0006461: protein complex assembly, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005515: protein binding		0.3523	0.4041	0.7566	1.088	9	9.35	9.4	9.75	10.08	9.81	3
33850_at	MAP4	microtubule-associated protein 4	W28892	4134	Hs.517949	GO:0007026: negative regulation of microtubule depolymerization, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0005198: structural molecule activity		−0.0352	0.1418	0.4387	1.1535	8.06	8.03	8.21	8.5	9.22	8.81	3
35776_at	ITSN1	intersectin 1 (SH3 domain protein)	AF064243	6453	Hs.160324	GO:0007242: intracellular signaling cascade, GO:0035023: regulation of Rho protein signal transduction, GO:0048488: synaptic vesicle endocytosis, GO:0005622: intracellular, GO:0016020: membrane, GO:0019717: synaptosome, GO:0030054: cell junction, GO:0045202: synapse, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0005509: calcium ion binding, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.2216	0.3621	0.8626	1.1197	7.72	7.94	8.08	8.58	8.84	8.62	3
222043_at	CLU	clusterin	AI982754	1191	Hs.436657	GO:0006629: lipid metabolic process, GO:0006915: apoptosis, GO:0006958: complement activation, classical pathway, GO:0008219: cell death, GO:0045087: innate immune response, GO:0005615: extracellular space		0.7642	0.6077	0.7832	1.1653	8.61	9.37	9.22	9.39	9.77	9.53	3

(*Continued*)

TABLE E3. (*Continued*)

32259_at	EZH1	enhancer of zeste homolog 1 (Drosophila)	AB002386	2145	Hs.194669	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0009653: anatomical structure morphogenesis, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003682: chromatin binding, GO:0005515: protein binding		0.4796	0.6196	0.896	1.32	7.56	8.04	8.18	8.46	8.88	8.86	3
212706_at	RASA4	RAS p21 protein activator 4	AI738591	10156	Hs.654726, Hs.693633	GO:0007242: intracellular signaling cascade, GO:0051056: regulation of small GTPase mediated signal transduction, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0005096: GTPase activator activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.6636	0.8777	1.1599	1.0544	8.08	8.74	8.96	9.24	9.14	9.06	3
214298_x_at	6-Sep	septin 6	AL568374	23157	Hs.496666	GO:0000910: cytokinesis, GO:0007049: cell cycle, GO:0005575: cellular_component, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0005525: GTP binding		0.7447	0.6298	1.4926	1.1995	4.07	4.81	4.7	5.56	5.27	4.55	3
208868_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1	BF125756	23710	Hs.524250	GO:0005622: intracellular, GO:0005776: autophagic vacuole, GO:0005874: microtubule, GO:0005515: protein binding, GO:0005515: protein binding, GO:0048487: beta-tubulin binding, GO:0050811: GABA receptor binding	04140: Regulation of autophagy	0.8456	0.895	1.2706	1.2804	6.23	7.08	7.13	7.5	7.51	7.69	3
209596_at	MXRA5	matrix-remodelling associated 5	AF245505	25878	Hs.369422	GO:0005515: protein binding		0.4483	0.7323	1.3624	1.1954	10.55	11	11.29	11.92	11.75	11.07	3
202259_s_at	PFAAP5	phosphonoformate immuno-associated protein 5	NM_014887	10443	Hs.507680	GO:0008150: biological_process, GO:0005575: cellular_component, GO:0003674: molecular_function		0.6064	0.7296	1.0797	1.0084	7.6	8.21	8.33	8.68	8.61	9.23	3
202992_at	C7	complement component 7	NM_000587	730	Hs.78065	GO:0006957: complement activation, alternative pathway, GO:0006958: complement activation, classical pathway, GO:0019835: cytolysis, GO:0005579: membrane attack complex	04610: Complement and coagulation cascades	0.1075	0.767	1.3558	1.6436	6.97	7.07	7.73	8.32	8.61	9.06	3
209612_s_at	ADH1B	alcohol dehydrogenase IB (class I), beta polypeptide	M24317	125	Hs.4	GO:0006069: ethanol oxidation, GO:0005737: cytoplasm, GO:0004024: alcohol dehydrogenase activity, zinc-dependent, GO:0008270: zinc ion binding, GO:0009055: electron carrier activity, GO:0046872: metal ion binding	00010: Glycolysis / Gluconeogenesis, 00071: Fatty acid metabolism, 00120: Bile acid biosynthesis, 00350: Tyrosine metabolism, 00561: Glycerolipid metabolism, 00624: 1- and 2-Methylnaphthalene degradation, 00980: Metabolism of xenobiotics by cytochrome P450	1.2021	1.3966	1.9945	1.8771	8.4	9.61	9.8	10.4	10.28	11.14	3
209613_s_at	ADH1B	alcohol dehydrogenase IB (class I), beta polypeptide	M21692	125	Hs.4	GO:0006069: ethanol oxidation, GO:0005737: cytoplasm, GO:0004024: alcohol dehydrogenase activity, zinc-dependent, GO:0008270: zinc ion binding, GO:0009055: electron carrier activity, GO:0046872: metal ion binding	00010: Glycolysis / Gluconeogenesis, 00071: Fatty acid metabolism, 00120: Bile acid biosynthesis, 00350: Tyrosine metabolism, 00561: Glycerolipid metabolism, 00624: 1- and 2-Methylnaphthalene degradation, 00980: Metabolism of xenobiotics by cytochrome P450	1.3581	1.6723	2.2764	2.3296	8.71	10.07	10.39	10.99	11.04	11.66	3
203240_at	FCGBP	Fc fragment of IgG binding protein	NM_003890	8857	Hs.111732	GO:0007155: cell adhesion, GO:0007339: binding of sperm to zona pellucida, GO:0016020: membrane		1.2873	1.756	1.9933	2.1222	7.96	9.25	9.72	9.96	10.09	9.96	3

(*Continued*)

TABLE E3. (*Continued*)

205357_s_at	AGTR1	angiotensin II receptor, type 1	NM_000685	185	Hs.477887, Hs.654382	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007200: G-protein signaling, coupled to IP3 second messenger (phospholipase C activating), GO:0007204: elevation of cytosolic calcium ion concentration, GO:0007589: fluid secretion, GO:0008015: circulation, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016021: integral to membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004945: angiotensin type II receptor activity, GO:0004945: angiotensin type II receptor activity, GO:0004947: bradykinin receptor activity, GO:0016494: C-X-C chemokine receptor activity	04020: Calcium signaling pathway, 04080: Neuroactive ligand-receptor interaction, 04614: Renin-angiotensin system	1.2891	1.5526	2.4402	2.0428	6.58	7.87	8.14	9.02	8.63	9.27	3
202073_at	OPTN	optineurin	AV757675	10133	Hs.332706, Hs.695379	GO:0000042: protein targeting to Golgi, GO:0007030: Golgi organization and biogenesis, GO:0007165: signal transduction, GO:0008219: cell death, GO:0043001: Golgi to plasma membrane protein transport, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0008022: protein C-terminus binding		0.6182	0.769	0.993	1.0033	8.08	8.7	8.85	9.07	9.09	9.33	3
210113_s_at	NLRP1	NLR family, pyrin domain containing 1	AF310105	22861	Hs.104305, Hs.652273	GO:0006917: induction of apoptosis, GO:0006919: caspase activation, GO:0006952: defense response, GO:0042981: regulation of apoptosis, GO:0051402: neuron apoptosis, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008656: caspase activator activity, GO:0019899: enzyme binding		0.2217	0.322	0.684	1.048	6.8	7.03	7.13	7.49	7.85	7.76	3
210102_at	LOH11CR2A	loss of heterozygosity, 11, chromosomal region 2, gene A	BC001234	4013	Hs.152944	GO:0007049: cell cycle, GO:0045786: negative regulation of progression through cell cycle		0.619	0.7494	1.1141	0.9595	7.08	7.7	7.83	8.2	8.04	8.24	3
213258_at	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	BF511231	7035	Hs.516578	GO:0007596: blood coagulation, GO:0007596: blood coagulation, GO:0005576: extracellular region, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0030414: protease inhibitor activity	04610: Complement and coagulation cascades	0.6456	0.7078	1.299	0.9508	7.55	8.2	8.26	8.85	8.5	8.65	3
204639_at	ADA	adenosine deaminase	NM_000022	100	Hs.654536	GO:0006163: purine nucleotide metabolic process, GO:0006955: immune response, GO:0009168: purine ribonucleoside monophosphate biosynthetic process, GO:0005737: cytoplasm, GO:0004000: adenosine deaminase activity, GO:0016787: hydrolase activity	00230: Purine metabolism	0.5394	0.5661	1.0109	0.8186	6.47	7.01	7.04	7.48	7.29	6.91	3
205079_s_at	MPDZ	multiple PDZ domain protein	NM_003829	8777	Hs.169378	GO:0005923: tight junction, GO:0016020: membrane, GO:0019717: synaptosome, GO:0030054: cell junction, GO:0042995: cell projection, GO:0045202: synapse, GO:0005515: protein binding	04530: Tight junction	0.3171	0.7299	1.3538	0.9872	3.49	3.8	4.22	4.84	4.47	4.1	3
201009_s_at	TXNIP	thioredoxin interacting protein	NM_006472	10628	Hs.533977	GO:0030216: keratinocyte differentiation, GO:0005737: cytoplasm, GO:0005515: protein binding		0.5917	0.6622	1.0096	0.9938	10.67	11.26	11.33	11.68	11.66	11.8	3
201034_at	ADD3	adducin 3 (gamma)	BE545756	120	Hs.501012	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0016020: membrane, GO:0005200: structural constituent of cytoskeleton, GO:0005516: calmodulin binding, GO:0046872: metal ion binding		0.5778	0.5781	1.0365	0.8577	10.61	11.19	11.19	11.65	11.47	11.61	3
221511_x_at	CCPG1	cell cycle progression 1	AF212228	9236	Hs.612814			0.5651	0.9436	1.1534	1.1045	6.88	7.45	7.83	8.04	7.99	8.04	3

(*Continued*)

TABLE E3. (*Continued*)

221564_at	PRMT2	protein arginine methyltransferase 2	AL570294	3275	Hs.154163	GO:0006479: protein amino acid methylation, GO:0007165: signal transduction, GO:0005634: nucleus, GO:0004871: signal transducer activity, GO:0008168: methyltransferase activity, GO:0016740: transferase activity, GO:0042802: identical protein binding	00150: Androgen and estrogen metabolism, 00340: Histidine metabolism, 00350: Tyrosine metabolism, 00380: Tryptophan metabolism, 00440: Aminophosphonate metabolism, 00450: Selenoamino acid metabolism, 00626: Naphthalene and anthracene degradation	0.7354	0.941	1.2234	1.1328	7.25	7.98	8.19	8.47	8.38	8.59	3
217707_x_at	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	AI535683	6595	Hs.298990	GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0005654: nucleoplasm, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003713: transcription coactivator activity, GO:0004386: helicase activity, GO:0004386: helicase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016787: hydrolase activity	00500: Starch and sucrose metabolism, 00790: Folate biosynthesis	0.651	0.837	1.074	1.1304	9.1	9.75	9.94	10.17	10.23	10.32	3
219935_at	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5 (aggrecanase-2)	NM_007038	11096	Hs.58324	GO:0006508: proteolysis, GO:0005578: proteinaceous extracellular matrix, GO:0004222: metalloendopeptidase activity, GO:0005178: integrin binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		1.019	1.0742	1.6586	1.5876	7.03	8.05	8.11	8.69	8.62	8.46	3
213375_s_at	CG018	hypothetical gene CG018	N80918	90634	Hs.161220			0.9799	1.0534	1.4607	1.3203	7.76	8.74	8.82	9.23	9.08	9.4	3
217047_s_at	FAM13A1	family with sequence similarity 13, member A1	AK027138	10144	Hs.97270	GO:0007165: signal transduction, GO:0005622: intracellular		0.9075	1.01	1.5975	1.4612	6.97	7.88	7.98	8.57	8.43	9.08	3
218613_at	PSD3	pleckstrin and Sec7 domain containing 3	NM_018422	23362	Hs.434255	GO:0032012: regulation of ARF protein signal transduction, GO:0005622: intracellular, GO:0005086: ARF guanyl-nucleotide exchange factor activity		0.418	0.7823	1.1813	0.9276	6.66	7.08	7.45	7.85	7.59	7.72	3
222156_x_at	CCPG1	cell cycle progression 1	AK022459	9236	Hs.612814			0.3723	0.7072	1.0647	0.8604	5.69	6.06	6.39	6.75	6.55	6.79	3
213306_at	MPDZ	multiple PDZ domain protein	AA917899	8777	Hs.169378	GO:0005923: tight junction, GO:0016020: membrane, GO:0019717: synaptosome, GO:0030054: cell junction, GO:0042995: cell projection, GO:0045202: synapse, GO:0005515: protein binding	04530: Tight junction	0.5132	0.8631	1.341	0.9959	7.6	8.11	8.46	8.94	8.59	8.83	3
213429_at			AW025579					0.4464	0.7054	1.1876	0.8791	7.16	7.61	7.87	8.35	8.04	7.88	3
203603_s_at	ZEB2	zinc finger E-box binding homeobox 2	NM_014795	9839	Hs.34871	GO:0001755: neural crest cell migration, GO:0001756: somitogenesis, GO:0001843: neural tube closure, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007417: central nervous system development, GO:0016481: negative regulation of transcription, GO:0048598: embryonic morphogenesis, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0008270: zinc ion binding, GO:0019208: phosphatase regulator activity, GO:0043565: sequence-specific DNA binding, GO:0046332: SMAD binding, GO:0046872: metal ion binding		0.3773	0.8405	1.2525	1.0483	7.92	8.3	8.76	9.17	8.97	9.07	3
204796_at	EML1	echinoderm microtubule associated protein like 1	NM_004434	2009	Hs.12451	GO:0007601: visual perception, GO:0005737: cytoplasm, GO:0005874: microtubule, GO:0005875: microtubule associated complex		0.1324	0.7751	1.1353	1.0423	5.61	5.74	6.38	6.74	6.65	6.96	3
201801_s_at	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	NM_004955	2030	Hs.25450	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006810: transport, GO:0015858: nucleoside transport, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0005337: nucleoside transmembrane transporter activity, GO:0005515: protein binding		0.4335	1.057	1.4472	0.9941	6.06	6.5	7.12	7.51	7.06	7.66	3

(*Continued*)

TABLE E3. (*Continued*)

201117_s_at	CPE	carboxypeptidase E	NM_001873	1363	Hs.75360	GO:0006464: protein modification process, GO:0006508: proteolysis, GO:0007218: neuropeptide signaling pathway, GO:0008152: metabolic process, GO:0030070: insulin processing, GO:0005886: plasma membrane, GO:0004180: carboxypeptidase activity, GO:0004182: carboxypeptidase A activity, GO:0004183: carboxypeptidase E activity, GO:0008237: metallopeptidase activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	04940: Type I diabetes mellitus	0.3977	0.944	1.4979	1.3896	9.93	10.33	10.88	11.43	11.32	11.5	3
219317_at	POLI	polymerase (DNA directed) iota	NM_007195	11201	Hs.438533	GO:0006260: DNA replication, GO:0006281: DNA repair, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0000287: magnesium ion binding, GO:0003677: DNA binding, GO:0016000: iota DNA polymerase activity, GO:0016740: transferase activity	03030: DNA polymerase	0.8321	1.1383	1.4393	1.4188	5.54	6.37	6.68	6.98	6.96	7.2	3
219908_at	DKK2	dickkopf homolog 2 (Xenopus laevis)	NM_014421	27123	Hs.211869	GO:0007275: multicellular organismal development, GO:0016055: Wnt receptor signaling pathway, GO:0030178: negative regulation of Wnt receptor signaling pathway, GO:0005576: extracellular region, GO:0005615: extracellular space	04310: Wnt signaling pathway	0.5366	1.174	2.1315	1.6186	6.59	7.12	7.76	8.72	8.21	8.02	3
213068_at	DPT	dermatopontin	AI146848	1805	Hs.80552	GO:0007155: cell adhesion, GO:0005578: proteinaceous extracellular matrix, GO:0005515: protein binding		0.7125	1.3729	2.0612	1.6099	8.16	8.88	9.54	10.23	9.77	9.38	3
213880_at	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5	AL524520	8549	Hs.658889	GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0005515: protein binding, GO:0016500: protein-hormone receptor activity		0.5429	1.5271	2.0956	1.6759	5.19	5.73	6.71	7.28	6.86	8.45	3
207977_s_at	DPT	dermatopontin	NM_001937	1805	Hs.80552	GO:0007155: cell adhesion, GO:0005578: proteinaceous extracellular matrix, GO:0005515: protein binding		0.6546	1.1782	1.6479	1.2297	8.02	8.67	9.2	9.67	9.25	8.99	3
209199_s_at	MEF2C	myocyte enhancer factor 2C	L08895	4208	Hs.654474	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0007399: nervous system development, GO:0007517: muscle development, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0003713: transcription coactivator activity, GO:0043565: sequence-specific DNA binding	04010: MAPK signaling pathway	0.5623	1.1552	1.6304	1.1989	6.3	6.86	7.45	7.93	7.5	7.84	3
204017_at	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	NM_006855	11015	Hs.693805	GO:0006621: protein retention in ER, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0015031: protein transport, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004872: receptor activity, GO:0046923: ER retention sequence binding		0.2919	1.0384	1.5985	1.3191	7.91	8.2	8.95	9.51	9.23	8.73	3

(*Continued*)

TABLE E3. (*Continued*)

205407_at	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	NM_021111	8434	Hs.388918	GO:0007049: cell cycle, GO:0045786: negative regulation of progression through cell cycle, GO:0000300: peripheral to membrane of membrane fraction, GO:0016020: membrane, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding, GO:0008191: metalloendopeptidase inhibitor activity, GO:0048503: GPI anchor binding		0.4963	1.0493	1.6029	1.2155	8.18	8.67	9.23	9.78	9.39	9.86	3
212486_s_at	FYN	FYN oncogene related to SRC, FGR, YES	N20923	2534	Hs.390567	GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0007242: intracellular signaling cascade, GO:0007243: protein kinase cascade, GO:0007275: multicellular organismal development, GO:0007612: learning, GO:0007631: feeding behavior, GO:0050852: T cell receptor signaling pathway, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0004713: protein-tyrosine kinase activity, GO:0004713: protein-tyrosine kinase activity, GO:0005524: ATP binding, GO:0016740: transferase activity, GO:0030145: manganese ion binding, GO:0042802: identical protein binding, GO:0046872: metal ion binding	04360: Axon guidance, 04510: Focal adhesion, 04520: Adherens junction, 04650: Natural killer cell mediated cytotoxicity, 04660: T cell receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 05130: Pathogenic Escherichia coli infection - EHEC, 05131: Pathogenic Escherichia coli infection - EPEC	0.7707	1.0699	1.9065	1.4288	4.46	5.23	5.53	6.37	5.89	6.06	3
220783_at	MMP27	matrix metallopeptidase 27	NM_022122	64066	Hs.534479	GO:0000270: peptidoglycan metabolic process, GO:0006508: proteolysis, GO:0030574: collagen catabolic process, GO:0005578: proteinaceous extracellular matrix, GO:0004222: metalloendopeptidase activity, GO:0005509: calcium ion binding, GO:0008270: zinc ion binding		0.9184	1.4279	2.1202	1.6493	3.26	4.18	4.69	5.38	4.91	4.76	3
202321_at	GGPS1	geranylgeranyl diphosphate synthase 1	AW299507	9453	Hs.647791	GO:0008299: isoprenoid biosynthetic process, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0004161: dimethylallyltranstransferase activity, GO:0004311: farnesyltranstransferase activity, GO:0004337: geranyltranstransferase activity, GO:0016740: transferase activity	00100: Biosynthesis of steroids, 00900: Terpenoid biosynthesis	0.4411	0.8134	1.0374	0.9166	5.95	6.39	6.77	6.99	6.87	7.18	3
213125_at	OLFML2B	olfactomedin-like 2B	AW007573	25903	Hs.507515	GO:0016020: membrane, GO:0016524: latrotoxin receptor activity		0.4255	0.3509	1.1507	0.8978	7.5	7.92	7.85	8.65	8.39	7.93	3
212148_at	PBX1	pre-B-cell leukemia homeobox 1	AL049381	5087	Hs.654412	GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0006700: C21-steroid hormone biosynthetic process, GO:0007548: sex differentiation, GO:0009790: embryonic development, GO:0030154: cell differentiation, GO:0030902: hindbrain development, GO:0045898: regulation of transcriptional preinitiation complex assembly, GO:0005634: nucleus, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0043565: sequence-specific DNA binding		0.5294	0.8819	1.1185	1.054	8.45	8.98	9.33	9.57	9.51	9.42	3
212310_at	MIA3	melanoma inhibitory activity family, member 3	D87742	375056	Hs.118474	GO:0016020: membrane, GO:0016021: integral to membrane		0.4428	0.6931	1.0915	1.2526	3.21	3.66	3.91	4.3	4.46	4.78	3
205158_at	RNASE4	ribonuclease, RNase A family, 4	NM_002937	6038	Hs.283749	GO:0006379: mRNA cleavage, GO:0005575: cellular_component, GO:0003676: nucleic acid binding, GO:0004519: endonuclease activity, GO:0004522: pancreatic ribonuclease activity, GO:0016787: hydrolase activity		0.8495	1.477	1.8882	1.9065	7.39	8.23	8.86	9.27	9.29	9.8	3
212730_at	DMN	desmuslin	AK026420	23336	Hs.207106	GO:0005737: cytoplasm, GO:0005882: intermediate filament, GO:0005515: protein binding, GO:0008307: structural constituent of muscle		0.2344	1.1369	1.6086	2.0326	8.04	8.28	9.18	9.65	10.08	10.08	3

(*Continued*)

TABLE E3. (*Continued*)

221024_s_at	SLC2A10	solute carrier family 2 (facilitated glucose transporter), member 10	NM_030777	81031	Hs.305971	GO:0008643: carbohydrate transport, GO:0015758: glucose transport, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005215: transporter activity, GO:0005351: sugar:hydrogen ion symporter activity		0.5604	0.893	1.7415	1.2325	5.12	5.68	6.01	6.86	6.35	6.18	3
221833_at	LONP2	lon peptidase 2, peroxisomal	AV700132	83752	Hs.694785	GO:0006508: proteolysis, GO:0006510: ATP-dependent proteolysis, GO:0007031: peroxisome organization and biogenesis, GO:0005777: peroxisome, GO:0000166: nucleotide binding, GO:0004176: ATP-dependent peptidase activity, GO:0004252: serine-type endopeptidase activity, GO:0005524: ATP binding, GO:0017111: nucleoside-triphosphatase activity		0.3226	0.7581	1.2891	1.7315	6.44	6.76	7.2	7.73	8.17	8.06	3
219243_at	GIMAP4	GTPase, IMAP family member 4	NM_018326	55303	Hs.647101	GO:0000166: nucleotide binding, GO:0005525: GTP binding		0.8322	0.7175	1.2789	1.2418	5.89	6.72	6.6	7.17	7.13	6.95	3
219689_at	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	NM_020163	56920	Hs.59729	GO:0007275: multicellular organismal development, GO:0016020: membrane, GO:0004872: receptor activity	04360: Axon guidance	0.5246	0.9423	1.4136	2.478	6.47	7	7.41	7.89	8.95	8.67	3
203501_at	PGCP	plasma glutamate carboxypeptidase	NM_006102	10404	Hs.156178	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0006518: peptide metabolic process, GO:0005615: extracellular space, GO:0005737: cytoplasm, GO:0004180: carboxypeptidase activity, GO:0008233: peptidase activity, GO:0043275: glutamate carboxypeptidase II activity		0.5217	0.8028	1.2184	1.0349	8.4	8.92	9.2	9.62	9.43	9.62	3
203801_at	MRPS14	mitochondrial ribosomal protein S14	BG254653	63931	Hs.508524	GO:0006412: translation, GO:0005622: intracellular, GO:0005739: mitochondrion, GO:0005761: mitochondrial ribosome, GO:0005840: ribosome, GO:0003735: structural constituent of ribosome		0.2969	0.6408	1.0707	1.2183	6.24	6.53	6.88	7.31	7.45	7.31	3
206101_at	ECM2	extracellular matrix protein 2, female organ and adipocyte specific	NM_001393	1842	Hs.117060	GO:0007160: cell-matrix adhesion, GO:0005578: proteinaceous extracellular matrix, GO:0005178: integrin binding, GO:0005515: protein binding		1.0388	1.4507	2.0811	1.9352	8.16	9.2	9.61	10.24	10.1	10.02	3
204755_x_at	HLF	hepatic leukemia factor	NM_002126	3131	Hs.196952	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0007275: multicellular organismal development, GO:0048511: rhythmic process, GO:0005634: nucleus, GO:0003690: double-stranded DNA binding, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity		0.5593	1.1678	1.3482	1.3831	6.33	6.89	7.5	7.68	7.71	7.88	3
215239_x_at	ZNF273	zinc finger protein 273	AU132789	10793	Hs.520889	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003676: nucleic acid binding, GO:0003677: DNA binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.6335	1.1307	1.4092	1.4227	7.93	8.56	9.06	9.34	9.35	9.96	3
218370_s_at	S100PBP	S100P binding protein	NM_022753	64766	Hs.440880	GO:0005634: nucleus, GO:0048306: calcium-dependent protein binding		0.8063	1.1397	1.5687	1.3897	4.32	5.12	5.46	5.88	5.71	6.01	3
213150_at	HOXA10	homeobox A10	BF792917	3206	Hs.592166	GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0007283: spermatogenesis, GO:0005634: nucleus, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding		0.5705	1.0934	1.3846	1.3148	5.38	5.95	6.47	6.76	6.69	6.79	3
213158_at			BG251521					0.8424	1.1323	1.6774	1.593	8.1	8.94	9.23	9.77	9.69	9.63	3
221756_at	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	BE042976	113791	Hs.26670	GO:0016020: membrane, GO:0016021: integral to membrane		0.9497	0.8087	1.017	1.1976	6.56	7.51	7.37	7.58	7.76	7.3	3

(*Continued*)

TABLE E3. (*Continued*)

211732_x_at	HNMT	histamine N-methyltransferase	BC005907	3176	Hs.42151	GO:0007585: respiratory gaseous exchange, GO:0005737: cytoplasm, GO:0008168: methyltransferase activity, GO:0016740: transferase activity, GO:0046539: histamine N-methyltransferase activity	00340: Histidine metabolism	0.5139	0.6537	1.0172	0.8801	3.69	4.2	4.34	4.7	4.57	4.66	3
213247_at	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	AA716107	79987	Hs.29040, Hs.522334, Hs.606771	GO:0005509: calcium ion binding, GO:0005529: sugar binding		0.2678	0.4761	1.2344	0.9955	7.49	7.76	7.97	8.73	8.49	8.73	3
213435_at	SATB2	SATB homeobox 2	AB028957	23314	Hs.516617	GO:0006355: regulation of transcription, DNA-dependent, GO:0005634: nucleus, GO:0003677: DNA binding, GO:0003700: transcription factor activity, GO:0043565: sequence-specific DNA binding		0.0742	0.2128	1.1137	0.8774	3.15	3.22	3.36	4.26	4.03	3.7	3
207714_s_at	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	NM_004353	871	Hs.596449	GO:0006457: protein folding, GO:0006986: response to unfolded protein, GO:0005783: endoplasmic reticulum, GO:0005793: ER-Golgi intermediate compartment, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005518: collagen binding, GO:0051082: unfolded protein binding		−0.0249	0.4286	1.1446	0.9101	8.59	8.57	9.02	9.74	9.5	8.76	3
209466_x_at	PTN	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	M57399	5764	Hs.371249	GO:0000074: regulation of progression through cell cycle, GO:0007185: transmembrane receptor protein tyrosine phosphatase signaling pathway, GO:0007399: nervous system development, GO:0007612: learning, GO:0008283: cell proliferation, GO:0008284: positive regulation of cell proliferation, GO:0030282: bone mineralization, GO:0005615: extracellular space, GO:0005783: endoplasmic reticulum, GO:0004864: protein phosphatase inhibitor activity, GO:0005125: cytokine activity, GO:0008083: growth factor activity, GO:0008201: heparin binding		0.1547	0.3069	1.1365	0.9522	6.27	6.43	6.58	7.41	7.22	6.67	3
219427_at	FAT4	FAT tumor suppressor homolog 4 (Drosophila)	NM_024582	79633	Hs.694841	GO:0007156: homophilic cell adhesion, GO:0016020: membrane, GO:0005509: calcium ion binding		0.033	0.3442	1.1145	0.9642	5.62	5.65	5.96	6.73	6.58	6.19	3
219895_at	FAM70A	family with sequence similarity 70, member A	NM_017938	55026	Hs.437563	GO:0016020: membrane, GO:0016021: integral to membrane		−0.0476	0.3937	1.0447	0.8847	2.74	2.7	3.14	3.79	3.63	4.63	3
222316_at	VDP	vesicle docking protein p115	AW973253	8615	Hs.292689	GO:0006886: intracellular protein transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0006904: vesicle docking during exocytosis, GO:0000139: Golgi membrane, GO:0005737: cytoplasm, GO:0016020: membrane, GO:0005488: binding, GO:0005515: protein binding, GO:0008565: protein transporter activity		0.049	0.4993	1.1415	1.001	7.32	7.36	7.81	8.46	8.32	8.58	3
49452_at	ACACB	acetyl-Coenzyme A carboxylase beta	AI057637	32	Hs.234898	GO:0006633: fatty acid biosynthetic process, GO:0008152: metabolic process, GO:0016020: membrane, GO:0000166: nucleotide binding, GO:0003989: acetyl-CoA carboxylase activity, GO:0004075: biotin carboxylase activity, GO:0005524: ATP binding, GO:0009374: biotin binding, GO:0016874: ligase activity, GO:0030145: manganese ion binding, GO:0046872: metal ion binding	00061: Fatty acid biosynthesis, 00620: Pyruvate metabolism, 00640: Propanoate metabolism, 04910: Insulin signaling pathway, 04920: Adipocytokine signaling pathway	0.577	0.9968	1.4241	2.3462	6.2	6.78	7.2	7.63	8.55	8.16	3
61734_at	RCN3	reticulocalbin 3, EF-hand calcium binding domain	AI797684	57333	Hs.567550	GO:0005783: endoplasmic reticulum, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.0015	0.7083	1.2927	1.1006	5.9	5.9	6.61	7.19	7	6.38	3

(*Continued*)

TABLE E3. (*Continued*)

201278_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	N21202	1601	Hs.481980	GO:0000904: cellular morphogenesis during differentiation, GO:0001701: in utero embryonic development, GO:0006898: receptor-mediated endocytosis, GO:0006907: pinocytosis, GO:0007588: excretion, GO:0008283: cell proliferation, GO:0005905: coated pit, GO:0016020: membrane, GO:0031410: cytoplasmic vesicle, GO:0008022: protein C-terminus binding	0.3686	0.5535	1.1016	0.8574	9.28	9.65	9.83	10.38	10.13	9.97	3
220351_at	CCRL1	chemokine (C-C motif) receptor-like 1	NM_016557	51554	Hs.310512	GO:0006935: chemotaxis, GO:0006955: immune response, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0016493: C-C chemokine receptor activity	0.303	0.8121	1.2517	1.1252	7.15	7.45	7.96	8.4	8.28	8.7	3
220988_s_at	C1QTNF3	C1q and tumor necrosis factor related protein 3	NM_030945	114899	Hs.171929	GO:0006817: phosphate transport, GO:0005737: cytoplasm, GO:0005739: mitochondrion	0.3734	0.9853	1.7933	1.5562	7.69	8.07	8.68	9.49	9.25	8.62	3
214954_at	SUSD5	sushi domain containing 5	BF977837	26032	Hs.196647	GO:0007155: cell adhesion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005540: hyaluronic acid binding	0.2271	0.7351	1.1526	1.0199	5.35	5.58	6.09	6.51	6.37	6.32	3
218162_at	OLFML3	olfactomedin-like 3	NM_020190	56944	Hs.9315		0.4181	0.736	1.2817	1.4981	8.79	9.21	9.53	10.07	10.29	9.98	3
212865_s_at	COL14A1	collagen, type XIV, alpha 1 (undulin)	BF449063	7373	Hs.409662	GO:0006817: phosphate transport, GO:0016337: cell-cell adhesion, GO:0030199: collagen fibril organization, GO:0005581: collagen, GO:0005596: collagen type XIV, GO:0005737: cytoplasm, GO:0005201: extracellular matrix structural constituent, GO:0005518: collagen binding, GO:0030674: protein binding, bridging	0.2974	0.6678	1.5094	1.166	8.76	9.05	9.42	10.26	9.92	9.17	3
213909_at	LRRC15	leucine rich repeat containing 15	AU147799	131578	Hs.288467	GO:0016020: membrane, GO:0016021: integral to membrane, GO:0005515: protein binding	0.3489	0.7746	1.6798	1.4469	7.59	7.94	8.36	9.27	9.03	8.06	3
210298_x_at	FHL1	four and a half LIM domains 1	AF098518	2273	Hs.435369	GO:0007275: multicellular organismal development, GO:0007517: muscle development, GO:0009887: organ morphogenesis, GO:0016049: cell growth, GO:0030154: cell differentiation, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0003674: molecular_function, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	0.2767	0.9667	1.3095	1.2516	7.77	8.04	8.73	9.08	9.02	9.66	3
210571_s_at	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase)	AF074480	8418	Hs.484918	GO:0008150: biological_process, GO:0005737: cytoplasm, GO:0030338: CMP-N-acetylneuraminate monooxygenase activity	0.0604	0.8463	1.4196	1.2357	3.89	3.95	4.74	5.31	5.13	6.57	3
209465_x_at	PTN	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	AL565812	5764	Hs.371249	GO:0000074: regulation of progression through cell cycle, GO:0007185: transmembrane receptor protein tyrosine phosphatase signaling pathway, GO:0007399: nervous system development, GO:0007612: learning, GO:0008283: cell proliferation, GO:0008284: positive regulation of cell proliferation, GO:0030282: bone mineralization, GO:0005615: extracellular space, GO:0005783: endoplasmic reticulum, GO:0004864: protein phosphatase inhibitor activity, GO:0005125: cytokine activity, GO:0008083: growth factor activity, GO:0008201: heparin binding	0.2497	0.7107	1.6509	1.4052	6.2	6.45	6.91	7.85	7.61	7.11	3
209501_at	CDR2	cerebellar degeneration-related protein 2, 62kDa	AL582414	1039	Hs.513430	GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0003674: molecular_function, GO:0005515: protein binding	0.3003	0.9155	1.2946	1.2957	6.26	6.56	7.17	7.55	7.55	7.91	3

(*Continued*)

TABLE E3. (*Continued*)

205857_at	SLC18A2	solute carrier family 18 (vesicular monoamine), member 2	AI269290	6571	Hs.654476	GO:0015844: monoamine transport, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0031410: cytoplasmic vesicle, GO:0005215: transporter activity, GO:0008504: monoamine transmembrane transporter activity		0.2508	0.8181	1.4466	1.3519	4.4	4.65	5.21	5.84	5.75	6.15	3
206726_at	PGDS	prostaglandin D2 synthase, hematopoietic	NM_014485	27306	Hs.128433	GO:0001516: prostaglandin biosynthetic process, GO:0006633: fatty acid biosynthetic process, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0007626: locomotory behavior, GO:0005737: cytoplasm, GO:0004667: prostaglandin-D synthase activity, GO:0016853: isomerase activity	00590: Arachidonic acid metabolism	0.3566	0.8997	1.6856	1.4573	3.19	3.55	4.09	4.88	4.65	5.21	3
205422_s_at	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	NM_004791	9358	Hs.584836	GO:0007155: cell adhesion, GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0008305: integrin complex, GO:0004872: receptor activity, GO:0005488: binding		0.2719	0.9496	1.664	1.6537	7.74	8.01	8.69	9.41	9.4	9.12	3
205803_s_at	TRPC1	transient receptor potential cation channel, subfamily C, member 1	NM_003304	7220	Hs.250687	GO:0006811: ion transport, GO:0006816: calcium ion transport, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005216: ion channel activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0015279: store-operated calcium channel activity	04020: Calcium signaling pathway	0.6731	0.8371	1.5331	1.2544	5.14	5.82	5.98	6.68	6.4	6.74	3
205051_s_at	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	NM_000222	3815	Hs.479754	GO:0006468: protein amino acid phosphorylation, GO:0006470: protein amino acid dephosphorylation, GO:0007165: signal transduction, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007243: protein kinase cascade, GO:0009314: response to radiation, GO:0018108: peptidyl-tyrosine phosphorylation, GO:0019221: cytokine and chemokine mediated signaling pathway, GO:0030097: hemopoiesis, GO:0048066: pigmentation during development, GO:0009897: external side of plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0000166: nucleotide binding, GO:0004716: receptor signaling protein tyrosine kinase activity, GO:0004872: receptor activity, GO:0005020: stem cell factor receptor activity, GO:0005021: vascular endothelial growth factor receptor activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016740: transferase activity	04060: Cytokine-cytokine receptor interaction, 04640: Hematopoietic cell lineage, 04916: Melanogenesis, 05221: Acute myeloid leukemia	0.3476	0.745	1.129	1.0318	8.23	8.58	8.98	9.36	9.26	9.83	3
205382_s_at	CFD	complement factor D (adipsin)	NM_001928	1675	Hs.155597	GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0006957: complement activation, alternative pathway, GO:0003817: complement factor D activity, GO:0003817: complement factor D activity, GO:0016787: hydrolase activity	04610: Complement and coagulation cascades	0.2436	0.6419	1.0671	1.4528	12.05	12.29	12.69	13.12	13.5	13.42	3

(*Continued*)

TABLE E3. (*Continued*)

