*Original article*

# Clinical efficacy and immune regulation with peanut oral immunotherapy

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**Background: Oral immunotherapy (OIT) has been thought to induce clinical desensitization to allergenic foods, but trials coupling the clinical response and immunologic effects of peanut OIT have not been reported.**
**Objective: The study objective was to investigate the clinical efficacy and immunologic changes associated with OIT.**
**Methods: Children with peanut allergy underwent an OIT protocol including initial day escalation, buildup, and maintenance phases, and then oral food challenge. Clinical response and immunologic changes were evaluated.**
**Results: Of 29 subjects who completed the protocol, 27 ingested 3.9 g peanut protein during food challenge. Most symptoms noted during OIT resolved spontaneously or with antihistamines. By 6 months, titrated skin prick tests and activation of basophils significantly declined. Peanut-specific IgE decreased by 12 to 18 months, whereas $IgG_4$ increased significantly. Serum factors inhibited IgE–peanut complex formation in an IgE-facilitated allergen binding assay. Secretion of IL-10, IL-5, IFN-γ, and TNF-α from PBMCs increased over a period of 6 to 12 months. Peanut-specific forkhead box protein 3 T cells increased until 12 months and decreased thereafter. In addition, T-cell microarrays showed downregulation of genes in apoptotic pathways.**
**Conclusion: Oral immunotherapy induces clinical desensitization to peanut, with significant longer-term humoral and cellular changes. Microarray data suggest a novel role for apoptosis in OIT. (J Allergy Clin Immunol ■■■■;■■■:■■■-■■■.)**

***Key words:*** *Peanut hypersensitivity, immunotherapy, immune tolerance, apoptosis, IgE, IgG, IL-5, IL-10*

In industrialized countries, peanut allergy affects 0.8% of children and 0.5% to 1% of the general population,[1-3] and the prevalence appears to be increasing. Peanuts and tree nuts account for the vast majority of life-threatening or fatal reactions to foods.[4,5] Currently, the primary treatment for peanut allergy is a peanut-free diet and ready access to self-injectable epinephrine and antihistamines.[6] Strict avoidance diets can be complicated by difficulty in interpreting labels[7] and undeclared allergens in commercially prepared foods.[8,9] As many as 50% of patients with food allergy have an allergic reaction during a given 2-year period.[10] The combination of avoidance diets and risks of accidental exposures and life-threatening reactions creates a tremendous burden to patients and families.

Traditional subcutaneous immunotherapy is useful in treating forms of inhalant allergen sensitivity such as allergic rhinoconjunctivitis and asthma[11] but is unsafe in food allergy.[12,13] Oral immunotherapy (OIT) and sublingual immunotherapy have been reported by our group and others to result in induction of clinical tolerance to a variety of food proteins.[14-16] Yet most studies have not attempted to couple clinical efficacy with long-term immunologic changes.

We conducted an open-label study of peanut OIT in children with peanut allergy. Our goals were to evaluate the ability of peanut OIT to induce clinical desensitization and to investigate the immunologic mechanisms associated with clinical efficacy. The term *desensitization* was used to mean a change in threshold

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*Abbreviations used*
FAB: Facilitated allergen binding
FoxP3: Forkhead box protein 3
MIP: Macrophage inflammatory protein
OFC: Oral food challenge
OIT: Oral immunotherapy
PBMC: Peripheral blood mononuclear cell
SPT: Skin prick test
Treg: Regulatory T cell

of ingested food antigen needed to cause allergic symptoms, whereas *tolerance* referred to the induction of long-term immunologic changes associated with the ability to ingest food without symptoms and without ongoing therapy. We hypothesized that subjects with peanut allergy who underwent OIT would be shifted toward a $T_H1$-type profile.

## METHODS

### Subject recruitment

Subjects age 1 to 16 years were recruited from the allergy and immunology clinics or surrounding community physician offices at Duke University Medical Center and Arkansas Children's Hospital. Ethics approval was obtained through the Institutional Review Boards at Duke University Medical Center and University of Arkansas for Medical Sciences. Written informed consent was obtained in accordance with each institution's ethics guidelines for research in children.

### Subject selection

Included subjects had a clinical history of reaction to peanut within 60 minutes of ingestion, a positive peanut skin prick test ([SPT] $\geq$3 mm of negative control), and a peanut CAP FEIA $\geq$15 kU/L (Phadia AB; Pharmacia, Inc, Uppsala, Sweden). Subjects were also included if they had a CAP FEIA $\geq$7 kU/L and a clinical reaction within the previous 6 months. Subjects were excluded for history of severe, life-threatening anaphylaxis (with hypotension) to peanut, severe or poorly controlled asthma, or a medical condition preventing undergoing a food challenge.

### Peanut flour and dosing

Peanut protein (from Partially Defatted Peanut Flour 12% Fat Light Roast; Golden Peanut Company, Alpharetta, Ga; 2 g flour = 1 g peanut protein) doses were premeasured and mixed in a food vehicle of the subject's choosing and taken in 2 or 3 bites. Approximately 240 mg peanut protein equals 1 whole peanut.[17]

### OIT protocol

Peanut OIT consisted of 3 phases: initial day escalation, buildup, and maintenance. Patients were instructed to eliminate peanut protein otherwise from their diets. During dosing, subjects were asked to keep a diary of any missed doses or adverse symptoms. Self-administered epinephrine was provided to all patients. A member of the study team was available by pager and phone at all times throughout the study.

**Initial day escalation phase.** The initial day escalation phase was undertaken at the research unit at each institution. Intramuscular epinephrine, oral and intravenous doses of diphenhydramine, and albuterol were at the bedside at all times. Dosing began at 0.1 mg peanut protein, followed by an approximate doubling every 30 minutes, up to 50 mg. The highest tolerated single dose was the starting dose for the buildup phase, which was initiated in the research unit the following day.

**Buildup phase.** Subjects were instructed to ingest the daily dose of peanut protein with other safe foods in 2 or 3 bites at home every day. Doses were increased 25 mg every 2 weeks until 300 mg was reached. Subjects returned to the clinic for dose escalations. For subjects who stopped dosing at lower than 50 mg on the initial day escalation, their doses were doubled every 2 weeks until they reached 50 mg, and then the increases were 25 mg. Buildup dosing was delayed if subjects had evidence of illness (eg, viral infection) at the time of scheduled up-dosing; therefore, the time to reach maintenance dosing varied between subjects.

**Maintenance phase.** After reaching 300 mg peanut protein daily, subjects continued this dose until the food challenge. After oral food challenge, subjects were increased to a daily OIT dose of 1800 mg if the peanut IgE remained >2 kU/L after 12 months on maintenance dose (this escalation occurred in all subjects reported). Subjects were evaluated every 4 months while on continued maintenance dosing (total of 36 months).

### Oral food challenge

The first cohort of subjects (n = 7) underwent an open oral food challenge (OFC) to peanut protein after 13 to 22 months of maintenance OIT, and the second cohort (n = 22) did after 4 to 7 months. The time to OFC was reduced because early basophil and skin test data as well as OFC data indicated a lack of clinical reactivity sooner than hypothesized. Before the OFC, subjects were asked to restrict use of antihistamines (short-acting, 72 hours; long-acting, 7 days), β-agonists (12 hours), theophylline (12 hours), and montelukast (12 hours). The OFC consisted of 4 doses (300 mg, 600 mg, 1200 mg, 1800 mg) of peanut protein given every 30 minutes up to a total of 3.9 g peanut protein (7.8 g peanut flour). The OFC was discontinued at 3.9 g or with objective symptoms.

### Purified peanut protein reagent

Peanut proteins were extracted from defatted peanut flour (Golden Peanut Co) in PBS, clarified by centrifugation (30,000*g* for 30 minutes), and sterilized by filtration.

The major peanut allergen, Ara h 2, was purified and lyophilized as previously described,[18] diluted in PBS, and sterilized. All protein concentrations were determined by using the bicinchoninic acid assay (BCA; Pierce, Rockford, Ill).

### Titrated skin prick testing

Titrated skin prick tests (SPTs) with peanut extract (Greer Laboratories, Inc, Lenoir, NC) and saline and histamine controls were performed at enrollment, after 4 months of maintenance therapy, and every 4 months thereafter. Tests to peanut were measured and followed at the same dilution (1:20, 1:200, 1:2000, or 1:20,000) that initially showed a wheal >5 mm. Wheal size was the average of the largest diameter and the perpendicular midpoint diameter. Data were analyzed using a mixed-model repeated-measures ANOVA. The response variable was the highest dilution causing >5 mm wheal at enrollment. Time and subject were treated as factors. Inferences about wheal size changes over time were made by comparing the mean at each time point back to time 0 using a multiple comparisons procedure. Restricted maximum likelihood was used to fit the ANOVA model and estimate model parameters.

### Basophil activation assay

Basophil activation was measured as previously described.[19] Briefly, peripheral blood was collected in sodium heparin tubes, aliquoted, and stimulated for 30 minutes with basophil medium alone (RPMI with 4 ng/mL human IL-3) or the medium with 10, 1, or 0.1 μg/mL peanut extract; 1 μg/mL anti-IgE (polyclonal rabbit antihuman; Bethyl Laboratories, Montgomery, Tx); or 2 μmol/L fMLP (VWR Scientific, West Chester, Pa). Cells were stained for 30 minutes at 4°C with the following mAbs: CD63–fluorescein isothiocyanate (clone H5C6), CD203c-phycoerythrin (IM3575), CD123 phycoerythrin-Cy5 (9F5), CD69-APC-Cy7 (FN50), CD3-allophycocyanin (SK7), CD14-APC (M5E2), CD19-APC (H1B19), CD41a-allophycocyanin (HIP8), and HLA-DR–phycoerythrin–Cy7 (L243) (IM3575, Beckman Coulter, Fullerton, Calif; all others, BD Biosciences, San Jose, Calif). CD63 upregulation was assessed by flow

cytometry. CD3, CD14, CD19, and CD41a–positive events were excluded, and a minimum 1000 $CD123^{+}HLA\text{-}DR^{-}$ events were acquired. Data were analyzed by using FlowJo software (TreeStar, Ashland, Ore).

## Assays for IgE, IgG, and $IgG_4$

Peanut-specific IgE, IgG, and $IgG_4$ levels were measured in serum samples by using the ImmunoCAP 100 instrument (Phadia AB) according to the manufacturer's instructions. The same statistical approach as for the titrated skin tests analysis was carried out, except that the natural log of the immunoglobulin concentrations was taken to meet the constant variance and normality assumptions of the ANOVA model better.