204154_at	CDO1	cysteine dioxygenase, type I	NM_001801	1036	Hs.442378	GO:0000097: sulfur amino acid biosynthetic process, GO:0006118: electron transport, GO:0006954: inflammatory response, GO:0042412: taurine biosynthetic process, GO:0046439: L-cysteine metabolic process, GO:0005829: cytosol, GO:0005506: iron ion binding, GO:0016491: oxidoreductase activity, GO:0017172: cysteine dioxygenase activity, GO:0046872: metal ion binding	00272: Cysteine metabolism, 00430: Taurine and hypotaurine metabolism	0.2786	0.7788	1.1295	1.1404	5.37	5.64	6.14	6.5	6.51	6.97	3
204160_s_at	ENPP4	ectonucleotide pyrophosphatase/ phosphodiesterase 4 (putative function)	NM_014936	22875	Hs.643497	GO:0008152: metabolic process, GO:0009117: nucleotide metabolic process, GO:0016787: hydrolase activity		0.4019	0.4923	1.4135	1.2194	3.8	4.2	4.29	5.22	5.02	5.94	3
203874_s_at	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	M88163	6594	Hs.152292	GO:0006338: chromatin remodeling, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007420: brain development, GO:0030182: neuron differentiation, GO:0043193: positive regulation of gene-specific transcription, GO:0005634: nucleus, GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0004386: helicase activity, GO:0004386: helicase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0008094: DNA-dependent ATPase activity, GO:0016787: hydrolase activity, GO:0030528: transcription regulator activity		0.5813	0.7402	1.2947	1.157	5.58	6.16	6.32	6.87	6.74	6.9	3
203886_s_at	FBLN2	fibulin 2	NM_001998	2199	Hs.198862	GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005201: extracellular matrix structural constituent, GO:0005509: calcium ion binding, GO:0005509: calcium ion binding, GO:0005515: protein binding		0.3389	0.5508	1.1043	1.2379	9.48	9.82	10.04	10.59	10.72	10.3	3
211737_x_at	PTN	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	BC005916	5764	Hs.371249	GO:0000074: regulation of progression through cell cycle, GO:0007185: transmembrane receptor protein tyrosine phosphatase signaling pathway, GO:0007399: nervous system development, GO:0007612: learning, GO:0008283: cell proliferation, GO:0008284: positive regulation of cell proliferation, GO:0030282: bone mineralization, GO:0005615: extracellular space, GO:0005783: endoplasmic reticulum, GO:0004864: protein phosphatase inhibitor activity, GO:0005125: cytokine activity, GO:0008083: growth factor activity, GO:0008201: heparin binding		0.3564	1.039	1.8495	1.7507	6.18	6.53	7.22	8.03	7.93	7.3	3
212670_at	ELN	elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)	AA479278	2006	Hs.647061	GO:0007585: respiratory gaseous exchange, GO:0008015: circulation, GO:0008283: cell proliferation, GO:0009887: organ morphogenesis, GO:0005578: proteinaceous extracellular matrix, GO:0005578: proteinaceous extracellular matrix, GO:0005737: cytoplasm, GO:0005201: extracellular matrix structural constituent, GO:0005525: GTP binding, GO:0030023: extracellular matrix constituent conferring elasticity		0.5961	2.0902	3.5423	2.7686	5.7	6.29	7.79	9.24	8.47	7.02	3
209406_at	BAG2	BCL2-associated athanogene 2	AF095192	9532	Hs.55220	GO:0006457: protein folding, GO:0006915: apoptosis, GO:0019538: protein metabolic process, GO:0005515: protein binding, GO:0030188: chaperone regulator activity		0.4176	1.1908	1.8697	1.5143	4.42	4.83	5.61	6.29	5.93	6.11	3

(*Continued*)

TABLE E3. (*Continued*)

211062_s_at	CPZ	carboxypeptidase Z	BC006393	8532	Hs.78068	GO:0006508: proteolysis, GO:0016055: Wnt receptor signaling pathway, GO:0005578: proteinaceous extracellular matrix, GO:0004182: carboxypeptidase A activity, GO:0008237: metallopeptidase activity, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		0.4267	1.5445	2.9967	2.6094	4.26	4.68	5.8	7.25	6.87	4.67	3
205498_at	GHR	growth hormone receptor	NM_000163	2690	Hs.125180	GO:0001501: skeletal development, GO:0006897: endocytosis, GO:0040007: growth, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0004872: receptor activity, GO:0004903: growth hormone receptor activity, GO:0005515: protein binding	04060: Cytokine-cytokine receptor interaction, 04080: Neuroactive ligand-receptor interaction, 04630: Jak-STAT signaling pathway	0.9781	1.3393	1.3835	1.7104	6.32	7.29	7.66	7.7	8.03	8.22	3
205907_s_at	OMD	osteomodulin	AI765819	4958	Hs.94070	GO:0007155: cell adhesion, GO:0005578: proteinaceous extracellular matrix, GO:0005515: protein binding		0.7745	1.5923	2.4087	1.9423	5.82	6.59	7.41	8.23	7.76	7.86	3
202733_at	P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	NM_004199	8974	Hs.519568	GO:0018401: peptidyl-proline hydroxylation to 4-hydroxy-L-proline, GO:0019538: protein metabolic process, GO:0005783: endoplasmic reticulum, GO:0004656: procollagen-proline 4-dioxygenase activity, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0009055: electron carrier activity, GO:0016702: oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, GO:0016706: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors, GO:0031418: L-ascorbic acid binding, GO:0046872: metal ion binding	00330: Arginine and proline metabolism	0.2801	0.6541	1.0896	0.9815	8.22	8.5	8.87	9.31	9.2	8.93	3
207543_s_at	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	NM_000917	5033	Hs.500047	GO:0019538: protein metabolic process, GO:0005783: endoplasmic reticulum, GO:0004656: procollagen-proline 4-dioxygenase activity, GO:0005488: binding, GO:0005506: iron ion binding, GO:0016491: oxidoreductase activity, GO:0016702: oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, GO:0016706: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors, GO:0031418: L-ascorbic acid binding, GO:0046872: metal ion binding	00330: Arginine and proline metabolism	0.2602	0.5472	1.1505	0.9314	7.24	7.5	7.78	8.39	8.17	8.31	3
219284_at	HSPBAP1	HSPB (heat shock 27kDa) associated protein 1	NM_024610	79663	Hs.29169	GO:0005737: cytoplasm		0.6355	0.8079	0.8929	1.0278	7.22	7.85	8.03	8.11	8.25	8.15	3
220711_at			NM_024978					−0.1313	0.0761	0.2757	1.4441	3.08	2.95	3.16	3.36	4.53	4	3

Fold change >2 for any time point; FDR <0.05.

TABLE E4. Genes modulated differently in responders and non-responders by etanercept in responders

R_0	Mean expression value estimate (Log2) for Responders in LS skin
R_1	Mean expression value estimate (Log2) for Responders in LS at Wk 1
R_2	Mean expression value estimate (Log2) for Responders in LS at Wk 2
R_4	Mean expression value estimate (Log2) for Responders in LS at Wk 4
R_12	Mean expression value estimate (Log2) for Responders in LS at Wk 12
R_NL	Mean expression value estimate (Log2) for Responders in NL skin at baseline
NR_0	Mean expression value estimate (Log2) for Non-Responders in LS skin
NR_1	Mean expression value estimate (Log2) for Non-Responders in LS at Wk 1
NR_2	Mean expression value estimate (Log2) for Non-Responders in LS at Wk 2
NR_4	Mean expression value estimate (Log2) for Non-Responders in LS at Wk 4
NR_12	Mean expression value estimate (Log2) for Non-Responders in LS at Wk 12
NR_NL	Mean expression value estimate (Log2) for Non-Responders in LS at Wk 12
Cluster	Final cluster membership

Probe	Symbol	Description	GenBank	Gene	UniGene	Gene Ontology	Pathway	R_0	R_1	R_2	R_4	R_12	R_NL	NR_0	NR_1	NR_2	NR_4	NR_12	NR_NL	Cluster
208018_s_at	HCK	hemopoietic cell kinase	NM_002110	3055	Hs.655210	GO:0000166: nucleotide binding, GO:0004715: non-membrane spanning protein tyrosine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005737: cytoplasm, GO:0006468: protein amino acid phosphorylation, GO:0007498: mesoderm development, GO:0016020: membrane, GO:0016740: transferase activity, GO:0044419: interspecies interaction between organisms		7.01	7.37	7.02	6.84	6.30	5.87	5.89	6.78	6.73	7.23	6.66	5.93	1
203058_s_at	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	AW299958	9060	Hs.524491	GO:0000103: sulfate assimilation, GO:0000166: nucleotide binding, GO:0001501: skeletal development, GO:0004020: adenylylsulfate kinase activity, GO:0004781: sulfate adenylyltransferase (ATP) activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0016779: nucleotidyltransferase activity	00230: Purine metabolism, 00450: Selenoamino acid metabolism, 00920: Sulfur metabolism	4.00	4.59	4.07	3.85	3.96	3.39	3.79	4.30	4.25	5.22	4.03	3.53	1
208813_at	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	BC000498	2805	Hs.500756	GO:0004069: aspartate transaminase activity, GO:0004069: aspartate transaminase activity, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0006520: amino acid metabolic process, GO:0006533: aspartate catabolic process, GO:0009058: biosynthetic process, GO:0030170: pyridoxal phosphate binding, GO:0032869: cellular response to insulin stimulus, GO:0051384: response to glucocorticoid stimulus	00251: Glutamate metabolism, 00252: Alanine and aspartate metabolism, 00272: Cysteine metabolism, 00330: Arginine and proline metabolism, 00350: Tyrosine metabolism, 00360: Phenylalanine metabolism, 00400: Phenylalanine, tyrosine and tryptophan biosynthesis, 00401: Novobiocin biosynthesis, 00710: Carbon fixation, 00950: Alkaloid biosynthesis I	9.87	9.74	9.50	8.85	8.71	8.95	9.64	9.40	9.45	9.66	9.10	8.86	1

(*Continued*)

TABLE E4. (*Continued*)

219198_at	GTF3C4	general transcription factor IIIC, polypeptide 4, 90kDa	NM_012204	9329	Hs.656646	GO:0000127: transcription factor TFIIIC complex, GO:0003677: DNA binding, GO:0003709: RNA polymerase III transcription factor activity, GO:0004406: H3/H4 histone acetyltransferase activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006351: transcription, DNA-dependent, GO:0006384: transcription initiation from RNA polymerase III promoter, GO:0008047: enzyme activator activity, GO:0008415: acyltransferase activity, GO:0016740: transferase activity, GO:0042791: 5S class rRNA transcription, GO:0042797: tRNA transcription from RNA polymerase III promoter		6.15	5.86	5.97	5.51	5.40	5.83	5.81	5.63	5.93	5.68	6.14	5.63	1
219956_at	GALNT6	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	NM_007210	11226	Hs.505575	GO:0000139: Golgi membrane, GO:0004653: polypeptide N-acetylgalactosaminyltransferase activity, GO:0005509: calcium ion binding, GO:0005529: sugar binding, GO:0005794: Golgi apparatus, GO:0006493: protein amino acid O-linked glycosylation, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016757: transferase activity, transferring glycosyl groups, GO:0030145: manganese ion binding, GO:0048471: perinuclear region of cytoplasm	00512: O-Glycan biosynthesis, 01030: Glycan structures - biosynthesis 1	8.11	7.36	7.07	6.11	5.70	5.47	7.64	7.16	7.21	7.29	7.39	5.48	1
206562_s_at	CSNK1A1	casein kinase 1, alpha 1	NM_001892	1452	Hs.529862, Hs.712555	GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004681: casein kinase I activity, GO:0005524: ATP binding, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0016055: Wnt receptor signaling pathway, GO:0016740: transferase activity	04310: Wnt signaling pathway, 04340: Hedgehog signaling pathway	11.98	11.81	11.70	11.24	10.23	10.71	11.86	11.80	11.64	11.94	11.43	10.67	1
206643_at	HAL	histidine ammonia-lyase	NM_002108	3034	Hs.190783	GO:0004397: histidine ammonia-lyase activity, GO:0004397: histidine ammonia-lyase activity, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0006548: histidine catabolic process, GO:0009058: biosynthetic process, GO:0016211: ammonia ligase activity, GO:0016829: lyase activity	00340: Histidine metabolism, 00910: Nitrogen metabolism	12.50	12.79	12.57	12.09	10.87	10.67	12.67	12.31	12.42	12.71	12.11	10.58	1

(*Continued*)

TABLE E4. (*Continued*)

206036_s_at	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	NM_002908	5966 Hs.631886	GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade	9.89	9.95	9.84	9.40	8.96	8.98	9.52	9.66	9.62	9.97	9.74	8.32	1
206125_s_at	KLK8	kallikrein-related peptidase 8	NM_007196	11202 Hs.104570	GO:0004252: serine-type endopeptidase activity, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0006508: proteolysis, GO:0007613: memory, GO:0008219: cell death, GO:0008233: peptidase activity, GO:0009611: response to wounding, GO:0031642: negative regulation of myelination, GO:0043616: keratinocyte proliferation, GO:0048681: negative regulation of axon regeneration, GO:0048812: neurite morphogenesis, GO:0050807: regulation of synapse organization and biogenesis	11.90	11.76	11.69	11.23	10.69	10.71	11.98	11.40	11.61	11.67	11.79	10.98	1
204331_s_at	MRPS12	mitochondrial ribosomal protein S12	AA587905	6183 Hs.411125	GO:0003735: structural constituent of ribosome, GO:0005515: protein binding, GO:0005622: intracellular, GO:0005739: mitochondrion, GO:0005761: mitochondrial ribosome, GO:0005840: ribosome, GO:0006412: translation, GO:0015935: small ribosomal subunit	9.58	9.32	9.01	8.67	8.24	8.44	9.13	8.84	9.03	9.29	8.96	8.41	1
205064_at	SPRR1B	small proline-rich protein 1B (cornifin)	NM_003125	6699 Hs.1076	GO:0001533: cornified envelope, GO:0005198: structural molecule activity, GO:0005737: cytoplasm, GO:0008544: epidermis development, GO:0018149: peptide cross-linking, GO:0030216: keratinocyte differentiation, GO:0030674: protein binding, bridging, GO:0031424: keratinization	14.20	14.05	13.86	13.36	12.83	12.64	14.02	13.94	13.89	13.94	13.86	12.80	1
204174_at	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	NM_001629	241 Hs.507658	GO:0005488: binding, GO:0006954: inflammatory response, GO:0008047: enzyme activator activity, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0019370: leukotriene biosynthetic process	7.80	8.21	7.95	7.82	6.50	6.91	7.15	7.77	7.71	8.37	7.83	6.60	1

(*Continued*)

TABLE E4. (*Continued*)

204203_at	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	NM_001806	1054 Hs.429666	GO:0001889: liver development, GO:0003700: transcription factor activity, GO:0005634: nucleus, GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006955: immune response, GO:0008134: transcription factor binding, GO:0030183: B cell differentiation, GO:0042267: natural killer cell mediated cytotoxicity, GO:0043353: enucleate erythrocyte differentiation, GO:0043433: negative regulation of transcription factor activity, GO:0043565: sequence-specific DNA binding, GO:0045078: positive regulation of interferon-gamma biosynthetic process, GO:0045739: positive regulation of DNA repair, GO:0046982: protein heterodimerization activity, GO:0051091: positive regulation of transcription factor activity		10.01	9.79	9.64	9.24	8.81	9.01	10.00	9.78	9.80	9.86	9.82	9.16	1
203740_at	MPHOSPH6	M-phase phosphoprotein 6	NM_005792	10200 Hs.344400	GO:0000087: M phase of mitotic cell cycle, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm		11.01	10.88	10.57	10.03	9.37	9.40	10.83	10.59	10.50	10.82	10.32	9.18	1
203888_at	THBD	thrombomodulin	NM_000361	7056 Hs.2030	GO:0004888: transmembrane receptor activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005615: extracellular space, GO:0005886: plasma membrane, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0007565: female pregnancy, GO:0007596: blood coagulation, GO:0009790: embryonic development, GO:0010165: response to X-ray, GO:0032496: response to lipopolysaccharide, GO:0051591: response to cAMP	04610: Complement and coagulation cascades	10.09	9.68	9.59	9.30	9.10	9.60	9.82	9.84	9.97	9.95	9.85	9.86	1
202917_s_at	S100A8	S100 calcium binding protein A8	NM_002964	6279 Hs.416073	GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0006954: inflammatory response		15.40	15.36	15.28	15.01	13.89	13.75	15.24	15.28	15.14	15.25	15.13	13.43	1
203535_at	S100A9	S100 calcium binding protein A9	NM_002965	6280 Hs.112405	GO:0004871: signal transducer activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0006954: inflammatory response, GO:0007267: cell-cell signaling, GO:0030595: leukocyte chemotaxis, GO:0031532: actin cytoskeleton reorganization, GO:0045113: regulation of integrin biosynthetic process		15.58	15.56	15.39	14.39	11.99	11.78	15.46	15.32	14.95	15.44	14.63	11.46	1

(*Continued*)

TABLE E4. (*Continued*)

202264_s_at	TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	NM_006114	10452 Hs.655909	GO:0003674: molecular_function, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0006626: protein targeting to mitochondrion, GO:0006820: anion transport, GO:0008308: voltage-gated anion channel activity, GO:0015031: protein transport, GO:0016021: integral to membrane, GO:0019867: outer membrane		9.05	8.63	8.56	8.17	8.26	8.12	8.57	8.49	8.35	8.67	8.88	8.17	1
202787_s_at	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	NM_004635	7867 Hs.234521	GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004708: MAP kinase kinase activity, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0006468: protein amino acid phosphorylation, GO:0006950: response to stress, GO:0007242: intracellular signaling cascade, GO:0007265: Ras protein signal transduction, GO:0016740: transferase activity	04010: MAPK signaling pathway, 04370: VEGF signaling pathway	9.39	9.44	9.14	8.66	8.02	8.01	9.01	8.76	8.97	9.12	8.68	7.66	1
201516_at	SRM	spermidine synthase	NM_003132	6723 Hs.76244	GO:0004766: spermidine synthase activity, GO:0008295: spermidine biosynthetic process, GO:0016740: transferase activity	00220: Urea cycle and metabolism of amino groups, 00271: Methionine metabolism, 00410: beta-Alanine metabolism	9.58	9.20	9.07	8.77	8.81	8.65	8.98	8.92	8.96	9.16	9.36	8.45	1
201912_s_at	GSPT1	G1 to S phase transition 1	NM_002094	2935 Hs.528780	GO:0000082: G1/S transition of mitotic cell cycle, GO:0000166: nucleotide binding, GO:0000184: mRNA catabolic process, nonsense-mediated decay, GO:0003747: translation release factor activity, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0005622: intracellular, GO:0006412: translation, GO:0006919: caspase activation, GO:0016567: protein ubiquitination, GO:0042981: regulation of apoptosis		10.77	10.51	10.25	9.96	9.29	9.54	10.48	10.30	10.22	10.53	10.16	9.50	1
201196_s_at	AMD1	adenosylmethionine decarboxylase 1	M21154	262 Hs.159118	GO:0004014: adenosylmethionine decarboxylase activity, GO:0004014: adenosylmethionine decarboxylase activity, GO:0005575: cellular_component, GO:0006597: spermine biosynthetic process, GO:0006597: spermine biosynthetic process, GO:0008295: spermidine biosynthetic process, GO:0008295: spermidine biosynthetic process, GO:0016829: lyase activity	00220: Urea cycle and metabolism of amino groups, 00271: Methionine metabolism	10.43	10.06	10.03	9.63	8.60	9.47	10.44	10.28	10.14	10.34	9.66	9.43	1

(*Continued*)

TABLE E4. (*Continued*)

201490_s_at	PPIF	peptidylprolyl isomerase F (cyclophilin F)	NM_005729	10105 Hs.381072	GO:0003755: peptidyl-prolyl cis-trans isomerase activity, GO:0005624: membrane fraction, GO:0005739: mitochondrion, GO:0005759: mitochondrial matrix, GO:0006457: protein folding, GO:0016853: isomerase activity, GO:0042277: peptide binding		10.81	10.54	10.03	9.18	7.48	8.05	10.34	10.09	9.97	10.41	9.47	7.82	1
211572_s_at	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	AF092511	9962 Hs.516866	GO:0005215: transporter activity, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006810: transport, GO:0006811: ion transport, GO:0006814: sodium ion transport, GO:0008523: sodium-dependent multivitamin transmembrane transporter activity, GO:0015205: nucleobase transmembrane transporter activity, GO:0015293: symporter activity, GO:0015851: nucleobase transport, GO:0015993: molecular hydrogen transport, GO:0016020: membrane, GO:0019852: L-ascorbic acid metabolic process, GO:0031402: sodium ion binding		3.83	2.75	2.35	2.37	2.33	2.32	2.67	2.35	3.02	3.17	2.36	2.31	1
220745_at	IL19	interleukin 19	NM_013371	29949 Hs.661017	GO:0005125: cytokine activity, GO:0005125: cytokine activity, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0006800: oxygen and reactive oxygen species metabolic process, GO:0006915: apoptosis, GO:0006917: induction of apoptosis, GO:0006955: immune response, GO:0006955: immune response, GO:0007165: signal transduction, GO:0042226: interleukin-6 biosynthetic process	04060: Cytokine-cytokine receptor interaction, 04630: Jak-STAT signaling pathway	4.07	2.40	1.89	1.98	1.99	1.82	2.42	2.16	2.88	2.98	1.88	1.81	1

(*Continued*)

TABLE E4. (*Continued*)

221245_s_at	FZD5	frizzled homolog 5 (Drosophila)	NM_030804	7855	Hs.17631	GO:0000139: Golgi membrane, GO:0004872: receptor activity, GO:0004926: non-G-protein coupled 7TM receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0005515: protein binding, GO:0005794: Golgi apparatus, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0007164: establishment of tissue polarity, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007275: multicellular organismal development, GO:0016055: Wnt receptor signaling pathway, GO:0048469: cell maturation	04310: Wnt signaling pathway, 04916: Melanogenesis, 05210: Colorectal cancer, 05217: Basal cell carcinoma	8.65	8.33	7.65	7.31	7.03	7.05	8.14	8.22	7.98	8.26	7.51	6.84	1
221704_s_at	VPS37B	vacuolar protein sorting 37 homolog B (S. cerevisiae)	BC005882	79720	Hs.507162	GO:0005737: cytoplasm, GO:0005768: endosome, GO:0015031: protein transport, GO:0016020: membrane, GO:0031902: late endosome membrane		8.14	7.74	7.51	7.34	7.68	7.51	7.60	7.58	7.86	7.96	7.36	7.72	1
219795_at	SLC6A14	solute carrier family 6 (amino acid transporter), member 14	NM_007231	11254	Hs.522109	GO:0005328: neurotransmitter:sodium symporter activity, GO:0005887: integral to plasma membrane, GO:0006520: amino acid metabolic process, GO:0006836: neurotransmitter transport, GO:0006865: amino acid transport, GO:0015171: amino acid transmembrane transporter activity, GO:0015293: symporter activity, GO:0016020: membrane		11.71	11.33	10.57	9.00	7.46	8.03	11.06	10.96	10.24	11.19	9.00	7.83	1
220249_at	HYAL4	hyalurono-glucosaminidase 4	NM_012269	23553	Hs.28673	GO:0004415: hyaluronoglucosaminidase activity, GO:0005975: carbohydrate metabolic process, GO:0006027: glycosaminoglycan catabolic process, GO:0007342: fusion of sperm to egg plasma membrane, GO:0008152: metabolic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016798: hydrolase activity, acting on glycosyl bonds		6.23	6.69	5.60	4.32	3.71	3.44	5.52	4.90	5.11	6.00	4.65	3.38	1
216905_s_at	ST14	suppression of tumorigenicity 14 (colon carcinoma)	U20428	6768	Hs.504315	GO:0004252: serine-type endopeptidase activity, GO:0005576: extracellular region, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0006508: proteolysis, GO:0019897: extrinsic to plasma membrane		7.47	7.09	6.76	6.52	6.20	6.23	7.11	6.70	6.96	7.24	6.63	6.03	1

(*Continued*)

TABLE E4. (*Continued*)

217738_at	NAMPT	nicotinamide phosphoribosyl-transferase	NM_005746	10135 Hs.489615	GO:0005125: cytokine activity, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0008284: positive regulation of cell proliferation, GO:0016757: transferase activity, transferring glycosyl groups, GO:0019363: pyridine nucleotide biosynthetic process, GO:0019674: NAD metabolic process, GO:0047280: nicotinamide phosphoribosyltransferase activity, GO:0047280: nicotinamide phosphoribosyltransferase activity	00760: Nicotinate and nicotinamide metabolism	11.36	11.16	10.73	10.18	9.14	9.86	10.83	10.99	10.59	11.02	9.82	9.49	1
216316_x_at	GK	glycerol kinase	X78713	2710 Hs.1466	GO:0000166: nucleotide binding, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0005524: ATP binding, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0005829: cytosol, GO:0005975: carbohydrate metabolic process, GO:0006072: glycerol-3-phosphate metabolic process, GO:0016020: membrane, GO:0016740: transferase activity	00561: Glycerolipid metabolism, 03320: PPAR signaling pathway	5.43	5.91	4.74	3.77	2.90	2.98	5.01	4.79	4.94	5.73	4.05	2.65	1
216834_at	RGS1	regulator of G-protein signaling 1	S59049	5996 Hs.75256	GO:0004871: signal transducer activity, GO:0005096: GTPase activator activity, GO:0005516: calmodulin binding, GO:0005886: plasma membrane, GO:0006955: immune response, GO:0007193: G-protein signaling, adenylate cyclase inhibiting pathway, GO:0009968: negative regulation of signal transduction		5.86	5.35	4.58	3.99	2.86	2.44	4.63	5.01	4.29	6.05	3.41	2.39	1
215966_x_at	GK3P	glycerol kinase 3 pseudogene	AA292874	2713 Hs.654557	GO:0000166: nucleotide binding, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0005524: ATP binding, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0005975: carbohydrate metabolic process, GO:0006072: glycerol-3-phosphate metabolic process, GO:0016020: membrane, GO:0016740: transferase activity		7.58	7.71	6.86	6.02	5.13	4.96	7.18	7.05	7.21	7.75	5.93	4.63	1

(*Continued*)

TABLE E4. (*Continued*)

215977_x_at	GK	glycerol kinase	X68285	2710	Hs.1466	GO:0000166: nucleotide binding, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0005524: ATP binding, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0005829: cytosol, GO:0005975: carbohydrate metabolic process, GO:0006072: glycerol-3-phosphate metabolic process, GO:0016020: membrane, GO:0016740: transferase activity	00561: Glycerolipid metabolism, 03320: PPAR signaling pathway	6.80	6.88	5.49	4.39	3.40	3.10	6.16	5.38	6.03	6.64	4.50	3.07	1
215103_at	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	AW192911	1562	Hs.511872	GO:0004497: monooxygenase activity, GO:0004497: monooxygenase activity, GO:0005506: iron ion binding, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005792: microsome, GO:0009055: electron carrier activity, GO:0016020: membrane, GO:0019825: oxygen binding, GO:0020037: heme binding, GO:0046872: metal ion binding, GO:0050381: unspecific monooxygenase activity	00590: Arachidonic acid metabolism, 00591: Linoleic acid metabolism, 00830: Retinol metabolism, 00980: Metabolism of xenobiotics by cytochrome P450, 00982: NA	5.03	4.94	4.97	4.39	4.30	4.21	5.29	4.74	4.96	5.82	4.91	4.43	1
215223_s_at	SOD2	superoxide dismutase 2, mitochondrial	W46388	6648	Hs.487046	GO:0000303: response to superoxide, GO:0001315: age-dependent response to reactive oxygen species, GO:0001315: age-dependent response to reactive oxygen species, GO:0001836: release of cytochrome c from mitochondria, GO:0004784: superoxide dismutase activity, GO:0004784: superoxide dismutase activity, GO:0005739: mitochondrion, GO:0005743: mitochondrial inner membrane, GO:0005759: mitochondrial matrix, GO:0006302: double-strand break repair, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006801: superoxide metabolic process, GO:0006801: superoxide metabolic process, GO:0006979: response to oxidative stress, GO:0016491: oxidoreductase activity, GO:0030145: manganese ion binding, GO:0042542: response to hydrogen peroxide, GO:0043066: negative regulation of apoptosis, GO:0046872: metal ion binding		10.50	10.09	8.85	7.93	6.40	6.99	9.68	9.37	8.35	9.74	7.56	6.30	1
212976_at	LRRC8B	leucine rich repeat containing 8 family, member B	R41498	23507	Hs.482017, Hs.632420, Hs.652456	GO:0005515: protein binding, GO:0016020: membrane, GO:0016021: integral to membrane		4.00	3.76	3.65	3.50	3.43	3.60	3.35	3.57	3.92	4.32	3.61	3.46	1

(*Continued*)

TABLE E4. (*Continued*)

213523_at	CCNE1	cyclin E1	AI671049	898 Hs.244723	GO:0000082: G1/S transition of mitotic cell cycle, GO:0003713: transcription coactivator activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0005829: cytosol, GO:0007049: cell cycle, GO:0030521: androgen receptor signaling pathway, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0050681: androgen receptor binding, GO:0051301: cell division	04110: Cell cycle, 04115: p53 signaling pathway, 05215: Prostate cancer, 05222: Small cell lung cancer	6.66	6.48	5.93	5.14	4.87	4.78	6.55	6.42	6.06	6.47	5.73	5.01	1
210827_s_at	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	U73844	1999 Hs.67928	GO:0003700: transcription factor activity, GO:0003713: transcription coactivator activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0006954: inflammatory response, GO:0008544: epidermis development, GO:0009653: anatomical structure morphogenesis, GO:0009790: embryonic development, GO:0016564: transcription repressor activity, GO:0030198: extracellular matrix organization and biogenesis, GO:0030855: epithelial cell differentiation, GO:0043565: sequence-specific DNA binding, GO:0060056: mammary gland involution		6.32	5.79	5.32	4.70	4.47	4.37	5.93	5.53	5.09	5.82	5.21	4.35	1
211429_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	AF119873	5265 Hs.525557	GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0006953: acute-phase response, GO:0007596: blood coagulation, GO:0008233: peptidase activity, GO:0031093: platelet alpha granule lumen	04610: Complement and coagulation cascades	8.07	7.91	6.66	5.96	5.48	4.93	7.23	7.08	6.83	7.75	6.19	4.73	1

(*Continued*)

TABLE E4. (*Continued*)

210001_s_at	SOCS1	suppressor of cytokine signaling 1	AB005043	8651 Hs.50640	GO:0001558: regulation of cell growth, GO:0001932: regulation of protein amino acid phosphorylation, GO:0004860: protein kinase inhibitor activity, GO:0005159: insulin-like growth factor receptor binding, GO:0005515: protein binding, GO:0005737: cytoplasm, GO:0007242: intracellular signaling cascade, GO:0019221: cytokine and chemokine mediated signaling pathway, GO:0019901: protein kinase binding, GO:0042518: negative regulation of tyrosine phosphorylation of Stat3 protein, GO:0045444: fat cell differentiation, GO:0046426: negative regulation of JAK-STAT cascade, GO:0046426: negative regulation of JAK-STAT cascade, GO:0046627: negative regulation of insulin receptor signaling pathway	04120: Ubiquitin mediated proteolysis, 04630: Jak-STAT signaling pathway, 04910: Insulin signaling pathway, 04930: Type II diabetes mellitus	5.83	5.54	5.12	5.04	4.87	4.68	5.22	5.21	5.65	5.98	5.07	4.64	1
210567_s_at	SKP2	S-phase kinase-associated protein 2 (p45)	BC001441	6502 Hs.23348	GO:0000082: G1/S transition of mitotic cell cycle, GO:0005515: protein binding, GO:0008283: cell proliferation	04110: Cell cycle, 04120: Ubiquitin mediated proteolysis, 05222: Small cell lung cancer	4.99	4.67	4.45	4.16	4.04	4.20	5.09	4.84	4.72	5.53	4.49	4.09	1
209236_at	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	AL389886	9962 Hs.516866	GO:0005215: transporter activity, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006810: transport, GO:0006811: ion transport, GO:0006814: sodium ion transport, GO:0008523: sodium-dependent multivitamin transmembrane transporter activity, GO:0015205: nucleobase transmembrane transporter activity, GO:0015293: symporter activity, GO:0015851: nucleobase transport, GO:0015993: molecular hydrogen transport, GO:0016020: membrane, GO:0019852: L-ascorbic acid metabolic process, GO:0031402: sodium ion binding		9.34	9.12	8.33	8.38	7.75	7.58	8.26	8.30	8.40	8.73	7.72	7.39	1
209853_s_at	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	BC001423	10197 Hs.152978	GO:0000502: proteasome complex, GO:0005829: cytosol, GO:0008537: proteasome activator complex, GO:0008538: proteasome activator activity, GO:0031145: anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process, GO:0042802: identical protein binding, GO:0051436: negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle, GO:0051437: positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle	04612: Antigen processing and presentation	8.87	8.70	8.52	7.78	7.21	7.59	8.80	8.64	8.88	8.79	7.78	7.63	1

(*Continued*)

TABLE E4. (*Continued*)

207500_at	CASP5	caspase 5, apoptosis-related cysteine peptidase	NM_004347	838	Hs.213327	GO:0005515: protein binding, GO:0005515: protein binding, GO:0005622: intracellular, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0008234: cysteine-type peptidase activity, GO:0008234: cysteine-type peptidase activity, GO:0042981: regulation of apoptosis		3.45	3.40	3.08	3.04	3.15	3.05	3.10	3.05	3.26	3.72	3.40	3.00	1
209100_at	IFRD2	interferon-related developmental regulator 2	BC001327	7866	Hs.315177, Hs.534543	GO:0005488: binding, GO:0005575: cellular_component, GO:0008283: cell proliferation, GO:0030154: cell differentiation		8.65	8.30	8.13	7.73	7.64	7.60	8.23	8.29	8.25	8.34	8.12	7.62	1
206336_at	CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	NM_002993	6372	Hs.164021	GO:0003964: RNA-directed DNA polymerase activity, GO:0005575: cellular_component, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0006278: RNA-dependent DNA replication, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0008009: chemokine activity, GO:0008201: heparin binding	04060: Cytokine-cytokine receptor interaction	3.51	3.00	2.59	2.60	2.63	2.60	2.58	2.59	2.87	4.22	2.79	2.56	1
206529_x_at	SLC26A4	solute carrier family 26, member 4	NM_000441	5172	Hs.571246	GO:0005215: transporter activity, GO:0006810: transport, GO:0007605: sensory perception of sound, GO:0008271: secondary active sulfate transmembrane transporter activity, GO:0008272: sulfate transport, GO:0015108: chloride transmembrane transporter activity, GO:0015111: iodide transmembrane transporter activity, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0031404: chloride ion binding		4.62	4.01	3.45	3.48	3.85	3.50	3.51	3.47	4.23	4.93	4.16	3.34	1
205239_at	AREG	amphiregulin	NM_001657	374	Hs.270833	GO:0005125: cytokine activity, GO:0005615: extracellular space, GO:0007267: cell-cell signaling, GO:0008083: growth factor activity, GO:0008283: cell proliferation, GO:0016020: membrane, GO:0016021: integral to membrane	04012: ErbB signaling pathway	7.40	6.72	6.07	4.75	4.27	4.72	6.83	6.75	6.15	6.68	5.39	4.43	1
205633_s_at	ALAS1	aminolevulinate, delta-, synthase 1	NM_000688	211	Hs.476308	GO:0003870: 5-aminolevulinate synthase activity, GO:0005739: mitochondrion, GO:0005759: mitochondrial matrix, GO:0006783: heme biosynthetic process, GO:0008415: acyltransferase activity, GO:0009058: biosynthetic process, GO:0016769: transferase activity, transferring nitrogenous groups, GO:0030170: pyridoxal phosphate binding, GO:0033014: tetrapyrrole biosynthetic process	00260: Glycine, serine and threonine metabolism, 00860: Porphyrin and chlorophyll metabolism	10.56	10.37	9.99	9.78	9.41	9.49	10.05	10.17	9.90	10.34	9.82	9.40	1

(*Continued*)

TABLE E4. (*Continued*)

204440_at	CD83	CD83 molecule	NM_004233	9308	Hs.654558	GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0006952: defense response, GO:0006959: humoral immune response, GO:0007165: signal transduction		7.47	7.30	7.10	6.83	6.57	6.14	6.66	7.05	6.90	7.62	6.51	6.17	1
204858_s_at	TYMP	thymidine phosphorylase	NM_001953	1890	Hs.531314, Hs.592212	GO:0000002: mitochondrial genome maintenance, GO:0001525: angiogenesis, GO:0005161: platelet-derived growth factor receptor binding, GO:0005829: cytosol, GO:0006206: pyrimidine base metabolic process, GO:0006213: pyrimidine nucleoside metabolic process, GO:0006220: pyrimidine nucleotide metabolic process, GO:0006260: DNA replication, GO:0006935: chemotaxis, GO:0007275: multicellular organismal development, GO:0008083: growth factor activity, GO:0008152: metabolic process, GO:0009032: thymidine phosphorylase activity, GO:0030154: cell differentiation	00230: Purine metabolism, 00240: Pyrimidine metabolism, 00983: NA, 05219: Bladder cancer	10.86	10.68	10.05	8.83	7.89	7.37	10.62	10.34	9.87	10.89	9.46	7.50	1

(*Continued*)

TABLE E4. (*Continued*)

203665_at	HMOX1	heme oxygenase (decycling) 1	NM_002133	3162 Hs.517581	GO:0001666: response to hypoxia, GO:0001935: endothelial cell proliferation, GO:0002246: healing during inflammatory response, GO:0002686: negative regulation of leukocyte migration, GO:0004392: heme oxygenase (decyclizing) activity, GO:0004630: phospholipase D activity, GO:0004871: signal transducer activity, GO:0005506: iron ion binding, GO:0005615: extracellular space, GO:0005624: membrane fraction, GO:0005634: nucleus, GO:0005730: nucleolus, GO:0005783: endoplasmic reticulum, GO:0005792: microsome, GO:0005829: cytosol, GO:0006788: heme oxidation, GO:0007243: protein kinase cascade, GO:0007264: small GTPase mediated signal transduction, GO:0007588: excretion, GO:0008217: regulation of blood pressure, GO:0008219: cell death, GO:0008285: negative regulation of cell proliferation, GO:0008630: DNA damage response, signal transduction resulting in induction of apoptosis, GO:0014806: smooth muscle hyperplasia, GO:0016491: oxidoreductase activity, GO:0019899: enzyme binding, GO:0020037: heme binding, GO:0031670: cellular response to nutrient, GO:0032764: negative regulation of mast cell cytokine production, GO:0034101: erythrocyte homeostasis, GO:0035094: response to nicotine, GO:0042167: heme catabolic process, GO:0042542: response to hydrogen peroxide, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0043305: negative regulation of mast cell degranulation, GO:0043433: negative regulation of transcription factor activity, GO:0043619: regulation of transcription from RNA polymerase II promoter in response to oxidative stress, GO:0043627: response to estrogen stimulus, GO:0045080: positive regulation of chemokine biosynthetic process, GO:0045765: regulation of angiogenesis, GO:0045768: positive regulation of anti-apoptosis, GO:0045909: positive regulation of vasodilation, GO:0046872: metal ion binding, GO:0050896: response to stimulus, GO:0055072: iron ion homeostasis, GO:0055072: iron ion homeostasis	00860: Porphyrin and chlorophyll metabolism	10.09	10.23	9.81	9.25	8.61	8.37	10.06	9.77	9.90	10.33	9.53	8.55	1

(*Continued*)

TABLE E4. (*Continued*)

203904_x_at	CD82	CD82 molecule	NM_002231	3732 Hs.527778	GO:0005515: protein binding, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0016020: membrane, GO:0016021: integral to membrane	04115: p53 signaling pathway	10.42	10.10	9.78	9.52	9.46	9.59	9.98	10.10	9.94	10.24	9.76	9.47	1
203234_at	UPP1	uridine phosphorylase 1	NM_003364	7378 Hs.488240	GO:0004850: uridine phosphorylase activity, GO:0004850: uridine phosphorylase activity, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0009116: nucleoside metabolic process, GO:0009166: nucleotide catabolic process, GO:0016757: transferase activity, transferring glycosyl groups	00240: Pyrimidine metabolism, 00983: NA	9.26	8.68	7.53	6.72	6.33	5.99	8.71	8.17	7.75	8.45	7.27	6.05	1
203499_at	EPHA2	EPH receptor A2	NM_004431	1969 Hs.171596	GO:0000166: nucleotide binding, GO:0004872: receptor activity, GO:0005003: ephrin receptor activity, GO:0005524: ATP binding, GO:0005887: integral to plasma membrane, GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007169: transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007275: multicellular organismal development, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016740: transferase activity, GO:0030182: neuron differentiation, GO:0048013: ephrin receptor signaling pathway	04360: Axon guidance	8.57	8.01	7.55	7.16	6.69	6.69	8.11	7.92	7.79	8.35	7.28	6.76	1
203127_s_at	SPTLC2	serine palmitoyl-transferase, long chain base subunit 2	BC005123	9517 Hs.435661	GO:0004758: serine C-palmitoyltransferase activity, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0008415: acyltransferase activity, GO:0009058: biosynthetic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016769: transferase activity, transferring nitrogenous groups, GO:0030170: pyridoxal phosphate binding	00600: Sphingolipid metabolism	8.44	8.20	7.48	6.15	5.20	4.99	8.28	7.99	7.86	8.40	6.82	4.86	1
203233_at	IL4R	interleukin 4 receptor	NM_000418	3566 Hs.513457	GO:0004872: receptor activity, GO:0004896: hematopoietin/ interferon-class (D200-domain) cytokine receptor activity, GO:0004913: interleukin-4 receptor activity, GO:0005057: receptor signaling protein activity, GO:0005515: protein binding, GO:0005576: extracellular region, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0006955: immune response, GO:0007165: signal transduction	04060: Cytokine-cytokine receptor interaction, 04630: Jak-STAT signaling pathway, 04640: Hematopoietic cell lineage	9.91	9.60	9.22	8.91	8.83	8.50	9.43	9.47	9.26	9.70	9.06	8.22	1

(*Continued*)

TABLE E4. (*Continued*)

202833_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	NM_000295	5265	Hs.525557	GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0006953: acute-phase response, GO:0007596: blood coagulation, GO:0008233: peptidase activity, GO:0031093: platelet alpha granule lumen	04610: Complement and coagulation cascades	6.15	5.76	4.82	3.87	3.47	3.22	5.30	5.19	4.51	5.71	4.12	3.23	1
202988_s_at	RGS1	regulator of G-protein signaling 1	NM_002922	5996	Hs.75256	GO:0004871: signal transducer activity, GO:0005096: GTPase activator activity, GO:0005516: calmodulin binding, GO:0005886: plasma membrane, GO:0006955: immune response, GO:0007193: G-protein signaling, adenylate cyclase inhibiting pathway, GO:0009968: negative regulation of signal transduction		4.12	3.66	3.56	3.39	3.43	3.34	3.46	3.41	3.50	3.99	3.71	3.27	1
202575_at	CRABP2	cellular retinoic acid binding protein 2	NM_001878	1382	Hs.405662	GO:0005215: transporter activity, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006355: regulation of transcription, DNA-dependent, GO:0006810: transport, GO:0007165: signal transduction, GO:0008289: lipid binding, GO:0008544: epidermis development, GO:0016918: retinal binding, GO:0019841: retinol binding		12.76	12.68	12.39	11.53	10.68	10.16	12.16	11.98	11.90	12.36	11.16	10.28	1
202779_s_at	UBE2S	ubiquitin-conjugating enzyme E2S	NM_014501	27338	Hs.396393	GO:0004842: ubiquitin-protein ligase activity, GO:0016874: ligase activity, GO:0019787: small conjugating protein ligase activity, GO:0051246: regulation of protein metabolic process	04120: Ubiquitin mediated proteolysis	8.64	8.30	7.90	7.66	7.13	7.36	8.17	7.91	7.76	8.27	7.64	7.40	1
201243_s_at	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	NM_001677	481	Hs.291196, Hs.706952	GO:0001666: response to hypoxia, GO:0005391: sodium:potassium-exchanging ATPase activity, GO:0005515: protein binding, GO:0005886: plasma membrane, GO:0005890: sodium:potassium-exchanging ATPase complex, GO:0006811: ion transport, GO:0006813: potassium ion transport, GO:0006814: sodium ion transport, GO:0016021: integral to membrane, GO:0016323: basolateral plasma membrane, GO:0030955: potassium ion binding, GO:0031402: sodium ion binding		12.60	12.63	12.34	11.87	11.41	11.88	11.87	12.21	11.91	12.36	11.57	11.53	1

(*Continued*)

TABLE E4. (*Continued*)

201473_at	JUNB	jun B proto-oncogene	NM_002229	3726 Hs.25292	GO:0000785: chromatin, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0003713: transcription coactivator activity, GO:0003714: transcription corepressor activity, GO:0005634: nucleus, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0009987: cellular process, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity		10.15	9.74	9.57	8.98	8.62	8.85	9.51	9.59	9.38	9.77	8.88	8.83	1
203968_s_at	CDC6	cell division cycle 6 homolog (S. cerevisiae)	NM_001254	990 Hs.405958	GO:0000076: DNA replication checkpoint, GO:0000079: regulation of cyclin-dependent protein kinase activity, GO:0000166: nucleotide binding, GO:0003682: chromatin binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0005737: cytoplasm, GO:0005819: spindle, GO:0005829: cytosol, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007089: traversing start control point of mitotic cell cycle, GO:0008156: negative regulation of DNA replication, GO:0008285: negative regulation of cell proliferation, GO:0017111: nucleoside-triphosphatase activity, GO:0051301: cell division	04110: Cell cycle	4.18	3.32	3.07	2.93	2.78	2.89	3.30	3.94	3.78	3.90	3.48	2.80	1
38037_at	HBEGF	heparin-binding EGF-like growth factor	M60278	1839 Hs.799, Hs.592942	GO:0004872: receptor activity, GO:0005154: epidermal growth factor receptor binding, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005887: integral to plasma membrane, GO:0007165: signal transduction, GO:0007173: epidermal growth factor receptor signaling pathway, GO:0007517: muscle development, GO:0008016: regulation of heart contraction, GO:0008083: growth factor activity, GO:0008201: heparin binding, GO:0009986: cell surface, GO:0016020: membrane, GO:0035313: wound healing, spreading of epidermal cells, GO:0048661: positive regulation of smooth muscle cell proliferation, GO:0051549: positive regulation of keratinocyte migration	04012: ErbB signaling pathway, 04912: GnRH signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection	4.81	3.66	3.67	3.48	3.45	3.43	3.64	4.43	3.87	4.05	3.59	3.43	1

(*Continued*)

TABLE E4. (*Continued*)

203821_at	HBEGF	heparin-binding EGF-like growth factor	NM_001945	1839	Hs.799, Hs.592942	GO:0004872: receptor activity, GO:0005154: epidermal growth factor receptor binding, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005887: integral to plasma membrane, GO:0007165: signal transduction, GO:0007173: epidermal growth factor receptor signaling pathway, GO:0007517: muscle development, GO:0008016: regulation of heart contraction, GO:0008083: growth factor activity, GO:0008201: heparin binding, GO:0009986: cell surface, GO:0016020: membrane, GO:0035313: wound healing, spreading of epidermal cells, GO:0048661: positive regulation of smooth muscle cell proliferation, GO:0051549: positive regulation of keratinocyte migration	04012: ErbB signaling pathway, 04912: GnRH signaling pathway, 05120: Epithelial cell signaling in Helicobacter pylori infection	8.55	7.50	7.27	6.71	6.42	6.55	7.33	7.91	7.26	7.58	6.90	6.42	1
208893_s_at	DUSP6	dual specificity phosphatase 6	BC003143	1848	Hs.298654, Hs.712581	GO:0000188: inactivation of MAPK activity, GO:0004722: protein serine/threonine phosphatase activity, GO:0004725: protein tyrosine phosphatase activity, GO:0004725: protein tyrosine phosphatase activity, GO:0005625: soluble fraction, GO:0005654: nucleoplasm, GO:0005737: cytoplasm, GO:0006470: protein amino acid dephosphorylation, GO:0016787: hydrolase activity, GO:0017017: MAP kinase tyrosine/serine/threonine phosphatase activity	04010: MAPK signaling pathway	7.17	6.58	6.38	6.32	6.36	6.38	6.16	6.79	6.43	6.27	6.36	6.11	1
205015_s_at	TGFA	transforming growth factor, alpha	NM_003236	7039	Hs.170009	GO:0000187: activation of MAPK activity, GO:0001525: angiogenesis, GO:0001948: glycoprotein binding, GO:0004708: MAP kinase kinase activity, GO:0004871: signal transducer activity, GO:0005155: epidermal growth factor receptor activating ligand activity, GO:0005576: extracellular region, GO:0005886: plasma membrane, GO:0008083: growth factor activity, GO:0008283: cell proliferation, GO:0016021: integral to membrane, GO:0045741: positive regulation of epidermal growth factor receptor activity, GO:0045840: positive regulation of mitosis, GO:0050679: positive regulation of epithelial cell proliferation	04012: ErbB signaling pathway, 05211: Renal cell carcinoma, 05212: Pancreatic cancer, 05214: Glioma, 05215: Prostate cancer, 05223: Non-small cell lung cancer	4.25	3.97	3.44	3.00	2.76	2.62	3.40	3.65	4.01	4.44	3.31	2.63	1

(*Continued*)

TABLE E4. (*Continued*)

209237_s_at	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	AF164142	9962 Hs.516866	GO:0005215: transporter activity, GO:0005624: membrane fraction, GO:0005887: integral to plasma membrane, GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006810: transport, GO:0006811: ion transport, GO:0006814: sodium ion transport, GO:0008523: sodium-dependent multivitamin transmembrane transporter activity, GO:0015205: nucleobase transmembrane transporter activity, GO:0015293: symporter activity, GO:0015851: nucleobase transport, GO:0015993: molecular hydrogen transport, GO:0016020: membrane, GO:0019852: L-ascorbic acid metabolic process, GO:0031402: sodium ion binding		3.88	2.61	2.17	1.95	1.86	1.87	2.08	1.91	2.39	3.44	1.89	1.85	1
222223_s_at	IL1F5	interleukin 1 family, member 5 (delta)	AF216693	26525 Hs.516301	GO:0005152: interleukin-1 receptor antagonist activity, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0006954: inflammatory response, GO:0006955: immune response		12.63	12.50	12.15	11.24	10.34	10.35	12.60	12.27	12.17	12.56	11.79	10.78	1
204493_at	BID	BH3 interacting domain death agonist	NM_001196	637 Hs.591054	GO:0001836: release of cytochrome c from mitochondria, GO:0005123: death receptor binding, GO:0005515: protein binding, GO:0005624: membrane fraction, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0005829: cytosol, GO:0005829: cytosol, GO:0008625: induction of apoptosis via death domain receptors, GO:0008633: activation of pro-apoptotic gene products, GO:0016020: membrane, GO:0051402: neuron apoptosis	04115: p53 signaling pathway, 04210: Apoptosis, 04650: Natural killer cell mediated cytotoxicity	4.22	3.86	3.45	3.20	3.01	2.86	3.10	3.37	3.60	3.86	3.21	2.71	1
220664_at	SPRR2C	small proline-rich protein 2C (pseudogene)	NM_006518	6702 Hs.2421	GO:0001533: cornified envelope, GO:0003676: nucleic acid binding, GO:0008544: epidermis development, GO:0009411: response to UV, GO:0030216: keratinocyte differentiation, GO:0046872: metal ion binding, GO:0046983: protein dimerization activity, GO:0051258: protein polymerization		13.44	13.24	12.46	10.21	8.22	7.97	12.86	12.57	11.87	13.04	11.23	7.94	1

(*Continued*)

TABLE E4. (*Continued*)

222037_at	MCM4	minichromosome maintenance complex component 4	AI859865	4173 Hs.460184	GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003678: DNA helicase activity, GO:0003697: single-stranded DNA binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0006260: DNA replication, GO:0006260: DNA replication, GO:0006268: DNA unwinding during replication, GO:0006270: DNA replication initiation, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0017111: nucleoside-triphosphatase activity	03030: DNA polymerase, 04110: Cell cycle	5.56	5.23	4.93	4.66	4.49	4.72	5.22	5.33	5.05	5.50	5.19	4.74	1
218810_at	ZC3H12A	zinc finger CCCH-type containing 12A	NM_025079	80149 Hs.656294	GO:0001525: angiogenesis, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006915: apoptosis, GO:0007275: multicellular organismal development, GO:0008270: zinc ion binding, GO:0030154: cell differentiation, GO:0046872: metal ion binding		10.27	10.08	9.50	8.12	6.10	6.37	9.54	9.33	9.12	9.89	7.71	6.07	1
219680_at	NLRX1	NLR family member X1	NM_024618	79671 Hs.524082	GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005737: cytoplasm		9.22	9.03	8.79	8.18	7.82	7.71	9.01	8.74	8.59	8.99	8.87	7.92	1
216212_s_at	DKC1	dyskeratosis congenita 1, dyskerin	AJ010395	1736 Hs.4747	GO:0001522: pseudouridine synthesis, GO:0003720: telomerase activity, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0005697: telomerase holoenzyme complex, GO:0005730: nucleolus, GO:0006364: rRNA processing, GO:0006396: RNA processing, GO:0007004: telomere maintenance via telomerase, GO:0008283: cell proliferation, GO:0009982: pseudouridine synthase activity, GO:0016853: isomerase activity		8.28	7.69	7.71	7.37	7.34	7.56	7.82	8.01	7.92	8.16	8.20	7.49	1
217185_s_at	LOC442240	similar to zinc finger protein 259	Z95118	442240 Hs.626676			6.36	5.77	5.77	5.37	5.08	5.17	5.88	5.74	5.58	6.04	5.96	5.11	1

(*Continued*)

TABLE E4. (*Continued*)

213421_x_at	PRSS3	protease, serine, 3	AW007273	5646 Hs.654513	GO:0004252: serine-type endopeptidase activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007586: digestion, GO:0008233: peptidase activity, GO:0031638: zymogen activation, GO:0043542: endothelial cell migration	04080: Neuroactive ligand-receptor interaction	11.32	11.07	10.76	9.98	9.98	9.74	11.18	10.73	10.73	10.96	10.95	10.11	1
214011_s_at	HSPC111	hypothetical protein HSPC111	BE314601	51491 Hs.696283	GO:0005634: nucleus		9.92	9.49	9.37	9.00	8.71	9.16	9.44	9.50	9.51	9.57	9.25	9.00	1
210754_s_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	M79321	4067 Hs.699154	GO:0000166: nucleotide binding, GO:0004713: protein-tyrosine kinase activity, GO:0004715: non-membrane spanning protein tyrosine kinase activity, GO:0004716: receptor signaling protein tyrosine kinase activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0006468: protein amino acid phosphorylation, GO:0007242: intracellular signaling cascade, GO:0008284: positive regulation of cell proliferation, GO:0009725: response to hormone stimulus, GO:0016740: transferase activity, GO:0018108: peptidyl-tyrosine phosphorylation, GO:0030218: erythrocyte differentiation, GO:0042531: positive regulation of tyrosine phosphorylation of STAT protein, GO:0044419: interspecies interaction between organisms, GO:0045121: membrane raft	04662: B cell receptor signaling pathway, 04664: Fc epsilon RI signaling pathway, 04730: Long-term depression, 05120: Epithelial cell signaling in Helicobacter pylori infection	8.01	7.99	7.51	7.09	6.29	6.17	7.36	7.67	7.35	7.99	7.24	5.76	1
212141_at	MCM4	minichromosome maintenance complex component 4	AA604621	4173 Hs.460184	GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003678: DNA helicase activity, GO:0003697: single-stranded DNA binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0006260: DNA replication, GO:0006260: DNA replication, GO:0006268: DNA unwinding during replication, GO:0006270: DNA replication initiation, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0017111: nucleoside-triphosphatase activity	03030: DNA polymerase, 04110: Cell cycle	8.00	7.71	7.38	6.75	6.27	6.91	7.60	8.03	7.64	7.86	7.44	6.91	1
209792_s_at	KLK10	kallikrein-related peptidase 10	BC002710	5655 Hs.275464	GO:0004252: serine-type endopeptidase activity, GO:0005576: extracellular region, GO:0006508: proteolysis, GO:0045786: negative regulation of cell cycle		12.34	12.06	11.76	10.90	9.81	9.90	12.15	12.00	11.87	12.08	11.59	10.26	1

(*Continued*)

TABLE E4. (*Continued*)

209800_at	KRT16	keratin 16	AF061812	3868 Hs.655160	GO:0005200: structural constituent of cytoskeleton, GO:0005515: protein binding, GO:0005882: intermediate filament, GO:0007010: cytoskeleton organization and biogenesis, GO:0008283: cell proliferation, GO:0008544: epidermis development	01430: Cell Communication	14.28	13.52	12.71	11.49	10.25	10.11	13.97	13.28	12.92	13.66	12.48	10.78	1
209727_at	GM2A	GM2 ganglioside activator	M76477	2760 Hs.483873	GO:0005319: lipid transporter activity, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005764: lysosome, GO:0005889: hydrogen:potassium-exchanging ATPase complex, GO:0006689: ganglioside catabolic process, GO:0006869: lipid transport, GO:0007611: learning and/or memory, GO:0009313: oligosaccharide catabolic process, GO:0009898: internal side of plasma membrane, GO:0016004: phospholipase activator activity, GO:0019377: glycolipid catabolic process, GO:0019915: sequestering of lipid, GO:0030149: sphingolipid catabolic process, GO:0030290: sphingolipid activator protein activity, GO:0032428: beta-N-acetylgalactosaminidase activity, GO:0045179: apical cortex, GO:0050877: neurological system process, GO:0050885: neuromuscular process controlling balance, GO:0051345: positive regulation of hydrolase activity		9.35	9.33	8.02	7.35	5.71	5.73	8.61	8.77	7.98	8.75	7.22	5.55	1

(*Continued*)

TABLE E4. (*Continued*)

209772_s_at	CD24	CD24 molecule	X69397	100133941	Hs.644105, Hs.694721	GO:0001666: response to hypoxia, GO:0001775: cell activation, GO:0001959: regulation of cytokine and chemokine mediated signaling pathway, GO:0002237: response to molecule of bacterial origin, GO:0002768: immune response-regulating cell surface receptor signaling pathway, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0005886: plasma membrane, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0007274: neuromuscular synaptic transmission, GO:0008629: induction of apoptosis by intracellular signals, GO:0009897: external side of plasma membrane, GO:0016055: Wnt receptor signaling pathway, GO:0016337: cell-cell adhesion, GO:0016477: cell migration, GO:0019901: protein kinase binding, GO:0030246: carbohydrate binding, GO:0030296: protein tyrosine kinase activator activity, GO:0030856: regulation of epithelial cell differentiation, GO:0031225: anchored to membrane, GO:0031295: T cell costimulation, GO:0031362: anchored to external side of plasma membrane, GO:0032597: B cell receptor transport into membrane raft, GO:0032600: chemokine receptor transport out of membrane raft, GO:0032913: negative regulation of transforming growth factor-beta3 production, GO:0042104: positive regulation of activated T cell proliferation, GO:0042325: regulation of phosphorylation, GO:0042632: cholesterol homeostasis, GO:0043406: positive regulation of MAP kinase activity, GO:0043408: regulation of MAPKKK cascade, GO:0043627: response to estrogen stimulus, GO:0045121: membrane raft, GO:0045730: respiratory burst, GO:0048488: synaptic vesicle endocytosis		11.94	11.67	11.23	10.12	8.59	8.62	11.74	11.26	11.11	11.50	10.41	8.75	1
209126_x_at	KRT6B	keratin 6B	L42612	3854	Hs.709235	GO:0005200: structural constituent of cytoskeleton, GO:0005882: intermediate filament, GO:0007398: ectoderm development	01430: Cell Communication	14.91	14.57	14.01	13.29	12.57	12.47	14.65	14.34	14.15	14.48	13.91	12.87	1
209514_s_at	RAB27A	RAB27A, member RAS oncogene family	BE502030	5873	Hs.654978	GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0016020: membrane, GO:0030425: dendrite, GO:0042470: melanosome		9.24	9.30	8.74	7.91	6.02	6.29	9.28	8.94	8.84	9.58	8.07	6.41	1

(*Continued*)

TABLE E4. (*Continued*)

208992 _s_at	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	BC000627	6774 Hs.463059	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0004871: signal transducer activity, GO:0005062: hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006355: regulation of transcription, DNA-dependent, GO:0006928: cell motility, GO:0007165: signal transduction, GO:0007165: signal transduction, GO:0007259: JAK-STAT cascade, GO:0007399: nervous system development, GO:0008134: transcription factor binding, GO:0019221: cytokine and chemokine mediated signaling pathway, GO:0044419: interspecies interaction between organisms	04630: Jak-STAT signaling pathway, 04920: Adipocytokine signaling pathway, 05212: Pancreatic cancer, 05221: Acute myeloid leukemia	11.60	11.40	10.99	10.50	9.91	10.21	11.17	11.18	10.95	11.42	10.94	9.75	1
209093 _s_at	GBA	glucosidase, beta; acid (includes glucosylceramidase)	K02920	2629 Hs.282997	GO:0003824: catalytic activity, GO:0004348: glucosylceramidase activity, GO:0005515: protein binding, GO:0005764: lysosome, GO:0005765: lysosomal membrane, GO:0005975: carbohydrate metabolic process, GO:0006629: lipid metabolic process, GO:0006665: sphingolipid metabolic process, GO:0007040: lysosome organization and biogenesis, GO:0008152: metabolic process, GO:0016020: membrane, GO:0016798: hydrolase activity, acting on glycosyl bonds, GO:0043169: cation binding	00460: Cyanoamino acid metabolism, 00500: Starch and sucrose metabolism, 00600: Sphingolipid metabolism, 00940: Phenylpropanoid biosynthesis, 01032: Glycan structures - degradation	10.15	10.21	9.72	8.87	8.15	7.84	9.95	9.51	9.56	10.06	9.43	8.30	1
208002 _s_at	ACOT7	acyl-CoA thioesterase 7	NM_007274	11332 Hs.126137	GO:0000062: acyl-CoA binding, GO:0004091: carboxylesterase activity, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0006629: lipid metabolic process, GO:0016290: palmitoyl-CoA hydrolase activity, GO:0016787: hydrolase activity	01040: Polyunsaturated fatty acid biosynthesis	9.20	9.04	8.78	8.14	8.16	8.00	8.86	8.81	8.80	9.18	8.93	8.36	1

(*Continued*)

TABLE E4. (*Continued*)

208433_s_at	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	NM_017522	7804 Hs.576154	GO:0004888: transmembrane receptor activity, GO:0005509: calcium ion binding, GO:0005576: extracellular region, GO:0005886: plasma membrane, GO:0005901: caveola, GO:0006508: proteolysis, GO:0006629: lipid metabolic process, GO:0006897: endocytosis, GO:0007165: signal transduction, GO:0008034: lipoprotein binding, GO:0016021: integral to membrane, GO:0019221: cytokine and chemokine mediated signaling pathway, GO:0030227: apolipoprotein E receptor activity, GO:0030227: apolipoprotein E receptor activity, GO:0030229: very-low-density lipoprotein receptor activity		4.20	3.35	3.18	3.18	3.14	3.15	3.53	3.58	3.44	3.83	3.78	3.03	1
207381_at	ALOX12B	arachidonate 12-lipoxygenase, 12R type	NM_001139	242 Hs.136574	GO:0004052: arachidonate 12-lipoxygenase activity, GO:0005506: iron ion binding, GO:0006629: lipid metabolic process, GO:0008544: epidermis development, GO:0016165: lipoxygenase activity, GO:0016491: oxidoreductase activity, GO:0019370: leukotriene biosynthetic process, GO:0046872: metal ion binding	00590: Arachidonic acid metabolism	11.41	11.35	11.00	10.34	9.57	9.55	11.29	10.94	10.90	11.28	10.85	9.64	1
207463_x_at	PRSS3	protease, serine, 3	NM_002771	5646 Hs.654513	GO:0004252: serine-type endopeptidase activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007586: digestion, GO:0008233: peptidase activity, GO:0031638: zymogen activation, GO:0043542: endothelial cell migration	04080: Neuroactive ligand-receptor interaction	11.14	10.86	10.54	9.68	9.55	9.45	11.10	10.48	10.48	10.78	10.79	9.82	1
206788_s_at	CBFB	core-binding factor, beta subunit	AF294326	865 Hs.460988	GO:0003674: molecular_function, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0003713: transcription coactivator activity, GO:0005515: protein binding, GO:0005575: cellular_component, GO:0005634: nucleus, GO:0006366: transcription from RNA polymerase II promoter, GO:0008150: biological_process		7.13	7.05	6.89	6.71	5.84	6.15	6.84	7.41	7.00	7.56	6.94	6.10	1

(*Continued*)

TABLE E4. (*Continued*)

207367_at	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	NM_001676	479 Hs.147111	GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0005524: ATP binding, GO:0005889: hydrogen:potassium-exchanging ATPase complex, GO:0006813: potassium ion transport, GO:0008152: metabolic process, GO:0008900: hydrogen:potassium-exchanging ATPase activity, GO:0015077: monovalent inorganic cation transmembrane transporter activity, GO:0015662: ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, GO:0015992: proton transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016787: hydrolase activity, GO:0016820: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, GO:0030955: potassium ion binding	00190: Oxidative phosphorylation	10.82	11.09	9.97	7.82	5.20	4.85	9.50	9.54	8.83	10.31	7.40	4.04	1
206499_s_at	RCC1	regulator of chromosome condensation 1	NM_001269	1104 Hs.469723	GO:0000082: G1/S transition of mitotic cell cycle, GO:0000790: nuclear chromatin, GO:0000794: condensed nuclear chromosome, GO:0003682: chromatin binding, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005087: Ran guanyl-nucleotide exchange factor activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0007049: cell cycle, GO:0007052: mitotic spindle organization and biogenesis, GO:0007088: regulation of mitosis, GO:0007090: regulation of S phase of mitotic cell cycle, GO:0042393: histone binding, GO:0051301: cell division		7.20	7.04	6.76	6.35	5.62	5.93	6.87	6.93	6.99	7.21	7.14	6.21	1
206628_at	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	NM_000343	6523 Hs.1964	GO:0005215: transporter activity, GO:0005351: sugar:hydrogen symporter activity, GO:0005412: glucose:sodium symporter activity, GO:0005515: protein binding, GO:0005887: integral to plasma membrane, GO:0005903: brush border, GO:0006811: ion transport, GO:0006814: sodium ion transport, GO:0008643: carbohydrate transport, GO:0015293: symporter activity, GO:0015758: glucose transport, GO:0016020: membrane, GO:0016324: apical plasma membrane, GO:0031402: sodium ion binding, GO:0050892: intestinal absorption		8.39	8.41	7.78	6.36	5.14	5.48	8.49	7.93	7.88	8.41	7.49	5.45	1

(*Continued*)

TABLE E4. (*Continued*)

206008_at	TGM1	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)	NM_000359	7051 Hs.508950	GO:0001533: cornified envelope, GO:0003810: protein-glutamine gamma-glutamyltransferase activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005913: cell-cell adherens junction, GO:0006464: protein modification process, GO:0008415: acyltransferase activity, GO:0009887: organ morphogenesis, GO:0016020: membrane, GO:0016740: transferase activity, GO:0018149: peptide cross-linking, GO:0030216: keratinocyte differentiation, GO:0031224: intrinsic to membrane, GO:0031424: keratinization, GO:0043163: cell envelope organization and biogenesis	11.15	10.82	10.24	9.32	8.53	8.44	11.08	10.38	10.16	10.80	9.91	8.89	1
206472_s_at	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	NM_005078	7090 Hs.709205	GO:0005515: protein binding, GO:0005634: nucleus, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0009887: organ morphogenesis, GO:0016055: Wnt receptor signaling pathway, GO:0045449: regulation of transcription	8.87	8.72	8.52	7.90	7.50	7.23	8.69	8.43	8.54	8.81	8.49	7.29	1
205895_s_at	NOLC1	nucleolar and coiled-body phosphoprotein 1	NM_004741	9221 Hs.523238	GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005525: GTP binding, GO:0005634: nucleus, GO:0005730: nucleolus, GO:0005737: cytoplasm, GO:0006364: rRNA processing, GO:0007049: cell cycle, GO:0007067: mitosis	7.08	6.67	6.52	6.13	5.69	6.12	6.55	6.75	6.60	6.67	6.57	6.04	1
206004_at	TGM3	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)	NM_003245	7053 Hs.2022	GO:0000287: magnesium ion binding, GO:0003810: protein-glutamine gamma-glutamyltransferase activity, GO:0003924: GTPase activity, GO:0005509: calcium ion binding, GO:0005525: GTP binding, GO:0005737: cytoplasm, GO:0006464: protein modification process, GO:0008415: acyltransferase activity, GO:0016746: transferase activity, transferring acyl groups, GO:0018149: peptide cross-linking, GO:0019003: GDP binding, GO:0030216: keratinocyte differentiation, GO:0030216: keratinocyte differentiation, GO:0031069: hair follicle morphogenesis, GO:0031234: extrinsic to internal side of plasma membrane, GO:0031424: keratinization, GO:0043163: cell envelope organization and biogenesis, GO:0051262: protein tetramerization	12.32	12.01	11.70	10.79	10.08	10.42	12.31	11.90	11.91	12.19	11.53	10.47	1

(*Continued*)

TABLE E4. (*Continued*)

205595_at	DSG3	desmoglein 3 (pemphigus vulgaris antigen)	NM_001944	1830 Hs.1925	GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005829: cytosol, GO:0005886: plasma membrane, GO:0005886: plasma membrane, GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0016021: integral to membrane, GO:0030054: cell junction	01430: Cell Communication	12.10	11.67	11.21	10.74	10.17	10.50	12.05	11.90	11.52	11.81	11.26	10.46	1
205847_at	PRSS22	protease, serine, 22	NM_022119	64063 Hs.459709	GO:0004252: serine-type endopeptidase activity, GO:0005576: extracellular region, GO:0006508: proteolysis, GO:0008233: peptidase activity		9.01	8.75	8.00	7.16	6.71	6.94	8.78	8.55	8.40	8.78	7.93	7.27	1
205349_at	GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	NM_002068	2769 Hs.73797	GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0004871: signal transducer activity, GO:0005525: GTP binding, GO:0005834: heterotrimeric G-protein complex, GO:0005886: plasma membrane, GO:0006471: protein amino acid ADP-ribosylation, GO:0007165: signal transduction, GO:0007202: activation of phospholipase C activity, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0007207: muscarinic acetylcholine receptor, phospholipase C activating pathway, GO:0019001: guanyl nucleotide binding	04020: Calcium signaling pathway	10.39	10.00	9.74	9.17	8.93	8.98	10.15	9.95	9.71	10.06	9.81	9.15	1
205476_at	CCL20	chemokine (C-C motif) ligand 20	NM_004591	6364 Hs.75498	GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0006935: chemotaxis, GO:0006954: inflammatory response, GO:0006955: immune response, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0008009: chemokine activity, GO:0042742: defense response to bacterium	04060: Cytokine-cytokine receptor interaction	6.46	5.20	4.91	3.35	2.76	2.63	3.88	3.35	4.46	4.71	3.74	2.13	1
204767_s_at	FEN1	flap structure-specific endonuclease 1	BC000323	2237 Hs.409065	GO:0000287: magnesium ion binding, GO:0003684: damaged DNA binding, GO:0003690: double-stranded DNA binding, GO:0004519: endonuclease activity, GO:0004523: ribonuclease H activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006260: DNA replication, GO:0006302: double-strand break repair, GO:0008309: double-stranded DNA specific exodeoxyribonuclease activity, GO:0008409: 5'-3' exonuclease activity, GO:0009650: UV protection, GO:0016787: hydrolase activity, GO:0017108: 5'-flap endonuclease activity, GO:0030145: manganese ion binding, GO:0048015: phosphoinositide-mediated signaling	03030: DNA polymerase, 03410: NA, 03450: NA	7.67	7.33	7.03	6.67	6.51	6.51	7.38	7.17	7.42	7.42	7.24	6.89	1

(*Continued*)

TABLE E4. (*Continued*)

205014_at	FGFBP1	fibroblast growth factor binding protein 1	NM_005130	9982	Hs.1690	GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0005886: plasma membrane, GO:0007165: signal transduction, GO:0007267: cell-cell signaling, GO:0008201: heparin binding, GO:0008285: negative regulation of cell proliferation, GO:0019838: growth factor binding		11.28	10.54	10.11	9.42	9.24	9.78	10.61	10.45	10.03	10.38	10.18	10.03	1
203128_at	SPTLC2	serine palmitoyl-transferase, long chain base subunit 2	NM_004863	9517	Hs.435661	GO:0004758: serine C-palmitoyltransferase activity, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0008415: acyltransferase activity, GO:0009058: biosynthetic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016769: transferase activity, transferring nitrogenous groups, GO:0030170: pyridoxal phosphate binding	00600: Sphingolipid metabolism	6.59	6.67	6.16	5.64	5.30	4.86	6.49	7.10	6.34	7.08	6.36	5.25	1
203147_s_at	TRIM14	tripartite motif-containing 14	NM_014788	9830	Hs.575631	GO:0005515: protein binding, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0007386: compartment specification, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		6.57	6.42	6.35	6.16	5.93	6.00	5.74	6.34	6.13	6.45	6.41	5.70	1
202068_s_at	LDLR	low density lipoprotein receptor	NM_000527	3949	Hs.213289, Hs.714323	GO:0004872: receptor activity, GO:0004888: transmembrane receptor activity, GO:0005041: low-density lipoprotein receptor activity, GO:0005319: lipid transporter activity, GO:0005509: calcium ion binding, GO:0005768: endosome, GO:0005886: plasma membrane, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005905: coated pit, GO:0006493: protein amino acid O-linked glycosylation, GO:0006629: lipid metabolic process, GO:0006869: lipid transport, GO:0006897: endocytosis, GO:0008034: lipoprotein binding, GO:0008202: steroid metabolic process, GO:0008203: cholesterol metabolic process, GO:0010008: endosome membrane, GO:0030229: very-low-density lipoprotein receptor activity, GO:0030299: cholesterol absorption, GO:0030301: cholesterol transport, GO:0030669: clathrin-coated endocytic vesicle membrane, GO:0042157: lipoprotein metabolic process, GO:0042632: cholesterol homeostasis, GO:0044419: interspecies interaction between organisms		10.74	10.13	9.76	9.19	8.67	9.20	10.26	10.31	10.10	10.12	9.51	9.54	1
202712_s_at	CKMT1B	creatine kinase, mitochondrial 1B	NM_020990	1159	Hs.425633		00330: Arginine and proline metabolism	11.77	11.53	11.14	10.57	10.36	10.21	11.61	11.28	11.24	11.50	11.28	10.38	1

(*Continued*)

TABLE E4. (*Continued*)

201531_at	ZFP36	zinc finger protein 36, C3H type, homolog (mouse)	NM_003407	7538	Hs.534052, Hs.707878	GO:0000289: poly(A) tail shortening, GO:0003677: DNA binding, GO:0003727: single-stranded RNA binding, GO:0003729: mRNA binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0006402: mRNA catabolic process, GO:0007243: protein kinase cascade, GO:0008270: zinc ion binding, GO:0017091: AU-rich element binding, GO:0045638: negative regulation of myeloid cell differentiation, GO:0046872: metal ion binding, GO:0050728: negative regulation of inflammatory response, GO:0050779: RNA destabilization		10.48	10.01	9.85	9.52	9.30	9.54	9.87	10.01	9.92	10.04	9.72	9.51	1
201583_s_at	SEC23B	Sec23 homolog B (S. cerevisiae)	NM_006363	10483	Hs.369373, Hs.460238	GO:0000139: Golgi membrane, GO:0005515: protein binding, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005794: Golgi apparatus, GO:0006886: intracellular protein transport, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0008270: zinc ion binding, GO:0016020: membrane, GO:0016192: vesicle-mediated transport, GO:0030127: COPII vesicle coat, GO:0033116: ER-Golgi intermediate compartment membrane		8.86	8.61	8.39	7.93	7.49	7.89	8.65	8.53	8.61	8.88	8.46	7.80	1
200874_s_at	NOL5A	nucleolar protein 5A (56kDa with KKE/D repeat)	NM_006392	10528	Hs.376064	GO:0003723: RNA binding, GO:0005634: nucleus, GO:0005730: nucleolus, GO:0006364: rRNA processing		6.63	6.25	6.24	5.80	5.99	6.04	6.06	6.32	6.29	6.37	6.56	5.84	1
201489_at	PPIF	peptidylprolyl isomerase F (cyclophilin F)	BC005020	10105	Hs.381072	GO:0003755: peptidyl-prolyl cis-trans isomerase activity, GO:0005624: membrane fraction, GO:0005739: mitochondrion, GO:0005759: mitochondrial matrix, GO:0006457: protein folding, GO:0016853: isomerase activity, GO:0042277: peptide binding		11.66	11.40	10.96	10.28	9.39	9.36	11.32	11.07	10.87	11.32	10.61	9.36	1
200648_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	NM_002065	2752	Hs.518525	GO:0004356: glutamate-ammonia ligase activity, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0006542: glutamine biosynthetic process, GO:0006807: nitrogen compound metabolic process, GO:0016874: ligase activity	00251: Glutamate metabolism, 00550: Peptidoglycan biosynthesis, 00910: Nitrogen metabolism	11.61	11.72	11.21	10.87	9.77	10.12	11.12	11.27	11.25	11.73	10.78	9.96	1
200731_s_at	PTP4A1	protein tyrosine phosphatase type IVA, member 1	AW165960	7803	Hs.227777, Hs.715299	GO:0004725: protein tyrosine phosphatase activity, GO:0005737: cytoplasm, GO:0005769: early endosome, GO:0005783: endoplasmic reticulum, GO:0005819: spindle, GO:0005886: plasma membrane, GO:0006470: protein amino acid dephosphorylation, GO:0007049: cell cycle, GO:0007275: multicellular organismal development, GO:0016787: hydrolase activity		9.63	9.19	8.98	8.62	7.99	8.62	9.14	9.11	9.08	9.39	8.78	8.37	1