## IgE-facilitated allergen binding assay for peanut

Indicator serum containing high concentrations of peanut-specific IgE (RAST >100 IU/mL) was purchased from PlasmaLab, Everett, Wash. Equal volumes (10 μL) of serum obtained from the clinical study and indicator serum were incubated with peanut extract (0.04 μg/mL in 2.5 μL) for 1 hour at 37°C.[20] Results of flow cytometry are expressed as relative binding, where binding observed by indicator serum alone is normalized to 100%, and changes in binding caused by the addition of patients' serum to the indicator serum is related to this value. Statistical differences between pre-OIT and post-OIT sera were determined by using SPSS 15.0 for Windows (SPSS Inc, Chicago, Ill). The 2-tailed Wilcoxon signed-rank test was used to compare pre-OIT and post-OIT sera ability to inhibit peanut-specific facilitated allergen binding (FAB). $P$ values <.05 were considered statistically significant.

## Cytokine assay and regulatory T-cell analyses

Peripheral blood mononuclear cells (PBMCs) were isolated from ~25 mL heparinized blood by using Ficoll-based density separation (LymphoH; Atlanta Biologicals, Lawrenceville, Ga). For cytokine assays, suspended PBMCs were distributed into 96-well flat-bottom plates at a concentration of $4 \times 10^5$ cells/well in triplicate and incubated with crude peanut protein (40 μg/well), Ara h 2 (20 μg/well), concanavalin A (8 μg/well; Sigma, St Louis, Mo), or medium alone (RPMI-1640 with 2 mmol/L L-glutamine, 25 mmol/L HEPES buffer containing 10% human AB serum, 100 IU/mL penicillin, and 100 μg/mL streptomycin; Mediatech, Manassas, Va). Cells were cultured at 37°C in 5% $CO_2$ humidified atmosphere for 24, 48, and 96 hours. Culture supernatants were collected at each time point and analyzed in duplicate for 14 different analytes by using a multiplex bead assay (R&D Systems, Minneapolis, Minn) for the Luminex 100 platform. To analyze the cytokine data, linear mixed-effects models were run in Splus (Insightful Co, Palo Alto, Calif) with subject as the random effect, and fixed effects given by culture condition, culture condition × months on immunotherapy, and time of culture. The response variable was

$$log(y+1),$$

where $y$ is the mean cytokine concentration. Slope comparisons were against the null hypothesis that slope = 0 for RPMI. A positive or negative coefficient was considered statistically significant at the .05 level and was a measure of the trend over time of each cytokine.

For flow cytometry, PBMCs ($2 \times 10^6$ cells/well) were cultured in 24-well plates under the same stimulation conditions as described. After 6 days, cells were collected and stained with fluorescent mAbs: anti-CD3–PerCP, CD4–fluorescein isothiocyanate, and CD25-phycoerythrin (BD Biosciences). Additional intracellular staining with anti–forkhead box protein 3 (Foxp3)—allophycocyanin was carried out after fixation/permeabilization of the cells (eBioscience). Isotype controls were included for each condition. The samples were run for 3-color detection in a FACSCalibur flow cytometer (Beckman-Coulter). At least 10,000 events were acquired for each experimental condition, and data were analyzed by using the FlowJo software.

## Microarray analysis

RNA isolated from resting PBMC $CD3^{+}$ T cells (EasySep T-cell Enrichment; Stem Cell Technologies, Inc, Vancouver, British Columbia, Canada) with the RNeasy Total RNA Isolation kit (Qiagen, Inc, Valencia, Calif) was used for target preparation and hybridization with the GeneChip human genome U133 Plus 2.0 array (Affymetrix, Inc, Santa Clara, Calif) according to the manufacturer instructions. Hybridized microarrays were scanned by using an Affymetrix GeneChip 3000 scanner. Microarray assays and statistical analyses of experimental data were performed by Expression Analysis, Inc, Durham, NC, and included assessment of data quality by standard quality checks and principal components analysis by sample of the probe-level data, along with normalization and signal summarization using the robust multiarray algorithm. Determination of differential expression of genes in subject samples before and after OIT was performed by repeated-measures analysis accounting for multiple testing using a variant of Significance Analysis of Microarrays[21] to detect statistically significant transcripts. Enrichment analysis of the set of transcripts identified as differentially expressed between subjects by repeated-measures analysis was then performed by GeneGo, Inc, (St Joseph, Mich) using the MetaCore software suite (GeneGo, Inc). This enrichment analysis matched Entrez (National Center for Biotechnology Information, National Institutes of Health, Bethesda, Md) geneIDs for common, similar, and unique sets of the OIT subjects differentially expressed transcript list with Entrez geneIDs in functional ontologies in MetaCore. The ontologies included canonical pathway maps, GeneGo cellular processes, gene ontology cellular processes, and disease categories. The degree of relevance to different categories for the OIT subjects dataset was defined by $P$ values, so that the lower $P$ value received higher priority.

## Quantitative real-time PCR

Resting PBMC $CD3^{+}$ T-cell RNA isolated for microarray assays was used for cDNA synthesis and quantification of experimental and control (18s rRNA) transcripts by Expression Analysis, Inc, using a 7900 HT Fast Real-Time PCR System (Applied Biosystems, Foster City, Calif) and TaqMan Gene Expression Assay (Applied Biosystems) gene-specific primer and probe sets. Experimental transcript levels were normalized to those for 18s rRNA in each sample.

# RESULTS

## Subject demographics

Thirty-nine subjects were enrolled. Twenty five (64%) were male. The median age at enrollment was 57.5 months (range, 12-111 months). The median age at first reaction to peanut was 15 months (range, 8-48 months). All but 3 subjects had allergic disease other than food allergy, including atopic dermatitis (69%), asthma (62%), and allergic rhinitis (62%). Fifty-four percent had an additional food allergy: 38% tree nuts, 23% egg, 13% cow's milk, 5% fish, and 3% soy.

All 39 subjects completed the initial day escalation protocol. Ten (25%) subjects subsequently withdrew. Six discontinued for personal reasons, including transportation issues, parental anxiety, and failure to perform home dosing. These 6 had reactions during the initial escalation day that were similar to reactions of patients who continued in the study. The remaining 4 subjects discontinued because of allergic reactions to the OIT that did not resolve with continued treatment or dose reduction. Three had gastrointestinal complaints, and 1 had symptoms of asthma. Twenty-nine subjects completed all 3 phases of the study and peanut challenges.

## Clinical responses during initial day escalation

During the initial day escalation, 10 (26%) subjects tolerated the highest dose of 50 mg peanut protein (Table I), 15 (38%) tolerated 25 mg, 6 (15%) tolerated 12 mg, 5 (13%) tolerated 6 mg, 1 (3%) tolerated 3 mg, and 2 (5%) tolerated 1.5 mg. Thirty-six patients (92%) experienced some symptoms during the initial escalation day. Most common were upper respiratory symptoms, with

**TABLE I.** Clinical responses to peanut OIT

| | Initial day escalation (N = 39) | Buildup +maintenance (n = 29) | OFC (n = 29) |
|---|---|---|---|
| Dose (mg) first symptom, median (range) | 6 (0.1-50) | | 1800 (300-1800) |
| No. (%) reached highest dose | 10 (26) | | 27 (93) |
| No. (%) without symptoms | 3 (8) | | 11 (38) |
| Therapy received, n (%) | 22 (56) | | 11 (38) |
| None | 17 (44) | | 18 (62) |
| Diphenhydramine | 19 (49) | | 11 (38) |
| Albuterol | 5 (13) | | 1 (3) |
| Epinephrine | 4 (10) | | 1 (3) |
| Total home doses, n | | 14,773 | |
| Days with symptoms, n (% of total home doses) | | 545 (3.7) | |
| Days with home treatment, n (% of total home doses) | | 111 (0.8) | |

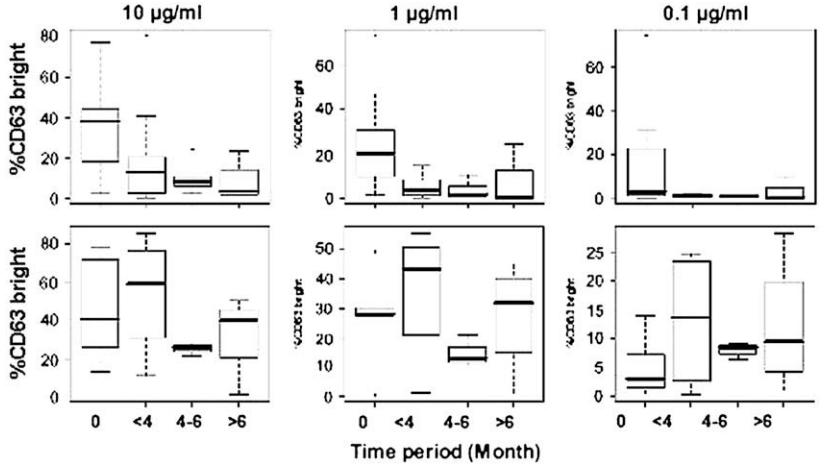


**FIG 1.** Effect of peanut OIT on basophil activation. *Top row,* Subjects who received peanut OIT. *Bottom row,* Subjects in an observational study of peanut allergy. At a peanut concentration of 10 µg/mL, OIT results in significant initial changes in basophil responsiveness (*$P < .001$).

27 patients (69%) reporting mild sneezing/itching and mild laryngeal symptoms. No patients experienced severe upper respiratory or laryngeal symptoms. Seventeen patients (44%) reported mild to moderate nausea or abdominal pain, and 8 patients (21%) had mild diarrhea/emesis. Twenty-four subjects (62%) had mild or moderate skin symptoms. A total of 6 patients experienced chest symptoms during the initial escalation day; all 6 had mild wheezing, and 2 progressed to moderate wheezing. Three of the subjects with chest symptoms during the initial day escalation also had a previous diagnosis of asthma.

## Buildup/maintenance

Subjects had symptoms after 46% of buildup doses. Subjects were on maintenance dosing at home prior to OFC for a median of 4.7 months (range, 4-22 months). All subjects experienced rare, and typically minor, symptoms during some point of home dosing (3.7% of 14,773 doses given; Table I). Upper respiratory (1.2%) and skin (1.1%) were the most common. Treatment was given with 0.8% of home doses. Only 2 subjects received epinephrine after home dosing, and each of the 2 had only 1 such incident.

## OFC

Twenty-nine subjects participated in the open OFC to peanut. Overall, 27 of 29 (93%) reached the total peanut dose of 3.9 g with no more than mild symptoms, suggesting successful desensitization to peanut protein. Two subjects did not ingest the maximal dose and stopped after 2.1 g. One stopped because of parental anxiety, and the other because of mild urticaria and 1 vomiting episode.

## Titrated SPTs

Titrated SPTs showed a significant decrease of 4 mm beginning at 6 months ($P < .0001$) and remained decreased throughout the study.

## Basophil activation

Basophil reactivity to peanut antigen was evaluated at 3 peanut concentrations: 10 µg/mL, 1 µg/mL, and 0.1 µg/mL; and 4 time points: before OIT (n = 15), <4 months (n = 9), 4 to 6 months (n = 6), and >6 months (n = 4; Fig 1). At a peanut concentration of 10 µg/mL, basophil activation was significantly reduced within 4 months ($P < .001$). We also evaluated basophil reactivity in subjects in an observational study of peanut allergy, and these patients did not experience reduced basophil activity.