(*Continued*)

TABLE E4. (*Continued*)

220599_s_at	CARD14	caspase recruitment domain family, member 14	NM_024110	79092	Hs.675480, Hs.696253	GO:0001934: positive regulation of protein amino acid phosphorylation, GO:0005515: protein binding, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0007250: activation of NF-kappaB-inducing kinase activity, GO:0042981: regulation of apoptosis, GO:0050700: CARD domain binding		8.66	8.49	8.29	7.59	6.84	7.16	8.42	8.05	8.17	8.30	7.99	7.05	1
39249_at	AQP3	aquaporin 3 (Gill blood group)	AB001325	360	Hs.234642	GO:0002684: positive regulation of immune system process, GO:0005215: transporter activity, GO:0006810: transport, GO:0006833: water transport, GO:0007588: excretion, GO:0015250: water channel activity, GO:0015254: glycerol channel activity, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016323: basolateral plasma membrane, GO:0032526: response to retinoic acid, GO:0033280: response to vitamin D, GO:0045616: regulation of keratinocyte differentiation, GO:0051592: response to calcium ion		12.01	11.52	11.30	11.11	10.72	11.26	11.95	11.52	11.47	11.61	11.67	11.27	1
220318_at	EPN3	epsin 3	NM_017957	55040	Hs.670090	GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0008289: lipid binding, GO:0031410: cytoplasmic vesicle		8.15	8.08	7.79	6.97	6.13	6.11	8.30	7.80	7.83	8.03	7.50	6.58	1
220322_at	IL1F9	interleukin 1 family, member 9	NM_019618	56300	Hs.211238	GO:0005152: interleukin-1 receptor antagonist activity, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0006955: immune response, GO:0007267: cell-cell signaling		12.80	12.61	12.01	10.53	7.71	8.04	12.42	12.12	11.63	12.38	11.05	8.43	1
219695_at	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	NM_024703	55512	Hs.368421	GO:0000137: Golgi cis cisterna, GO:0000139: Golgi membrane, GO:0000287: magnesium ion binding, GO:0004767: sphingomyelin phosphodiesterase activity, GO:0005794: Golgi apparatus, GO:0005886: plasma membrane, GO:0006685: sphingomyelin catabolic process, GO:0007049: cell cycle, GO:0007275: multicellular organismal development, GO:0016021: integral to membrane, GO:0016787: hydrolase activity, GO:0030072: peptide hormone secretion	00600: Sphingolipid metabolism	10.13	10.28	10.05	9.60	8.57	8.55	10.05	9.81	9.83	10.13	9.56	8.37	1
220013_at	ABHD9	abhydrolase domain containing 9	NM_024794	79852	Hs.156457	GO:0005575: cellular_component, GO:0008150: biological_process, GO:0016787: hydrolase activity		11.21	11.17	10.98	10.43	9.96	9.93	11.14	10.82	10.82	11.08	11.04	10.05	1
219403_s_at	HPSE	heparanase	AF155510	10855	Hs.44227	GO:0000287: magnesium ion binding, GO:0004566: beta-glucuronidase activity, GO:0005509: calcium ion binding, GO:0005576: extracellular region, GO:0005765: lysosomal membrane, GO:0006029: proteoglycan metabolic process, GO:0016020: membrane, GO:0016787: hydrolase activity	00531: Glycosaminoglycan degradation, 01032: Glycan structures - degradation	11.33	11.29	10.69	9.12	6.01	6.67	11.22	10.44	10.43	11.09	9.79	7.01	1

(*Continued*)

TABLE E4. (*Continued*)

219630_at	PDZK1IP1	PDZK1 interacting protein 1	NM_005764	10158	Hs.431099	GO:0016020: membrane, GO:0016021: integral to membrane		12.14	12.16	11.76	11.12	10.02	10.12	12.14	11.59	11.60	11.94	11.32	10.13	1
219272_at	TRIM62	tripartite motif-containing 62	NM_018207	55223	Hs.656006	GO:0005515: protein binding, GO:0005622: intracellular, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		6.69	6.60	6.41	5.85	5.56	5.58	6.70	6.30	6.56	6.74	6.69	5.68	1
219358_s_at	CENTA2	centaurin, alpha 2	NM_018404	55803	Hs.514063	GO:0005546: phosphatidylinositol-4,5-bisphosphate binding, GO:0005547: phosphatidylinositol-3,4,5-triphosphate binding, GO:0005737: cytoplasm, GO:0005740: mitochondrial envelope, GO:0005886: plasma membrane, GO:0007507: heart development, GO:0008060: ARF GTPase activator activity, GO:0008270: zinc ion binding, GO:0030674: protein binding, bridging, GO:0032312: regulation of ARF GTPase activity, GO:0043325: phosphatidylinositol-3,4-bisphosphate binding, GO:0043533: inositol 1,3,4,5 tetrakisphosphate binding, GO:0046872: metal ion binding		10.09	9.92	9.66	8.99	8.13	8.04	10.07	9.57	9.61	9.80	9.36	8.39	1
218295_s_at	NUP50	nucleoporin 50kDa	AF267865	10762	Hs.475103	GO:0005634: nucleus, GO:0005643: nuclear pore, GO:0005654: nucleoplasm, GO:0015031: protein transport, GO:0016020: membrane, GO:0031965: nuclear membrane, GO:0046907: intracellular transport, GO:0051028: mRNA transport, GO:0065002: intracellular protein transport across a membrane		7.72	7.52	7.27	6.73	5.34	5.83	7.86	7.77	7.51	7.86	7.13	5.82	1
218900_at	CNNM4	cyclin M4	NM_020184	26504	Hs.175043	GO:0005886: plasma membrane, GO:0006811: ion transport, GO:0016021: integral to membrane		7.11	7.42	7.04	6.33	5.24	5.03	6.80	6.19	6.54	6.82	6.34	4.74	1
217202_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	U08626	2752	Hs.518525	GO:0004356: glutamate-ammonia ligase activity, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0006542: glutamine biosynthetic process, GO:0006807: nitrogen compound metabolic process, GO:0016874: ligase activity	00251: Glutamate metabolism, 00550: Peptidoglycan biosynthesis, 00910: Nitrogen metabolism	10.22	10.33	9.92	9.52	8.50	8.69	9.63	9.93	9.88	10.20	9.49	8.55	1
217755_at	HN1	hematological and neurological expressed 1	AF060925	51155	Hs.532803	GO:0005634: nucleus		9.68	9.43	9.12	8.75	8.08	8.60	9.54	9.17	9.30	9.52	9.35	8.67	1
216684_s_at	SS18	synovial sarcoma translocation, chromosome 18	AF257501	6760	Hs.404263	GO:0005634: nucleus		8.53	8.33	8.26	7.97	7.14	7.76	8.39	8.24	8.21	8.47	8.10	7.60	1
217140_s_at	LOC 100132302	similar to Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	AJ002428	100132302				10.67	10.55	10.39	9.98	9.48	10.00	10.44	10.52	10.44	10.52	10.49	9.78	1

(*Continued*)

TABLE E4. (*Continued*)

216258 _s_at	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	BE148534	5275 Hs.241407	GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0009411: response to UV, GO:0030162: regulation of proteolysis		10.44	10.22	9.65	8.18	5.64	5.69	10.50	9.93	9.31	10.09	8.19	5.31	1
216379 _x_at			AK000168				13.79	13.67	13.42	12.88	12.14	12.13	13.67	13.50	13.32	13.58	13.14	12.21	1
215465 _at	ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12	AL080207	26154 Hs.134585	GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0006869: lipid transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016887: ATPase activity, GO:0019725: cellular homeostasis	02010: ABC transporters - General	11.43	11.56	11.25	10.52	9.36	9.69	11.55	11.15	11.03	11.49	10.86	9.77	1
215728 _s_at	ACOT7	acyl-CoA thioesterase 7	AL031848	11332 Hs.126137	GO:0000062: acyl-CoA binding, GO:0004091: carboxylesterase activity, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0006629: lipid metabolic process, GO:0016290: palmitoyl-CoA hydrolase activity, GO:0016787: hydrolase activity	01040: Polyunsaturated fatty acid biosynthesis	6.11	5.90	5.79	5.52	5.31	5.26	5.67	5.91	5.89	5.98	5.94	5.16	1
214490 _at	ARSF	arylsulfatase F	NM_004042	416 Hs.101674	GO:0004065: arylsulfatase activity, GO:0005509: calcium ion binding, GO:0005576: extracellular region, GO:0008152: metabolic process, GO:0016787: hydrolase activity		8.67	9.27	8.79	7.64	5.30	4.99	8.66	8.36	8.31	9.24	7.73	4.24	1
214549 _x_at	SPRR1A	small proline-rich protein 1A	NM_005987	6698 Hs.46320	GO:0001533: cornified envelope, GO:0005198: structural molecule activity, GO:0005737: cytoplasm, GO:0008544: epidermis development, GO:0018149: peptide cross-linking, GO:0030216: keratinocyte differentiation, GO:0030674: protein binding, bridging, GO:0031424: keratinization		14.39	14.05	13.80	12.91	12.29	12.05	14.27	13.93	13.79	13.97	13.73	12.16	1
214070 _s_at	ATP10B	ATPase, class V, type 10B	AW006935	23120 Hs.109358	GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004012: phospholipid-translocating ATPase activity, GO:0005524: ATP binding, GO:0006810: transport, GO:0015662: ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, GO:0015914: phospholipid transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016787: hydrolase activity		9.58	9.82	9.39	9.05	8.07	7.87	9.83	9.48	9.62	9.83	9.41	8.29	1
214205 _x_at	GLRX3	glutaredoxin 3	AK022131	10539 Hs.42644	GO:0005515: protein binding, GO:0005737: cytoplasm, GO:0009055: electron carrier activity, GO:0015035: protein disulfide oxidoreductase activity, GO:0045454: cell redox homeostasis		9.53	9.38	9.10	8.63	8.42	8.44	9.36	9.15	9.18	9.03	9.35	8.45	1

(*Continued*)

TABLE E4. (*Continued*)

213562_s_at	SQLE	squalene epoxidase	BF979497	6713 Hs.71465	GO:0004506: squalene monooxygenase activity, GO:0004506: squalene monooxygenase activity, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005789: endoplasmic reticulum membrane, GO:0005792: microsome, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016126: sterol biosynthetic process, GO:0016491: oxidoreductase activity	00100: Biosynthesis of steroids, 00900: Terpenoid biosynthesis	9.43	9.15	8.91	8.05	6.66	7.43	9.52	9.35	9.27	9.40	8.58	7.71	1
213796_at	SPRR1A	small proline-rich protein 1A	AI923984	6698 Hs.46320	GO:0001533: cornified envelope, GO:0005198: structural molecule activity, GO:0005737: cytoplasm, GO:0008544: epidermis development, GO:0018149: peptide cross-linking, GO:0030216: keratinocyte differentiation, GO:0030674: protein binding, bridging, GO:0031424: keratinization		13.98	13.66	13.50	12.58	11.98	11.98	13.86	13.48	13.48	13.56	13.42	12.26	1
213060_s_at	CHI3L2	chitinase 3-like 2	U58515	1117 Hs.514840	GO:0004568: chitinase activity, GO:0005615: extracellular space, GO:0005975: carbohydrate metabolic process, GO:0006032: chitin catabolic process, GO:0016787: hydrolase activity, GO:0043169: cation binding		10.28	10.57	9.84	8.67	6.01	6.79	9.84	9.65	9.13	10.26	8.62	4.79	1
213470_s_at	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	BF983406	3187 Hs.604001	GO:0000166: nucleotide binding, GO:0000398: nuclear mRNA splicing, via spliceosome, GO:0003676: nucleic acid binding, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005681: spliceosome, GO:0008266: poly(U) binding, GO:0008380: RNA splicing, GO:0030530: heterogeneous nuclear ribonucleoprotein complex		7.98	7.73	7.58	7.74	6.96	7.21	7.23	7.97	7.30	7.99	7.72	6.67	1
211367_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	U13699	834 Hs.2490	GO:0005515: protein binding, GO:0005515: protein binding, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007165: signal transduction, GO:0008234: cysteine-type peptidase activity, GO:0008656: caspase activator activity, GO:0042981: regulation of apoptosis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade	01510: Neurodegenerative Diseases, 05040: Huntington's disease, 05050: Dentatorubropallidoluysian atrophy (DRPLA)	9.19	9.39	9.14	8.66	7.73	7.99	9.18	9.22	9.34	9.43	8.78	8.20	1
212531_at	LCN2	lipocalin 2	NM_005564	3934 Hs.204238	GO:0005215: transporter activity, GO:0005488: binding, GO:0005576: extracellular region, GO:0006810: transport		12.21	12.23	11.30	9.22	6.39	6.53	11.28	11.24	10.46	11.70	9.47	5.67	1
211015_s_at	HSPA4	heat shock 70kDa protein 4	L12723	3308 Hs.90093	GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0005737: cytoplasm, GO:0006950: response to stress, GO:0006986: response to unfolded protein	04612: Antigen processing and presentation	10.76	10.52	10.31	9.92	9.62	9.71	10.62	10.48	10.48	10.63	10.52	9.77	1

(*Continued*)

TABLE E4. (*Continued*)

211366_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	U13698	834 Hs.2490	GO:0005515: protein binding, GO:0005515: protein binding, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0007165: signal transduction, GO:0008234: cysteine-type peptidase activity, GO:0008656: caspase activator activity, GO:0042981: regulation of apoptosis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade	01510: Neurodegenerative Diseases, 05040: Huntington's disease, 05050: Dentatorubropallidoluysian atrophy (DRPLA)	9.06	9.21	8.97	8.66	7.78	8.08	9.08	8.97	9.16	9.23	8.83	8.41	1
210663_s_at	KYNU	kynureninase (L-kynurenine hydrolase)	BC000879	8942 Hs.470126	GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005829: cytosol, GO:0005829: cytosol, GO:0006569: tryptophan catabolic process, GO:0006569: tryptophan catabolic process, GO:0008152: metabolic process, GO:0009435: NAD biosynthetic process, GO:0016787: hydrolase activity, GO:0019805: quinolinate biosynthetic process, GO:0030170: pyridoxal phosphate binding, GO:0030429: kynureninase activity, GO:0030429: kynureninase activity, GO:0030429: kynureninase activity, GO:0030429: kynureninase activity, GO:0042803: protein homodimerization activity, GO:0043420: anthranilate metabolic process	00380: Tryptophan metabolism	9.59	9.61	8.71	7.25	4.71	3.06	9.19	8.65	8.52	9.27	7.38	3.40	1
210951_x_at	RAB27A	RAB27A, member RAS oncogene family	AF125393	5873 Hs.654978	GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005525: GTP binding, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0016020: membrane, GO:0030425: dendrite, GO:0042470: melanosome		9.74	9.85	9.30	8.57	6.47	7.39	9.86	9.55	9.43	9.95	8.51	7.32	1
209872_s_at	PKP3	plakophilin 3	BF001503	11187 Hs.534395	GO:0005198: structural molecule activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0007155: cell adhesion, GO:0030057: desmosome		9.74	9.50	9.39	8.84	7.88	8.45	9.63	9.38	9.24	9.56	9.57	8.61	1
210413_x_at	SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	U19557	6318 Hs.123035	GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding, GO:0005576: extracellular region, GO:0005737: cytoplasm, GO:0006955: immune response, GO:0030162: regulation of proteolysis		14.46	14.36	13.90	12.15	9.54	8.53	14.11	13.96	13.39	14.08	12.86	9.71	1
209719_x_at	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	BC005224	6317 Hs.227948	GO:0004867: serine-type endopeptidase inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005515: protein binding, GO:0005737: cytoplasm		14.21	14.11	13.77	12.58	10.13	8.91	13.98	13.83	13.43	13.96	13.00	10.03	1
209771_x_at			AA761181				13.80	13.67	13.46	12.94	12.24	12.20	13.71	13.51	13.39	13.52	13.19	12.36	1

(*Continued*)

TABLE E4. (*Continued*)

208651_x_at	CD24	CD24 molecule	BG327863	100133941	Hs.644105, Hs.694721	GO:0001666: response to hypoxia, GO:0001775: cell activation, GO:0001959: regulation of cytokine and chemokine mediated signaling pathway, GO:0002237: response to molecule of bacterial origin, GO:0002768: immune response-regulating cell surface receptor signaling pathway, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0005886: plasma membrane, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0007274: neuromuscular synaptic transmission, GO:0008629: induction of apoptosis by intracellular signals, GO:0009897: external side of plasma membrane, GO:0016055: Wnt receptor signaling pathway, GO:0016337: cell-cell adhesion, GO:0016477: cell migration, GO:0019901: protein kinase binding, GO:0030246: carbohydrate binding, GO:0030296: protein tyrosine kinase activator activity, GO:0030856: regulation of epithelial cell differentiation, GO:0031225: anchored to membrane, GO:0031295: T cell costimulation, GO:0031362: anchored to external side of plasma membrane, GO:0032597: B cell receptor transport into membrane raft, GO:0032600: chemokine receptor transport out of membrane raft, GO:0032913: negative regulation of transforming growth factor-beta3 production, GO:0042104: positive regulation of activated T cell proliferation, GO:0042325: regulation of phosphorylation, GO:0042632: cholesterol homeostasis, GO:0043406: positive regulation of MAP kinase activity, GO:0043408: regulation of MAPKKK cascade, GO:0043627: response to estrogen stimulus, GO:0045121: membrane raft, GO:0045730: respiratory burst, GO:0048488: synaptic vesicle endocytosis		12.62	12.46	12.20	11.62	10.73	10.85	12.51	12.26	12.14	12.37	11.88	10.81	1
209372_x_at	TUBB2A	tubulin, beta 2A	BF971587	7280	Hs.654543	GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005198: structural molecule activity, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0005737: cytoplasm, GO:0005874: microtubule, GO:0007018: microtubule-based movement, GO:0007067: mitosis, GO:0030182: neuron differentiation, GO:0043234: protein complex, GO:0051258: protein polymerization	04540: Gap junction, 05130: Pathogenic Escherichia coli infection - EHEC, 05131: Pathogenic Escherichia coli infection - EPEC	9.36	8.73	8.82	8.37	7.98	8.29	9.26	8.85	8.90	8.75	9.05	8.37	1

(*Continued*)

TABLE E4. (*Continued*)

208596_s_at	UGT1A3	UDP glucuronosyltransferase 1 family, polypeptide A3				NM_019093	54659												
Hs.554822	GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005792: microsome, GO:0008152: metabolic process, GO:0015020:				glucuronosyltransferase activity, GO:0016020: membrane, GO:0016021: integral to membrane	00040: Pentose and glucuronate interconversions, 00150: Androgen and estrogen metabolism, 00500: Starch and sucrose metabolism, 00830: Retinol metabolism, 00860: Porphyrin and chlorophyll metabolism, 00980: Metabolism of xenobiotics by cytochrome P450, 00982: NA, 00983: NA	8.41	8.33	8.17	7.63	5.79	6.88	8.67	8.32	8.01	8.84	7.87	6.69	1
208650_s_at	CD24	CD24 molecule	BG327863	100133941	Hs.644105, Hs.694721	GO:0001666: response to hypoxia, GO:0001775: cell activation, GO:0001959: regulation of cytokine and chemokine mediated signaling pathway, GO:0002237: response to molecule of bacterial origin, GO:0002768: immune response-regulating cell surface receptor signaling pathway, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0005886: plasma membrane, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0007274: neuromuscular synaptic transmission, GO:0008629: induction of apoptosis by intracellular signals, GO:0009897: external side of plasma membrane, GO:0016055: Wnt receptor signaling pathway, GO:0016337: cell-cell adhesion, GO:0016477: cell migration, GO:0019901: protein kinase binding, GO:0030246: carbohydrate binding, GO:0030296: protein tyrosine kinase activator activity, GO:0030856: regulation of epithelial cell differentiation, GO:0031225: anchored to membrane, GO:0031295: T cell costimulation, GO:0031362: anchored to external side of plasma membrane, GO:0032597: B cell receptor transport into membrane raft, GO:0032600: chemokine receptor transport out of membrane raft, GO:0032913: negative regulation of transforming growth factor-beta3 production, GO:0042104: positive regulation of activated T cell proliferation, GO:0042325: regulation of phosphorylation, GO:0042632: cholesterol homeostasis, GO:0043406: positive regulation of MAP kinase activity, GO:0043408: regulation of MAPKKK cascade, GO:0043627: response to estrogen stimulus, GO:0045121: membrane raft, GO:0045730: respiratory burst, GO:0048488: synaptic vesicle endocytosis		13.50	13.28	12.99	12.11	10.81	10.94	13.39	13.04	12.81	13.17	12.30	10.90	1

(*Continued*)

TABLE E4. (*Continued*)

207622_s_at	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	NM_005692	10061	Hs.654958	GO:0000166: nucleotide binding, GO:0005215: transporter activity, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0005740: mitochondrial envelope, GO:0006810: transport, GO:0016887: ATPase activity, GO:0043190: ATP-binding cassette (ABC) transporter complex		9.09	8.77	8.66	8.24	7.99	8.23	8.79	8.82	8.82	8.89	8.75	8.37	1
208539_x_at	SPRR2D	small proline-rich protein 2D	NM_006945	6703	Hs.505327	GO:0001533: cornified envelope, GO:0005198: structural molecule activity, GO:0005737: cytoplasm, GO:0008544: epidermis development, GO:0030216: keratinocyte differentiation, GO:0031424: keratinization		15.59	15.59	15.36	14.51	12.69	13.13	15.45	15.43	15.02	15.52	14.79	12.09	1
216237_s_at	MCM5	minichromosome maintenance complex component 5	AA807529	4174	Hs.517582	GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0006260: DNA replication, GO:0006260: DNA replication, GO:0006270: DNA replication initiation, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent	03030: DNA polymerase, 04110: Cell cycle	8.61	8.34	8.11	7.80	7.71	7.48	8.33	7.99	8.46	8.56	8.03	8.00	1
217167_x_at	GK	glycerol kinase	AJ252550	2710	Hs.1466	GO:0000166: nucleotide binding, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0004370: glycerol kinase activity, GO:0005524: ATP binding, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0005829: cytosol, GO:0005975: carbohydrate metabolic process, GO:0006072: glycerol-3-phosphate metabolic process, GO:0016020: membrane, GO:0016740: transferase activity	00561: Glycerolipid metabolism, 03320: PPAR signaling pathway	5.70	5.97	4.55	3.72	2.81	2.79	5.09	4.37	5.09	5.79	3.70	2.59	1
205829_at	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	NM_000413	3292	Hs.654385, Hs.655222	GO:0004303: estradiol 17-beta-dehydrogenase activity, GO:0004303: estradiol 17-beta-dehydrogenase activity, GO:0005488: binding, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0005737: cytoplasm, GO:0006703: estrogen biosynthetic process, GO:0016491: oxidoreductase activity	00150: Androgen and estrogen metabolism	6.15	5.88	5.38	4.01	3.82	3.82	5.14	4.71	4.91	5.16	4.09	4.30	1
205863_at	S100A12	S100 calcium binding protein A12	NM_005621	6283	Hs.19413	GO:0005509: calcium ion binding, GO:0005626: insoluble fraction, GO:0005829: cytosol, GO:0006805: xenobiotic metabolic process, GO:0006954: inflammatory response, GO:0008270: zinc ion binding, GO:0042742: defense response to bacterium, GO:0050832: defense response to fungus		10.98	11.10	9.65	6.04	3.88	2.80	10.52	9.94	8.69	10.74	7.09	3.55	1

(*Continued*)

TABLE E4. (*Continued*)

218498_s_at	ERO1L	ERO1-like (S. cerevisiae)	NM_014584	30001	Hs.592304	GO:0005515: protein binding, GO:0005624: membrane fraction, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005792: microsome, GO:0006464: protein modification process, GO:0006467: protein thiol-disulfide exchange, GO:0006810: transport, GO:0009055: electron carrier activity, GO:0009266: response to temperature stimulus, GO:0016020: membrane, GO:0016491: oxidoreductase activity, GO:0016671: oxidoreductase activity, acting on sulfur group of donors, disulfide as acceptor, GO:0050660: FAD binding, GO:0051085: chaperone cofactor-dependent protein folding	05110: Cholera - Infection	8.44	8.06	7.64	7.34	6.73	6.98	7.93	8.15	7.68	8.38	6.02	6.74	2
207720_at	LOR	loricrin	NM_000427	4014	Hs.251680	GO:0001533: cornified envelope, GO:0005200: structural constituent of cytoskeleton, GO:0005626: insoluble fraction, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0009898: internal side of plasma membrane, GO:0018149: peptide cross-linking, GO:0030216: keratinocyte differentiation, GO:0030280: structural constituent of epidermis, GO:0030674: protein binding, bridging, GO:0031424: keratinization		13.77	14.19	14.52	14.57	14.56	14.44	14.03	13.28	14.24	13.77	14.57	14.53	2
210212_x_at	MTCP1	mature T-cell proliferation 1	BC002600	4515	Hs.6917	GO:0005739: mitochondrion, GO:0008283: cell proliferation		6.34	6.85	7.06	7.23	7.22	7.41	6.72	6.75	6.98	6.58	7.41	7.56	2
209205_s_at	LMO4	LIM domain only 4	BC003600	8543	Hs.436792, Hs.654822	GO:0001843: neural tube closure, GO:0003700: transcription factor activity, GO:0005667: transcription factor complex, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0008134: transcription factor binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		8.93	9.13	9.20	9.50	9.50	9.60	8.87	9.11	9.08	8.85	7.83	9.59	2
209206_at	SEC22B	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	AV701283	9554	Hs.632438	GO:0000139: Golgi membrane, GO:0005515: protein binding, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005794: Golgi apparatus, GO:0006888: ER to Golgi vesicle-mediated transport, GO:0015031: protein transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016192: vesicle-mediated transport, GO:0033116: ER-Golgi intermediate compartment membrane, GO:0042470: melanosome	04130: SNARE interactions in vesicular transport	9.24	9.33	9.55	9.71	9.62	9.76	9.47	9.65	9.52	9.51	8.75	9.66	2

(*Continued*)

TABLE E4. (*Continued*)

205467_at	CASP10	caspase 10, apoptosis-related cysteine peptidase	NM_001230	843 Hs.5353	GO:0005515: protein binding, GO:0006508:04210: Apoptosis proteolysis, GO:0008234: cysteine-type peptidase activity, GO:0008624: induction of apoptosis by extracellular signals, GO:0042802: identical protein binding, GO:0042981: regulation of apoptosis	4.30	4.50	4.20	4.28	4.09	3.94	4.64	4.29	4.59	4.55	3.24	3.92	2
206953_s_at	LPHN2	latrophilin 2	NM_012302	23266 Hs.24212	GO:0003674: molecular_function, GO:0004872: receptor activity, GO:0004930: G-protein coupled receptor activity, GO:0005529: sugar binding, GO:0005575: cellular_component, GO:0005886: plasma membrane, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007218: neuropeptide signaling pathway, GO:0008150: biological_process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016524: latrotoxin receptor activity	8.94	9.14	8.90	8.89	8.52	8.60	9.63	9.32	9.21	9.25	8.08	8.45	2
205074_at	SLC22A5	solute carrier family 22 (organic cation/ carnitine transporter), member 5	AB015050	6584 Hs.705425	GO:0000166: nucleotide binding, GO:0005215: transporter activity, GO:0005524: ATP binding, GO:0005886: plasma membrane, GO:0006810: transport, GO:0006811: ion transport, GO:0006814: sodium ion transport, GO:0015075: ion transmembrane transporter activity, GO:0015226: carnitine transporter activity, GO:0015293: symporter activity, GO:0015879: carnitine transport, GO:0016021: integral to membrane, GO:0031402: sodium ion binding	3.96	4.17	4.34	4.51	4.68	4.83	4.52	4.54	4.74	4.28	4.22	5.13	2
205191_at	RP2	retinitis pigmentosa 2 (X-linked recessive)	NM_006915	6102 Hs.44766	GO:0004550: nucleoside diphosphate kinase activity, GO:0005488: binding, GO:0005524: ATP binding, GO:0005886: plasma membrane, GO:0006183: GTP biosynthetic process, GO:0006228: UTP biosynthetic process, GO:0006241: CTP biosynthetic process, GO:0007025: beta-tubulin folding, GO:0007601: visual perception, GO:0050896: response to stimulus, GO:0051082: unfolded protein binding	6.95	6.95	7.20	7.36	7.02	7.47	7.14	7.35	7.16	7.24	6.18	7.12	2
203803_at	PCYOX1	prenylcysteine oxidase 1	N45309	51449 Hs.567502	GO:0001735: prenylcysteine oxidase activity, GO:0005488: binding, GO:0005764: lysosome, GO:0016491: oxidoreductase activity, GO:0016829: lyase activity, GO:0030328: prenylcysteine catabolic process	8.81	9.00	9.39	9.28	9.27	9.60	9.44	9.71	9.20	9.52	8.56	9.44	2

(*Continued*)

TABLE E4. (*Continued*)

203881_s_at	DMD	dystrophin	NM_004010	1756	Hs.495912	GO:0003779: actin binding, GO:0003779: actin binding, GO:0003779: actin binding, GO:0005200: structural constituent of cytoskeleton, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0007016: cytoskeletal anchoring, GO:0007016: cytoskeletal anchoring, GO:0007517: muscle development, GO:0008270: zinc ion binding, GO:0008307: structural constituent of muscle, GO:0008307: structural constituent of muscle, GO:0009986: cell surface, GO:0016010: dystrophin-associated glycoprotein complex, GO:0016010: dystrophin-associated glycoprotein complex, GO:0016010: dystrophin-associated glycoprotein complex, GO:0016020: membrane, GO:0043034: costamere, GO:0043043: peptide biosynthetic process		8.45	8.79	9.32	9.60	9.83	10.25	9.05	9.35	9.29	9.09	8.51	10.38	2
212148_at	PBX1	pre-B-cell leukemia homeobox 1	AL049381	5087	Hs.654412	GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0006700: C21-steroid hormone biosynthetic process, GO:0007530: sex determination, GO:0030154: cell differentiation, GO:0043565: sequence-specific DNA binding		8.45	8.98	9.33	9.57	9.51	9.42	9.06	9.05	9.09	8.83	8.67	9.27	2
212327_at	LIMCH1	LIM and calponin homology domains 1	AK026815	22998	Hs.335163	GO:0003779: actin binding, GO:0008270: zinc ion binding, GO:0031032: actomyosin structure organization and biogenesis, GO:0046872: metal ion binding		8.56	8.92	9.26	9.63	9.58	9.65	8.93	9.05	9.12	8.61	8.93	9.47	2
204041_at	MAOB	monoamine oxidase B	NM_000898	4129	Hs.654473	GO:0005739: mitochondrion, GO:0005740: mitochondrial envelope, GO:0005741: mitochondrial outer membrane, GO:0005743: mitochondrial inner membrane, GO:0008131: amine oxidase activity, GO:0009055: electron carrier activity, GO:0009055: electron carrier activity, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016491: oxidoreductase activity	00220: Urea cycle and metabolism of amino groups, 00260: Glycine, serine and threonine metabolism, 00340: Histidine metabolism, 00350: Tyrosine metabolism, 00360: Phenylalanine metabolism, 00380: Tryptophan metabolism, 00982: NA	6.98	6.85	6.90	7.15	7.48	7.43	7.54	7.56	6.97	6.56	6.47	7.27	2
204568_at	KIAA0831	KIAA0831	NM_014924	22863	Hs.414809			7.97	8.43	8.62	8.86	8.94	8.99	8.46	8.37	8.68	8.29	7.89	9.22	2
221188_s_at	CIDEB	cell death-inducing DFFA-like effector b	NM_014430	27141	Hs.642693, Hs.708040	GO:0005515: protein binding, GO:0005622: intracellular, GO:0005829: cytosol, GO:0006915: apoptosis, GO:0006917: induction of apoptosis, GO:0008630: DNA damage response, signal transduction resulting in induction of apoptosis		7.63	7.58	7.53	7.31	7.35	7.58	7.78	7.26	7.64	7.62	6.18	7.49	2
222111_at			AU145293					7.30	7.66	7.97	8.14	8.16	8.56	7.78	8.20	7.92	8.06	7.39	8.80	2

(*Continued*)

TABLE E4. (*Continued*)

213657_s_at			BE858194				5.42	5.75	5.86	6.18	6.48	6.65	5.88	5.45	6.22	5.61	6.35	6.78	2
203080_s_at	BAZ2B	bromodomain adjacent to zinc finger domain, 2B	NM_013450	29994 Hs.470369	GO:0003677: DNA binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		8.75	9.11	9.20	9.37	9.21	9.32	9.13	9.23	9.14	9.22	8.03	9.47	2
203202_at	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	AI950314	11103 Hs.645517	GO:0003723: RNA binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005732: small nucleolar ribonucleoprotein complex, GO:0006364: rRNA processing		7.90	8.09	8.08	8.10	7.99	8.16	8.28	8.58	8.33	8.38	7.27	8.40	2
201836_s_at	SUPT7L	suppressor of Ty 7 (S. cerevisiae)-like	AU154740	9913 Hs.6232	GO:0005515: protein binding, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0051457: maintenance of protein localization in nucleus		3.88	4.41	4.49	4.58	4.35	4.56	4.56	5.04	4.55	4.55	3.38	4.24	2
201843_s_at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	NM_004105	2202 Hs.76224	GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0007601: visual perception		8.17	8.75	8.98	9.38	9.49	9.91	8.45	8.87	8.74	8.46	7.59	10.17	2
201661_s_at	ACSL3	acyl-CoA synthetase long-chain family member 3	D89053	2181 Hs.655772	GO:0000287: magnesium ion binding, GO:0004321: fatty-acyl-CoA synthase activity, GO:0004467: long-chain-fatty-acid-CoA ligase activity, GO:0005515: protein binding, GO:0005739: mitochondrion, GO:0005741: mitochondrial outer membrane, GO:0005777: peroxisome, GO:0005778: peroxisomal membrane, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005792: microsome, GO:0006629: lipid metabolic process, GO:0006631: fatty acid metabolic process, GO:0008152: metabolic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016874: ligase activity	00071: Fatty acid metabolism, 03320: PPAR signaling pathway, 04920: Adipocytokine signaling pathway	8.02	8.21	8.39	8.74	9.02	9.31	8.02	8.68	8.40	8.65	7.67	8.90	2

(*Continued*)

TABLE E4. (*Continued*)

201824_at	RNF14	ring finger protein 14	AB022663	9604	Hs.483616	GO:0003713: transcription coactivator activity, GO:0003713: transcription coactivator activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007165: signal transduction, GO:0008270: zinc ion binding, GO:0016874: ligase activity, GO:0019787: small conjugating protein ligase activity, GO:0030521: androgen receptor signaling pathway, GO:0045893: positive regulation of transcription, DNA-dependent, GO:0046872: metal ion binding, GO:0050681: androgen receptor binding		7.06	7.32	7.48	7.69	7.44	7.93	7.45	7.57	7.42	7.54	6.55	7.81	2
201124_at	ITGB5	integrin, beta 5	AL048423	3693	Hs.536663	GO:0004872: receptor activity, GO:0005178: integrin binding, GO:0005515: protein binding, GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0008305: integrin complex, GO:0016020: membrane, GO:0016021: integral to membrane	04510: Focal adhesion, 04512: ECM-receptor interaction, 04810: Regulation of actin cytoskeleton	5.73	6.69	7.21	7.53	8.05	7.91	5.95	6.50	6.58	6.07	6.04	7.93	2
201449_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	AL567227	7072	Hs.413123	GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003723: RNA binding, GO:0006915: apoptosis, GO:0006917: induction of apoptosis, GO:0008143: poly(A) binding		7.32	7.57	7.74	7.88	7.93	8.00	7.64	7.72	7.81	7.69	6.84	8.02	2
200719_at	SKP1	S-phase kinase-associated protein 1	BE964043	6500	Hs.171626, Hs.710433	GO:0003674: molecular_function, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005575: cellular_component, GO:0005654: nucleoplasm, GO:0005829: cytosol, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0008150: biological_process, GO:0051437: positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle	04110: Cell cycle, 04120: Ubiquitin mediated proteolysis, 04310: Wnt signaling pathway, 04350: TGF-beta signaling pathway	8.54	8.68	8.84	8.92	9.11	9.34	8.53	8.64	8.79	8.65	7.69	9.39	2
200856_x_at	LOC 100133918	similar to nuclear receptor co-repressor 1	BF437948	100133918				5.40	5.54	5.67	6.01	6.03	6.26	6.05	6.04	6.05	6.00	5.20	6.82	2
221213_s_at	ZNF280D	zinc finger protein 280D	NM_017661	54816	Hs.511477	GO:0003677: DNA binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		5.87	6.09	6.43	6.79	6.61	6.91	6.27	6.37	6.49	6.14	5.91	6.99	2