## Peanut-specific serum IgE, IgG, and $IgG_4$

The initial median concentration of serum peanut-specific IgE was 85.4 kU/L (range, 9.1-840.0 kU/L). After 3 months of treatment, median peanut-specific IgE increased nearly 3-fold

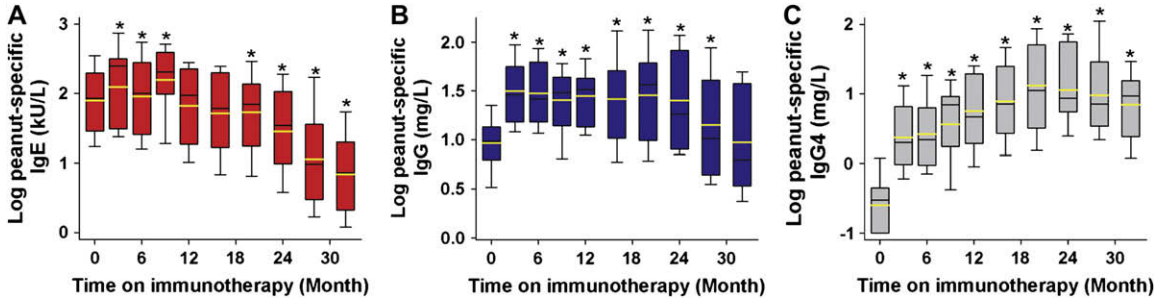


**FIG 2.** Serum levels of peanut-specific immunoglobulins during peanut OIT. In the serum of 28 subjects undergoing immunotherapy, peanut-specific IgE **(A)**, IgG **(B)**, and $IgG_4$ **(C)** were measured by using the ImmunoCAP instrument. Values are log-transformed, and median and mean values are represented by *black and yellow horizontal lines*, respectively. A mixed model, repeated-measures ANOVA was used to determine the statistical significance between baseline and treatment time points (*$P < .0005$).

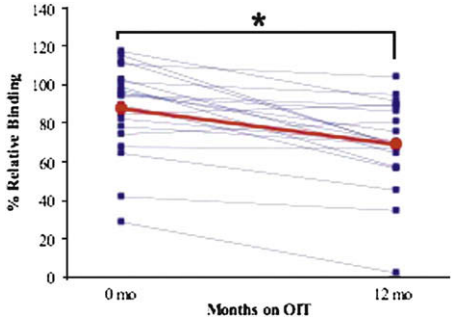


**FIG 3.** Peanut OIT leads to FAB inhibition. *Blue lines* represent individual data points, *red line* the mean. Statistical differences between pre-OIT and 12-month–post-OIT serum were determined by Wilcoxon signed-rank test (*$P < .001$).

(249.0 kU/L; $P < .0005$). At 12 and 18 months, no significant decrease from baseline was found, but for all subsequent time points (until 33 months), peanut-specific IgE levels were significantly decreased ($P < .0005$; Fig 2, *A*).

Median baseline serum peanut-specific IgG was 9.7 mg/L (range, 2.5-56.0 mg/L). A significant increase ($P < .0005$) in specific IgG levels also started at 3 months (Fig 2, *B*). Specific IgG levels remained high until 24 months and slowly returned to baseline by 33 months.

The peanut-specific $IgG_4$ followed a slightly different trend (Fig 2, *C*). Initial concentrations were low, with a median of 0.3 mg/L (range, 0.1-1.4 mg/L). Peanut-specific $IgG_4$ concentrations increased initially, reaching statistical significance at 3 months (2.0 mg/L vs 0.3 mg/L; $P < .0005$), and continued elevated at the end of the study ($P < .0005$).

## FAB assay

FAB inhibition by serum factors was tested in 20 patients at baseline and after 12 months of treatment. A decrease in percent relative binding after 12 months of OIT was measured in 18 of the 20 subjects (Fig 3). Subjects with peanut allergy from our egg OIT study[16] currently avoiding peanuts were used as controls and showed no change in relative binding (data not shown). For the peanut OIT subjects, the percent mean relative binding decreased from 87.6% ± 23.4% at baseline to 69.3% ± 23.3% by 12 months ($P < .001$).

## Secreted cytokines

A panel of 14 cytokines was measured in the supernatants of PBMCs incubated for 24, 48, and 96 hours with peanut, Ara h 2, ConA, or medium alone (RPMI) for the first 5 subjects every 6 months for a period of 2 years on OIT. As expected, a more robust secretion of cytokines was measured after ConA stimulation, enabling measurement of otherwise undetectable cytokines (Fig 4). Cytokines including IL-5, IL-10, IFN-γ, and TNF-α significantly increased, as did the growth factor G-CSF, whereas IL-2 declined. IL-4 and IL-17 were undetectable at baseline and remained so, whereas many inflammatory mediators (IL-1β, IL-6, IL-8, macrophage inflammatory protein [MIP] 1β, and GM-CSF) were found at saturating levels (data not shown).

After peanut stimulation, a number of inflammatory cytokines/chemokines were significantly increased over time, including IL-1β, IL-5, TNF-α, and MIP-1β, as well as the growth factors G-CSF and GM-CSF (Fig 5). Saturating levels of IL-6 and IL-8 prevented the delineation of a trend, and no significant change in monocyte chemotactic protein 1 was observed during immunotherapy (data not shown). After peanut stimulation, no detectable levels of secreted IL-2, IL-4, IL-10, IL-17, or IFN-γ were measured (data not shown). Cytokine levels detected after stimulation with a single allergen, Ara h 2, were not different from those with medium alone (data not shown).

## $FoxP3^+$ regulatory T cells

In 10 subjects who received peanut OIT for as long as 36 months, a subpopulation of $FoxP3^+$ T cells were investigated by flow cytometry in the lymphocyte gates of PBMCs incubated for 6 days with medium alone (RPMI), peanut, or Ara h 2 (Fig 6). During OIT, the number of FoxP3 T cells increased approximately 1.5-fold in peanut-stimulated cells at 6 and 12 months ($P < .05$) and decreased thereafter, returning to baseline levels by 20 months. Ara h 2 stimulation created a similar yet less pronounced increase.

## Microarray and quantitative real-time PCR analysis of patient T cells

Genome-wide oligonucleotide microarray analyses compared transcription patterns in T cells obtained from 6 unrelated subjects before starting OIT and 6 months after uncomplicated OIT. Differential expression of genes in subject samples before and

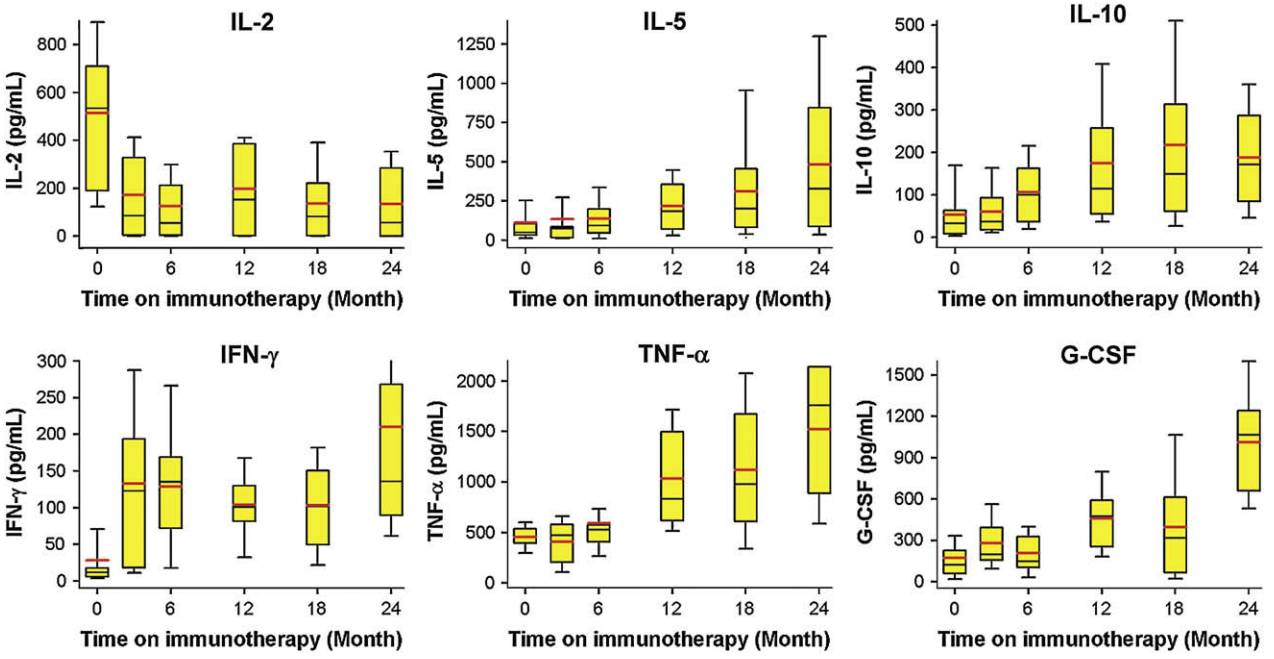


**FIG 4.** Cytokines secreted from PBMCs after ConA stimulation. The plotted 6 cytokines/chemokines all had statistically significant changes versus medium alone ($P < .05$). *Black lines* are median values; *red lines* are means.

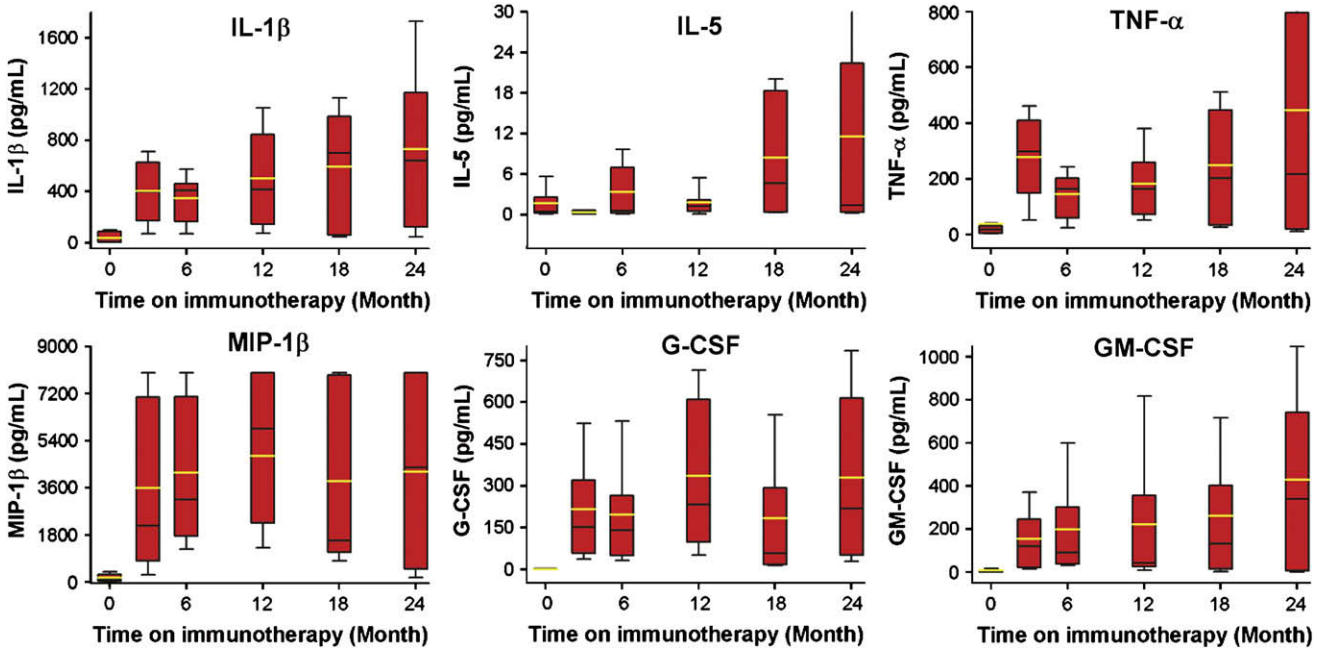


**FIG 5.** Cytokines secreted from PBMCs stimulated with crude peanut extract. The plotted 6 cytokines/chemokines all had statistically significant changes versus medium alone ($P < .05$). *Black lines* are median values; *yellow lines* are means.

after OIT was determined by repeated-measures analysis and yielded 450 transcripts with a false discovery rate of <7%. A reduced, nonrepetitive subset of 334 genes having a well described Entrez GeneID (see this article's Table E1 in the Online Repository at www.jacionline.org) was then submitted to GeneGo, Inc, for enrichment analysis. The 3 canonical signaling and metabolic pathways most affected by OIT were all involved in apoptosis, and all differentially expressed transcripts in these pathways were downregulated after 6 months of OIT (Table II). Quantitative real-time PCR of selected samples confirmed the observed downregulation of *BCL2L11*, *GADD45A*, *TNFSF8*, and *RELA* gene expression in 3 subjects after OIT (data not shown). Further enrichment analysis of 110 cellular and molecular processes whose content is defined and mapped by GeneGo, Inc,

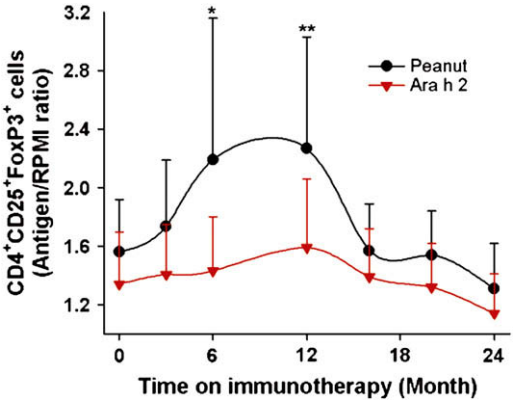


**FIG 6.** Changes of FoxP3$^+$ Treg cells during peanut oral immunotherapy. PBMCs from 10 subjects were cultured in presence of peanut proteins, Ara h 2, or medium alone (RPMI). Paired *t* tests were used to determine statistical differences between baseline and later time points ($P < .05$, 6 months; $P < .01$, 12 months).

with each process representing a preset network of protein interactions characteristic for the process, also demonstrated a statistically significant alteration of apoptosis networks after OIT.

**TABLE II.** Log decrease in expression of apoptosis-related genes with peanut OIT

| Pathway* | Gene symbol† | Entrez ID‡ | Log ratio§ |
|---|---|---|---|
| Regulation of apoptosis by mitochondrial proteins | *CASP9* | 842 | –0.5298 |
| | *VDAC1* | 7,416 | –0.9541 |
| | *BAK1* | 578 | –0.4894 |
| | *BCL2L11* | 10,018 | –1.3777 |
| p53-Dependent apoptosis | *GADD45A* | 1,647 | –1.1790 |
| | *TP73* | 7,161 | –0.3054 |
| | *CASP9* | 842 | –0.5298 |
| | *BCL2L11* | 10,018 | –1.3777 |
| Antiapoptotic TNFs/NF-κB/IAP pathway | *TNFSF8* | 944 | –1.0622 |
| | *REL* | 5,966 | –1.4996 |
| | *RELA* | 5,970 | –0.7671 |

*Canonical apoptosis and survival signaling and metabolic pathways as defined by GeneGo, Inc.
†HUGO Gene Nomenclature Database, European Molecular Biology Laboratory, European Bioinformatics Institute.
‡Entrez Gene Database, National Center for Biotechnology Information, National Institutes of Health.
§$Log_2$ (expression after 6 months OIT/expression before OIT), calculated from microarray data.

## DISCUSSION

In this clinical and mechanistic study, peanut OIT induced clinical desensitization in the 29 subjects with peanut allergy who completed the study. Ninety-three percent successfully completed an OFC to 3.9 g peanut protein, and all subjects had a significant increase in the amount of peanut they tolerated during food challenge. Peanut OIT was also safe; mild symptoms were relieved with diphenhydramine or albuterol. Our results are consistent with previous studies in which OIT led to clinical desensitization to foods such as egg and cow's milk.[14-16,22] Furthermore, the humoral and cellular responses associated with peanut OIT suggest that OIT also induces the transition from short-term desensitization to long-term tolerance. For this analysis, we did not perform OFCs after cessation of therapy, when sensitivity could return. Per the protocol, these definitive challenges are planned for subjects who complete 3 years of maintenance therapy and have a significant drop in serum IgE. However, compared with previous OIT studies, our study had a longer duration of maintenance therapy, which we hypothesize has a significant impact on the immunologic parameters indicative of long-term tolerance.

In our study, titrated SPTs showed a significant decrease at 6 months and remained decreased throughout the study. Similarly, basophil activation, a measure of IgE-dependent response, decreased significantly within 4 months, and the decline continued beyond 6 months. IgE-mediated hypersensitivity responses are known to be downregulated during drug desensitization,[23] and chronic FcεRI signaling induces a downregulation of Syk-dependent signal transduction *in vitro*.[24]

With peanut OIT, peanut-specific IgE, IgG, and $IgG_4$ increased by approximately 3 months, and then the IgE declined by 18 months. IgG began to decrease by the end of the study, whereas $IgG_4$ remained elevated. Increased levels of specific $IgG_4$ with or without decreased IgE have been associated with successful venom immunotherapy,[25] lower levels of atopy in the presence of parasite infection,[26] transient rather than persistent milk allergy,[27] and the apparent protective effect of high levels of cat allergen exposure.[28,29] Previous reports have demonstrated that fractionated $IgG_4$ antibodies from serum of patients who received grass pollen immunotherapy inhibit IgE–FAB binding to B cells,[30-33] suggesting a functional role of $IgG_4$ in inhibiting IgE–FAB.

Traditional allergen-injection immunotherapy appears to act through downregulation of allergen-specific $T_H2$ responses or increased $T_H1$ responses or through the induction of Treg cells. Populations of both thymus-derived CD25$^+$ natural T cells and antigen-specific T cells become CD25$^+$, express FoxP3, secrete IL-10, and have suppressive function. IL-10$^+$ T cells are induced during venom, dust mite, birch, and grass pollen immunotherapy.[34-36] In our study, FoxP3 regulatory T cells increased after the induction of OIT and then eventually decreased. IL-10 was significantly increased over a period of 6 to 12 months, as were a number of inflammatory cytokines/chemokines, such as IL-1β, IL-5, TNF-α, and MIP-1β, and the growth factors G-CSF and GM-CSF. These changes did not reflect the typical transition toward a $T_H1$ profile that we expected. However, the early induction of regulatory T cells expressing FoxP3 and the associated increase in IL-10 indicate an immunologic change induced by OIT, with transition away from a $T_H2$-type profile that was seen with both nonspecific (ConA) and antigen-specific (peanut) stimulation over time.

Our microarray data demonstrating downregulation of genes in several apoptosis pathways in patient T cells after 6 months of OIT are intriguing and may reflect involvement of programmed cell death in peanut OIT. However, it is unclear from these results whether the observed changes in total peripheral blood T-cell transcription patterns include altered apoptosis of antigen-specific T cells. To help clarify this point, studies are underway to compare transcript patterns before and after OIT in peanut-specific T cells isolated by using MHC class II/Ara h 2 peptide tetramers. The lack of treatment-related changes in expression of Treg-specific, $T_H1$-specific, or $T_H2$-specific genes by microarray versus by protein assays likely reflects the small number of FoxP3-producing cells and low cytokine transcription levels in unstimulated CD3$^+$ T cells analyzed in microarrays.

To our knowledge, no other oligonucleotide microarray analyses of patient T-cell transcription patterns pretreatment and posttreatment of food allergy have been reported. In 1 microarray study of PBMC transcripts in 8 subjects with allergic rhinitis, several apoptosis-related genes were underexpressed compared with control PBMCs before allergen immunotherapy.[37] A small number of studies have noted increased *in vitro* apoptosis of stimulated peripheral blood $T_H2$ cells after standard allergen immunotherapy in subjects with either grass pollen allergy[38,39] or dust mite–sensitive asthma.[40] We plan similar flow-cytometric analyses of apoptosis in patient T cells after *in vitro* stimulation with peanut antigen.

Taken together, our results suggest that OIT induces a progression toward tolerance starting with desensitization at approximately 3 months. During this time, the threshold of antigen needed to induce an allergic response changes drastically, as reflected by diminished reaction to SPTs and activation of basophils. Subsequent immunologic changes over a period of 6 to 12 months reflect a proinflammatory, rather than $T_H2$, profile.

In our study, results of titrated SPTs; levels of allergen-specific IgE, IgG, and $IgG_4$ over time; and FAB data are similar to those reported from studies of traditional subcutaneous immunotherapy.[25,30-36] Our cytokine data, with a significant increase in IL-10 and a number of inflammatory cytokines/chemokines, are not reflective of the typical transition toward a $T_H1$ profile. The increase in IL-10 could support an initial increase in Treg cells, leading to tolerance, but the overall increase in the inflammatory cytokines/chemokines is not really suggestive of this expected change. The inflammatory response may result from the oral versus subcutaneous route of exposure, although exactly how is unclear. No similar studies comparing OIT and traditional subcutaneous allergy immunotherapy have been performed that might provide a context for our basophil and microarray data.

Clinical desensitization, which we defined as raising the threshold of food antigen needed to cause allergic symptoms, can provide an improved margin of safety in case of accidental food ingestion. This is an important therapeutic benefit to patients and their families. Blind, placebo-controlled studies with peanut OIT are underway now, as are studies to determine the ability of OIT to induce long-term clinical tolerance after discontinuing OIT.

We acknowledge discussions about this project with the late Larry Katz, PhD (formerly J. B. Duke Professor of Neurobiology and Investigator, Howard Hughes Medical Institute).