(*Continued*)

TABLE E4. (*Continued*)

44783_s_at	HEY1	hairy/enhancer-of-split related with YRPW motif 1	R61374	23462 Hs.234434	GO:0001570: vasculogenesis, GO:0003677: DNA binding, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0007219: Notch signaling pathway, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0009887: organ morphogenesis, GO:0030528: transcription regulator activity		6.08	6.31	6.60	6.80	7.02	6.88	6.29	6.42	6.63	5.95	5.72	6.91	2
220351_at	CCRL1	chemokine (C-C motif) receptor-like 1	NM_016557	51554 Hs.310512	GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0006935: chemotaxis, GO:0006955: immune response, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0016493: C-C chemokine receptor activity		7.15	7.45	7.96	8.40	8.28	8.70	7.55	7.73	7.52	7.21	7.27	8.23	2
220988_s_at	C1QTNF3	C1q and tumor necrosis factor related protein 3	NM_030945	114899 Hs.171929	GO:0005576: extracellular region, GO:0005737: cytoplasm, GO:0006817: phosphate transport		7.69	8.07	8.68	9.49	9.25	8.62	8.03	8.17	8.51	8.33	8.04	8.56	2
219518_s_at	ELL3	elongation factor RNA polymerase II-like 3	NM_025165	80237 Hs.712675	GO:0005515: protein binding, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006368: RNA elongation from RNA polymerase II promoter, GO:0007283: spermatogenesis, GO:0008023: transcription elongation factor complex, GO:0008159: positive transcription elongation factor activity, GO:0016944: RNA polymerase II transcription elongation factor activity, GO:0045817: positive regulation of transcription from RNA polymerase II promoter, global		6.90	7.15	7.52	8.12	8.34	8.88	7.83	7.76	7.93	7.58	7.98	9.20	2
220244_at	LOH3CR2A	loss of heterozygosity, 3, chromosomal region 2, gene A	NM_013343	29931 Hs.591661			6.00	6.13	6.44	6.91	7.55	7.05	6.18	6.19	6.45	5.91	6.53	6.88	2
219213_at	JAM2	junctional adhesion molecule 2	NM_021219	58494 Hs.517227	GO:0005886: plasma membrane, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005923: tight junction, GO:0016337: cell-cell adhesion, GO:0030054: cell junction	04514: Cell adhesion molecules (CAMs), 04530: Tight junction, 04670: Leukocyte transendothelial migration, 05120: Epithelial cell signaling in Helicobacter pylori infection	6.69	7.12	7.34	8.10	8.34	7.80	6.87	6.73	7.15	7.02	6.52	7.50	2

(*Continued*)

TABLE E4. (*Continued*)

219517_at	ELL3	elongation factor RNA polymerase II-like 3	NM_025165	80237 Hs.712675	GO:0005515: protein binding, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006368: RNA elongation from RNA polymerase II promoter, GO:0007283: spermatogenesis, GO:0008023: transcription elongation factor complex, GO:0008159: positive transcription elongation factor activity, GO:0016944: RNA polymerase II transcription elongation factor activity, GO:0045817: positive regulation of transcription from RNA polymerase II promoter, global	8.47	8.61	8.82	9.26	9.64	9.87	9.27	9.03	9.26	9.01	9.38	10.19	2
218641_at	MGC3032	hypothetical protein MGC3032	NM_023941	65998 Hs.568945	GO:0005622: intracellular, GO:0008270: zinc ion binding	4.22	4.56	4.67	5.08	5.33	5.16	4.37	4.85	4.55	4.13	4.40	5.17	2
219132_at	PELI2	pellino homolog 2 (Drosophila)	NM_021255	57161 Hs.657926	GO:0005515: protein binding	3.73	4.01	4.24	4.63	5.12	5.16	4.19	3.90	4.05	3.74	4.02	4.81	2
218532_s_at	FAM134B	family with sequence similarity 134, member B	NM_019000	54463 Hs.481704	GO:0016020: membrane, GO:0016021: integral to membrane	7.08	7.39	7.57	8.20	8.57	8.90	7.72	7.77	7.83	7.31	7.80	9.19	2
218633_x_at	ABHD10	abhydrolase domain containing 10	NM_018394	55347 Hs.708240	GO:0004252: serine-type endopeptidase activity, GO:0005739: mitochondrion, GO:0008233: peptidase activity	5.86	6.62	6.77	6.96	6.81	7.10	6.79	6.82	6.90	6.71	6.14	7.24	2
218437_s_at	LZTFL1	leucine zipper transcription factor-like 1	AA843132	54585 Hs.30824		7.37	7.69	8.03	8.33	8.46	8.71	7.97	8.17	7.94	7.83	7.65	9.09	2
218490_s_at	ZNF302	zinc finger protein 302	NM_018443	55900 Hs.436350	GO:0003677: DNA binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	7.71	8.37	8.47	8.95	9.05	9.11	8.36	8.71	8.50	8.46	8.21	9.19	2
218309_at	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	NM_018584	55450 Hs.197922	GO:0004860: protein kinase inhibitor activity, GO:0008427: calcium-dependent protein kinase inhibitor activity, GO:0019717: synaptosome, GO:0019901: protein kinase binding, GO:0030054: cell junction, GO:0030425: dendrite, GO:0043025: cell soma, GO:0045202: synapse, GO:0045211: postsynaptic membrane	6.91	7.25	7.83	8.35	8.80	9.28	7.29	7.61	7.27	7.31	7.45	9.03	2
218370_s_at	S100PBP	S100P binding protein	NM_022753	64766 Hs.440880	GO:0005634: nucleus, GO:0048306: calcium-dependent protein binding	4.32	5.12	5.46	5.88	5.71	6.01	5.43	5.69	5.31	4.68	4.55	6.16	2
216320_x_at	MST1	macrophage stimulating 1 (hepatocyte growth factor-like)	U37055	4485 Hs.349110, Hs.512587	GO:0003824: catalytic activity, GO:0004252: serine-type endopeptidase activity, GO:0005509: calcium ion binding, GO:0005576: extracellular region, GO:0006508: proteolysis, GO:0007596: blood coagulation, GO:0008150: biological_process	3.89	4.44	4.81	5.10	5.86	5.56	5.34	4.89	5.01	4.63	5.32	6.21	2

(*Continued*)

TABLE E4. (*Continued*)

216331_at	ITGA7	integrin, alpha 7	AK022548	3679 Hs.524484, Hs.639559	GO:0004872: receptor activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0007155: cell adhesion, GO:0007160: cell-matrix adhesion, GO:0007229: integrin-mediated signaling pathway, GO:0007517: muscle development, GO:0008305: integrin complex, GO:0008360: regulation of cell shape, GO:0016020: membrane, GO:0016021: integral to membrane	04510: Focal adhesion, 04512: ECM-receptor interaction, 04810: Regulation of actin cytoskeleton	8.08	8.52	8.68	9.03	9.85	9.34	8.11	7.99	8.31	7.35	7.96	9.06	2
214152_at	CCPG1	cell cycle progression 1	AU144243	9236 Hs.285051	GO:0007049: cell cycle, GO:0016020: membrane, GO:0016021: integral to membrane		4.39	4.79	5.18	5.55	5.55	5.60	5.06	4.84	5.18	5.16	4.80	5.59	2
214454_at	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2	NM_014244	9509 Hs.591725	GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0006508: proteolysis, GO:0008270: zinc ion binding, GO:0030574: collagen catabolic process, GO:0046872: metal ion binding		4.48	4.69	4.87	5.48	5.65	4.84	4.77	4.63	4.40	4.45	4.39	4.73	2
213496_at	LPPR4	plasticity related gene 1	AW592563	9890 Hs.13245	GO:0008195: phosphatidate phosphatase activity, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016787: hydrolase activity		4.79	5.28	5.42	6.18	5.99	6.00	4.96	5.45	5.39	4.97	4.79	5.56	2
214151_s_at	CCPG1	cell cycle progression 1	AU144243	9236 Hs.285051	GO:0007049: cell cycle, GO:0016020: membrane, GO:0016021: integral to membrane		6.45	7.10	7.46	7.81	7.93	7.90	7.48	7.29	7.56	7.20	7.09	7.86	2
213106_at	ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	AI769688	10396 Hs.435052	GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004012: phospholipid-translocating ATPase activity, GO:0005524: ATP binding, GO:0006810: transport, GO:0008152: metabolic process, GO:0015662: ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, GO:0015914: phospholipid transport, GO:0015917: aminophospholipid transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016787: hydrolase activity, GO:0016820: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, GO:0019829: cation-transporting ATPase activity, GO:0031410: cytoplasmic vesicle		5.81	6.75	6.78	7.65	7.66	7.75	6.25	6.59	6.73	6.48	6.42	7.68	2

(*Continued*)

TABLE E4. (*Continued*)

213397_x_at	ANG	angiogenin, ribonuclease, RNase A family, 5	AI761728	283 Hs.283749	GO:0001525: angiogenesis, GO:0001525: angiogenesis, GO:0001541: ovarian follicle development, GO:0001556: oocyte maturation, GO:0001666: response to hypoxia, GO:0001666: response to hypoxia, GO:0001890: placenta development, GO:0001938: positive regulation of endothelial cell proliferation, GO:0003676: nucleic acid binding, GO:0003677: DNA binding, GO:0003779: actin binding, GO:0004519: endonuclease activity, GO:0004519: endonuclease activity, GO:0004522: pancreatic ribonuclease activity, GO:0004540: ribonuclease activity, GO:0005102: receptor binding, GO:0005507: copper ion binding, GO:0005576: extracellular region, GO:0005605: basal lamina, GO:0005615: extracellular space, GO:0005634: nucleus, GO:0005730: nucleolus, GO:0006651: diacylglycerol biosynthetic process, GO:0007154: cell communication, GO:0007202: activation of phospholipase C activity, GO:0007275: multicellular organismal development, GO:0008201: heparin binding, GO:0009303: rRNA transcription, GO:0009725: response to hormone stimulus, GO:0016477: cell migration, GO:0016787: hydrolase activity, GO:0017148: negative regulation of translation, GO:0019843: rRNA binding, GO:0030041: actin filament polymerization, GO:0030154: cell differentiation, GO:0030426: growth cone, GO:0032148: activation of protein kinase B activity, GO:0032311: angiogenin-PRI complex, GO:0032431: activation of phospholipase A2, GO:0042277: peptide binding, GO:0042327: positive regulation of phosphorylation, GO:0042592: homeostatic process, GO:0043025: cell soma, GO:0048662: negative regulation of smooth muscle cell proliferation, GO:0050714: positive regulation of protein secretion, GO:0050714: positive regulation of protein secretion	8.77	9.42	9.93	10.34	10.49	10.84	9.28	9.49	9.53	9.21	9.32	10.77	2
213010_at	PRKCDBP	protein kinase C, delta binding protein	AI088622	112464 Hs.434044	GO:0045786: negative regulation of cell cycle	7.25	7.41	7.68	7.93	8.55	8.17	7.35	7.66	7.42	6.77	7.46	8.12	2
213075_at	OLFML2A	olfactomedin-like 2A	AL050002	169611 Hs.357004	GO:0005576: extracellular region, GO:0016020: membrane	7.80	8.15	8.57	9.11	9.60	9.57	8.12	8.56	8.67	8.13	8.55	9.72	2
212675_s_at	CEP68	centrosomal protein 68kDa	AB011154	23177 Hs.709257	GO:0005813: centrosome	8.38	9.07	9.27	9.79	9.89	9.86	8.75	9.15	9.24	8.99	8.87	9.77	2

(*Continued*)

TABLE E4. (*Continued*)

212690_at	DDHD2	DDHD domain containing 2	AB018268	23259 Hs.434966	GO:0005737: cytoplasm, GO:0016042: lipid catabolic process, GO:0016787: hydrolase activity, GO:0046872: metal ion binding	7.73	8.36	8.59	8.96	9.04	9.10	8.33	8.67	8.54	8.34	8.39	9.13	2
212328_at	LIMCH1	LIM and calponin homology domains 1	AB029025	22998 Hs.335163	GO:0003779: actin binding, GO:0008270: zinc ion binding, GO:0031032: actomyosin structure organization and biogenesis, GO:0046872: metal ion binding	8.75	8.99	9.44	9.71	9.88	9.81	9.13	9.13	9.16	8.96	8.86	9.54	2
212503_s_at	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	N22859	22982 Hs.432397	GO:0003824: catalytic activity, GO:0005634: nucleus, GO:0008134: transcription factor binding, GO:0008152: metabolic process	6.59	7.09	7.50	8.09	8.21	8.16	6.64	7.23	7.32	6.73	6.60	8.01	2
210571_s_at	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	AF074480	8418 Hs.484918	GO:0005737: cytoplasm, GO:0008150: biological_ process, GO:0030338: CMP-N-acetylneuraminate monooxygenase activity, GO:0046381: CMP-N-acetylneuraminate metabolic process	3.89	3.95	4.74	5.31	5.13	6.57	4.94	4.43	5.12	3.93	4.21	7.05	2

(*Continued*)

TABLE E4. (*Continued*)

212097_at	CAV1	caveolin 1, caveolae protein, 22kDa	AU147399	857 Hs.74034	GO:0000139: Golgi membrane, GO:0000139: Golgi membrane, GO:0000139: Golgi membrane, GO:0000188: inactivation of MAPK activity, GO:0001570: vasculogenesis, GO:0001666: response to hypoxia, GO:0001937: negative regulation of endothelial cell proliferation, GO:0005198: structural molecule activity, GO:0005515: protein binding, GO:0005783: endoplasmic reticulum, GO:0005794: Golgi apparatus, GO:0005811: lipid particle, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005901: caveola, GO:0006641: triacylglycerol metabolic process, GO:0006816: calcium ion transport, GO:0006874: cellular calcium ion homeostasis, GO:0006897: endocytosis, GO:0006940: regulation of smooth muscle contraction, GO:0007519: skeletal muscle development, GO:0008104: protein localization, GO:0015485: cholesterol binding, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016050: vesicle organization and biogenesis, GO:0016504: protease activator activity, GO:0019217: regulation of fatty acid metabolic process, GO:0019915: sequestering of lipid, GO:0030193: regulation of blood coagulation, GO:0030301: cholesterol transport, GO:0030857: negative regulation of epithelial cell differentiation, GO:0033484: nitric oxide homeostasis, GO:0042632: cholesterol homeostasis, GO:0043409: negative regulation of MAPKKK cascade, GO:0045019: negative regulation of nitric oxide biosynthetic process, GO:0045907: positive regulation of vasoconstriction, GO:0045908: negative regulation of vasodilation, GO:0046426: negative regulation of JAK-STAT cascade, GO:0048471: perinuclear region of cytoplasm, GO:0048554: positive regulation of metalloenzyme activity, GO:0050998: nitric-oxide synthase binding, GO:0051260: protein homooligomerization, GO:0051899: membrane depolarization, GO:0052547: regulation of peptidase activity, GO:0060056: mammary gland involution	04510: Focal adhesion	12.05	12.23	12.52	12.86	13.08	13.05	12.24	12.39	12.32	12.02	12.26	12.91	2
209656_s_at	TMEM47	transmembrane protein 47	AL136550	83604 Hs.8769	GO:0005886: plasma membrane, GO:0016021: integral to membrane		8.38	9.03	9.47	10.08	10.36	10.48	8.61	9.25	8.91	8.55	8.67	10.32	2
210102_at	VWA5A	von Willebrand factor A domain containing 5A	BC001234	4013 Hs.152944	GO:0045786: negative regulation of cell cycle		7.08	7.70	7.83	8.20	8.04	8.24	7.58	7.96	8.00	7.55	7.20	8.22	2

(*Continued*)

TABLE E4. (*Continued*)

209200_at	MEF2C	myocyte enhancer factor 2C	AL536517	4208 Hs.653394	GO:0001568: blood vessel development, GO:0001649: osteoblast differentiation, GO:0001958: endochondral ossification, GO:0001974: blood vessel remodeling, GO:0002062: chondrocyte differentiation, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0007399: nervous system development, GO:0007507: heart development, GO:0007517: muscle development, GO:0043565: sequence-specific DNA binding, GO:0045941: positive regulation of transcription, GO:0045944: positive regulation of transcription from RNA polymerase II promoter	04010: MAPK signaling pathway	5.36	5.96	6.18	6.70	6.92	6.58	5.16	5.81	5.78	5.05	5.31	5.99	2
209291_at	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	AW157094	3400 Hs.519601	GO:0003714: transcription corepressor activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0007405: neuroblast proliferation, GO:0008284: positive regulation of cell proliferation, GO:0030528: transcription regulator activity, GO:0045449: regulation of transcription, GO:0045665: negative regulation of neuron differentiation, GO:0048712: negative regulation of astrocyte differentiation	04350: TGF-beta signaling pathway	10.37	10.69	11.16	11.51	11.92	12.25	10.66	10.88	10.97	10.68	11.03	12.54	2
205609_at	ANGPT1	angiopoietin 1	NM_001146	284 Hs.369675	GO:0001525: angiogenesis, GO:0005102: receptor binding, GO:0005102: receptor binding, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0007165: signal transduction, GO:0007165: signal transduction, GO:0007275: multicellular organismal development, GO:0030154: cell differentiation		3.29	3.71	4.25	5.05	5.74	5.26	4.09	4.98	4.40	3.85	3.42	4.78	2
208760_at	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	AL031714	7329 Hs.302903	GO:0000795: synaptonemal complex, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0007049: cell cycle, GO:0007059: chromosome segregation, GO:0007067: mitosis, GO:0016605: PML body, GO:0016874: ligase activity, GO:0019787: small conjugating protein ligase activity, GO:0043398: HLH domain binding, GO:0044419: interspecies interaction between organisms, GO:0051246: regulation of protein metabolic process, GO:0051301: cell division	04120: Ubiquitin mediated proteolysis	5.53	6.03	6.50	6.83	7.21	7.17	6.12	6.21	6.14	5.82	6.56	7.32	2

(*Continued*)

TABLE E4. (*Continued*)

205158_at	RNASE4	ribonuclease, RNase A family, 4	NM_002937	6038 Hs.283749	GO:0003676: nucleic acid binding, GO:0004519: endonuclease activity, GO:0004522: pancreatic ribonuclease activity, GO:0005576: extracellular region, GO:0006379: mRNA cleavage, GO:0016787: hydrolase activity		7.39	8.23	8.86	9.27	9.29	9.80	8.01	8.32	8.20	7.93	7.93	9.85	2
205225_at	ESR1	estrogen receptor 1	NM_000125	2099 Hs.208124	GO:0003677: DNA binding, GO:0003700: transcription factor activity, GO:0003707: steroid hormone receptor activity, GO:0004872: receptor activity, GO:0005496: steroid binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006355: regulation of transcription, DNA-dependent, GO:0007165: signal transduction, GO:0008270: zinc ion binding, GO:0016585: chromatin remodeling complex, GO:0030235: nitric-oxide synthase regulator activity, GO:0030284: estrogen receptor activity, GO:0030315: T-tubule, GO:0030520: estrogen receptor signaling pathway, GO:0042562: hormone binding, GO:0043005: neuron projection, GO:0043195: terminal button, GO:0043204: perikaryon, GO:0043526: neuroprotection, GO:0043565: sequence-specific DNA binding, GO:0045885: positive regulation of survival gene product activity, GO:0046872: metal ion binding, GO:0047485: protein N-terminus binding		2.51	2.76	3.06	3.47	3.46	3.10	3.27	3.30	3.17	2.90	3.06	3.04	2
204992_s_at	PFN2	profilin 2	NM_002628	5217 Hs.91747	GO:0003779: actin binding, GO:0005515: protein binding, GO:0005546: phosphatidylinositol-4,5-bisphosphate binding, GO:0005737: cytoplasm, GO:0007010: cytoskeleton organization and biogenesis, GO:0008064: regulation of actin polymerization and/or depolymerization, GO:0015629: actin cytoskeleton, GO:0030036: actin cytoskeleton organization and biogenesis	04810: Regulation of actin cytoskeleton	8.15	8.62	8.87	9.24	9.41	9.50	8.37	8.71	8.68	8.23	8.20	9.31	2
205076_s_at	MTMR11	myotubularin related protein 11	NM_006697	10903 Hs.425144			5.78	6.30	6.44	6.80	6.93	7.13	6.46	6.26	6.20	6.08	6.36	7.16	2
204797_s_at	EML1	echinoderm microtubule associated protein like 1	NM_004434	2009 Hs.12451	GO:0005509: calcium ion binding, GO:0005737: cytoplasm, GO:0005874: microtubule, GO:0005875: microtubule associated complex		7.40	7.71	8.11	8.38	8.48	8.59	8.49	8.32	8.35	8.06	8.07	8.83	2

(*Continued*)

TABLE E4. (*Continued*)

204838_s_at	MLH3	mutL homolog 3 (E. coli)	NM_014381	27030 Hs.436650	GO:0003696: satellite DNA binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0006298: mismatch repair, GO:0006298: mismatch repair, GO:0007131: meiotic recombination, GO:0030983: mismatched DNA binding	03430: NA	4.69	5.08	5.12	5.69	5.69	5.66	5.70	5.34	5.48	5.28	5.21	5.85	2
204686_at	IRS1	insulin receptor substrate 1	NM_005544	3667 Hs.471508	GO:0004871: signal transducer activity, GO:0005069: transmembrane receptor protein tyrosine kinase docking protein activity, GO:0005158: insulin receptor binding, GO:0005159: insulin-like growth factor receptor binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005792: microsome, GO:0005886: plasma membrane, GO:0005901: caveola, GO:0007165: signal transduction, GO:0008286: insulin receptor signaling pathway, GO:0019901: protein kinase binding, GO:0042169: SH2 domain binding, GO:0043434: response to peptide hormone stimulus, GO:0043491: protein kinase B signaling cascade, GO:0043548: phosphoinositide 3-kinase binding, GO:0043548: phosphoinositide 3-kinase binding, GO:0043552: positive regulation of phosphoinositide 3-kinase activity, GO:0048009: insulin-like growth factor receptor signaling pathway	04910: Insulin signaling pathway, 04920: Adipocytokine signaling pathway, 04930: Type II diabetes mellitus	7.06	7.19	7.73	8.13	8.50	8.73	7.69	8.02	7.89	7.31	7.49	8.66	2
204788_s_at	PPOX	protoporphyrinogen oxidase	NM_000309	5498 Hs.517373	GO:0004729: protoporphyrinogen oxidase activity, GO:0004729: protoporphyrinogen oxidase activity, GO:0005739: mitochondrion, GO:0005758: mitochondrial intermembrane space, GO:0006783: heme biosynthetic process, GO:0009055: electron carrier activity, GO:0016020: membrane, GO:0016491: oxidoreductase activity, GO:0031304: intrinsic to mitochondrial inner membrane, GO:0050660: FAD binding	00860: Porphyrin and chlorophyll metabolism	6.94	7.08	7.38	7.68	8.28	8.25	7.37	6.95	7.16	7.05	7.71	8.68	2

(*Continued*)

TABLE E4. (*Continued*)

203919_at	TCEA2	transcription elongation factor A (SII), 2	NM_003195	6919	Hs.505004, Hs.711562	GO:0003677: DNA binding, GO:0003702: RNA polymerase II transcription factor activity, GO:0003711: transcription elongation regulator activity, GO:0003711: transcription elongation regulator activity, GO:0003746: translation elongation factor activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006350: transcription, GO:0006354: RNA elongation, GO:0006354: RNA elongation, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0008023: transcription elongation factor complex, GO:0008270: zinc ion binding, GO:0030528: transcription regulator activity, GO:0046872: metal ion binding		3.44	3.93	4.34	4.87	5.55	4.94	3.61	3.99	4.08	3.68	4.30	5.01	2
204276_at	TK2	thymidine kinase 2, mitochondrial	BE895437	7084	Hs.512619	GO:0000166: nucleotide binding, GO:0004797: thymidine kinase activity, GO:0005524: ATP binding, GO:0005739: mitochondrion, GO:0005743: mitochondrial inner membrane, GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0006260: DNA replication, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0016773: phosphotransferase activity, alcohol group as acceptor	00240: Pyrimidine metabolism, 00983: NA	6.34	6.73	7.14	7.60	7.64	7.65	6.74	7.01	6.96	6.73	6.54	7.53	2
203723_at	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	NM_002221	3707	Hs.528087, Hs.659396	GO:0000166: nucleotide binding, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0007165: signal transduction, GO:0008440: inositol trisphosphate 3-kinase activity, GO:0016301: kinase activity, GO:0016740: transferase activity	00562: Inositol phosphate metabolism, 04020: Calcium signaling pathway, 04070: Phosphatidylinositol signaling system	7.53	7.72	7.95	8.41	8.76	8.75	7.64	7.76	7.79	7.13	7.69	8.76	2
203874_s_at	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	M88163	6594	Hs.152292	GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0004386: helicase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007420: brain development, GO:0008094: DNA-dependent ATPase activity, GO:0016585: chromatin remodeling complex, GO:0016787: hydrolase activity, GO:0030182: neuron differentiation, GO:0030528: transcription regulator activity, GO:0031491: nucleosome binding, GO:0043044: ATP-dependent chromatin remodeling, GO:0043193: positive regulation of gene-specific transcription		5.58	6.16	6.32	6.87	6.74	6.90	6.05	6.09	6.26	6.10	5.62	6.82	2

(*Continued*)

TABLE E4. (*Continued*)

203065_s_at	CAV1	caveolin 1, caveolae protein, 22kDa	NM_001753	857	Hs.74034	GO:0000139: Golgi membrane, GO:0000139: Golgi membrane, GO:0000139: Golgi membrane, GO:0000188: inactivation of MAPK activity, GO:0001570: vasculogenesis, GO:0001666: response to hypoxia, GO:0001937: negative regulation of endothelial cell proliferation, GO:0005198: structural molecule activity, GO:0005515: protein binding, GO:0005783: endoplasmic reticulum, GO:0005794: Golgi apparatus, GO:0005811: lipid particle, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005901: caveola, GO:0006641: triacylglycerol metabolic process, GO:0006816: calcium ion transport, GO:0006874: cellular calcium ion homeostasis, GO:0006897: endocytosis, GO:0006940: regulation of smooth muscle contraction, GO:0007519: skeletal muscle development, GO:0008104: protein localization, GO:0015485: cholesterol binding, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016050: vesicle organization and biogenesis, GO:0016504: protease activator activity, GO:0019217: regulation of fatty acid metabolic process, GO:0019915: sequestering of lipid, GO:0030193: regulation of blood coagulation, GO:0030301: cholesterol transport, GO:0030857: negative regulation of epithelial cell differentiation, GO:0033484: nitric oxide homeostasis, GO:0042632: cholesterol homeostasis, GO:0043409: negative regulation of MAPKKK cascade, GO:0045019: negative regulation of nitric oxide biosynthetic process, GO:0045907: positive regulation of vasoconstriction, GO:0045908: negative regulation of vasodilation, GO:0046426: negative regulation of JAK-STAT cascade, GO:0048471: perinuclear region of cytoplasm, GO:0048554: positive regulation of metalloenzyme activity, GO:0050998: nitric-oxide synthase binding, GO:0051260: protein homooligomerization, GO:0051899: membrane depolarization, GO:0052547: regulation of peptidase activity, GO:0060056: mammary gland involution	04510: Focal adhesion	10.56	10.73	11.02	11.46	11.76	11.63	10.71	11.01	10.87	10.58	10.87	11.37	2

(*Continued*)

TABLE E4. (*Continued*)

203335_at	PHYH	phytanoyl-CoA 2-hydroxylase	NM_006214	5264	Hs.498732	GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0005777: peroxisome, GO:0006629: lipid metabolic process, GO:0007399: nervous system development, GO:0007601: visual perception, GO:0007605: sensory perception of sound, GO:0009055: electron carrier activity, GO:0031418: L-ascorbic acid binding, GO:0048244: phytanoyl-CoA dioxygenase activity, GO:0050896: response to stimulus		7.78	8.25	8.78	9.17	9.37	9.69	8.35	8.24	8.44	8.09	8.21	9.56	2
202468_s_at	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	NM_003798	8727	Hs.58488	GO:0005198: structural molecule activity, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0007155: cell adhesion, GO:0015629: actin cytoskeleton, GO:0045296: cadherin binding		8.24	8.41	8.87	9.09	9.37	9.62	9.26	8.74	8.97	8.78	9.15	9.86	2
202973_x_at	FAM13A1	family with sequence similarity 13, member A1	NM_014883	10144	Hs.97270	GO:0005622: intracellular, GO:0007165: signal transduction		7.73	8.60	8.74	9.14	9.33	9.67	8.44	8.83	8.82	8.55	8.43	9.85	2
202321_at	GGPS1	geranylgeranyl diphosphate synthase 1	AW299507	9453	Hs.647791	GO:0004161: dimethylallyltranstransferase activity, GO:0004311: farnesyltranstransferase activity, GO:0004337: geranyltranstransferase activity, GO:0005625: soluble fraction, GO:0005737: cytoplasm, GO:0008299: isoprenoid biosynthetic process, GO:0016740: transferase activity	00100: Biosynthesis of steroids, 00900: Terpenoid biosynthesis	5.95	6.39	6.77	6.99	6.87	7.18	6.56	6.43	6.35	6.32	5.70	6.99	2
202350_s_at	MATN2	matrilin 2	NM_002380	4147	Hs.189445, Hs.660622	GO:0003674: molecular_function, GO:0005509: calcium ion binding, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0008150: biological_process		9.21	9.60	10.01	10.35	10.60	10.63	9.68	9.77	9.97	9.57	10.05	10.66	2
201117_s_at	CPE	carboxypeptidase E	NM_001873	1363	Hs.712551	GO:0004180: carboxypeptidase activity, GO:0005576: extracellular region, GO:0005886: plasma membrane, GO:0006464: protein modification process, GO:0006508: proteolysis, GO:0007218: neuropeptide signaling pathway, GO:0008152: metabolic process, GO:0008237: metallopeptidase activity, GO:0008270: zinc ion binding, GO:0030070: insulin processing, GO:0046872: metal ion binding	04940: Type I diabetes mellitus	9.93	10.33	10.88	11.43	11.32	11.50	10.21	10.82	10.61	10.26	10.33	11.16	2
202125_s_at	TRAK2	trafficking protein, kinesin binding 2	NM_015049	66008	Hs.152774	GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0050811: GABA receptor binding		8.26	8.88	9.19	9.55	9.76	9.72	8.82	9.09	9.11	8.80	8.97	9.73	2
205614_x_at	MST1	macrophage stimulating 1 (hepatocyte growth factor-like)	NM_020998	4485	Hs.349110, Hs.512587	GO:0003824: catalytic activity, GO:0004252: serine-type endopeptidase activity, GO:0005509: calcium ion binding, GO:0005576: extracellular region, GO:0006508: proteolysis, GO:0007596: blood coagulation, GO:0008150: biological_process		3.14	4.12	4.04	4.35	4.92	4.72	4.34	3.86	4.16	3.78	4.67	5.49	2
221756_at	PIK3IP1	phosphoinositide -3-kinase interacting protein 1	BE042976	113791	Hs.26670	GO:0016020: membrane, GO:0016021: integral to membrane		6.56	7.51	7.37	7.58	7.76	7.30	7.13	7.05	7.20	7.19	7.10	7.46	2

(*Continued*)

TABLE E4. (*Continued*)

218418_s_at	KANK2	KN motif and ankyrin repeat domains 2	NM_015493	25959	Hs.284208, Hs.714335		7.38	7.97	8.39	8.95	9.37	9.02	7.55	8.23	8.29	7.62	8.55	8.92	2
219440_at	RAI2	retinoic acid induced 2	NM_021785	10742	Hs.446680, Hs.708804	GO:0003674: molecular_function, GO:0005575: cellular_component, GO:0009790: embryonic development	6.27	6.70	7.02	7.59	7.90	7.89	6.35	6.69	6.61	6.23	7.06	7.62	2
213369_at	PCDH21	protocadherin 21	AI825832	92211	Hs.137556	GO:0004872: receptor activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0007601: visual perception, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0050896: response to stimulus	8.13	8.21	8.72	9.31	10.49	10.85	9.15	9.17	9.37	8.39	10.18	11.39	2
213455_at	FAM114A1	family with sequence similarity 114, member A1	W87466	92689	Hs.476517	GO:0005737: cytoplasm	8.45	8.84	9.17	9.44	9.59	9.43	8.79	9.18	9.12	8.76	9.23	9.52	2
212299_at	NEK9	NIMA (never in mitosis gene a)- related kinase 9	AL117502	91754	Hs.7200	GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006468: protein amino acid phosphorylation, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0016740: transferase activity, GO:0051301: cell division	7.06	7.57	7.71	8.05	8.04	8.05	7.38	7.70	7.85	7.37	7.39	8.26	2
213249_at	FBXL7	F-box and leucine-rich repeat protein 7	AU145127	23194	Hs.433057	GO:0000151: ubiquitin ligase complex, GO:0004842: ubiquitin-protein ligase activity, GO:0005515: protein binding, GO:0006511: ubiquitin-dependent protein catabolic process	6.30	6.32	6.73	7.08	7.32	6.90	5.85	6.35	6.31	5.40	6.54	6.60	2
208158_s_at	OSBPL1A	oxysterol binding protein-like 1A	NM_018030	114876	Hs.370725	GO:0005543: phospholipid binding, GO:0005622: intracellular, GO:0006869: lipid transport, GO:0008202: steroid metabolic process, GO:0008203: cholesterol metabolic process, GO:0016192: vesicle-mediated transport	8.60	8.91	9.23	9.46	9.72	9.60	8.82	8.77	9.06	8.63	9.22	9.60	2
210135_s_at	SHOX2	short stature homeobox 2	AF022654	6474	Hs.55967	GO:0001501: skeletal development, GO:0003700: transcription factor activity, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0007507: heart development, GO:0043565: sequence-specific DNA binding	4.35	4.84	5.02	6.16	5.86	5.33	4.33	4.70	4.63	4.56	4.65	4.95	2

(*Continued*)

TABLE E4. (*Continued*)

205932_s_at	MSX1	msh homeobox 1	NM_002448	4487 Hs.424414	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0007517: muscle development, GO:0009887: organ morphogenesis, GO:0016564: transcription repressor activity, GO:0030326: embryonic limb morphogenesis, GO:0030900: forebrain development, GO:0030901: midbrain development, GO:0043565: sequence-specific DNA binding, GO:0051216: cartilage development		5.43	5.57	6.29	6.93	7.54	7.05	5.41	6.32	5.94	5.37	6.17	6.69	2
206149_at	CHP2	calcineurin B homologous protein 2	NM_022097	63928 Hs.178589	GO:0005509: calcium ion binding		8.23	8.74	9.46	9.99	10.58	11.06	9.28	8.84	9.38	8.85	10.28	11.53	2
204151_x_at	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	NM_001353	1645 Hs.460260	GO:0004033: aldo-keto reductase activity, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0006805: xenobiotic metabolic process, GO:0007586: digestion, GO:0008206: bile acid metabolic process, GO:0015721: bile acid and bile salt transport, GO:0016491: oxidoreductase activity, GO:0030299: cholesterol absorption, GO:0032052: bile acid binding, GO:0042632: cholesterol homeostasis, GO:0047006: 20-alpha-hydroxysteroid dehydrogenase activity, GO:0047042: 3-alpha-hydroxysteroid dehydrogenase (B-specific) activity, GO:0047115: trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity, GO:0051260: protein homooligomerization	00980: Metabolism of xenobiotics by cytochrome P450	10.86	11.08	11.31	11.46	11.89	11.74	11.34	11.49	11.13	10.80	11.43	11.69	2
204939_s_at	PLN	phospholamban	NM_002667	5350 Hs.170839	GO:0002026: regulation of the force of heart contraction, GO:0005246: calcium channel regulator activity, GO:0005515: protein binding, GO:0006874: cellular calcium ion homeostasis, GO:0008015: blood circulation, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016529: sarcoplasmic reticulum, GO:0042030: ATPase inhibitor activity, GO:0045822: negative regulation of heart contraction, GO:0048738: cardiac muscle development, GO:0051924: regulation of calcium ion transport	04020: Calcium signaling pathway	6.18	6.97	8.00	8.69	9.05	9.05	6.60	7.43	7.11	5.83	6.83	8.53	2
202500_at	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2	NM_006736	3300 Hs.77768	GO:0006457: protein folding, GO:0006986: response to unfolded protein, GO:0031072: heat shock protein binding, GO:0051082: unfolded protein binding		7.68	7.86	8.19	8.46	8.93	9.08	8.24	8.04	8.04	7.69	8.75	9.37	2

(*Continued*)

TABLE E4. (*Continued*)

202733_at	P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	NM_004199	8974	Hs.519568	GO:0004656: procollagen-proline 4-dioxygenase activity, GO:0005506: iron ion binding, GO:0005515: protein binding, GO:0005783: endoplasmic reticulum, GO:0005788: endoplasmic reticulum lumen, GO:0009055: electron carrier activity, GO:0016491: oxidoreductase activity, GO:0016702: oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, GO:0016706: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors, GO:0019538: protein metabolic process, GO:0031418: L-ascorbic acid binding, GO:0046872: metal ion binding	00330: Arginine and proline metabolism	8.22	8.50	8.87	9.31	9.20	8.93	8.56	8.75	8.70	8.61	8.74	9.12	2
65472_at	C2orf68	chromosome 2 open reading frame 68	AI161338	388969	Hs.516159			4.45	4.57	4.83	5.19	5.80	5.46	4.80	4.73	5.01	4.67	5.04	6.00	2
202289_s_at	TACC2	transforming, acidic coiled-coil containing protein 2	NM_006997	10579	Hs.501252, Hs.713875	GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005813: centrosome, GO:0035257: nuclear hormone receptor binding		10.41	10.54	10.78	11.06	11.42	11.56	11.08	10.77	10.93	10.70	11.28	11.79	2
45297_at	EHD2	EH-domain containing 2	AI417917	30846	Hs.714795	GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003924: GTPase activity, GO:0005509: calcium ion binding, GO:0005524: ATP binding, GO:0005525: GTP binding, GO:0005624: membrane fraction, GO:0005634: nucleus, GO:0005886: plasma membrane, GO:0006897: endocytosis, GO:0019904: protein domain specific binding, GO:0030866: cortical actin cytoskeleton organization and biogenesis		7.07	7.20	7.56	7.91	8.79	8.14	6.88	7.17	7.23	6.56	7.15	8.20	2
64942_at	GPR153	G protein-coupled receptor 153	AI937160	387509	Hs.531581	GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0005886: plasma membrane, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0016021: integral to membrane		7.06	7.13	7.27	7.48	7.73	7.41	6.98	6.92	7.24	6.71	6.37	7.44	2
38892_at	KIAA0240	KIAA0240	D87077	23506	Hs.658033			8.18	8.35	8.63	8.83	8.98	9.03	8.52	8.57	8.64	8.56	8.22	9.19	2
40446_at	PHF1	PHD finger protein 1	AL021366	5252	Hs.166204	GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		6.31	6.72	7.01	7.21	7.79	7.42	6.40	6.69	6.73	6.43	6.60	7.63	2
222156_x_at	CCPG1	cell cycle progression 1	AK022459	9236	Hs.285051	GO:0007049: cell cycle, GO:0016020: membrane, GO:0016021: integral to membrane		5.69	6.06	6.39	6.75	6.55	6.79	6.08	6.17	6.36	6.22	5.65	6.78	2

(*Continued*)

TABLE E4. (*Continued*)

222273_at	PAPOLG	poly(A) polymerase gamma	AI419423	64895	Hs.387471	GO:0003723: RNA binding, GO:0004652: polynucleotide adenylyltransferase activity, GO:0005634: nucleus, GO:0006350: transcription, GO:0006397: mRNA processing, GO:0016740: transferase activity, GO:0043631: RNA polyadenylation		7.04	7.31	7.36	7.59	7.74	7.90	7.48	7.68	7.45	7.28	7.02	8.38	2
221974_at	SNRPN	small nuclear ribonucleoprotein polypeptide N	AW770748	6638	Hs.555970, Hs.564847, Hs.578619, Hs.585703, Hs.621316, Hs.632166	GO:0003674: molecular_function, GO:0003676: nucleic acid binding, GO:0003723: RNA binding, GO:0005575: cellular_component, GO:0005634: nucleus, GO:0005681: spliceosome, GO:0008150: biological_process, GO:0008380: RNA splicing, GO:0016071: mRNA metabolic process, GO:0030529: ribonucleoprotein complex, GO:0030532: small nuclear ribonucleoprotein complex, GO:0042802: identical protein binding		3.34	3.61	3.65	3.99	4.44	4.38	3.32	3.84	3.65	3.58	3.17	4.25	2
222125_s_at	PH-4	hypoxia-inducible factor prolyl 4-hydroxylase	BC000580	54681	Hs.654944	GO:0005506: iron ion binding, GO:0005509: calcium ion binding, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0016020: membrane, GO:0016491: oxidoreductase activity, GO:0016702: oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, GO:0016706: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors, GO:0019538: protein metabolic process, GO:0031418: L-ascorbic acid binding		6.61	6.92	7.10	7.30	7.79	7.66	6.80	6.74	6.95	6.50	6.73	7.81	2
221833_at	SIAH1	seven in absentia homolog 1 (Drosophila)	AV700132	6477	Hs.295923	GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006508: proteolysis, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006915: apoptosis, GO:0007049: cell cycle, GO:0007275: multicellular organismal development, GO:0007283: spermatogenesis, GO:0007399: nervous system development, GO:0007411: axon guidance, GO:0008022: protein C-terminus binding, GO:0008270: zinc ion binding, GO:0009653: anatomical structure morphogenesis, GO:0016874: ligase activity, GO:0030154: cell differentiation, GO:0030163: protein catabolic process, GO:0046872: metal ion binding	04115: p53 signaling pathway, 04120: Ubiquitin mediated proteolysis, 04310: Wnt signaling pathway	6.44	6.76	7.20	7.73	8.17	8.06	6.06	6.51	6.66	6.03	6.05	7.77	2
221864_at	ORAI3	ORAI calcium release-activated calcium modulator 3	AW517464	93129	Hs.460617	GO:0016020: membrane, GO:0016021: integral to membrane		6.35	6.78	7.04	7.19	7.62	7.29	6.48	6.37	6.69	6.54	6.42	7.47	2

(*Continued*)

TABLE E4. (*Continued*)

221735_at	WDR48	WD repeat domain 48	H04342	57599	Hs.706774	GO:0005764: lysosome, GO:0044419: interspecies interaction between organisms		8.06	8.18	8.21	8.39	8.47	8.42	8.01	8.22	8.08	8.02	7.32	8.34	2
221749_at	YTHDF3	YTH domain family, member 3	AU157915	253943	Hs.491861	GO:0005737: cytoplasm		9.99	10.20	10.34	10.47	10.27	10.55	10.40	10.45	10.36	10.37	9.47	10.59	2
221589_s_at	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	AW612403	4329	Hs.293970	GO:0000062: acyl-CoA binding, GO:0004491: methylmalonate-semialdehyde dehydrogenase (acylating) activity, GO:0005739: mitochondrion, GO:0006573: valine metabolic process, GO:0016491: oxidoreductase activity, GO:0018478: malonate-semialdehyde dehydrogenase (acetylating) activity, GO:0019859: thymine metabolic process	00031: Inositol metabolism, 00280: Valine, leucine and isoleucine degradation, 00640: Propanoate metabolism	7.38	8.09	8.15	8.61	8.73	8.98	7.98	8.01	8.39	8.20	7.36	8.82	2
221645_s_at	ZNF83	zinc finger protein 83	M27877	55769	Hs.467210, Hs.659798, Hs.665751, Hs.710125	GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		7.65	8.09	8.40	8.90	9.04	9.19	7.74	8.40	8.26	8.11	7.97	9.33	2
221543_s_at	ERLIN2	ER lipid raft associated 2	AL442077	11160	Hs.705490	GO:0003674: molecular_function, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0008150: biological_process, GO:0016020: membrane, GO:0016021: integral to membrane		8.83	9.15	9.14	9.31	9.27	9.47	9.11	9.29	9.36	9.23	8.35	9.49	2
221554_at	LYK5	protein kinase LYK5	AF308302	92335	Hs.514402	GO:0000166: nucleotide binding, GO:0004672: protein kinase activity, GO:0004672: protein kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0006611: protein export from nucleus, GO:0007049: cell cycle, GO:0016740: transferase activity, GO:0032147: activation of protein kinase activity	04150: mTOR signaling pathway	6.64	6.82	6.76	6.90	7.04	7.07	6.86	6.75	6.85	6.82	6.14	7.26	2
221511_x_at	CCPG1	cell cycle progression 1	AF212228	9236	Hs.285051	GO:0007049: cell cycle, GO:0016020: membrane, GO:0016021: integral to membrane		6.88	7.45	7.83	8.04	7.99	8.04	7.44	7.56	7.67	7.46	6.94	8.25	2
221523_s_at	RRAGD	Ras-related GTP binding D	AL138717	58528	Hs.485938	GO:0000166: nucleotide binding, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0005634: nucleus, GO:0005737: cytoplasm		7.44	7.63	7.95	8.31	8.50	9.02	7.93	8.32	8.15	8.02	7.48	8.84	2
221208_s_at	C11orf61	chromosome 11 open reading frame 61	NM_024631	79684	Hs.146079			7.16	7.27	7.65	8.10	7.94	8.20	7.41	7.75	7.71	7.50	6.65	8.07	2

(*Continued*)

TABLE E4. (*Continued*)

221510_s_at	GLS	glutaminase	AI828035	2744	Hs.116448	GO:0004359: glutaminase activity, GO:0004359: glutaminase activity, GO:0005739: mitochondrion, GO:0005759: mitochondrial matrix, GO:0006543: glutamine catabolic process, GO:0016787: hydrolase activity	00251: Glutamate metabolism, 00471: D-Glutamine and D-glutamate metabolism, 00910: Nitrogen metabolism	9.73	9.82	9.99	10.25	9.98	10.46	9.80	10.27	9.91	10.13	8.94	10.25	2
221090_s_at	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	NM_018233	55239	Hs.231883	GO:0005506: iron ion binding, GO:0016491: oxidoreductase activity, GO:0016702: oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, GO:0016706: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors, GO:0019538: protein metabolic process, GO:0031418: L-ascorbic acid binding, GO:0046872: metal ion binding		7.21	7.18	7.20	7.17	7.17	7.27	7.20	7.29	7.51	7.35	5.97	7.23	2
221156_x_at	CCPG1	cell cycle progression 1	NM_004748	9236	Hs.285051	GO:0007049: cell cycle, GO:0016020: membrane, GO:0016021: integral to membrane		7.50	7.56	7.69	7.91	7.82	7.94	7.62	7.69	7.63	7.62	6.85	7.74	2
220974_x_at	SFXN3	sideroflexin 3	NM_030971	81855	Hs.283844	GO:0005506: iron ion binding, GO:0005739: mitochondrion, GO:0006812: cation transport, GO:0006826: iron ion transport, GO:0008324: cation transmembrane transporter activity, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0031966: mitochondrial membrane		8.84	8.95	9.17	9.53	9.80	9.73	8.79	8.89	9.06	8.68	8.70	9.77	2
221014_s_at	RAB33B	RAB33B, member RAS oncogene family	NM_031296	83452	Hs.591679	GO:0000139: Golgi membrane, GO:0000166: nucleotide binding, GO:0005525: GTP binding, GO:0005794: Golgi apparatus, GO:0007264: small GTPase mediated signal transduction, GO:0015031: protein transport, GO:0016020: membrane		6.94	7.14	7.39	7.58	7.77	7.88	7.28	7.49	7.63	7.49	6.41	7.95	2

(*Continued*)

TABLE E4. (*Continued*)

220432_s_at	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	NM_016593	51302	Hs.387367	GO:0004497: monooxygenase activity, GO:0005506: iron ion binding, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005789: endoplasmic reticulum membrane, GO:0005792: microsome, GO:0006629: lipid metabolic process, GO:0006699: bile acid biosynthetic process, GO:0006707: cholesterol catabolic process, GO:0007586: digestion, GO:0008202: steroid metabolic process, GO:0008387: steroid 7-alpha-hydroxylase activity, GO:0008396: oxysterol 7-alpha-hydroxylase activity, GO:0008396: oxysterol 7-alpha-hydroxylase activity, GO:0009055: electron carrier activity, GO:0016020: membrane, GO:0020037: heme binding, GO:0030573: bile acid catabolic process, GO:0033782: 24-hydroxycholesterol 7alpha-hydroxylase activity, GO:0046872: metal ion binding		7.00	7.29	7.60	7.96	8.31	8.65	8.15	7.73	8.21	7.99	7.69	9.18	2
220744_s_at	IFT122	intraflagellar transport 122 homolog (Chlamydomonas)	NM_018262	55764	Hs.655284	GO:0005737: cytoplasm, GO:0019861: flagellum		4.02	4.41	4.69	5.02	6.03	5.78	4.30	4.16	4.74	4.30	4.68	5.94	2
219909_at	MMP28	matrix metallopeptidase 28	NM_024302	79148	Hs.380710	GO:0004222: metalloendopeptidase activity, GO:0004222: metalloendopeptidase activity, GO:0005509: calcium ion binding, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005578: proteinaceous extracellular matrix, GO:0006508: proteolysis, GO:0006508: proteolysis, GO:0008152: metabolic process, GO:0008270: zinc ion binding		2.85	2.91	3.03	3.44	4.66	4.60	2.90	3.39	3.03	3.16	3.33	4.91	2
220402_at	P53AIP1	p53-regulated apoptosis-inducing protein 1	NM_022112	63970	Hs.160953, Hs.711194	GO:0003674: molecular_function, GO:0005739: mitochondrion, GO:0006915: apoptosis	04115: p53 signaling pathway	7.68	7.83	7.90	7.74	7.81	7.78	7.90	7.85	7.83	7.87	6.70	7.86	2
219833_s_at	EFHC1	EF-hand domain (C-terminal) containing 1	NM_018100	114327	Hs.403171	GO:0005509: calcium ion binding, GO:0005929: cilium, GO:0005930: axoneme, GO:0008022: protein C-terminus binding, GO:0019861: flagellum, GO:0043025: cell soma		5.43	6.03	6.44	6.95	7.28	7.16	6.57	6.27	6.58	6.52	5.77	7.65	2
219848_s_at	ZNF432	zinc finger protein 432	NM_014650	9668	Hs.655934	GO:0003677: DNA binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		6.61	7.20	7.30	7.54	7.98	7.93	6.90	7.02	6.96	7.00	6.44	7.92	2
219765_at	ZNF329	zinc finger protein 329	NM_024620	79673	Hs.458377	GO:0003677: DNA binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		4.83	4.98	5.07	5.62	5.97	5.81	4.91	5.17	5.26	5.14	4.66	5.84	2
219802_at	PYROXD1	pyridine nucleotide-disulphide oxidoreductase domain 1	NM_024854	79912	Hs.709545	GO:0009055: electron carrier activity, GO:0016491: oxidoreductase activity		7.80	7.96	8.08	8.34	8.23	8.54	8.41	8.17	8.25	8.28	7.77	8.65	2

(*Continued*)

TABLE E4. (*Continued*)

219407_s_at	LAMC3	laminin, gamma 3	NM_006059	10319	Hs.201805	GO:0005198: structural molecule activity, GO:0005515: protein binding, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0005604: basement membrane, GO:0007155: cell adhesion, GO:0016020: membrane	01430: Cell Communication, 04510: Focal adhesion, 04512: ECM-receptor interaction, 05222: Small cell lung cancer	2.56	2.65	2.84	3.43	4.71	4.37	2.47	2.50	2.93	2.32	2.58	3.98	2
219487_at	BBS10	Bardet-Biedl syndrome 10	NM_024685	79738	Hs.96322	GO:0000166: nucleotide binding, GO:0001895: retinal homeostasis, GO:0005524: ATP binding, GO:0006457: protein folding, GO:0035058: sensory cilium biogenesis, GO:0045494: photoreceptor cell maintenance, GO:0050896: response to stimulus, GO:0051082: unfolded protein binding		5.00	5.08	5.48	5.69	5.67	5.90	5.46	5.64	5.42	5.34	5.10	5.95	2
219376_at	ZNF322A	zinc finger protein 322A	NM_024639	79692	Hs.126280, Hs.530271	GO:0003677: DNA binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		3.82	3.92	3.96	4.22	4.06	4.12	4.07	4.44	3.98	4.00	3.09	4.10	2
219401_at	XYLT2	xylosyltransferase II	NM_022167	64132	Hs.699363	GO:0000139: Golgi membrane, GO:0005575: cellular_component, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005794: Golgi apparatus, GO:0006024: glycosaminoglycan biosynthetic process, GO:0008375: acetylglucosaminyltransferase activity, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016757: transferase activity, transferring glycosyl groups, GO:0030158: protein xylosyltransferase activity	00532: Chondroitin sulfate biosynthesis, 01030: Glycan structures - biosynthesis 1	4.77	4.88	4.95	5.18	5.56	5.14	5.05	5.00	5.04	4.72	4.61	5.39	2
219284_at	HSPBAP1	HSPB (heat shock 27kDa) associated protein 1	NM_024610	79663	Hs.29169	GO:0005737: cytoplasm		7.22	7.85	8.03	8.11	8.25	8.15	7.74	7.73	7.91	7.83	7.12	8.23	2
219353_at	NHLRC2	NHL repeat containing 2	NM_017687	374354	Hs.369924, Hs.594372			7.56	7.90	8.00	8.27	8.19	8.45	7.95	8.27	8.08	8.02	7.51	8.42	2
219069_at	ANKRD49	ankyrin repeat domain 49	NM_017704	54851	Hs.29052			8.21	8.52	8.58	8.62	8.52	8.67	8.49	8.51	8.62	8.35	7.48	8.79	2
219274_at	TSPAN12	tetraspanin 12	NM_012338	23554	Hs.16529	GO:0005624: membrane fraction, GO:0016020: membrane, GO:0016021: integral to membrane		4.22	4.04	4.41	4.85	5.24	4.79	4.23	4.63	4.47	4.31	3.88	4.50	2

(*Continued*)

TABLE E4. (*Continued*)

218878_s_at	SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	NM_012238	23411	Hs.369779	GO:0003677: DNA binding, GO:0003950: NAD+ ADP-ribosyltransferase activity, GO:0005634: nucleus, GO:0005677: chromatin silencing complex, GO:0006342: chromatin silencing, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006471: protein amino acid ADP-ribosylation, GO:0006476: protein amino acid deacetylation, GO:0006915: apoptosis, GO:0006974: response to DNA damage stimulus, GO:0007275: multicellular organismal development, GO:0007519: skeletal muscle development, GO:0008022: protein C-terminus binding, GO:0008270: zinc ion binding, GO:0017136: NAD-dependent histone deacetylase activity, GO:0019213: deacetylase activity, GO:0030154: cell differentiation, GO:0033158: regulation of protein import into nucleus, translocation, GO:0044419: interspecies interaction between organisms, GO:0046872: metal ion binding, GO:0051097: negative regulation of helicase activity, GO:0051287: NAD binding		8.45	8.70	8.79	8.92	8.60	9.03	8.91	8.94	8.59	8.79	7.77	9.00	2
218909_at	RPS6KC1	ribosomal protein S6 kinase, 52kDa, polypeptide 1	NM_012424	26750	Hs.591416	GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005737: cytoplasm, GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0016020: membrane, GO:0016740: transferase activity, GO:0035091: phosphoinositide binding		5.71	6.24	6.27	6.54	6.40	6.52	6.46	6.30	6.67	6.63	5.47	6.56	2
218761_at	RNF111	ring finger protein 111	NM_017610	54778	Hs.404423	GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0007275: multicellular organismal development, GO:0008270: zinc ion binding, GO:0016874: ligase activity, GO:0046872: metal ion binding		8.15	8.42	8.42	8.58	8.55	8.66	8.35	8.57	8.53	8.51	7.36	8.85	2
218789_s_at	C11orf71	chromosome 11 open reading frame 71	NM_019021	54494	Hs.91816, Hs.715083			5.91	6.33	6.58	6.68	6.50	6.68	6.59	6.11	6.30	6.52	5.50	6.72	2
218718_at	PDGFC	platelet derived growth factor C	NM_016205	56034	Hs.570855	GO:0005576: extracellular region, GO:0007417: central nervous system development, GO:0008083: growth factor activity, GO:0008283: cell proliferation, GO:0016020: membrane	04060: Cytokine-cytokine receptor interaction, 04510: Focal adhesion, 04540: Gap junction, 05215: Prostate cancer, 05218: Melanoma	7.94	8.39	8.79	9.18	9.40	9.76	8.01	8.47	8.54	8.46	7.86	9.87	2

(*Continued*)

TABLE E4. (*Continued*)

218757_s_at	UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)	NM_023010	65109	Hs.103832	GO:0000166: nucleotide binding, GO:0000184: mRNA catabolic process, nonsense-mediated decay, GO:0000398: nuclear mRNA splicing, via spliceosome, GO:0003723: RNA binding, GO:0005487: nucleocytoplasmic transporter activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006810: transport, GO:0051028: mRNA transport	7.49	8.04	8.03	8.10	7.87	8.02	8.29	8.37	8.19	8.10	6.82	8.28	2
218694_at	ARMCX1	armadillo repeat containing, X-linked 1	NM_016608	51309	Hs.9728	GO:0005488: binding, GO:0016020: membrane, GO:0016021: integral to membrane	9.27	9.55	9.82	10.07	10.12	10.22	9.44	9.83	9.67	9.49	9.21	10.14	2
218701_at	LACTB2	lactamase, beta 2	NM_016027	51110	Hs.118554	GO:0008270: zinc ion binding, GO:0016787: hydrolase activity, GO:0046872: metal ion binding	7.38	7.37	7.55	7.51	7.14	7.83	7.98	7.87	7.95	7.69	6.08	8.06	2
218651_s_at	LARP6	La ribonucleoprotein domain family, member 6	NM_018357	55323	Hs.416755	GO:0003676: nucleic acid binding, GO:0003723: RNA binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006396: RNA processing, GO:0030529: ribonucleoprotein complex	2.72	2.83	2.93	3.10	4.01	3.65	2.75	3.10	2.75	2.80	2.89	3.45	2
218683_at	PTBP2	polypyrimidine tract binding protein 2	NM_021190	58155	Hs.591430, Hs.596061	GO:0000166: nucleotide binding, GO:0003676: nucleic acid binding, GO:0003723: RNA binding, GO:0005634: nucleus, GO:0006397: mRNA processing, GO:0008380: RNA splicing	8.41	8.77	8.88	9.25	9.11	9.13	8.82	8.99	9.03	8.86	8.21	9.02	2
218574_s_at	LMCD1	LIM and cysteine-rich domains 1	NM_014583	29995	Hs.475353	GO:0000122: negative regulation of transcription from RNA polymerase II promoter, GO:0003674: molecular_function, GO:0003714: transcription corepressor activity, GO:0005515: protein binding, GO:0005575: cellular_component, GO:0005634: nucleus, GO:0008150: biological_process, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	6.99	7.15	7.33	7.93	8.35	8.12	6.79	7.21	7.18	6.80	6.43	7.89	2
218637_at	IMPACT	Impact homolog (mouse)	NM_018439	55364	Hs.515317	GO:0003674: molecular_function, GO:0005575: cellular_component, GO:0006417: regulation of translation, GO:0008150: biological_process	7.26	7.61	7.89	8.08	7.97	8.12	7.71	7.67	7.98	7.88	6.85	8.10	2
218528_s_at	RNF38	ring finger protein 38	NM_022781	152006	Hs.333503	GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	8.64	9.06	9.18	9.52	9.56	9.65	9.04	9.26	9.13	9.03	8.79	9.72	2
218546_at	C1orf115	chromosome 1 open reading frame 115	NM_024709	79762	Hs.519839	GO:0016020: membrane, GO:0016021: integral to membrane	5.96	6.79	7.15	7.58	8.23	8.19	6.32	7.00	6.78	6.83	6.61	7.81	2
218456_at	CAPRIN2	caprin family member 2	NM_023925	65981	Hs.234355	GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0030308: negative regulation of cell growth	7.71	8.03	8.30	8.64	8.69	8.75	8.01	7.94	8.20	7.98	7.69	8.84	2
218491_s_at	THYN1	thymocyte nuclear protein 1	NM_014174	29087	Hs.13645	GO:0005634: nucleus	7.50	7.86	7.88	8.19	8.20	8.41	7.97	7.71	7.93	7.78	7.57	8.28	2
218352_at	RCBTB1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	NM_018191	55213	Hs.508021	GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007049: cell cycle, GO:0016568: chromatin modification	7.61	8.02	8.15	8.47	8.32	8.91	8.03	8.45	8.36	8.22	6.81	8.61	2

(*Continued*)

TABLE E4. (*Continued*)

218361_at	GOLPH3L	golgi phosphoprotein 3-like	NM_018178	55204	Hs.203699	GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0016020: membrane		8.33	8.34	8.34	8.42	8.54	8.59	8.65	8.61	8.37	8.37	7.68	8.76	2
218304 _s_at	OSBPL11	oxysterol binding protein-like 11	NM_022776	114885	Hs.477440	GO:0006869: lipid transport, GO:0008202: steroid metabolic process		8.02	8.07	8.24	8.42	8.01	8.44	8.56	8.58	8.50	8.38	7.03	8.60	2
218346 _s_at	SESN1	sestrin 1	NM_014454	27244	Hs.591336	GO:0005634: nucleus, GO:0005634: nucleus, GO:0006974: response to DNA damage stimulus, GO:0007050: cell cycle arrest, GO:0007050: cell cycle arrest, GO:0008285: negative regulation of cell proliferation	04115: p53 signaling pathway	8.19	8.70	8.76	8.99	8.94	9.04	8.43	8.39	8.62	8.56	8.02	9.18	2
218168 _s_at	CABC1	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	NM_020247	56997	Hs.118241	GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0005739: mitochondrion, GO:0008219: cell death, GO:0016301: kinase activity, GO:0016740: transferase activity		7.70	8.31	8.39	8.49	8.87	8.92	8.03	7.95	8.17	8.13	8.05	8.87	2
218285 _s_at	BDH2	3-hydroxybutyrate dehydrogenase, type 2	NM_020139	56898	Hs.124696	GO:0003858: 3-hydroxybutyrate dehydrogenase activity, GO:0005488: binding, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0006635: fatty acid beta-oxidation, GO:0016491: oxidoreductase activity, GO:0051287: NAD binding	00072: Synthesis and degradation of ketone bodies, 00650: Butanoate metabolism	8.70	9.02	9.06	9.31	9.33	9.37	8.94	8.96	8.95	8.95	8.55	9.43	2
217935 _s_at	UQCC	ubiquinol-cytochrome c reductase complex chaperone	NM_018244	55245	Hs.714359	GO:0031410: cytoplasmic vesicle		7.19	7.36	7.41	7.53	7.31	7.31	7.54	7.61	7.55	7.67	6.12	7.54	2
217954 _s_at	PHF3	PHD finger protein 3	NM_015153	23469	Hs.348921	GO:0003674: molecular_function, GO:0005515: protein binding, GO:0005575: cellular_component, GO:0006350: transcription, GO:0007275: multicellular organismal development, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		8.59	9.02	9.18	9.50	9.42	9.72	9.13	9.40	9.24	9.18	8.59	9.73	2
217853_at	TNS3	tensin 3	NM_022748	64759	Hs.520814	GO:0005515: protein binding, GO:0005515: protein binding, GO:0030054: cell junction		8.35	9.07	9.17	9.47	9.65	9.49	8.51	9.10	9.10	8.91	8.69	9.52	2
217894_at	KCTD3	potassium channel tetramerisation domain containing 3	NM_016121	51133	Hs.335139	GO:0005249: voltage-gated potassium channel activity, GO:0005515: protein binding, GO:0006813: potassium ion transport, GO:0008076: voltage-gated potassium channel complex, GO:0016020: membrane		9.12	9.17	9.38	9.49	9.30	9.60	9.30	9.49	9.44	9.37	8.41	9.43	2

(*Continued*)

TABLE E4. (*Continued*)

216321_s_at	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	X03348	2908	Hs.122926	GO:0003700: transcription factor activity, GO:0004883: glucocorticoid receptor activity, GO:0005496: steroid binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005759: mitochondrial matrix, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0007165: signal transduction, GO:0007530: sex determination, GO:0008270: zinc ion binding, GO:0016568: chromatin modification, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding	04080: Neuroactive ligand-receptor interaction	10.16	10.53	10.77	11.10	11.04	11.13	10.55	10.82	10.84	10.62	10.18	11.19	2
217800_s_at	NDFIP1	Nedd4 family interacting protein 1	NM_030571	80762	Hs.9788, Hs.653510	GO:0000139: Golgi membrane, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade		10.09	10.32	10.67	10.92	10.66	10.99	10.02	10.47	10.51	10.33	9.19	10.57	2
214843_s_at	USP33	ubiquitin specific peptidase 33	AK022864	23032	Hs.480597	GO:0004221: ubiquitin thiolesterase activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005737: cytoplasm, GO:0006511: ubiquitin-dependent protein catabolic process, GO:0008234: cysteine-type peptidase activity, GO:0008270: zinc ion binding, GO:0016579: protein deubiquitination, GO:0016579: protein deubiquitination, GO:0030891: VCB complex, GO:0046872: metal ion binding		8.00	8.29	8.41	8.47	8.56	8.55	8.32	8.54	8.60	8.67	7.57	8.69	2
215012_at	ZNF451	zinc finger protein 451	AU144775	26036	Hs.485628, Hs.705485	GO:0003677: DNA binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		7.37	7.42	7.72	7.93	8.13	8.13	7.66	7.70	7.65	7.54	7.10	8.20	2
214724_at	DIXDC1	DIX domain containing 1	AF070621	85458	Hs.655626	GO:0003779: actin binding, GO:0004871: signal transducer activity, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0007275: multicellular organismal development, GO:0016055: Wnt receptor signaling pathway, GO:0030054: cell junction		7.37	7.46	8.07	8.58	9.08	9.10	7.34	7.99	7.48	7.24	7.32	8.94	2
214749_s_at	ARMCX6	armadillo repeat containing, X-linked 6	AK000818	54470	Hs.83530	GO:0016020: membrane, GO:0016021: integral to membrane		8.58	8.89	8.97	9.20	9.33	9.39	8.75	8.92	9.07	8.82	8.17	9.67	2

(*Continued*)

TABLE E4. (*Continued*)

214683_s_at	CLK1	CDC-like kinase 1	AI251890	1195	Hs.433732	GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0004715: non-membrane spanning protein tyrosine kinase activity, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0006468: protein amino acid phosphorylation, GO:0008283: cell proliferation, GO:0016740: transferase activity		10.36	10.65	10.73	11.03	10.73	10.90	10.71	10.90	10.47	10.71	10.05	10.94	2
214686_at	ZNF266	zinc finger protein 266	AA868898	10781	Hs.656185	GO:0003677: DNA binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		8.89	9.25	9.41	9.58	9.81	9.65	8.92	8.82	9.07	8.85	8.55	9.62	2
214132_at	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	BG232034	509	Hs.271135	GO:0000275: mitochondrial proton-transporting ATP synthase complex, catalytic core F(1), GO:0005739: mitochondrion, GO:0005759: mitochondrial matrix, GO:0006811: ion transport, GO:0015986: ATP synthesis coupled proton transport, GO:0015992: proton transport, GO:0016020: membrane, GO:0016469: proton-transporting two-sector ATPase complex, GO:0016887: ATPase activity, GO:0016887: ATPase activity, GO:0046872: metal ion binding, GO:0046933: hydrogen ion transporting ATP synthase activity, rotational mechanism, GO:0046961: hydrogen ion transporting ATPase activity, rotational mechanism	00190: Oxidative phosphorylation	6.70	7.27	7.29	7.59	7.27	7.60	7.27	7.45	7.28	7.15	6.28	7.68	2
214186_s_at	3.8-1	MHC class I mRNA fragment 3.8-1	AI346483	352961	Hs.132807			6.32	6.47	6.67	7.21	6.97	7.28	6.72	6.81	6.75	6.55	6.19	7.55	2
213982_s_at	RABGAP1L	RAB GTPase activating protein 1-like	BG107203	9910	Hs.585378	GO:0005097: Rab GTPase activator activity, GO:0005097: Rab GTPase activator activity, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005769: early endosome, GO:0005794: Golgi apparatus, GO:0032313: regulation of Rab GTPase activity, GO:0032880: regulation of protein localization		6.45	7.01	7.11	7.41	7.74	7.53	6.95	7.21	7.12	7.13	7.00	7.78	2
214036_at			BE464799					6.02	6.33	6.46	6.77	7.45	7.52	6.47	6.72	6.72	5.86	5.95	7.73	2
213675_at			W61005					6.21	6.44	6.75	7.23	8.12	7.80	6.18	6.63	6.67	6.20	6.75	7.54	2
213895_at	EMP1	epithelial membrane protein 1	BF445047	2012	Hs.713606	GO:0005624: membrane fraction, GO:0007275: multicellular organismal development, GO:0008283: cell proliferation, GO:0008544: epidermis development, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016049: cell growth		6.20	5.89	6.14	6.75	7.13	7.50	6.53	6.69	6.52	6.23	5.97	7.85	2

(*Continued*)

TABLE E4. (*Continued*)

213592_at	APLNR	apelin receptor	X89271	187 Hs.438311	GO:0001584: rhodopsin-like receptor activity, GO:0004872: receptor activity, GO:0004872: receptor activity, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0016021: integral to membrane	04080: Neuroactive ligand-receptor interaction	6.44	6.79	6.86	7.30	7.73	6.80	6.42	6.60	6.73	6.66	6.33	6.60	2
213626_at	CBR4	carbonyl reductase 4	AL049442	84869 Hs.659311	GO:0005488: binding, GO:0005737: cytoplasm, GO:0016491: oxidoreductase activity		8.01	8.33	8.45	8.74	8.49	8.76	8.60	8.71	8.66	8.59	7.55	9.01	2
213480_at	VAMP4	vesicle-associated membrane protein 4	AF052100	8674 Hs.6651	GO:0000139: Golgi membrane, GO:0005764: lysosome, GO:0005768: endosome, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016192: vesicle-mediated transport	04130: SNARE interactions in vesicular transport	8.30	8.48	8.73	8.93	8.98	9.17	8.50	8.63	8.81	8.50	7.91	9.36	2
213500_at			AI307760				6.45	6.48	6.66	6.73	6.80	6.89	6.54	6.83	6.76	6.62	5.84	7.13	2
213304_at	FAM179B	family with sequence similarity 179, member B	AI823592	23116 Hs.371078	GO:0005488: binding		7.26	7.70	7.86	8.32	8.00	8.31	7.98	8.11	8.03	7.97	7.01	8.37	2
213331_s_at	NEK1	NIMA (never in mitosis gene a)-related kinase 1	AV700007	4750 Hs.481181	GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004674: protein serine/threonine kinase activity, GO:0004674: protein serine/threonine kinase activity, GO:0004713: protein-tyrosine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005575: cellular_component, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0016740: transferase activity, GO:0051301: cell division		5.82	6.14	6.16	6.42	6.38	6.32	5.99	6.22	6.23	6.31	5.37	6.32	2
213169_at	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	BG109855	9037 Hs.27621	GO:0004872: receptor activity, GO:0007155: cell adhesion, GO:0007267: cell-cell signaling, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030154: cell differentiation	04360: Axon guidance	5.70	6.34	6.31	6.85	6.90	6.74	5.78	6.59	6.19	6.29	5.42	6.42	2
213213_at	DIDO1	death inducer-obliterator 1	AL035669	11083 Hs.517172	GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006350: transcription, GO:0006915: apoptosis, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		6.20	6.63	6.56	6.73	7.17	7.06	6.69	6.77	6.62	6.38	6.63	7.17	2

(*Continued*)

TABLE E4. (*Continued*)

212984_at	ATF2	activating transcription factor 2	BE786164	1386	Hs.592510	GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0003713: transcription coactivator activity, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005829: cytosol, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0043565: sequence-specific DNA binding, GO:0046872: metal ion binding, GO:0046983: protein dimerization activity	04010: MAPK signaling pathway	9.09	9.40	9.61	9.90	9.82	9.91	9.43	9.68	9.62	9.56	9.03	9.83	2
213020_at	GOSR1	golgi SNAP receptor complex member 1	AI814252	9527	Hs.462680	GO:0000139: Golgi membrane, GO:0005484: SNAP receptor activity, GO:0005794: Golgi apparatus, GO:0006886: intracellular protein transport, GO:0006891: intra-Golgi vesicle-mediated transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016192: vesicle-mediated transport, GO:0031201: SNARE complex, GO:0042147: retrograde transport, endosome to Golgi	04130: SNARE interactions in vesicular transport	7.60	7.66	7.78	7.89	7.81	8.00	7.97	7.93	7.96	7.94	6.94	8.01	2
212981_s_at	FAM115A	family with sequence similarity 115, member A	BF030508	9747	Hs.406492, Hs.709470			8.21	8.48	8.68	8.96	8.94	9.08	8.56	8.92	8.82	8.63	8.14	8.93	2
212982_at	ZDHHC17	zinc finger, DHHC-type containing 17	AI621223	23390	Hs.4014	GO:0000139: Golgi membrane, GO:0004871: signal transducer activity, GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0005794: Golgi apparatus, GO:0008270: zinc ion binding, GO:0008415: acyltransferase activity, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016740: transferase activity, GO:0019706: protein-cysteine S-palmitoleyltransferase activity, GO:0030659: cytoplasmic vesicle membrane, GO:0031410: cytoplasmic vesicle, GO:0042953: lipoprotein transport, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0046872: metal ion binding		9.29	9.63	9.74	10.09	10.04	9.99	9.45	9.79	9.83	9.69	8.88	10.13	2
212847_at	FUBP1	far upstream element (FUSE) binding protein 1	AL036840	8880	Hs.567380	GO:0003697: single-stranded DNA binding, GO:0003700: transcription factor activity, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter		8.06	8.29	8.52	8.86	8.71	8.94	8.04	8.71	8.58	8.45	7.32	8.97	2

(*Continued*)

TABLE E4. (*Continued*)

212893_at	ZZZ3	zinc finger, ZZ-type containing 3	AL080063	26009	Hs.480506	GO:0003677: DNA binding, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		7.58	8.06	8.12	8.26	8.13	8.29	8.28	8.23	8.35	8.19	6.41	8.47	2
212761_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	AI703074	6934	Hs.593995	GO:0001568: blood vessel development, GO:0003677: DNA binding, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006916: anti-apoptosis, GO:0007050: cell cycle arrest, GO:0008013: beta-catenin binding, GO:0008283: cell proliferation, GO:0016566: specific transcriptional repressor activity, GO:0031016: pancreas development, GO:0032024: positive regulation of insulin secretion, GO:0032350: regulation of hormone metabolic process, GO:0042593: glucose homeostasis, GO:0045444: fat cell differentiation, GO:0048625: myoblast cell fate commitment, GO:0060070: Wnt receptor signaling pathway through beta-catenin	04310: Wnt signaling pathway, 04520: Adherens junction, 04916: Melanogenesis, 05210: Colorectal cancer, 05213: Endometrial cancer, 05215: Prostate cancer, 05216: Thyroid cancer, 05217: Basal cell carcinoma, 05221: Acute myeloid leukemia	9.73	10.29	10.51	10.88	11.12	11.08	10.10	10.36	10.48	10.29	10.35	11.03	2
212762_s_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	AI375916	6934	Hs.593995	GO:0001568: blood vessel development, GO:0003677: DNA binding, GO:0003700: transcription factor activity, GO:0003702: RNA polymerase II transcription factor activity, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006916: anti-apoptosis, GO:0007050: cell cycle arrest, GO:0008013: beta-catenin binding, GO:0008283: cell proliferation, GO:0016566: specific transcriptional repressor activity, GO:0031016: pancreas development, GO:0032024: positive regulation of insulin secretion, GO:0032350: regulation of hormone metabolic process, GO:0042593: glucose homeostasis, GO:0045444: fat cell differentiation, GO:0048625: myoblast cell fate commitment, GO:0060070: Wnt receptor signaling pathway through beta-catenin	04310: Wnt signaling pathway, 04520: Adherens junction, 04916: Melanogenesis, 05210: Colorectal cancer, 05213: Endometrial cancer, 05215: Prostate cancer, 05216: Thyroid cancer, 05217: Basal cell carcinoma, 05221: Acute myeloid leukemia	7.62	7.90	8.52	8.80	8.98	9.24	7.67	8.37	8.23	8.28	7.66	8.90	2

(*Continued*)

TABLE E4. (*Continued*)

212752_at	CLASP1	cytoplasmic linker associated protein 1	AA176798	23332	Hs.469840	GO:0000777: condensed chromosome kinetochore, GO:0001578: microtubule bundle formation, GO:0005515: protein binding, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0005828: kinetochore microtubule, GO:0005856: cytoskeleton, GO:0005881: cytoplasmic microtubule, GO:0007026: negative regulation of microtubule depolymerization, GO:0007026: negative regulation of microtubule depolymerization, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0007163: establishment and/or maintenance of cell polarity, GO:0010458: exit from mitosis, GO:0030981: cortical microtubule cytoskeleton, GO:0031592: centrosomal corona, GO:0043515: kinetochore binding, GO:0051010: microtubule plus-end binding, GO:0051301: cell division		8.79	8.93	9.04	9.20	9.21	9.24	9.15	8.87	9.22	9.21	8.32	9.36	2
212756_s_at	UBR2	ubiquitin protein ligase E3 component n-recognin 2	AI761518	23304	Hs.529925	GO:0004842: ubiquitin-protein ligase activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0008270: zinc ion binding, GO:0016874: ligase activity, GO:0030163: protein catabolic process, GO:0046872: metal ion binding		7.00	7.31	7.22	7.28	7.36	7.24	7.54	7.45	7.73	7.48	6.59	7.58	2
212631_at	STX7	syntaxin 7	AI566082	8417	Hs.593148, Hs.605992	GO:0005484: SNAP receptor activity, GO:0005768: endosome, GO:0006886: intracellular protein transport, GO:0006892: post-Golgi vesicle-mediated transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016192: vesicle-mediated transport, GO:0031901: early endosome membrane	04130: SNARE interactions in vesicular transport	8.01	8.43	8.47	8.57	8.31	8.62	8.39	8.51	8.52	8.41	6.59	8.62	2
212669_at	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	AI093569	818	Hs.699281	GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004683: calmodulin-dependent protein kinase activity, GO:0004723: calcium-dependent protein serine/threonine phosphatase activity, GO:0005516: calmodulin binding, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0005575: cellular_component, GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0030073: insulin secretion	04012: ErbB signaling pathway, 04020: Calcium signaling pathway, 04310: Wnt signaling pathway, 04720: Long-term potentiation, 04740: Olfactory transduction, 04912: GnRH signaling pathway, 04916: Melanogenesis, 05214: Glioma	4.28	4.34	4.55	4.68	5.06	4.61	4.37	4.37	4.18	4.14	4.10	4.68	2

(*Continued*)

TABLE E4. (*Continued*)

212549_at	STAT5B	signal transducer and activator of transcription 5B	BE645861	6777	Hs.714309	GO:0001553: luteinization, GO:0001779: natural killer cell differentiation, GO:0003700: transcription factor activity, GO:0004871: signal transducer activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0007165: signal transduction, GO:0007259: JAK-STAT cascade, GO:0007565: female pregnancy, GO:0007595: lactation, GO:0008284: positive regulation of cell proliferation, GO:0019218: regulation of steroid metabolic process, GO:0019221: cytokine and chemokine mediated signaling pathway, GO:0019915: sequestering of lipid, GO:0030155: regulation of cell adhesion, GO:0030856: regulation of epithelial cell differentiation, GO:0040018: positive regulation of multicellular organism growth, GO:0042104: positive regulation of activated T cell proliferation, GO:0042448: progesterone metabolic process, GO:0043029: T cell homeostasis, GO:0043066: negative regulation of apoptosis, GO:0045086: positive regulation of interleukin-2 biosynthetic process, GO:0045579: positive regulation of B cell differentiation, GO:0045647: negative regulation of erythrocyte differentiation, GO:0045885: positive regulation of survival gene product activity, GO:0045931: positive regulation of mitotic cell cycle, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0046543: development of secondary female sexual characteristics, GO:0046544: development of secondary male sexual characteristics, GO:0050729: positive regulation of inflammatory response	04012: ErbB signaling pathway, 04630: Jak-STAT signaling pathway, 05220: Chronic myeloid leukemia	7.37	7.58	7.60	8.04	8.19	8.12	7.34	7.72	7.56	7.54	6.89	8.19	2
212628_at	PKN2	protein kinase N2	BG292065	5586	Hs.440833	GO:0000166: nucleotide binding, GO:0004672: protein kinase activity, GO:0004697: protein kinase C activity, GO:0005524: ATP binding, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0006468: protein amino acid phosphorylation, GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007165: signal transduction, GO:0016740: transferase activity		9.44	9.57	9.58	9.76	9.36	9.75	9.62	9.72	9.67	9.69	8.52	9.74	2

(*Continued*)

TABLE E4. (*Continued*)

212510 _at	GPD1L	glycerol-3-phosphate dehydrogenase 1-like	AA135522	23171	Hs.82432	GO:0004367: glycerol-3-phosphate dehydrogenase (NAD+) activity, GO:0005488: binding, GO:0005737: cytoplasm, GO:0005975: carbohydrate metabolic process, GO:0009331: glycerol-3-phosphate dehydrogenase complex, GO:0046168: glycerol-3-phosphate catabolic process, GO:0051287: NAD binding	00564: Glycerophospholipid metabolism	7.21	7.68	7.77	8.19	8.47	8.79	7.43	7.67	7.79	7.56	6.95	8.75	2
212511 _at	PICALM	phosphatidylinositol binding clathrin assembly protein	AI766247	8301	Hs.163893	GO:0005543: phospholipid binding, GO:0005545: phosphatidylinositol binding, GO:0005545: phosphatidylinositol binding, GO:0005794: Golgi apparatus, GO:0005905: coated pit, GO:0005905: coated pit, GO:0006898: receptor-mediated endocytosis, GO:0006898: receptor-mediated endocytosis, GO:0016020: membrane, GO:0030118: clathrin coat, GO:0030276: clathrin binding, GO:0030276: clathrin binding, GO:0031410: cytoplasmic vesicle, GO:0048268: clathrin cage assembly		8.48	8.54	8.51	8.67	8.80	8.79	8.62	8.82	8.71	8.75	7.81	8.75	2
212310 _at	MIA3	melanoma inhibitory activity family, member 3	D87742	375056	Hs.118474	GO:0002687: positive regulation of leukocyte migration, GO:0005515: protein binding, GO:0007162: negative regulation of cell adhesion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030336: negative regulation of cell migration, GO:0042060: wound healing		3.21	3.66	3.91	4.30	4.46	4.78	3.55	3.84	3.73	3.57	3.40	4.85	2
212504 _at	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	N31807	22982	Hs.432397	GO:0003824: catalytic activity, GO:0005634: nucleus, GO:0008134: transcription factor binding, GO:0008152: metabolic process		6.04	6.37	6.65	7.13	7.75	7.47	6.33	6.45	6.35	6.26	6.10	7.64	2
212243 _at	GRINL1A	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	BE645501	81488	Hs.437256	GO:0004872: receptor activity, GO:0005635: nuclear envelope		7.69	8.16	8.08	8.19	7.80	8.07	7.92	8.08	8.10	8.12	7.01	8.03	2
212305 _s_at	MIA3	melanoma inhibitory activity family, member 3	AK025122	375056	Hs.118474	GO:0002687: positive regulation of leukocyte migration, GO:0005515: protein binding, GO:0007162: negative regulation of cell adhesion, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030336: negative regulation of cell migration, GO:0042060: wound healing		6.55	6.61	6.61	6.76	6.80	6.83	6.68	6.89	6.73	6.60	5.73	6.82	2
212122 _at	RHOQ	ras homolog gene family, member Q	AW771590	23433	Hs.709193	GO:0000166: nucleotide binding, GO:0003924: GTPase activity, GO:0005515: protein binding, GO:0005525: GTP binding, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0007264: small GTPase mediated signal transduction, GO:0008150: biological_process, GO:0008360: regulation of cell shape	04910: Insulin signaling pathway	7.55	7.73	8.04	8.26	8.38	8.40	7.87	7.92	8.01	7.67	7.06	8.49	2
212158 _at	SDC2	syndecan 2	AL577322	6383	Hs.1501, Hs.598247	GO:0003674: molecular_function, GO:0005887: integral to plasma membrane, GO:0008092: cytoskeletal protein binding, GO:0008150: biological_process, GO:0016020: membrane	04512: ECM-receptor interaction, 04514: Cell adhesion molecules (CAMs)	8.96	9.37	9.84	10.26	10.47	10.55	9.03	9.51	9.47	9.13	8.94	10.21	2

(*Continued*)

TABLE E4. (*Continued*)

212060_at	SR140	U2-associated SR140 protein	AU152088	23350	Hs.596572	GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0006396: RNA processing		8.35	8.31	8.53	8.52	8.40	8.68	8.49	8.65	8.67	8.50	7.43	8.69	2
212061_at	SR140	U2-associated SR140 protein	AB002330	23350	Hs.596572	GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0006396: RNA processing		7.58	7.91	8.03	8.33	8.35	8.73	7.59	8.17	8.07	7.88	7.22	8.68	2
210346_s_at	CLK4	CDC-like kinase 4	AF212224	57396	Hs.406557	GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0004713: protein-tyrosine kinase activity, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0006468: protein amino acid phosphorylation, GO:0016740: transferase activity		9.15	9.48	9.50	9.68	9.49	9.58	9.55	9.68	9.35	9.60	8.29	9.62	2
211105_s_at	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	U80918	4772	Hs.534074, Hs.701518	GO:0003700: transcription factor activity, GO:0005528: FK506 binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0007242: intracellular signaling cascade, GO:0016563: transcription activator activity	04310: Wnt signaling pathway, 04360: Axon guidance, 04370: VEGF signaling pathway, 04650: Natural killer cell mediated cytotoxicity, 04660: T cell receptor signaling pathway, 04662: B cell receptor signaling pathway	4.52	4.79	5.11	5.60	6.40	6.23	4.53	4.65	4.89	4.51	4.88	6.17	2
209894_at	LEPR	leptin receptor	U50748	3953	Hs.705413	GO:0004896: hematopoietin/interferon-class (D200-domain) cytokine receptor activity, GO:0005515: protein binding, GO:0005576: extracellular region, GO:0005886: plasma membrane, GO:0006112: energy reserve metabolic process, GO:0007166: cell surface receptor linked signal transduction, GO:0007275: multicellular organismal development, GO:0016021: integral to membrane	04060: Cytokine-cytokine receptor interaction, 04080: Neuroactive ligand-receptor interaction, 04630: Jak-STAT signaling pathway, 04920: Adipocytokine signaling pathway	8.91	9.71	10.09	10.51	10.89	11.76	9.56	10.05	10.10	9.76	8.85	11.49	2
210239_at	IRX5	iroquois homeobox 5	U90304	10265	Hs.435730	GO:0003700: transcription factor activity, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0043565: sequence-specific DNA binding, GO:0048468: cell development		7.33	7.69	7.89	7.96	7.78	7.99	7.39	7.83	7.64	7.82	6.27	8.08	2
209815_at	PTCH1	patched homolog 1 (Drosophila)	BG054916	5727	Hs.494538, Hs.638946	GO:0004872: receptor activity, GO:0005515: protein binding, GO:0005887: integral to plasma membrane, GO:0007165: signal transduction, GO:0008158: hedgehog receptor activity, GO:0008283: cell proliferation, GO:0008589: regulation of smoothened signaling pathway, GO:0009887: organ morphogenesis, GO:0009953: dorsal/ventral pattern formation, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016485: protein processing, GO:0030326: embryonic limb morphogenesis, GO:0040015: negative regulation of multicellular organism growth, GO:0045786: negative regulation of cell cycle	04340: Hedgehog signaling pathway, 05217: Basal cell carcinoma	6.43	6.91	7.33	7.75	8.18	8.21	6.63	7.90	7.34	7.35	6.92	8.53	2

(*Continued*)

TABLE E4. (*Continued*)

209884 _s_at	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	AF047033	9497	Hs.250072	GO:0005215: transporter activity, GO:0005452: inorganic anion exchanger activity, GO:0005515: protein binding, GO:0006814: sodium ion transport, GO:0006820: anion transport, GO:0008509: anion transmembrane transporter activity, GO:0008510: sodium:bicarbonate symporter activity, GO:0015293: symporter activity, GO:0015701: bicarbonate transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016323: basolateral plasma membrane, GO:0016324: apical plasma membrane, GO:0031402: sodium ion binding, GO:0042995: cell projection		8.14	8.25	8.21	8.39	8.00	8.11	8.24	8.33	8.17	8.42	6.90	7.90	2
209537 _at	EXTL2	exostoses (multiple)-like 2	AF000416	2135	Hs.357637	GO:0001888: glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity, GO:0005576: extracellular region, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0006044: N-acetylglucosamine metabolic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016757: transferase activity, transferring glycosyl groups, GO:0019276: UDP-N-acetylgalactosamine metabolic process, GO:0030145: manganese ion binding, GO:0035248: alpha-1,4-N-acetylgalactosaminyltransferase activity, GO:0046872: metal ion binding	00534: Heparan sulfate biosynthesis, 01030: Glycan structures - biosynthesis 1	6.76	7.19	7.54	7.73	7.47	7.65	7.24	7.51	7.41	7.28	6.14	7.81	2
209568 _s_at	RGL1	ral guanine nucleotide dissociation stimulator-like 1	AF186779	23179	Hs.497148	GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005515: protein binding, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0007165: signal transduction, GO:0008321: Ral guanyl-nucleotide exchange factor activity, GO:0051056: regulation of small GTPase mediated signal transduction		7.39	8.23	8.18	8.46	8.35	7.92	7.29	7.85	7.98	7.95	6.83	7.70	2
209497 _s_at	RBM4B	RNA binding motif protein 4B	BC003503	83759	Hs.618713	GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005634: nucleus, GO:0006397: mRNA processing, GO:0008270: zinc ion binding, GO:0008380: RNA splicing, GO:0046872: metal ion binding		4.65	4.99	4.84	5.20	4.90	5.00	5.11	4.94	4.80	4.84	3.90	5.39	2
209501 _at	CDR2	cerebellar degeneration-related protein 2, 62kDa	AL582414	1039	Hs.513430	GO:0003674: molecular_function, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm		6.26	6.56	7.17	7.55	7.55	7.91	6.96	6.97	7.21	6.88	5.93	8.10	2
209484 _s_at	NSL1	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	AF201941	25936	Hs.497692	GO:0000444: MIS12/MIND type complex, GO:0003676: nucleic acid binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0007049: cell cycle, GO:0007059: chromosome segregation, GO:0007067: mitosis, GO:0008168: methyltransferase activity, GO:0032259: methylation, GO:0051301: cell division		7.98	8.25	8.31	8.50	8.19	8.45	8.27	8.43	8.40	8.37	6.58	8.58	2

(*Continued*)

TABLE E4. (*Continued*)

209487_at	RBPMS	RNA binding protein with multiple splicing	D84109	11030 Hs.334587	GO:0000166: nucleotide binding, GO:0003723: RNA binding, GO:0005515: protein binding, GO:0006396: RNA processing	7.26	7.62	7.88	8.00	8.70	8.42	7.18	7.82	7.57	7.07	7.06	7.87	2
209323_at	PRKRIR	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	AF081567	5612 Hs.503315	GO:0003677: DNA binding, GO:0006950: response to stress, GO:0007165: signal transduction, GO:0008270: zinc ion binding, GO:0008285: negative regulation of cell proliferation, GO:0046872: metal ion binding, GO:0046983: protein dimerization activity	8.88	9.12	9.27	9.43	9.41	9.65	9.12	9.36	9.16	9.17	8.25	9.53	2
209422_at	PHF20	PHD finger protein 20	AY027523	51230 Hs.517044	GO:0003676: nucleic acid binding, GO:0003677: DNA binding, GO:0005515: protein binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	9.13	9.27	9.47	9.67	9.85	9.95	9.47	9.52	9.53	9.27	9.05	10.03	2
209300_s_at	NECAP1	NECAP endocytosis associated 1	BC002888	25977 Hs.555927	GO:0005515: protein binding, GO:0005886: plasma membrane, GO:0005905: coated pit, GO:0006897: endocytosis, GO:0015031: protein transport, GO:0030125: clathrin vesicle coat, GO:0031410: cytoplasmic vesicle	7.53	7.66	7.70	7.84	7.81	8.02	7.54	7.63	7.69	7.74	6.54	7.98	2
209307_at	SWAP70	SWAP-70 protein	AB014540	23075 Hs.153026	GO:0003677: DNA binding, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0016444: somatic cell DNA recombination, GO:0042995: cell projection, GO:0045190: isotype switching	9.11	9.37	9.59	9.89	9.60	9.89	9.62	9.80	9.72	9.66	8.80	9.98	2
209268_at	VPS45	vacuolar protein sorting 45 homolog (S. cerevisiae)	AF165513	11311 Hs.443750	GO:0000139: Golgi membrane, GO:0005764: lysosome, GO:0005768: endosome, GO:0005794: Golgi apparatus, GO:0005798: Golgi-associated vesicle, GO:0006886: intracellular protein transport, GO:0006904: vesicle docking during exocytosis, GO:0006954: inflammatory response, GO:0010008: endosome membrane, GO:0016020: membrane, GO:0016192: vesicle-mediated transport	8.60	8.83	8.83	8.95	8.89	8.95	8.84	8.68	8.93	8.79	8.12	8.98	2

(*Continued*)

TABLE E4. (*Continued*)

209298 _s_at	ITSN1	intersectin 1 (SH3 domain protein)	AF114488	6453 Hs.160324	GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005089: Rho guanyl-nucleotide exchange factor activity, GO:0005509: calcium ion binding, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005622: intracellular, GO:0007242: intracellular signaling cascade, GO:0012505: endomembrane system, GO:0016020: membrane, GO:0019717: synaptosome, GO:0030054: cell junction, GO:0035023: regulation of Rho protein signal transduction, GO:0042995: cell projection, GO:0045202: synapse, GO:0048488: synaptic vesicle endocytosis		6.03	6.46	6.90	7.58	7.56	7.67	6.23	6.84	6.76	6.53	6.12	7.50	2
209112 _at	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	BC001971	1027 Hs.238990	GO:0000082: G1/S transition of mitotic cell cycle, GO:0004860: protein kinase inhibitor activity, GO:0004861: cyclin-dependent protein kinase inhibitor activity, GO:0005072: transforming growth factor beta receptor, cytoplasmic mediator activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0005829: cytosol, GO:0006813: potassium ion transport, GO:0006917: induction of apoptosis, GO:0007049: cell cycle, GO:0007050: cell cycle arrest, GO:0007605: sensory perception of sound, GO:0008284: positive regulation of cell proliferation, GO:0030308: negative regulation of cell growth, GO:0031116: positive regulation of microtubule polymerization, GO:0042326: negative regulation of phosphorylation, GO:0045736: negative regulation of cyclin-dependent protein kinase activity, GO:0048102: autophagic cell death, GO:0048839: inner ear development, GO:0050680: negative regulation of epithelial cell proliferation, GO:0051271: negative regulation of cell motility	04012: ErbB signaling pathway, 04110: Cell cycle, 05215: Prostate cancer, 05220: Chronic myeloid leukemia, 05222: Small cell lung cancer	10.08	10.50	10.63	10.84	10.74	10.91	10.57	10.67	10.56	10.64	10.20	10.97	2
209167 _at	GPM6B	glycoprotein M6B	AI419030	2824 Hs.495710	GO:0003674: molecular_function, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0030154: cell differentiation		6.33	6.53	6.76	7.19	7.37	7.56	6.49	6.77	6.62	6.52	5.72	7.18	2

(*Continued*)

TABLE E4. (*Continued*)

209031_at	CADM1	cell adhesion molecule 1	AL519710	23705	Hs.370510	GO:0001913: T cell mediated cytotoxicity, GO:0005102: receptor binding, GO:0005102: receptor binding, GO:0005886: plasma membrane, GO:0005911: intercellular junction, GO:0006915: apoptosis, GO:0006955: immune response, GO:0007155: cell adhesion, GO:0007156: homophilic cell adhesion, GO:0007157: heterophilic cell adhesion, GO:0007275: multicellular organismal development, GO:0007283: spermatogenesis, GO:0008022: protein C-terminus binding, GO:0008037: cell recognition, GO:0008037: cell recognition, GO:0016021: integral to membrane, GO:0016323: basolateral plasma membrane, GO:0030154: cell differentiation, GO:0030165: PDZ domain binding, GO:0042271: susceptibility to natural killer cell mediated cytotoxicity, GO:0042271: susceptibility to natural killer cell mediated cytotoxicity, GO:0042803: protein homodimerization activity, GO:0045786: negative regulation of cell cycle, GO:0050715: positive regulation of cytokine secretion, GO:0050798: activated T cell proliferation, GO:0051606: detection of stimulus, GO:0051606: detection of stimulus	04514: Cell adhesion molecules (CAMs)	7.97	8.21	8.26	8.70	8.91	8.82	8.04	8.30	8.61	8.17	7.34	9.05	2
209064_x_at	LOC645139	hypothetical LOC645139	BF248165	645139	Hs.567929			8.55	8.85	8.94	8.92	8.86	9.25	8.78	8.86	9.02	8.89	7.14	9.11	2
208986_at	TCF12	transcription factor 12	AL559478	6938	Hs.511504	GO:0003677: DNA binding, GO:0003702: RNA polymerase II transcription factor activity, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006955: immune response, GO:0007275: multicellular organismal development, GO:0007517: muscle development, GO:0030528: transcription regulator activity, GO:0045449: regulation of transcription		9.49	9.82	10.04	10.43	10.19	10.40	9.79	10.00	10.08	9.96	9.47	10.37	2
209005_at	FBXL5	F-box and leucine-rich repeat protein 5	AF157323	26234	Hs.643433	GO:0000151: ubiquitin ligase complex, GO:0004842: ubiquitin-protein ligase activity, GO:0005515: protein binding, GO:0016567: protein ubiquitination		6.06	6.40	6.74	7.00	7.29	7.19	6.26	6.32	6.36	6.15	5.76	7.14	2

(*Continued*)

TABLE E4. (*Continued*)

208913_at	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	AA868560	23062 Hs.460336	GO:0005515: protein binding, GO:0005622: intracellular, GO:0005768: endosome, GO:0005794: Golgi apparatus, GO:0005802: trans-Golgi network, GO:0006886: intracellular protein transport, GO:0010008: endosome membrane, GO:0016020: membrane, GO:0016192: vesicle-mediated transport, GO:0030117: membrane coat, GO:0030131: clathrin adaptor complex, GO:0030306: ADP-ribosylation factor binding		6.63	7.04	7.06	7.42	7.65	7.45	6.84	7.07	7.04	7.13	6.76	7.69	2
208939_at	SEPHS1	selenophosphate synthetase 1	AV682679	22929 Hs.124027	GO:0000166: nucleotide binding, GO:0003824: catalytic activity, GO:0004756: selenide, water dikinase activity, GO:0005524: ATP binding, GO:0005524: ATP binding, GO:0005525: GTP binding, GO:0006464: protein modification process, GO:0008430: selenium binding, GO:0016740: transferase activity	00450: Selenoamino acid metabolism	7.06	7.43	7.61	7.80	7.35	7.72	7.55	7.79	7.69	7.62	6.23	7.92	2
208398_s_at	TBPL1	TBP-like 1	NM_004865	9519 Hs.486507	GO:0003677: DNA binding, GO:0003702: RNA polymerase II transcription factor activity, GO:0003713: transcription coactivator activity, GO:0005488: binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005669: transcription factor TFIID complex, GO:0005737: cytoplasm, GO:0006355: regulation of transcription, DNA-dependent, GO:0006367: transcription initiation from RNA polymerase II promoter	03022: Basal transcription factors	7.65	7.93	8.04	8.02	7.92	8.05	8.14	8.17	8.06	8.09	7.01	8.10	2
208848_at	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	M30471	128 Hs.78989	GO:0001523: retinoid metabolic process, GO:0004022: alcohol dehydrogenase activity, GO:0005488: binding, GO:0005504: fatty acid binding, GO:0005737: cytoplasm, GO:0006069: ethanol oxidation, GO:0008270: zinc ion binding, GO:0009055: electron carrier activity, GO:0016491: oxidoreductase activity, GO:0046872: metal ion binding, GO:0051903: S-(hydroxymethyl)glutathione dehydrogenase activity	00010: Glycolysis / Gluconeogenesis, 00071: Fatty acid metabolism, 00120: Bile acid biosynthesis, 00350: Tyrosine metabolism, 00624: 1- and 2-Methylnaphthalene degradation, 00641: 3-Chloroacrylic acid degradation, 00680: Methane metabolism, 00830: Retinol metabolism, 00980: Metabolism of xenobiotics by cytochrome P450, 00982: NA	8.78	9.07	9.14	9.30	9.01	9.21	8.92	9.24	9.06	8.95	7.36	8.98	2
207719_x_at	CEP170	centrosomal protein 170kDa	NM_014812	9859 Hs.533635	GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005874: microtubule		7.99	8.43	8.51	9.03	8.61	8.72	8.10	8.51	8.40	8.31	6.45	8.29	2

(*Continued*)

TABLE E4. (*Continued*)

207753_at	ZNF304	zinc finger protein 304	NM_020657	57343 Hs.287374	GO:0003676: nucleic acid binding, GO:0003677: DNA binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		6.84	7.05	7.28	7.58	7.66	7.83	7.18	7.02	7.31	7.33	6.08	7.77	2
206555_s_at	THUMPD1	THUMP domain containing 1	NM_017736	55623 Hs.460232			9.18	9.12	9.37	9.58	9.83	9.73	9.18	9.46	9.54	9.53	8.67	9.86	2
207625_s_at	CBFA2T2	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	NM_005093	9139 Hs.153934	GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0008283: cell proliferation, GO:0046872: metal ion binding		5.16	5.30	5.49	5.52	6.09	6.06	5.45	5.47	5.88	5.40	5.23	6.26	2
205928_at	ZNF443	zinc finger protein 443	NM_005815	10224 Hs.631623	GO:0003677: DNA binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006917: induction of apoptosis, GO:0006950: response to stress, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		6.34	6.51	6.74	6.76	6.90	7.13	6.78	7.18	6.71	6.85	5.98	7.19	2
206539_s_at	CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12	NM_023944	66002 Hs.591000	GO:0004497: monooxygenase activity, GO:0005506: iron ion binding, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005792: microsome, GO:0009055: electron carrier activity, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0020037: heme binding, GO:0046872: metal ion binding, GO:0050381: unspecific monooxygenase activity		7.65	8.06	8.12	8.22	8.61	8.71	8.66	8.17	8.45	8.30	8.00	9.25	2
205726_at	DIAPH2	diaphanous homolog 2 (Drosophila)	NM_006729	1730 Hs.226483	GO:0000910: cytokinesis, GO:0003779: actin binding, GO:0005102: receptor binding, GO:0005737: cytoplasm, GO:0005769: early endosome, GO:0007275: multicellular organismal development, GO:0016043: cellular component organization and biogenesis, GO:0017048: Rho GTPase binding, GO:0030036: actin cytoskeleton organization and biogenesis, GO:0030154: cell differentiation, GO:0048477: oogenesis	04810: Regulation of actin cytoskeleton	7.14	7.69	7.94	8.11	8.52	8.22	7.45	7.83	7.83	7.63	7.07	8.18	2
205794_s_at	NOVA1	neuro-oncological ventral antigen 1	NM_002515	4857 Hs.31588	GO:0003723: RNA binding, GO:0005634: nucleus, GO:0007268: synaptic transmission, GO:0007626: locomotory behavior, GO:0008380: RNA splicing		5.69	6.00	6.65	7.17	7.28	7.63	5.83	6.86	6.38	6.14	5.85	6.92	2

(*Continued*)

TABLE E4. (*Continued*)

205664_at	KIN	KIN, antigenic determinant of recA protein homolog (mouse)	NM_012311	22944 Hs.397918	GO:0003677: DNA binding, GO:0003690: double-stranded DNA binding, GO:0003723: RNA binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006260: DNA replication, GO:0006281: DNA repair, GO:0006310: DNA recombination, GO:0006397: mRNA processing, GO:0008270: zinc ion binding, GO:0016363: nuclear matrix, GO:0044419: interspecies interaction between organisms, GO:0046872: metal ion binding		7.36	7.42	7.54	7.51	7.38	7.63	7.65	7.83	7.55	7.53	6.48	7.53	2
205684_s_at	DENND4C	DENN/MADD domain containing 4C	NM_017925	55667 Hs.249591	GO:0016020: membrane, GO:0016021: integral to membrane		9.06	9.38	9.51	9.60	9.69	9.91	9.58	9.48	9.55	9.46	9.03	10.01	2
205516_x_at	CIZ1	CDKN1A interacting zinc finger protein 1	NM_012127	25792 Hs.212395	GO:0003676: nucleic acid binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005634: nucleus, GO:0008270: zinc ion binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		8.45	8.47	8.64	8.83	9.23	9.26	8.48	8.40	8.71	8.37	8.17	9.43	2
205558_at	TRAF6	TNF receptor-associated factor 6	NM_004620	7189 Hs.591983	GO:0000209: protein polyubiquitination, GO:0002726: positive regulation of T cell cytokine production, GO:0004842: ubiquitin-protein ligase activity, GO:0005515: protein binding, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0007165: signal transduction, GO:0007250: activation of NF-kappaB-inducing kinase activity, GO:0008270: zinc ion binding, GO:0032743: positive regulation of interleukin-2 production, GO:0042981: regulation of apoptosis, GO:0043123: positive regulation of I-kappaB kinase/NF-kappaB cascade, GO:0046872: metal ion binding, GO:0050852: T cell receptor signaling pathway, GO:0050870: positive regulation of T cell activation	04010: MAPK signaling pathway, 04120: Ubiquitin mediated proteolysis, 04620: Toll-like receptor signaling pathway, 05222: Small cell lung cancer	4.35	4.59	4.60	4.49	4.69	4.59	4.63	4.57	4.53	4.45	3.93	4.44	2
205437_at	ZNF211	zinc finger protein 211	NM_006385	10520 Hs.590977	GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		3.50	3.93	3.96	4.17	4.43	4.41	4.18	4.16	4.03	4.01	3.76	4.54	2

(*Continued*)

TABLE E4. (*Continued*)

205453_at	HOXB2	homeobox B2	NM_002145	3212 Hs.514289	GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0005634: nucleus, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0007275: multicellular organismal development, GO:0008015: blood circulation, GO:0043565: sequence-specific DNA binding	5.68	5.86	5.88	6.04	6.32	6.16	6.46	6.56	6.35	6.08	5.96	7.04	2
205003_at	DOCK4	dedicator of cytokinesis 4	NM_014705	9732 Hs.654652	GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005515: protein binding, GO:0012505: endomembrane system, GO:0016020: membrane, GO:0030165: PDZ domain binding, GO:0030675: Rac GTPase activator activity, GO:0032420: stereocilium, GO:0048365: Rac GTPase binding	5.74	6.56	6.75	7.45	7.46	7.57	6.04	6.94	6.94	6.37	5.58	7.13	2
205006_s_at	NMT2	N-myristoyl-transferase 2	NM_004808	9397 Hs.60339	GO:0004379: glycylpeptide N-tetradecanoyltransferase activity, GO:0005737: cytoplasm, GO:0006499: N-terminal protein myristoylation, GO:0008415: acyltransferase activity, GO:0009249: protein lipoylation, GO:0016740: transferase activity	6.62	6.72	7.10	7.17	7.63	7.79	6.65	6.81	6.78	6.68	6.59	7.86	2
204643_s_at	ENOX2	ecto-NOX disulfide-thiol exchanger 2	NM_006375	10495 Hs.171458	GO:0000166: nucleotide binding, GO:0001558: regulation of cell growth, GO:0003676: nucleic acid binding, GO:0005507: copper ion binding, GO:0005576: extracellular region, GO:0005829: cytosol, GO:0005886: plasma membrane, GO:0006810: transport, GO:0007624: ultradian rhythm, GO:0009897: external side of plasma membrane, GO:0015035: protein disulfide oxidoreductase activity, GO:0016491: oxidoreductase activity	4.68	4.94	4.89	4.84	5.14	4.89	5.05	5.19	5.08	5.21	4.28	5.25	2
204937_s_at	ZNF274	zinc finger protein 274	NM_016325	10782 Hs.83761	GO:0003700: transcription factor activity, GO:0003714: transcription corepressor activity, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005730: nucleolus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	8.01	8.18	8.36	8.46	8.59	8.97	8.50	8.35	8.56	8.32	7.99	9.31	2

(*Continued*)

TABLE E4. (*Continued*)

204464_s_at	EDNRA	endothelin receptor type A	NM_001957	1909	Hs.183713	GO:0001584: rhodopsin-like receptor activity, GO:0001599: endothelin-A receptor activity, GO:0004435: phosphoinositide phospholipase C activity, GO:0004872: receptor activity, GO:0005515: protein binding, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0006939: smooth muscle contraction, GO:0007165: signal transduction, GO:0007186: G-protein coupled receptor protein signaling pathway, GO:0007190: activation of adenylate cyclase activity, GO:0007202: activation of phospholipase C activity, GO:0007204: elevation of cytosolic calcium ion concentration, GO:0007585: respiratory gaseous exchange, GO:0008283: cell proliferation, GO:0015758: glucose transport	04020: Calcium signaling pathway, 04080: Neuroactive ligand-receptor interaction	8.71	8.86	9.10	9.36	9.45	9.18	8.75	9.22	9.14	8.47	7.83	8.99	2
204523_at	ZNF140	zinc finger protein 140	NM_003440	7699	Hs.181552	GO:0003676: nucleic acid binding, GO:0003700: transcription factor activity, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		8.16	8.27	8.33	8.54	8.53	8.61	8.40	8.39	8.24	8.37	7.53	8.68	2
204291_at	ZNF518A	zinc finger protein 518A	NM_014803	9849	Hs.657337	GO:0003677: DNA binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		7.16	7.40	7.59	7.85	7.41	7.91	7.64	7.83	7.61	7.60	6.78	7.93	2
204303_s_at	KIAA0427	KIAA0427	NM_014772	9811	Hs.145230	GO:0005515: protein binding, GO:0016070: RNA metabolic process		3.53	3.45	3.60	3.67	4.73	4.03	3.54	3.44	3.71	3.29	3.68	4.50	2
204176_at	KLHL20	kelch-like 20 (Drosophila)	AA808694	27252	Hs.495035	GO:0003779: actin binding, GO:0005515: protein binding, GO:0007010: cytoskeleton organization and biogenesis, GO:0009986: cell surface, GO:0015629: actin cytoskeleton		7.42	7.67	7.90	8.13	7.57	8.16	7.92	7.81	7.84	7.94	6.16	8.07	2
204237_at	GULP1	GULP, engulfment adaptor PTB domain containing 1	NM_016315	51454	Hs.470887, Hs.712910	GO:0004871: signal transducer activity, GO:0005515: protein binding, GO:0005737: cytoplasm, GO:0006869: lipid transport, GO:0006911: phagocytosis, engulfment, GO:0006915: apoptosis		7.88	8.20	8.53	8.80	8.60	8.64	8.12	8.21	8.48	7.90	7.46	8.44	2
204062_s_at	ULK2	unc-51-like kinase 2 (C. elegans)	BG526973	9706	Hs.168762	GO:0000166: nucleotide binding, GO:0004674: protein serine/threonine kinase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0006468: protein amino acid phosphorylation, GO:0007165: signal transduction, GO:0007409: axonogenesis, GO:0016740: transferase activity	04140: Regulation of autophagy, 04150: mTOR signaling pathway	7.16	7.53	7.56	7.70	7.50	7.68	7.66	7.94	7.50	7.69	6.88	7.97	2

(*Continued*)

TABLE E4. (*Continued*)

204069_at	MEIS1	Meis homeobox 1	NM_002398	4211	Hs.526754, Hs.603755	GO:0003700: transcription factor activity, GO:0003705: RNA polymerase II transcription factor activity, enhancer binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005667: transcription factor complex, GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0043565: sequence-specific DNA binding		4.61	5.06	5.19	5.52	5.63	5.56	5.00	5.55	5.08	5.06	4.94	6.06	2
203981_s_at	ABCD4	ATP-binding cassette, sub-family D (ALD), member 4	AL574660	5826	Hs.94395	GO:0000166: nucleotide binding, GO:0005215: transporter activity, GO:0005524: ATP binding, GO:0005777: peroxisome, GO:0005778: peroxisomal membrane, GO:0006810: transport, GO:0006810: transport, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016887: ATPase activity, GO:0042626: ATPase activity, coupled to transmembrane movement of substances, GO:0043190: ATP-binding cassette (ABC) transporter complex	02010: ABC transporters - General	7.00	7.48	7.44	7.85	7.87	7.87	7.52	7.31	7.71	7.59	7.33	7.76	2
204030_s_at	SCHIP1	schwannomin interacting protein 1	NM_014575	29970	Hs.134665	GO:0003674: molecular_function, GO:0005575: cellular_component, GO:0005737: cytoplasm, GO:0008150: biological_process, GO:0042802: identical protein binding		5.56	5.63	5.96	6.60	6.81	6.37	5.61	6.13	5.84	5.66	5.02	5.98	2
203905_at	PARN	poly(A)-specific ribonuclease (deadenylation nuclease)	NM_002582	5073	Hs.253197	GO:0000166: nucleotide binding, GO:0000184: mRNA catabolic process, nonsense-mediated decay, GO:0000287: magnesium ion binding, GO:0003723: RNA binding, GO:0003730: mRNA 3'-UTR binding, GO:0004527: exonuclease activity, GO:0004535: poly(A)-specific ribonuclease activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0007292: female gamete generation, GO:0009451: RNA modification, GO:0016787: hydrolase activity		7.75	7.99	8.15	8.19	8.09	8.29	8.30	8.26	8.07	8.10	7.44	8.62	2

(*Continued*)

TABLE E4. (*Continued*)

203935_at	ACVR1	activin A receptor, type I	L02911	90 Hs.470316	GO:0000082: G1/S transition of mitotic cell cycle, GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0001569: patterning of blood vessels, GO:0001655: urogenital system development, GO:0001701: in utero embryonic development, GO:0001707: mesoderm formation, GO:0001755: neural crest cell migration, GO:0002526: acute inflammatory response, GO:0004872: receptor activity, GO:0005024: transforming growth factor beta receptor activity, GO:0005524: ATP binding, GO:0006468: protein amino acid phosphorylation, GO:0007179: transforming growth factor beta receptor signaling pathway, GO:0007281: germ cell development, GO:0007368: determination of left/right symmetry, GO:0007369: gastrulation, GO:0007498: mesoderm development, GO:0007507: heart development, GO:0016020: membrane, GO:0016361: activin receptor activity, type I, GO:0016740: transferase activity, GO:0030145: manganese ion binding, GO:0030278: regulation of ossification, GO:0030501: positive regulation of bone mineralization, GO:0030509: BMP signaling pathway, GO:0032926: negative regulation of activin receptor signaling pathway, GO:0042803: protein homodimerization activity, GO:0043066: negative regulation of apoptosis, GO:0045177: apical part of cell, GO:0045669: positive regulation of osteoblast differentiation, GO:0045941: positive regulation of transcription, GO:0046332: SMAD binding, GO:0048179: activin receptor complex, GO:0048184: follistatin binding, GO:0048185: activin binding, GO:0048641: regulation of skeletal muscle development, GO:0050431: transforming growth factor beta binding, GO:0051145: smooth muscle cell differentiation	04060: Cytokine-cytokine receptor interaction, 04350: TGF-beta signaling pathway	8.83	9.01	9.13	9.20	9.01	9.03	9.00	9.20	9.09	8.94	7.88	8.94	2
203825_at	BRD3	bromodomain containing 3	NM_007371	8019 Hs.522472	GO:0003674: molecular_function, GO:0005634: nucleus, GO:0008150: biological_process		8.34	8.52	8.79	9.07	9.56	9.30	8.64	8.80	8.71	8.60	8.83	9.50	2
203855_at	WDR47	WD repeat domain 47	NM_014969	22911 Hs.654760			9.72	9.85	10.07	10.29	10.21	10.63	10.21	10.27	10.11	10.01	9.30	10.62	2
203810_at	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	BG252490	11080 Hs.13852	GO:0006457: protein folding, GO:0006986: response to unfolded protein, GO:0009408: response to heat, GO:0031072: heat shock protein binding, GO:0051082: unfolded protein binding		6.99	6.99	7.31	7.78	7.92	8.24	7.27	7.43	7.21	7.24	6.48	7.90	2

(*Continued*)

TABLE E4. (*Continued*)

203822_s_at	ELF2	E74-like factor 2 (ets domain transcription factor)	NM_006874	1998 Hs.634040	GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0016563: transcription activator activity, GO:0043565: sequence-specific DNA binding		8.46	8.76	8.81	9.01	8.76	8.99	8.77	8.84	8.85	8.85	7.75	8.90	2
203710_at	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	NM_002222	3708 Hs.567295, Hs.712541	GO:0005216: ion channel activity, GO:0005220: inositol 1,4,5-triphosphate-sensitive calcium-release channel activity, GO:0005262: calcium channel activity, GO:0005262: calcium channel activity, GO:0005509: calcium ion binding, GO:0005515: protein binding, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005887: integral to plasma membrane, GO:0006811: ion transport, GO:0006816: calcium ion transport, GO:0007165: signal transduction, GO:0008095: inositol-1,4,5-triphosphate receptor activity, GO:0008219: cell death, GO:0015085: calcium ion transmembrane transporter activity, GO:0016020: membrane, GO:0031095: platelet dense tubular network membrane	04020: Calcium signaling pathway, 04070: Phosphatidylinositol signaling system, 04540: Gap junction, 04720: Long-term potentiation, 04730: Long-term depression, 04912: GnRH signaling pathway	7.40	7.42	7.62	7.73	7.82	7.87	7.31	7.68	7.62	7.57	6.72	7.69	2
203794_at	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	NM_014826	8476 Hs.35433	GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0004674: protein serine/threonine kinase activity, GO:0005083: small GTPase regulator activity, GO:0005524: ATP binding, GO:0005737: cytoplasm, GO:0005911: intercellular junction, GO:0006468: protein amino acid phosphorylation, GO:0007242: intracellular signaling cascade, GO:0008270: zinc ion binding, GO:0016301: kinase activity, GO:0016740: transferase activity, GO:0019992: diacylglycerol binding, GO:0031252: leading edge, GO:0031532: actin cytoskeleton reorganization, GO:0042802: identical protein binding, GO:0051056: regulation of small GTPase mediated signal transduction		4.42	4.75	5.11	5.52	6.07	5.64	4.43	5.07	5.03	4.55	4.55	5.64	2
203614_at	UTP14C	UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)	NM_021645	9724 Hs.512963	GO:0005634: nucleus, GO:0006364: rRNA processing, GO:0007126: meiosis, GO:0007275: multicellular organismal development, GO:0007283: spermatogenesis, GO:0030154: cell differentiation, GO:0032040: small subunit processome		7.74	8.05	7.99	8.27	8.18	8.49	8.25	8.31	8.21	8.06	7.19	8.61	2

(*Continued*)

TABLE E4. (*Continued*)

203680_at	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	NM_002736	5577	Hs.433068	GO:0000166: nucleotide binding, GO:0001932: regulation of protein amino acid phosphorylation, GO:0005952: cAMP-dependent protein kinase complex, GO:0008603: cAMP-dependent protein kinase regulator activity, GO:0009755: hormone-mediated signaling, GO:0030552: cAMP binding	04210: Apoptosis, 04910: Insulin signaling pathway	6.70	7.58	8.11	8.24	8.29	8.81	7.37	7.87	7.66	7.61	6.63	8.30	2
203556_at	ZHX2	zinc fingers and homeoboxes 2	NM_014943	22882	Hs.658443, Hs.714291	GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006402: mRNA catabolic process, GO:0008270: zinc ion binding, GO:0043565: sequence-specific DNA binding, GO:0045892: negative regulation of transcription, DNA-dependent, GO:0046872: metal ion binding		7.36	7.67	7.91	8.25	8.32	8.37	7.34	7.73	7.96	7.28	6.69	8.33	2
203562_at	FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	NM_005103	9638	Hs.224008	GO:0005515: protein binding, GO:0005737: cytoplasm, GO:0005813: centrosome, GO:0005886: plasma membrane, GO:0007155: cell adhesion, GO:0007399: nervous system development, GO:0007411: axon guidance, GO:0043015: gamma-tubulin binding		6.70	7.35	7.54	7.93	8.01	7.75	6.65	7.17	7.17	6.61	6.42	7.49	2
203494_s_at	CEP57	centrosomal protein 57kDa	NM_014679	9702	Hs.101014	GO:0000060: protein import into nucleus, translocation, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0005813: centrosome, GO:0005874: microtubule, GO:0007286: spermatid development, GO:0008543: fibroblast growth factor receptor signaling pathway, GO:0017134: fibroblast growth factor binding, GO:0042803: protein homodimerization activity		8.10	8.78	8.86	8.99	9.18	9.09	8.84	8.73	8.85	8.63	8.09	9.24	2
203521_s_at	ZNF318	zinc finger protein 318	NM_014345	24149	Hs.509718	GO:0003676: nucleic acid binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007126: meiosis, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		4.28	4.63	4.81	5.06	5.36	5.35	4.60	5.01	5.09	4.92	4.49	5.54	2

(*Continued*)

TABLE E4. (*Continued*)

203448_s_at	TERF1	telomeric repeat binding factor (NIMA-interacting) 1	AI347136	7013 Hs.442707	GO:0000781: chromosome, telomeric region, GO:0003677: DNA binding, GO:0003677: DNA binding, GO:0003691: double-stranded telomeric DNA binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0005694: chromosome, GO:0005819: spindle, GO:0007004: telomere maintenance via telomerase, GO:0007004: telomere maintenance via telomerase, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0042162: telomeric DNA binding, GO:0042802: identical protein binding, GO:0045449: regulation of transcription, GO:0051301: cell division		5.99	6.00	6.11	6.23	6.39	6.36	6.05	6.17	6.19	6.09	5.34	6.57	2
203449_s_at	TERF1	telomeric repeat binding factor (NIMA-interacting) 1	NM_017489	7013 Hs.442707	GO:0000781: chromosome, telomeric region, GO:0003677: DNA binding, GO:0003677: DNA binding, GO:0003691: double-stranded telomeric DNA binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005634: nucleus, GO:0005654: nucleoplasm, GO:0005694: chromosome, GO:0005819: spindle, GO:0007004: telomere maintenance via telomerase, GO:0007004: telomere maintenance via telomerase, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0042162: telomeric DNA binding, GO:0042802: identical protein binding, GO:0045449: regulation of transcription, GO:0051301: cell division		7.78	8.10	8.29	8.48	8.34	8.70	8.19	8.30	8.44	8.32	7.66	8.61	2
203284_s_at	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	AW151887	9653 Hs.48823	GO:0000139: Golgi membrane, GO:0005794: Golgi apparatus, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016740: transferase activity	00534: Heparan sulfate biosynthesis, 01030: Glycan structures - biosynthesis 1	6.95	7.57	7.57	7.59	6.81	7.48	7.61	7.88	7.82	7.62	4.87	7.60	2

(*Continued*)

TABLE E4. (*Continued*)

203323_at	CAV2	caveolin 2	BF197655	858 Hs.212332, Hs.603096	GO:0000139: Golgi membrane, GO:0001764: neuron migration, GO:0001937: negative regulation of endothelial cell proliferation, GO:0004713: protein-tyrosine kinase activity, GO:0005515: protein binding, GO:0005624: membrane fraction, GO:0005625: soluble fraction, GO:0005739: mitochondrion, GO:0005794: Golgi apparatus, GO:0005829: cytosol, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005901: caveola, GO:0005925: focal adhesion, GO:0006906: vesicle fusion, GO:0007005: mitochondrion organization and biogenesis, GO:0007029: endoplasmic reticulum organization and biogenesis, GO:0007268: synaptic transmission, GO:0007420: brain development, GO:0007595: lactation, GO:0009925: basal plasma membrane, GO:0016050: vesicle organization and biogenesis, GO:0016324: apical plasma membrane, GO:0019861: flagellum, GO:0019900: kinase binding, GO:0019905: syntaxin binding, GO:0030133: transport vesicle, GO:0030317: sperm motility, GO:0030321: transepithelial chloride transport, GO:0030324: lung development, GO:0030659: cytoplasmic vesicle membrane, GO:0031116: positive regulation of microtubule polymerization, GO:0042311: vasodilation, GO:0042493: response to drug, GO:0042803: protein homodimerization activity, GO:0043434: response to peptide hormone stimulus, GO:0043627: response to estrogen stimulus, GO:0046777: protein amino acid autophosphorylation, GO:0048278: vesicle docking, GO:0048471: perinuclear region of cytoplasm, GO:0048741: skeletal muscle fiber development, GO:0050998: nitric-oxide synthase binding, GO:0051259: protein oligomerization	04510: Focal adhesion	10.60	10.64	11.08	11.25	11.50	11.67	10.87	11.06	11.03	10.74	10.71	11.63	2

(*Continued*)

TABLE E4. (*Continued*)

202979_s_at	CREBZF	CREB/ATF bZIP transcription factor	NM_021212	58487	Hs.535319, Hs.595940	GO:0003700: transcription factor activity, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0009615: response to virus, GO:0016481: negative regulation of transcription, GO:0016566: specific transcriptional repressor activity, GO:0043565: sequence-specific DNA binding, GO:0045814: negative regulation of gene expression, epigenetic, GO:0046983: protein dimerization activity, GO:0051090: regulation of transcription factor activity		8.08	8.41	8.67	8.98	8.39	8.93	8.66	8.91	8.68	8.76	7.38	9.07	2
202983_at	HLTF	helicase-like transcription factor	AI760760	6596	Hs.3068	GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003702: RNA polymerase II transcription factor activity, GO:0004386: helicase activity, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005634: nucleus, GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0008270: zinc ion binding, GO:0016563: transcription activator activity, GO:0016568: chromatin modification, GO:0016787: hydrolase activity, GO:0016887: ATPase activity, GO:0046872: metal ion binding		7.92	8.38	8.43	8.76	8.41	8.75	8.21	8.88	8.60	8.50	7.52	8.58	2
202732_at	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	NM_007066	11142	Hs.472831	GO:0004860: protein kinase inhibitor activity, GO:0004862: cAMP-dependent protein kinase inhibitor activity, GO:0005515: protein binding, GO:0006469: negative regulation of protein kinase activity		8.09	8.25	8.65	8.96	9.35	9.12	7.96	8.30	8.27	7.93	8.22	8.98	2
202769_at	CCNG2	cyclin G2	AW134535	901	Hs.13291	GO:0000075: cell cycle checkpoint, GO:0005737: cytoplasm, GO:0007049: cell cycle, GO:0007067: mitosis, GO:0051301: cell division	04115: p53 signaling pathway	9.91	10.32	10.20	10.24	10.03	10.03	10.38	10.54	10.06	10.36	9.30	10.07	2
202651_at	LPGAT1	lysophosphatidylglycerol acyltransferase 1	NM_014873	9926	Hs.654626	GO:0003674: molecular_function, GO:0005737: cytoplasm, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0008152: metabolic process, GO:0008415: acyltransferase activity, GO:0008654: phospholipid biosynthetic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016740: transferase activity		8.40	8.67	8.77	9.16	8.74	8.97	8.83	9.11	8.98	8.90	7.91	8.87	2

(*Continued*)

TABLE E4. (*Continued*)

202660_at	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	AA834576	3709 Hs.512235	GO:0005216: ion channel activity, GO:0005220: inositol 1,4,5-triphosphate-sensitive calcium-release channel activity, GO:0005262: calcium channel activity, GO:0005509: calcium ion binding, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005886: plasma membrane, GO:0006811: ion transport, GO:0006816: calcium ion transport, GO:0007165: signal transduction, GO:0008095: inositol-1,4,5-triphosphate receptor activity, GO:0015085: calcium ion transmembrane transporter activity, GO:0016021: integral to membrane	04020: Calcium signaling pathway, 04070: Phosphatidylinositol signaling system, 04540: Gap junction, 04720: Long-term potentiation, 04730: Long-term depression, 04912: GnRH signaling pathway	9.12	9.22	9.42	9.60	9.85	10.60	9.90	9.68	9.73	9.94	9.14	10.79	2
202598_at	S100A13	S100 calcium binding protein A13	NM_005979	6284 Hs.516505	GO:0005509: calcium ion binding, GO:0005575: cellular_component, GO:0030154: cell differentiation		8.89	9.18	9.29	9.52	9.86	9.57	8.83	9.14	9.10	8.87	8.76	9.50	2
202630_at	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	AA046411	10513 Hs.84084	GO:0003777: microtubule motor activity, GO:0005488: binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0006886: intracellular protein transport, GO:0016020: membrane		7.87	8.36	8.58	8.86	8.85	9.11	7.89	8.50	8.33	8.27	7.75	9.04	2
202551_s_at	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	BG546884	51232 Hs.699247	GO:0001558: regulation of cell growth, GO:0004857: enzyme inhibitor activity, GO:0004867: serine-type endopeptidase inhibitor activity, GO:0005010: insulin-like growth factor receptor activity, GO:0005520: insulin-like growth factor binding, GO:0005576: extracellular region, GO:0005886: plasma membrane, GO:0007399: nervous system development, GO:0016021: integral to membrane		9.98	10.05	10.17	10.64	10.51	10.91	10.05	10.52	10.32	10.11	9.23	10.61	2
202557_at	HSPA13	heat shock protein 70kDa family, member 13	AI718418	6782 Hs.352341	GO:0000166: nucleotide binding, GO:0005524: ATP binding, GO:0005783: endoplasmic reticulum, GO:0005792: microsome		7.52	7.51	7.67	7.71	7.45	7.78	7.93	8.18	7.72	8.07	6.33	7.58	2

(*Continued*)

TABLE E4. (*Continued*)

202409_at	IGF2	insulin-like growth factor 2 (somatomedin A)	X07868	3481	Hs.523414, Hs.700350, Hs.706973	GO:0001501: skeletal development, GO:0005158: insulin receptor binding, GO:0005159: insulin-like growth factor receptor binding, GO:0005179: hormone activity, GO:0005576: extracellular region, GO:0006349: genetic imprinting, GO:0007275: multicellular organismal development, GO:0008083: growth factor activity, GO:0008283: cell proliferation, GO:0008286: insulin receptor signaling pathway, GO:0032583: regulation of gene-specific transcription		5.97	6.60	7.06	7.79	8.63	8.08	5.66	6.28	6.41	5.73	6.17	7.26	2
202512_s_at	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	AK001899	9474	Hs.486063	GO:0005515: protein binding, GO:0005737: cytoplasm, GO:0005776: autophagic vacuole, GO:0006914: autophagy, GO:0006915: apoptosis	04140: Regulation of autophagy	4.49	4.90	5.11	5.46	5.73	5.89	4.81	5.18	5.27	5.08	4.55	5.66	2
202265_at	BMI1	BMI1 polycomb ring finger oncogene	NM_005180	648	Hs.380403	GO:0005515: protein binding, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0007379: segment specification, GO:0008270: zinc ion binding, GO:0010468: regulation of gene expression, GO:0016568: chromatin modification, GO:0046872: metal ion binding, GO:0048146: positive regulation of fibroblast proliferation		9.58	9.89	10.02	10.34	10.16	10.26	9.95	10.24	10.18	10.03	9.36	10.14	2
202342_s_at	TRIM2	tripartite motif-containing 2	NM_015271	23321	Hs.435711	GO:0005515: protein binding, GO:0005622: intracellular, GO:0005737: cytoplasm, GO:0008150: biological_ process, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		7.37	7.61	7.79	8.31	8.10	8.76	7.22	7.77	7.53	7.52	6.10	8.52	2
202173_s_at	VEZF1	vascular endothelial zinc finger 1	NM_007146	7716	Hs.463569	GO:0001525: angiogenesis, GO:0001885: endothelial cell development, GO:0003677: DNA binding, GO:0003704: specific RNA polymerase II transcription factor activity, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006968: cellular defense response, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		8.81	8.76	9.34	9.52	9.74	9.89	8.92	9.30	9.05	9.22	8.20	9.46	2
202260_s_at	STXBP1	syntaxin binding protein 1	NM_003165	6812	Hs.288229	GO:0005737: cytoplasm, GO:0006904: vesicle docking during exocytosis, GO:0015031: protein transport, GO:0016020: membrane, GO:0016192: vesicle-mediated transport		7.18	7.54	7.45	7.58	8.01	8.08	7.29	7.32	7.59	7.22	6.79	7.97	2

(*Continued*)

TABLE E4. (*Continued*)

202073_at	OPTN	optineurin	AV757675	10133 Hs.332706	GO:0000042: protein targeting to Golgi, GO:0005737: cytoplasm, GO:0005794: Golgi apparatus, GO:0007030: Golgi organization and biogenesis, GO:0007165: signal transduction, GO:0008022: protein C-terminus binding, GO:0008219: cell death, GO:0043001: Golgi to plasma membrane protein transport	8.08	8.70	8.85	9.07	9.09	9.33	8.60	8.82	8.87	8.77	8.43	9.45	2
202172_at	VEZF1	vascular endothelial zinc finger 1	BG035116	7716 Hs.463569	GO:0001525: angiogenesis, GO:0001885: endothelial cell development, GO:0003677: DNA binding, GO:0003704: specific RNA polymerase II transcription factor activity, GO:0005622: intracellular, GO:0005634: nucleus, GO:0006350: transcription, GO:0006357: regulation of transcription from RNA polymerase II promoter, GO:0006968: cellular defense response, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	7.61	7.96	8.26	8.68	9.02	8.96	7.88	8.24	8.13	8.01	7.44	9.07	2
201918_at	SLC25A36	solute carrier family 25, member 36	AI927944	55186 Hs.144130	GO:0005215: transporter activity, GO:0005488: binding, GO:0005739: mitochondrion, GO:0005743: mitochondrial inner membrane, GO:0006810: transport, GO:0006839: mitochondrial transport, GO:0016020: membrane, GO:0016021: integral to membrane	6.11	6.45	6.72	7.09	6.96	7.10	6.80	7.13	6.78	6.71	6.08	7.03	2
201986_at	MED13	mediator complex subunit 13	AB011165	9969 Hs.282678	GO:0000119: mediator complex, GO:0004872: receptor activity, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006367: transcription initiation from RNA polymerase II promoter, GO:0016455: RNA polymerase II transcription mediator activity, GO:0030374: ligand-dependent nuclear receptor transcription coactivator activity, GO:0030521: androgen receptor signaling pathway, GO:0042809: vitamin D receptor binding, GO:0045944: positive regulation of transcription from RNA polymerase II promoter, GO:0046966: thyroid hormone receptor binding	8.59	8.43	8.61	8.69	8.81	9.04	8.66	8.89	8.54	8.71	7.15	8.99	2

(*Continued*)

TABLE E4. (*Continued*)

204294_at	AMT	aminomethyl-transferase	NM_000481	275 Hs.102	GO:0004047: aminomethyltransferase activity, GO:0005737: cytoplasm, GO:0005739: mitochondrion, GO:0006546: glycine catabolic process, GO:0006546: glycine catabolic process, GO:0008483: transaminase activity, GO:0016740: transferase activity	00260: Glycine, serine and threonine metabolism, 00670: One carbon pool by folate, 00910: Nitrogen metabolism	4.84	5.84	6.20	6.72	7.02	6.92	5.10	5.56	5.80	5.33	5.30	6.97	2
204671_s_at	ANKRD6	ankyrin repeat domain 6	BE677131	22881 Hs.702213	GO:0005515: protein binding		3.77	3.86	4.36	5.13	5.48	5.11	3.98	4.27	4.44	4.05	4.51	5.00	2
221470_s_at	IL1F7	interleukin 1 family, member 7 (zeta)	NM_014439	27178 Hs.166371	GO:0005152: interleukin-1 receptor antagonist activity, GO:0005576: extracellular region, GO:0005576: extracellular region, GO:0005615: extracellular space, GO:0006955: immune response		6.87	7.74	8.43	9.08	9.58	10.24	7.67	6.73	8.23	7.47	8.43	10.43	2
203249_at	EZH1	enhancer of zeste homolog 1 (Drosophila)	AB002386	2145 Hs.194669	GO:0003677: DNA binding, GO:0003682: chromatin binding, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0009653: anatomical structure morphogenesis		7.15	7.70	7.86	8.06	8.60	8.47	7.71	7.79	7.79	7.51	8.05	8.71	2
213118_at	UHRF1BP1L	UHRF1 binding protein 1-like	AL136821	23074 Hs.620701			6.97	7.17	7.22	7.18	7.25	7.36	7.52	7.22	7.50	7.41	6.57	7.00	2
211379_x_at	B3GALNT1	beta-1,3-N-acetylgalacto-saminyltransferase 1 (globoside blood group)	AB050855	8706 Hs.418062	GO:0000139: Golgi membrane, GO:0000287: magnesium ion binding, GO:0005794: Golgi apparatus, GO:0006486: protein amino acid glycosylation, GO:0008378: galactosyltransferase activity, GO:0008499: UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity, GO:0009312: oligosaccharide biosynthetic process, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016757: transferase activity, transferring glycosyl groups, GO:0047273: galactosylgalactosylglucosylceramide beta-D-acetylgalactosaminyltransferase activity	00603: Glycosphingolipid biosynthesis - globoseries, 01031: Glycan structures - biosynthesis 2	4.39	4.35	4.67	4.96	4.55	4.73	4.73	4.71	4.54	4.72	3.86	4.15	2

(*Continued*)

TABLE E4. (*Continued*)

212985_at	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	BF115739	323	Hs.479602	GO:0001540: beta-amyloid binding, GO:0005634: nucleus, GO:0007050: cell cycle arrest, GO:0007242: intracellular signaling cascade, GO:0008134: transcription factor binding, GO:0016020: membrane, GO:0030027: lamellipodium, GO:0030308: negative regulation of cell growth, GO:0030426: growth cone, GO:0045202: synapse, GO:0045449: regulation of transcription, GO:0045749: negative regulation of S phase of mitotic cell cycle		7.57	7.91	8.20	8.62	8.62	8.65	7.76	8.15	7.99	7.72	6.97	8.48	2
220369_at	SMEK1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	NM_017936	55671	Hs.533887	GO:0005515: protein binding, GO:0016020: membrane, GO:0016021: integral to membrane		3.54	3.38	3.69	3.58	3.05	3.35	3.66	3.71	3.70	3.59	4.40	3.29	3
221715_at			Z25437					3.97	3.73	3.59	3.61	3.76	3.72	3.61	3.65	3.60	3.72	4.69	3.60	3
211466_at	NFIB	nuclear factor I/B	U70862	4781	Hs.644095	GO:0003700: transcription factor activity, GO:0003700: transcription factor activity, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005634: nucleus, GO:0006260: DNA replication, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent		3.68	3.59	3.51	3.50	3.77	3.62	3.50	3.50	3.52	3.54	4.59	3.51	3
217695_x_at			BF942161					4.61	4.36	4.25	4.24	4.60	4.33	4.17	4.20	4.24	4.28	5.36	4.27	3
210282_at	ZMYM2	zinc finger, MYM-type 2	AL136621	7750	Hs.644041	GO:0005515: protein binding, GO:0005575: cellular_component, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0008150: biological_process, GO:0008270: zinc ion binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		3.19	3.04	3.05	3.21	3.37	3.16	2.96	3.03	3.00	3.10	4.32	3.52	3
210985_s_at	SP100	SP100 nuclear antigen	AF056322	6672	Hs.369056	GO:0000785: chromatin, GO:0003677: DNA binding, GO:0005634: nucleus, GO:0005694: chromosome, GO:0006355: regulation of transcription, DNA-dependent, GO:0016605: PML body, GO:0019904: protein domain specific binding		4.33	4.09	4.24	4.10	4.22	4.21	4.11	4.18	4.18	4.10	5.07	4.02	3
206757_at	PDE5A	phosphodiesterase 5A, cGMP-specific	NM_001083	8654	Hs.587281, Hs.647971	GO:0000166: nucleotide binding, GO:0000287: magnesium ion binding, GO:0003824: catalytic activity, GO:0004114: 3',5'-cyclic-nucleotide phosphodiesterase activity, GO:0005575: cellular_component, GO:0007165: signal transduction, GO:0007165: signal transduction, GO:0008150: biological_process, GO:0008270: zinc ion binding, GO:0009187: cyclic nucleotide metabolic process, GO:0016787: hydrolase activity, GO:0030553: cGMP binding, GO:0047555: 3',5'-cyclic-GMP phosphodiesterase activity	00230: Purine metabolism	3.53	3.28	3.34	3.37	3.45	3.44	3.19	3.34	3.24	3.28	4.15	3.25	3

(*Continued*)

TABLE E4. (*Continued*)

208262_x_at	MEFV	Mediterranean fever	NM_000243	4210 Hs.632221	GO:0003779: actin binding, GO:0005515: protein binding, GO:0005622: intracellular, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0006954: inflammatory response, GO:0008270: zinc ion binding, GO:0046872: metal ion binding		4.00	3.69	3.65	3.64	3.79	3.70	3.60	3.57	3.62	3.65	4.84	3.64	3
206438_x_at	TCTN2	tectonic family member 2	NM_024809	79867 Hs.167165	GO:0016020: membrane, GO:0016021: integral to membrane		7.19	7.00	6.94	7.01	7.28	7.15	6.96	6.98	6.95	6.83	8.29	7.06	3
206514_s_at	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	D12620	4051 Hs.106242	GO:0004497: monooxygenase activity, GO:0005506: iron ion binding, GO:0005783: endoplasmic reticulum, GO:0005789: endoplasmic reticulum membrane, GO:0005792: microsome, GO:0006691: leukotriene metabolic process, GO:0009055: electron carrier activity, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0020037: heme binding, GO:0046872: metal ion binding, GO:0050051: leukotriene-B4 20-monooxygenase activity	00590: Arachidonic acid metabolism	4.25	4.12	3.83	3.95	3.96	3.81	3.78	3.87	3.76	3.86	4.71	3.72	3
211133_x_at	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	AF009643	11025 Hs.631592	GO:0004888: transmembrane receptor activity, GO:0005887: integral to plasma membrane, GO:0006952: defense response, GO:0006955: immune response, GO:0007166: cell surface receptor linked signal transduction, GO:0016020: membrane	04662: B cell receptor signaling pathway	5.25	5.09	4.84	4.79	5.03	4.69	4.62	4.96	5.09	4.79	5.64	5.14	3
221712_s_at	WDR74	WD repeat domain 74	BC006351	54663 Hs.654620	GO:0005634: nucleus		6.69	6.38	6.27	6.08	6.28	6.42	6.41	6.47	6.45	6.38	7.14	6.65	3
203672_x_at	TPMT	thiopurine S-methyltransferase	U12387	7172 Hs.444319	GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, GO:0008119: thiopurine S-methyltransferase activity, GO:0008152: metabolic process, GO:0008168: methyltransferase activity, GO:0016740: transferase activity, GO:0046498: S-adenosylhomocysteine metabolic process, GO:0046500: S-adenosylmethionine metabolic process	00983: NA	7.10	7.00	6.78	6.73	6.54	6.68	6.70	6.78	6.89	7.14	7.85	6.47	3

(*Continued*)

TABLE E4. (*Continued*)

213006_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	AV655640	1052 Hs.440829	GO:0003700: transcription factor activity, GO:0005634: nucleus, GO:0006350: transcription, GO:0006355: regulation of transcription, DNA-dependent, GO:0006366: transcription from RNA polymerase II promoter, GO:0043565: sequence-specific DNA binding, GO:0046983: protein dimerization activity	4.03	4.02	3.45	3.25	3.43	3.30	3.81	3.69	3.86	4.26	4.36	3.23	3
211712_s_at	ANXA9	annexin A9	BC005830	8416 Hs.3346	GO:0001786: phosphatidylserine binding, GO:0005509: calcium ion binding, GO:0005544: calcium-dependent phospholipid binding, GO:0005829: cytosol, GO:0009986: cell surface, GO:0015464: acetylcholine receptor activity, GO:0016337: cell-cell adhesion, GO:0042803: protein homodimerization activity	8.65	9.58	9.67	9.50	8.90	8.66	8.88	8.21	9.00	9.09	9.29	8.53	4
202179_at	BLMH	bleomycin hydrolase	NM_000386	642 Hs.371914	GO:0004177: aminopeptidase activity, GO:0004180: carboxypeptidase activity, GO:0005625: soluble fraction, GO:0005634: nucleus, GO:0005737: cytoplasm, GO:0006508: proteolysis, GO:0009636: response to toxin, GO:0042493: response to drug	11.09	11.45	11.99	11.62	11.12	11.13	11.74	11.09	11.63	11.51	12.24	11.31	4
210085_s_at	ANXA9	annexin A9	AF230929	8416 Hs.3346	GO:0001786: phosphatidylserine binding, GO:0005509: calcium ion binding, GO:0005544: calcium-dependent phospholipid binding, GO:0005829: cytosol, GO:0009986: cell surface, GO:0015464: acetylcholine receptor activity, GO:0016337: cell-cell adhesion, GO:0042803: protein homodimerization activity	8.93	9.69	9.79	9.61	8.46	8.59	9.05	8.34	8.92	9.19	9.31	8.09	4
213707_s_at	DLX5	distal-less homeobox 5	NM_005221	1749 Hs.99348	GO:0001501: skeletal development, GO:0003700: transcription factor activity, GO:0005515: protein binding, GO:0005634: nucleus, GO:0006355: regulation of transcription, DNA-dependent, GO:0007275: multicellular organismal development, GO:0007399: nervous system development, GO:0007409: axonogenesis, GO:0030326: embryonic limb morphogenesis, GO:0042472: inner ear morphogenesis, GO:0043565: sequence-specific DNA binding, GO:0045669: positive regulation of osteoblast differentiation	6.55	6.83	6.96	6.17	5.86	6.02	7.52	6.75	6.77	6.58	7.04	6.51	4

(*Continued*)

TABLE E4. (*Continued*)

220413_at	SLC39A2	solute carrier family 39 (zinc transporter), member 2	NM_014579	29986 Hs.175783	GO:0005385: zinc ion transmembrane transporter activity, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0006811: ion transport, GO:0006829: zinc ion transport, GO:0008270: zinc ion binding, GO:0030001: metal ion transport, GO:0046873: metal ion transmembrane transporter activity		8.91	9.46	9.27	8.92	8.37	8.19	9.53	8.89	9.18	9.42	9.37	8.36	4
205464_at	SCNN1B	sodium channel, nonvoltage-gated 1, beta	NM_000336	6338 Hs.414614	GO:0001666: response to hypoxia, GO:0002028: regulation of sodium ion transport, GO:0005216: ion channel activity, GO:0005515: protein binding, GO:0006811: ion transport, GO:0007588: excretion, GO:0009986: cell surface, GO:0015280: amiloride-sensitive sodium channel activity, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0016324: apical plasma membrane, GO:0031402: sodium ion binding, GO:0035313: wound healing, spreading of epidermal cells, GO:0050896: response to stimulus, GO:0050909: sensory perception of taste	04742: Taste transduction	5.33	5.98	5.99	5.76	5.58	5.57	5.59	5.01	5.50	5.83	5.45	5.79	4
213820_s_at	STARD5	StAR-related lipid transfer (START) domain containing 5	T54159	80765 Hs.513075	GO:0005829: cytosol, GO:0006694: steroid biosynthetic process, GO:0006694: steroid biosynthetic process, GO:0006869: lipid transport, GO:0008289: lipid binding, GO:0015485: cholesterol binding, GO:0017127: cholesterol transporter activity		8.40	8.74	8.56	8.34	8.27	8.27	8.71	8.02	8.59	8.75	8.46	8.56	4
210015_s_at	MAP2	microtubule-associated protein 2	U89330	4133 Hs.368281	GO:0003674: molecular_function, GO:0005198: structural molecule activity, GO:0005516: calmodulin binding, GO:0005737: cytoplasm, GO:0005856: cytoskeleton, GO:0005874: microtubule, GO:0005875: microtubule associated complex, GO:0005875: microtubule associated complex, GO:0007026: negative regulation of microtubule depolymerization, GO:0008150: biological_process		4.34	4.40	4.48	4.04	3.98	3.99	5.27	4.06	4.85	4.21	4.46	4.59	4
210052_s_at	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	AF098158	22974 Hs.244580, Hs.708960	GO:0000922: spindle pole, GO:0005515: protein binding, GO:0005524: ATP binding, GO:0005525: GTP binding, GO:0005634: nucleus, GO:0007067: mitosis, GO:0008283: cell proliferation		7.86	7.90	7.79	7.54	6.64	6.69	8.34	7.06	7.64	7.87	7.30	7.15	4
214077_x_at	MEIS3P1	Meis homeobox 3 pseudogene 1	H15129	4213 Hs.356135			7.30	7.10	7.74	7.91	7.96	7.98	6.60	7.61	7.20	7.27	6.99	7.60	5

(*Continued*)

TABLE E4. (*Continued*)

218541_s_at	C8orf4	chromosome 8 open reading frame 4	NM_020130	56892	Hs.591849	GO:0006915: apoptosis	5.26	4.80	4.98	5.37	5.60	4.94	4.20	5.46	4.53	4.95	4.65	4.59	5
204075_s_at	KIAA0562	KIAA0562	AI936976	9731	Hs.133089, Hs.509017	GO:0005488: binding	8.28	7.85	8.15	8.30	8.46	8.68	7.94	8.57	8.48	8.21	8.24	8.67	5
205169_at	RBBP5	retinoblastoma binding protein 5	NM_005057	5929	Hs.519230	GO:0005515: protein binding, GO:0005634: nucleus, GO:0035097: histone methyltransferase complex	4.87	4.25	4.57	4.68	4.66	4.52	4.69	5.36	4.49	5.06	4.89	4.69	5
219446_at	RIC8B	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	NM_018157	55188	Hs.131306	GO:0001965: G-protein alpha-subunit binding, GO:0005085: guanyl-nucleotide exchange factor activity, GO:0005488: binding, GO:0005737: cytoplasm, GO:0005829: cytosol, GO:0005886: plasma membrane, GO:0008277: regulation of G-protein coupled receptor protein signaling pathway	4.73	4.67	4.64	4.96	4.91	5.13	4.66	5.61	4.78	4.91	4.66	4.96	5
222162_s_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	AK023795	9510	Hs.643357	GO:0004222: metalloendopeptidase activity, GO:0005576: extracellular region, GO:0005578: proteinaceous extracellular matrix, GO:0006508: proteolysis, GO:0007229: integrin-mediated signaling pathway, GO:0008201: heparin binding, GO:0008270: zinc ion binding, GO:0008285: negative regulation of cell proliferation, GO:0046872: metal ion binding	8.19	7.57	7.66	7.91	7.97	8.52	7.35	8.18	8.05	7.81	7.47	8.24	5
209426_s_at	AMACR	alpha-methylacyl -CoA racemase	AF047020	23600	Hs.508343	GO:0003824: catalytic activity, GO:0005739: mitochondrion, GO:0005777: peroxisome, GO:0008111: alpha-methylacyl-CoA racemase activity, GO:0008152: metabolic process, GO:0016491: oxidoreductase activity, GO:0016853: isomerase activity	2.97	3.27	3.41	3.22	3.07	3.35	4.09	3.04	3.68	3.17	3.07	2.98	6

Fold change >2 for any time point; FDR <0.05.

TABLE E5. GSEA table responders versus nonresponders

Gene set	Size	ES	Normalized ES	*P* value	FDR
IL-17 and TNF	36	−0.91	−2.95	.000	0.000
IL-17–specific	19	−0.84	−2.33	.000	0.000
IFN-γ	1184	−0.42	−2.12	.000	0.000
TNF-specific	557	−0.38	−1.82	.000	0.001

TABLE E6. GSEA table for responders

Gene set	Size	ES	Normalized ES	*P* value	FDR
IL-17 and TNF	36	−0.90	−2.84	.000	0.000
IL-17–specific	19	−0.86	−2.38	.000	0.000
IFN-γ	1184	−0.41	−2.10	.000	0.000
TNF-specific	557	−0.38	−1.86	.000	0.003