**Key messages**

- **Peanut OIT resulted in clinical desensitization for the vast majority (27/29) of children with peanut allergy who completed more than 8 months of therapy.**
- **Evaluation of immunologic changes throughout peanut OIT suggests that desensitization develops by 6 months and is followed by the downregulation of the $T_H2$ response to peanut. By 6 months, diminished reaction to SPTs and activation of basophils occurred. Over 6 to 12 months, secretion of IL-10, IL-5, IFN-γ, and TNF-α from PBMCs increased. Peanut-specific FoxP3 T cells increased until 12 months and then decreased thereafter. By 12 to 18 months, peanut-specific IgE decreased, whereas $IgG_4$ increased.**
- **During peanut OIT, T-cell microarrays showed downregulation of genes in apoptotic pathways. This finding is novel and may provide insight into the mechanism of oral immunotherapy.**

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**TABLE E1.** T cell Microarray Data

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 207978_s_at | -2.878692667 | 8013 | NR4A3 | nuclear receptor subfamily 4, group A, member 3 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement | 3700 // transcription factor activity // inferred from electronic annotation /// 3707 // steroid hormone receptor activity // inferred from electronic annotation /// 3707 // steroid hormone receptor activity // traceable author statement /// 4879 // ligand-dependent nuclear receptor activity // inferred from electronic annotation /// 4887 // thyroid hormone receptor activity // traceable author statement /// 5488 // binding // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 3677 // DNA binding // non-traceable author statement |
| 227613_at | -2.356654833 | 55422 | ZNF331 | zinc finger protein 331 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // non-traceable author statement /// 8270 // zinc ion binding // non-traceable author statement /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 207630_s_at | -2.1808985 | 1390 | CREM | cAMP responsive element modulator | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from direct assay /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 7165 // signal transduction // traceable author statement | 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5634 // nucleus // traceable author statement | 3700 // transcription factor activity // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8140 // cAMP response element binding protein binding // non-traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3677 // DNA binding // non-traceable author statement |
| 218880_at | -2.1591505 | 2355 | FOSL2 | FOS-like antigen 2 | 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 8219 // cell death // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 228284_at | -2.053828833 | 7088 | TLE1 | Transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) | 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7222 // frizzled signaling pathway // inferred from electronic annotation /// 7275 // development // traceable author statement /// 9887 // organ morphogenesis // traceable author statement /// 16481 // negative regulation of transcription // inferred from direct assay /// 30178 // negative regulation of Wnt receptor signaling pathway // non-traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 16055 // Wnt receptor signaling pathway // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation | 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 8134 // transcription factor binding // inferred from direct assay /// 5515 // protein binding // inferred from physical interaction |
| 204141_at | -1.975228333 | 7280 | TUBB2A | tubulin, beta 2A | 7018 // microtubule-based movement // inferred from electronic annotation /// 51258 // protein polymerization // inferred from electronic annotation | 5737 // cytoplasm // inferred from electronic annotation /// 5856 // cytoskeleton // not recorded /// 5874 // microtubule // inferred from electronic annotation /// 43234 // protein complex // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // inferred from electronic annotation /// 5198 // structural molecule activity // inferred from electronic annotation /// 5200 // structural constituent of cytoskeleton // not recorded /// 5525 // GTP binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 211423_s_at | -1.895904833 | 6309 | SC5DL | sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like | 6629 // lipid metabolism // traceable author statement /// 8152 // metabolism // inferred from electronic annotation /// 16126 // sterol biosynthesis // inferred from electronic annotation /// 6694 // steroid biosynthesis // inferred from electronic annotation /// 8610 // lipid biosynthesis // inferred from electronic annotation | 5783 // endoplasmic reticulum // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | 248 // C-5 sterol desaturase activity // traceable author statement /// 3824 // catalytic activity // inferred from electronic annotation /// 5506 // iron ion binding // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation |
| 224836_at | -1.8171125 | 58476 | TP53INP2 | tumor protein p53 inducible nuclear protein 2 | — | 5634 // nucleus // inferred from electronic annotation | — |
| 200730_s_at | -1.794823667 | 7803 | PTP4A1 | protein tyrosine phosphatase type IVA, member 1 | 6470 // protein amino acid dephosphorylation // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation | 5783 // endoplasmic reticulum // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation | 4725 // protein tyrosine phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation |
| 206648_at | -1.789139 | 51276 | ZNF571 | zinc finger protein 571 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |

*(Continued)*

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 216236_s_at | -1.787462167 | 6515 | SLC2A3 | solute carrier family 2 (facilitated glucose transporter), member 3 | 5975 // carbohydrate metabolism // non-traceable author statement /// 8643 // carbohydrate transport // inferred from electronic annotation /// 15758 // glucose transport // traceable author statement /// 6810 // transport // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7283 // spermatogenesis // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation | 5624 // membrane fraction // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 16021 // integral to membrane // not recorded | 5215 // transporter activity // inferred from electronic annotation /// 5351 // sugar porter activity // inferred from electronic annotation /// 5355 // glucose transporter activity // inferred from electronic annotation /// 5355 // glucose transporter activity // traceable author statement |
| 210837_s_at | -1.738381167 | 5144 | PDE4D | Phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) | 7165 // signal transduction // inferred from electronic annotation | 5625 // soluble fraction // traceable author statement /// 5626 // insoluble fraction // traceable author statement | 4114 // 3',5'-cyclic-nucleotide phosphodiesterase activity // non-traceable author statement /// 4115 // 3',5'-cyclic-AMP phosphodiesterase activity // traceable author statement /// 16787 // hydrolase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4114 // 3',5'-cyclic-nucleotide phosphodiesterase activity // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation |
| 227029_at | -1.737881333 | 283635 | C14orf24 | chromosome 14 open reading frame 24 | — | — | 3998 // acylphosphatase activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 202464_s_at | -1.734775833 | 5209 | PFKFB3 | 6-phosphofructo-2-kinase/ fructose-2,6-biphosphatase 3 | 6003 // fructose 2,6-bisphosphate metabolism // inferred from electronic annotation /// 6003 // fructose 2,6-bisphosphate metabolism // non-traceable author statement /// 8152 // metabolism // inferred from electronic annotation | — | 166 // nucleotide binding // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation /// 3873 // 6-phosphofructo-2-kinase activity // inferred from electronic annotation /// 3873 // 6-phosphofructo-2-kinase activity // non-traceable author statement /// 4331 // fructose-2,6-bisphosphate 2-phosphatase activity // inferred from electronic annotation /// 4331 // fructose-2,6-bisphosphate 2-phosphatase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 42802 // identical protein binding // inferred from physical interaction |
| 221140_s_at | -1.718265667 | 29933 | GPR132 | G protein-coupled receptor 132 | 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation | 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 211302_s_at | -1.6801025 | 5142 | PDE4B | phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) | 7165 // signal transduction // inferred from electronic annotation | 5625 // soluble fraction // traceable author statement /// 5626 // insoluble fraction // traceable author statement | 3824 // catalytic activity // inferred from electronic annotation /// 4114 // 3',5'-cyclic-nucleotide phosphodiesterase activity // inferred from electronic annotation /// 4115 // 3',5'-cyclic-AMP phosphodiesterase activity // traceable author statement /// 16787 // hydrolase activity // inferred from electronic annotation |
| 221704_s_at | -1.601305 | 79720 | VPS37B | vacuolar protein sorting 37 homolog B (S. cerevisiae) /// vacuolar protein sorting 37 homolog B (S. cerevisiae) | — | — | — |
| 213452_at | -1.599954833 | 7738 | ZNF184 | zinc finger protein 184 | 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement | 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3677 // DNA binding // non-traceable author statement /// 8270 // zinc ion binding // non-traceable author statement |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 241985_at | -1.595948167 | 133746 | JMY | junction-mediating and regulatory protein | 6357 // regulation of transcription from RNA polymerase II promoter // inferred from sequence or structural similarity /// 6917 // induction of apoptosis // inferred from sequence or structural similarity /// 7050 // cell cycle arrest // inferred from sequence or structural similarity /// 43620 // regulation of transcription in response to stress // inferred from sequence or structural similarity /// 51091 // positive regulation of transcription factor activity // inferred from sequence or structural similarity /// 43065 // positive regulation of apoptosis // inferred from sequence or structural similarity | 5634 // nucleus // inferred from sequence or structural similarity | 3713 // transcription coactivator activity // inferred from sequence or structural similarity /// 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from sequence or structural similarity |
| 216248_s_at | -1.584516667 | 4929 | NR4A2 | nuclear receptor subfamily 4, group A, member 2 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7165 // signal transduction // non-traceable author statement /// 19735 // antimicrobial humoral response (sensu Vertebrata) // traceable author statement | 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // traceable author statement | 3700 // transcription factor activity // inferred from electronic annotation /// 3707 // steroid hormone receptor activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4879 // ligand-dependent nuclear receptor activity // inferred from electronic annotation /// 4879 // ligand-dependent nuclear receptor activity // traceable author statement |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 203574_at | -1.580138667 | 4783 | NFIL3 | nuclear factor, interleukin 3 regulated | 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // traceable author statement /// 6955 // immune response // traceable author statement | 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // traceable author statement /// 3714 // transcription corepressor activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 3677 // DNA binding // traceable author statement |
| 216350_s_at | -1.567034667 | 7556 | ZNF10 | zinc finger protein 10 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |
| 208868_s_at | -1.533629833 | 23710 | GABARAPL1 | GABA(A) receptor-associated protein like 1 | 6605 // protein targeting // inferred from sequence or structural similarity /// 7268 // synaptic transmission // inferred from sequence or structural similarity | 5776 // autophagic vacuole // inferred from direct assay /// 5874 // microtubule // inferred from electronic annotation /// 5886 // plasma membrane // inferred from sequence or structural similarity | 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from sequence or structural similarity /// 48487 // beta-tubulin binding // inferred from sequence or structural similarity /// 50811 // GABA receptor binding // inferred from sequence or structural similarity |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 1556499_s_at | -1.521649667 | 1277 | COL1A1 | collagen, type I, alpha 1 | 1501 // skeletal development // traceable author statement /// 6817 // phosphate transport // inferred from electronic annotation /// 7605 // sensory perception of sound // inferred from electronic annotation /// 8544 // epidermis development // traceable author statement | 5581 // collagen // inferred from electronic annotation /// 5584 // collagen type I // not recorded /// 5737 // cytoplasm // inferred from electronic annotation /// 5578 // extracellular matrix (sensu Metazoa) // inferred from electronic annotation | 5201 // extracellular matrix structural constituent // inferred from electronic annotation /// 8147 // structural constituent of bone // not recorded /// 5198 // structural molecule activity // inferred from electronic annotation |
| 1555167_s_at | -1.513607 | 10135 | PBEF1 | pre-B-cell colony enhancing factor 1 | 7165 // signal transduction // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement /// 19363 // pyridine nucleotide biosynthesis // inferred from electronic annotation | — | 4516 // nicotinate phosphoribosyltransferase activity // inferred from electronic annotation /// 5125 // cytokine activity // traceable author statement /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 47280 // nicotinamide phosphoribosyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation |
| 206036_s_at | -1.499682 | 5966 | REL | v-rel reticuloendotheliosis viral oncogene homolog (avian) | 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // not recorded /// 43123 // positive regulation of I-kappaB kinase/ NF-kappaB cascade // inferred from expression pattern /// 6350 // transcription // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // non-traceable author statement /// 4871 // signal transducer activity // inferred from expression pattern /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 222846_at | -1.454860833 | 51762 | RAB8B | RAB8B, member RAS oncogene family | 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 15031 // protein transport // non-traceable author statement /// 15031 // protein transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 8134 // transcription factor binding // inferred from electronic annotation |
| 1553267_a_at | -1.421095833 | 246175 | CNOT6L | CCR4-NOT transcription complex, subunit 6-like | — | — | — |
| 218273_s_at | -1.3857885 | 54704 | PPM2C | protein phosphatase 2C, magnesium-dependent, catalytic subunit | 16311 // dephosphorylation // inferred from sequence or structural similarity /// 6470 // protein amino acid dephosphorylation // inferred from electronic annotation | 5739 // mitochondrion // inferred from sequence or structural similarity /// 8287 // protein serine/threonine phosphatase complex // inferred from electronic annotation /// 5739 // mitochondrion // inferred from electronic annotation | 287 // magnesium ion binding // inferred from sequence or structural similarity /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 3824 // catalytic activity // inferred from electronic annotation /// 4722 // protein serine/threonine phosphatase activity // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation /// 4741 // [pyruvate dehydrogenase (lipoamide)] phosphatase activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 224978_s_at | -1.378553 | 57602 | USP36 | ubiquitin specific peptidase 36 | 6511 // ubiquitin-dependent protein catabolism // inferred from electronic annotation /// 6512 // ubiquitin cycle // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4221 // ubiquitin thiolesterase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation |
| 1558143_a_at | -1.377738167 | 10018 | BCL2L11 | BCL2-like 11 (apoptosis facilitator) | 6915 // apoptosis // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 43065 // positive regulation of apoptosis // inferred from electronic annotation | 5624 // membrane fraction // traceable author statement /// 16020 // membrane // inferred from electronic annotation | 5515 // protein binding // inferred from physical interaction |
| 201340_s_at | -1.371434333 | 8507 | ENC1 | ectodermal-neural cortex (with BTB-like domain) | 7275 // development // traceable author statement /// 7399 // nervous system development // traceable author statement /// 7275 // development // inferred from electronic annotation | 5634 // nucleus // traceable author statement /// 5856 // cytoskeleton // inferred from electronic annotation | 3779 // actin binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation |
| 219312_s_at | -1.365253167 | 65986 | ZBTB10 | zinc finger and BTB domain containing 10 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 209694_at | -1.358417167 | 5805 | PTS | 6-pyruvoyltetrahydropterin synthase | 6520 // amino acid metabolism // traceable author statement /// 6559 // L-phenylalanine catabolism // inferred from electronic annotation /// 6729 // tetrahydrobiopterin biosynthesis // traceable author statement /// 7417 // central nervous system development // traceable author statement /// 6729 // tetrahydrobiopterin biosynthesis // inferred from electronic annotation | — | 3874 // 6-pyruvoyltetrahydropterin synthase activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 16829 // lyase activity // inferred from electronic annotation /// 42802 // identical protein binding // inferred from physical interaction /// 46872 // metal ion binding // inferred from electronic annotation /// 3874 // 6-pyruvoyltetrahydropterin synthase activity // inferred from electronic annotation |
| 225539_at | -1.347026 | 49854 | ZNF295 | zinc finger protein 295 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |
| 202684_s_at | -1.341559167 | 8731 | RNMT | RNA (guanine-7-) methyltransferase | 6370 // mRNA capping // inferred from electronic annotation /// 6370 // mRNA capping // traceable author statement | 5634 // nucleus // traceable author statement | 3723 // RNA binding // traceable author statement /// 4482 // mRNA (guanine-N7-)-methyltransferase activity // traceable author statement /// 8168 // methyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 210001_s_at | -1.340937 | 8651 | SOCS1 | suppressor of cytokine signaling 1 | 1558 // regulation of cell growth // inferred from electronic annotation /// 1932 // regulation of protein amino acid phosphorylation // inferred from sequence or structural similarity /// 6512 // ubiquitin cycle // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7259 // JAK-STAT cascade // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // inferred from sequence or structural similarity /// 42518 // negative regulation of tyrosine phosphorylation of Stat3 protein // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // non-traceable author statement /// 46627 // negative regulation of insulin receptor signaling pathway // inferred from sequence or structural similarity /// 9968 // negative regulation of signal transduction // inferred from el | 5737 // cytoplasm // traceable author statement | 4860 // protein kinase inhibitor activity // traceable author statement /// 5159 // insulin-like growth factor receptor binding // inferred from physical interaction /// 19901 // protein kinase binding // inferred from physical interaction /// 19210 // kinase inhibitor activity // inferred from sequence or structural similarity |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 223982_s_at | -1.339257833 | 50640 | PNPLA8 | patatin-like phospholipase domain containing 8 | 6631 // fatty acid metabolism // inferred from sequence or structural similarity /// 6631 // fatty acid metabolism // inferred from direct assay /// 6629 // lipid metabolism // inferred from electronic annotation | 5622 // intracellular // inferred from sequence or structural similarity /// 5624 // membrane fraction // inferred from sequence or structural similarity /// 5778 // peroxisomal membrane // inferred from sequence or structural similarity /// 5622 // intra | 5524 // ATP binding // inferred from sequence or structural similarity /// 47499 // calcium-independent phospholipase A2 activity // inferred from sequence or structural similarity /// 47499 // calcium-independent phospholipase A2 activity // inferred from direct assay /// 5488 // binding // inferred from electronic annotation /// 5524 // ATP binding // non-traceable author statement |
| 228536_at | -1.328323 | 90826 | LOC90826 | hypothetical protein BC004337 | — | — | 8168 // methyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation |
| 208881_x_at | -1.326290667 | 3422 | IDI1 | isopentenyl-diphosphate delta isomerase 1 | 6695 // cholesterol biosynthesis // inferred from electronic annotation /// 8299 // isoprenoid biosynthesis // traceable author statement /// 16117 // carotenoid biosynthesis // inferred from electronic annotation /// 6694 // steroid biosynthesis // inferred from electronic annotation /// 8299 // isoprenoid biosynthesis // inferred from electronic annotation /// 8610 // lipid biosynthesis // inferred from electronic annotation /// 16126 // sterol biosynthesis // inferred from electronic annotation | 5777 // peroxisome // traceable author statement /// 5777 // peroxisome // inferred from electronic annotation | 287 // magnesium ion binding // inferred from electronic annotation /// 4452 // isopentenyl-diphosphate delta-isomerase activity // traceable author statement /// 16853 // isomerase activity // inferred from electronic annotation /// 4452 // isopentenyl-diphosphate delta-isomerase activity // inferred from electronic annotation |
| 213138_at | -1.325532333 | 10865 | ARID5A | AT rich interactive domain 5A (MRF1-like) | 45892 // negative regulation of transcription, DNA-dependent // traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // Unknown | 3677 // DNA binding // inferred from electronic annotation /// 3677 // DNA binding // traceable author statement /// 16564 // transcriptional repressor activity // traceable author statement |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 219015_s_at | -1.324439667 | 55849 | GLT28D1 | glycosyltransferase 28 domain containing 1 | 5975 // carbohydrate metabolism // inferred from electronic annotation /// 30259 // lipid glycosylation // inferred from electronic annotation | — | 16740 // transferase activity // inferred from electronic annotation /// 16758 // transferase activity, transferring hexosyl groups // inferred from electronic annotation /// 30246 // carbohydrate binding // inferred from electronic annotation |
| 218013_x_at | -1.301145167 | 51164 | DCTN4 | dynactin 4 (p62) | — | 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5813 // centrosome // traceable author statement /// 5856 // cytoskeleton // inferred from electronic annotation /// 5869 // dynactin complex // not reco | — |
| 217127_at | -1.297697167 | 1491 | CTH | cystathionase (cystathionine gamma-lyase) | 8652 // amino acid biosynthesis // inferred from electronic annotation /// 19344 // cysteine biosynthesis // inferred from electronic annotation /// 6520 // amino acid metabolism // inferred from electronic annotation /// 6534 // cysteine metabolism // traceable author statement | — | 4123 // cystathionine gamma-lyase activity // inferred from electronic annotation /// 16829 // lyase activity // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 202932_at | -1.2854945 | 7525 | YES1 | v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 | 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 6464 // protein modification // traceable author statement | — | 166 // nucleotide binding // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 224215_s_at | -1.2774495 | 28514 | DLL1 | delta-like 1 (Drosophila) | 1701 // embryonic development (sensu Mammalia) // inferred from sequence or structural similarity /// 1709 // cell fate determination // non-traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 7219 // Notch signaling pathway // non-traceable author statement /// 7399 // nervous system development // inferred from sequence or structural similarity /// 9887 // organ morphogenesis // inferred from sequence or structural similarity /// 9912 // auditory receptor cell fate commitment // inferred from sequence or structural similarity /// 30097 // hemopoiesis // non-traceable author statement /// 30154 // cell differentiation // traceable author statement /// 30155 // regulation of cell adhesion // traceable author statement /// 42472 // inner ear morphogenesis // inferred from sequence or structural similarity /// 42475 // odontogenesis (sensu Vertebrata) // inferred from sequence or structural similarity /// 7219 // Notch signaling pathway // inferred from electroni | 5576 // extracellular region // non-traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electr | 5112 // Notch binding // inferred from physical interaction /// 5509 // calcium ion binding // inferred from electronic annotation |
| 213668_s_at | -1.260899 | 6659 | SOX4 | SRY (sex determining region Y)-box 4 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // traceable author statement /// 3677 // DNA binding // inferred from electronic annotation |
| 1555638_a_at | -1.258578167 | 64092 | SAMSN1 | SAM domain, SH3 domain and nuclear localisation signals, 1 | — | — | 1784 // phosphotyrosine binding // inferred from direct assay |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 204087_s_at | -1.255436 | 8884 | SLC5A6 | solute carrier family 5 (sodium-dependent vitamin transporter), member 6 | 6811 // ion transport // inferred from electronic annotation /// 6814 // sodium ion transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6810 // transport // traceable author statement | 5624 // membrane fraction // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annota | 5215 // transporter activity // inferred from electronic annotation /// 8523 // sodium-dependent multivitamin transporter activity // traceable author statement /// 15293 // symporter activity // inferred from electronic annotation /// 31402 // sodium ion binding // inferred from electronic annotation |
| 204952_at | -1.252561833 | 27076 | LYPD3 | LY6/PLAUR domain containing 3 | — | 16020 // membrane // inferred from electronic annotation /// 46658 // anchored to plasma membrane // traceable author statement | 48503 // GPI anchor binding // inferred from electronic annotation |
| 204093_at | -1.229745 | 902 | CCNH | cyclin H | 79 // regulation of cyclin-dependent protein kinase activity // not recorded /// 6281 // DNA repair // not recorded /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 74 // regulation of progression through cell cycle // inferred from electronic annotation | 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | — |
| 221425_s_at | -1.226083833 | 81689 | HBLD2 | HESB like domain containing 2 /// HESB like domain containing 2 | — | 5739 // mitochondrion // inferred from electronic annotation | 5506 // iron ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 51536 // iron-sulfur cluster binding // inferred from electronic annotation |
| 221712_s_at | -1.224328167 | 54663 | WDR74 | WD repeat domain 74 /// WD repeat domain 74 | — | 5634 // nucleus // inferred from electronic annotation | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 202558_s_at | -1.2236935 | 6782 | STCH | stress 70 protein chaperone, microsome-associated, 60kDa | — | 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5792 // microsome // traceable author statement /// 5792 // microsome // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation |
| 206976_s_at | -1.222607 | 10808 | HSPH1 | heat shock 105kDa/110kDa protein 1 | 6457 // protein folding // inferred from electronic annotation /// 6986 // response to unfolded protein // traceable author statement /// 6986 // response to unfolded protein // inferred from electronic annotation | 5737 // cytoplasm // traceable author statement | 166 // nucleotide binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation |
| 204472_at | -1.218162667 | 2669 | GEM | GTP binding protein overexpressed in skeletal muscle | 6955 // immune response // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 7264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement | 16020 // membrane // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 5516 // calmodulin binding // inferred from electronic annotation /// 5525 // GTP binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5525 // GTP binding // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 215438_x_at | -1.215578833 | 2935 | GSPT1 | G1 to S phase transition 1 | 82 // G1/S transition of mitotic cell cycle // traceable author statement /// 184 // mRNA catabolism, nonsense-mediated decay // traceable author statement /// 6412 // protein biosynthesis // inferred from electronic annotation /// 82 // G1/S transition of mitotic cell cycle // inferred from sequence or structural similarity /// 184 // mRNA catabolism, nonsense-mediated decay // inferred from sequence or structural similarity | 5622 // intracellular // non-traceable author statement /// 5622 // intracellular // inferred from sequence or structural similarity | 166 // nucleotide binding // inferred from electronic annotation /// 3747 // translation release factor activity // inferred from mutant phenotype /// 3924 // GTPase activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5525 // GTP binding // inferred from electronic annotation /// 3747 // translation release factor activity // inferred from sequence or structural similarity /// 3924 // GTPase activity // inferred from sequence or structural similarity /// 5515 // protein binding // inferred from sequence or structural similarity |
| 201739_at | -1.205856667 | 6446 | SGK | serum/glucocorticoid regulated kinase | 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // traceable author statement /// 6814 // sodium ion transport // traceable author statement /// 6915 // apoptosis // inferred from electronic annotation /// 6950 // response to stress // traceable author statement | 5634 // nucleus // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation |
| 230185_at | -1.2049305 | 79725 | THAP9 | THAP domain containing 9 | — | — | 3676 // nucleic acid binding // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 218113_at | -1.204014667 | 23670 | TMEM2 | transmembrane protein 2 | — | 16021 // integral to membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement | — |
| 36711_at | -1.202160667 | 23764 | MAFF | v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // traceable author statement /// 7567 // parturition // traceable author statement | 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation |
| 219099_at | -1.180585333 | 57103 | C12orf5 | chromosome 12 open reading frame 5 | 8152 // metabolism // inferred from electronic annotation | — | 16853 // isomerase activity // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation |
| 203725_at | -1.1790535 | 1647 | GADD45A | growth arrest and DNA-damage-inducible, alpha | 79 // regulation of cyclin-dependent protein kinase activity // traceable author statement /// 6281 // DNA repair // traceable author statement /// 6915 // apoptosis // traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7050 // cell cycle arrest // traceable author statement /// 6974 // response to DNA damage stimulus // inferred from electronic annotation /// 7050 // cell cycle arrest // inferred from electronic annotation /// 74 // regulation of progression through cell cycle // traceable author statement | 5634 // nucleus // traceable author statement | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 208810_at | -1.177939167 | 10049 | DNAJB6 | DnaJ (Hsp40) homolog, subfamily B, member 6 | 6457 // protein folding // inferred from electronic annotation /// 6986 // response to unfolded protein // non-traceable author statement | — | 31072 // heat shock protein binding // inferred from electronic annotation /// 51082 // unfolded protein binding // inferred from electronic annotation |
| 207001_x_at | -1.159597833 | 1831 | TSC22D3 | TSC22 domain family, member 3 | 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement | — | 3700 // transcription factor activity // inferred from electronic annotation /// 3700 // transcription factor activity // traceable author statement |
| 225582_at | -1.156030667 | 85450 | KIAA1754 | KIAA1754 | — | — | — |
| 1555281_x_at | -1.149420667 | 25852 | ARMC8 | armadillo repeat containing 8 | 7155 // cell adhesion // inferred from electronic annotation | 5856 // cytoskeleton // inferred from electronic annotation | 5198 // structural molecule activity // inferred from electronic annotation /// 5488 // binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation |
| 219343_at | -1.145858 | 55664 | CDC37L1 | CDC37 cell division cycle 37 homolog (S. cerevisiae)-like 1 | 74 // regulation of progression through cell cycle // inferred from electronic annotation /// 51301 // cell division // inferred from electronic annotation | — | — |
| 209362_at | -1.13266 | 9412 | SURB7 | SRB7 suppressor of RNA polymerase B homolog (yeast) | 6350 // transcription // inferred from electronic annotation /// 45944 // positive regulation of transcription from RNA polymerase II promoter // inferred from direct assay /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement | 119 // mediator complex // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation /// 5665 // DNA-directed RNA polymerase II, core complex // traceable author statement | 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 3713 // transcription coactivator activity // inferred from direct assay /// 3899 // DNA-directed RNA polymerase activity // traceable author statement |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 230492_s_at | -1.120679333 | 56261 | RP5-1022P6.2 | hypothetical protein KIAA1434 | 6071 // glycerol metabolism // inferred from electronic annotation /// 5975 // carbohydrate metabolism // inferred from electronic annotation | — | 8889 // glycerophosphodiester phosphodiesterase activity // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation /// 30246 // carbohydrate binding // inferred from electronic annotation |
| 222874_s_at | -1.116975 | 2055 | CLN8 | ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) | 7399 // nervous system development // traceable author statement | 5783 // endoplasmic reticulum // traceable author statement /// 5793 // ER-Golgi intermediate compartment // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author stat | — |
| 222815_at | -1.103659667 | 51132 | RNF12 | ring finger protein 12 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 16481 // negative regulation of transcription // non-traceable author statement /// 6512 // ubiquitin cycle // inferred from electronic annotation | 17053 // transcriptional repressor complex // non-traceable author statement | 3714 // transcription corepressor activity // non-traceable author statement /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 219347_at | -1.101665833 | 55270 | NUDT15 | nudix (nucleoside diphosphate linked moiety X)-type motif 15 | — | — | 287 // magnesium ion binding // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 30145 // manganese ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 202147_s_at | -1.0975745 | 3475 | IFRD1 | interferon-related developmental regulator 1 | 7518 // myoblast cell fate determination // traceable author statement /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation | — | 5488 // binding // inferred from electronic annotation |
| 227960_s_at | -1.096905 | 81889 | FAHD1 | fumarylacetoacetate hydrolase domain containing 1 | 8152 // metabolism // inferred from electronic annotation | — | 287 // magnesium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 201830_s_at | -1.095089 | 10276 | NET1 | neuroepithelial cell transforming gene 1 | 1558 // regulation of cell growth // non-traceable author statement /// 7165 // signal transduction // traceable author statement /// 35023 // regulation of Rho protein signal transduction // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 5089 // Rho guanyl-nucleotide exchange factor activity // inferred from electronic annotation /// 5085 // guanyl-nucleotide exchange factor activity // inferred from electronic annotation /// 5085 // guanyl-nucleotide exchange factor activity // traceable author statement |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 204958_at | -1.092619667 | 1263 | PLK3 | polo-like kinase 3 (Drosophila) | 74 // regulation of progression through cell cycle // traceable author statement /// 6468 // protein amino acid phosphorylation // traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation | — | 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // traceable author statement /// 5515 // protein binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation |
| 202314_at | -1.084398667 | 1595 | CYP51A1 | cytochrome P450, family 51, subfamily A, polypeptide 1 | 6118 // electron transport // inferred from electronic annotation /// 6695 // cholesterol biosynthesis // inferred from electronic annotation /// 6694 // steroid biosynthesis // inferred from electronic annotation /// 8610 // lipid biosynthesis // inferred from electronic annotation /// 16126 // sterol biosynthesis // inferred from electronic annotation | 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | 4497 // monooxygenase activity // inferred from electronic annotation /// 5506 // iron ion binding // inferred from electronic annotation /// 8398 // sterol 14-demethylase activity // inferred from electronic annotation /// 20037 // heme binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 8398 // sterol 14-demethylase activity // not recorded |
| 225557_at | -1.081168833 | 64651 | AXUD1 | AXIN1 up-regulated 1 | 6915 // apoptosis // non-traceable author statement /// 6915 // apoptosis // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 202647_s_at | -1.068950833 | 4893 | NRAS | neuroblastoma RAS viral (v-ras) oncogene homolog | 74 // regulation of progression through cell cycle // non-traceable author statement /// 7264 // small GTPase mediated signal transduction // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // not recorded /// 5525 // GTP binding // inferred from electronic annotation |
| 235735_at | -1.066199833 | 944 | TNFSF8 | Tumor necrosis factor (ligand) superfamily, member 8 | 6917 // induction of apoptosis // traceable author statement /// 6955 // immune response // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 8283 // cell proliferation // traceable author statement | 5615 // extracellular space // inferred from electronic annotation /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electr | 5164 // tumor necrosis factor receptor binding // inferred from electronic annotation /// 5125 // cytokine activity // inferred from electronic annotation /// 5102 // receptor binding // traceable author statement |
| 222763_s_at | -1.057171667 | 55339 | WDR33 | WD repeat domain 33 | 6301 // postreplication repair // non-traceable author statement /// 6817 // phosphate transport // inferred from electronic annotation /// 7283 // spermatogenesis // non-traceable author statement | 5634 // nucleus // inferred from direct assay /// 5737 // cytoplasm // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | — |
| 228468_at | -1.046991 | 84930 | MASTL | microtubule associated serine/threonine kinase-like | 6468 // protein amino acid phosphorylation // inferred from electronic annotation | — | 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 204541_at | -1.029213833 | 23541 | SEC14L2 | SEC14-like 2 (S. cerevisiae) | 6350 // transcription // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 45540 // regulation of cholesterol biosynthesis // non-traceable author statement /// 45893 // positive regulation of transcription, DNA-dependent // non-traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5737 // cytoplasm // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 5634 // | 5386 // carrier activity // non-traceable author statement /// 5543 // phospholipid binding // non-traceable author statement /// 8431 // vitamin E binding // non-traceable author statement /// 16563 // transcriptional activator activity // non-traceable author statement /// 5215 // transporter activity // inferred from electronic annotation /// 8289 // lipid binding // inferred from electronic annotation |
| 208622_s_at | -1.027501167 | 7430 | VIL2 | villin 2 (ezrin) | 7016 // cytoskeletal anchoring // non-traceable author statement /// 8360 // regulation of cell shape // inferred from electronic annotation /// 51017 // actin filament bundle formation // inferred from direct assay | 5737 // cytoplasm // inferred from electronic annotation /// 5856 // cytoskeleton // inferred from electronic annotation /// 5884 // actin filament // inferred from direct assay /// 5902 // microvillus // non-traceable author statement /// 16020 // membra | 5198 // structural molecule activity // inferred from electronic annotation /// 5488 // binding // inferred from electronic annotation /// 8092 // cytoskeletal protein binding // inferred from electronic annotation /// 51015 // actin filament binding // inferred from direct assay /// 5515 // protein binding // inferred from physical interaction |
| 201751_at | -1.023781167 | 9929 | JOSD1 | Josephin domain containing 1 | — | — | — |
| 222408_s_at | -1.018166667 | 51646 | YPEL5 | yippee-like 5 (Drosophila) | — | — | — |
| 218276_s_at | -1.017600167 | 60485 | SAV1 | salvador homolog 1 (Drosophila) | 7165 // signal transduction // inferred from electronic annotation | — | 5515 // protein binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 201409_s_at | -1.006632833 | 5500 | PPP1CB | protein phosphatase 1, catalytic subunit, beta isoform | 5975 // carbohydrate metabolism // inferred from electronic annotation /// 5977 // glycogen metabolism // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 51301 // cell division // inferred from electronic annotation | — | 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation /// 5506 // iron ion binding // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 30145 // manganese ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 212749_s_at | -1.005041 | 25898 | RCHY1 | ring finger and CHY zinc finger domain containing 1 | 6512 // ubiquitin cycle // inferred from electronic annotation | 5737 // cytoplasm // inferred from direct assay | 5515 // protein binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 224281_s_at | -0.994716333 | 51335 | NGRN | neugrin, neurite outgrowth associated | 30182 // neuron differentiation // non-traceable author statement /// 6464 // protein modification // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement | 3677 // DNA binding // inferred from electronic annotation /// 4835 // tubulin-tyrosine ligase activity // inferred from electronic annotation |
| 1562255_at | -0.989167 | 94120 | SYTL3 | synaptotagmin-like 3 | 6886 // intracellular protein transport // inferred from electronic annotation | — | 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 17137 // Rab GTPase binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 201574_at | -0.986441833 | 2107 | ETF1 | eukaryotic translation termination factor 1 | 6412 // protein biosynthesis // inferred from electronic annotation /// 6415 // translational termination // inferred from electronic annotation | 5737 // cytoplasm // inferred from electronic annotation | 5515 // protein binding // inferred from physical interaction /// 16149 // translation release factor activity, codon specific // inferred from electronic annotation /// 43022 // ribosome binding // traceable author statement /// 3747 // translation release factor activity // traceable author statement |
| 201926_s_at | -0.985534 | 1604 | CD55 | CD55 molecule, decay accelerating factor for complement (Cromer blood group) | 6958 // complement activation, classical pathway // inferred from electronic annotation /// 45087 // innate immune response // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation | 5625 // soluble fraction // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation | 48503 // GPI anchor binding // inferred from electronic annotation |
| 223070_at | -0.985048833 | 58515 | SELK | selenoprotein K | — | — | 8430 // selenium binding // inferred from electronic annotation |
| 223454_at | -0.984813333 | 58191 | CXCL16 | chemokine (C-X-C motif) ligand 16 | 6898 // receptor mediated endocytosis // non-traceable author statement /// 6935 // chemotaxis // non-traceable author statement /// 48247 // lymphocyte chemotaxis // non-traceable author statement /// 6935 // chemotaxis // inferred from electronic annotation | 5576 // extracellular region // non-traceable author statement /// 5615 // extracellular space // inferred from electronic annotation /// 16020 // membrane // traceable author statement /// 16021 // integral to membrane // non-traceable author statement / | 5041 // low-density lipoprotein receptor activity // inferred from sequence or structural similarity /// 5044 // scavenger receptor activity // traceable author statement /// 8009 // chemokine activity // inferred from sequence or structural similarity /// 5125 // cytokine activity // inferred from electronic annotation /// 5102 // receptor binding // non-traceable author statement |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 209161_at | -0.978153333 | 9128 | PRPF4 | PRP4 pre-mRNA processing factor 4 homolog (yeast) | 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 8380 // RNA splicing // non-traceable author statement /// 6397 // mRNA processing // inferred from electronic annotation /// 8380 // RNA splicing // inferred from electronic annotation /// 6396 // RNA processing // traceable author statement /// 8380 // RNA splicing // traceable author statement | 5634 // nucleus // traceable author statement /// 5681 // spliceosome complex // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation /// 5681 // spliceosome complex // inferred from electronic annotation | 31202 // RNA splicing factor activity, transesterification mechanism // non-traceable author statement |
| 218486_at | -0.97345 | 8462 | KLF11 | Kruppel-like factor 11 | 122 // negative regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // traceable author statement /// 8285 // negative regulation of cell proliferation // traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation |
| 212644_s_at | -0.968791333 | 93487 | C14orf32 | chromosome 14 open reading frame 32 | — | — | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 200958_s_at | -0.966464167 | 6386 | SDCBP | syndecan binding protein (syntenin) | 6612 // protein targeting to membrane // non-traceable author statement /// 6930 // substrate-bound cell migration, cell extension // non-traceable author statement /// 7242 // intracellular signaling cascade // non-traceable author statement /// 7268 // synaptic transmission // non-traceable author statement /// 30036 // actin cytoskeleton organization and biogenesis // non-traceable author statement | 5634 // nucleus // non-traceable author statement /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5856 // cytoskeleton // non-traceable author statement /// 5895 // interleukin-5 receptor complex // inferred from sequence or s | 5137 // interleukin-5 receptor binding // inferred from sequence or structural similarity /// 5515 // protein binding // inferred from electronic annotation /// 8093 // cytoskeletal adaptor activity // non-traceable author statement /// 42043 // neurexin binding // inferred from sequence or structural similarity /// 45545 // syndecan binding // non-traceable author statement /// 46982 // protein heterodimerization activity // inferred from physical interaction |
| 230380_at | -0.965570833 | 83591 | THAP2 | THAP domain containing, apoptosis associated protein 2 | — | — | 3677 // DNA binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |
| 228749_at | -0.9638685 | 57683 | KIAA1571 | KIAA1571 protein | — | — | 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation |
| 218189_s_at | -0.959609 | 54187 | NANS | N-acetylneuraminic acid synthase (sialic acid synthase) | 9103 // lipopolysaccharide biosynthesis // non-traceable author statement /// 16051 // carbohydrate biosynthesis // inferred from electronic annotation | 5737 // cytoplasm // non-traceable author statement | 8781 // N-acylneuraminate cytidylyltransferase activity // non-traceable author statement /// 16740 // transferase activity // inferred from electronic annotation /// 47444 // N-acylneuraminate-9-phosphate synthase activity // inferred from electronic annotation /// 50462 // N-acetylneuraminate synthase activity // inferred from electronic annotation |
| 201858_s_at | -0.958221667 | 5552 | PRG1 | proteoglycan 1, secretory granule | — | — | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 208078_s_at | -0.956521 | 150094 | SNF1LK | SNF1-like kinase /// SNF1-like kinase | 6468 // protein amino acid phosphorylation // inferred from sequence or structural similarity /// 7049 // cell cycle // inferred from electronic annotation /// 7243 // protein kinase cascade // inferred from sequence or structural similarity /// 7346 // regulation of progression through mitotic cell cycle // inferred from sequence or structural similarity /// 45595 // regulation of cell differentiation // inferred from sequence or structural similarity /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 122 // negative regulation of transcription from RNA polymerase II promoter // traceable author statem | 5737 // cytoplasm // inferred from sequence or structural similarity /// 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from sequence or structural similarity /// 4674 // protein serine/threonine kinase activity // inferred from sequence or structural similarity /// 5524 // ATP binding // inferred from sequence or structural similarity /// 16740 // transferase activity // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kin |
| 235440_at | -0.956198333 | 144108 | SPTY2D1 | SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae) | — | — | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 217140_s_at | -0.954184333 | 7416 | VDAC1 | voltage-dependent anion channel 1 | 6820 // anion transport // traceable author statement /// 8632 // apoptotic program // traceable author statement /// 6810 // transport // inferred from electronic annotation /// 6811 // ion transport // inferred from electronic annotation /// 6820 // anion transport // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation | 5739 // mitochondrion // traceable author statement /// 5741 // mitochondrial outer membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotatio | 8308 // voltage-gated ion-selective channel activity // inferred from electronic annotation /// 15283 // apoptogenic cytochrome c release channel activity // traceable author statement /// 15482 // voltage-gated anion channel porin activity // traceable author statement /// 15288 // porin activity // inferred from electronic annotation |
| 226321_at | -0.952975833 | 116068 | LYSMD3 | LysM, putative peptidoglycan-binding, domain containing 3 | 16998 // cell wall catabolism // inferred from electronic annotation | — | 4518 // nuclease activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation |

*(Continued)*



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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 200748_s_at | -0.946176667 | 2495 | FTH1 | ferritin, heavy polypeptide 1 | 6826 // iron ion transport // inferred from electronic annotation /// 6879 // iron ion homeostasis // inferred from electronic annotation /// 6880 // intracellular sequestering of iron ion // traceable author statement /// 6955 // immune response // inferred from direct assay /// 6955 // immune response // inferred from sequence or structural similarity /// 8283 // cell proliferation // traceable author statement /// 8285 // negative regulation of cell proliferation // inferred from direct assay /// 8285 // negative regulation of cell proliferation // inferred from sequence or structural similarity /// 6879 // iron ion homeostasis // traceable author statement /// 6928 // cell motility // traceable author statement /// 30041 // actin filament polymerization // traceable author statement /// 6461 // protein complex assembly // non-traceable author statement | 5886 // plasma membrane // inferred from sequence or structural similarity /// 5886 // plasma membrane // non-traceable author statement /// 8043 // ferritin complex // traceable author statement /// 5856 // cytoskeleton // inferred from electronic annota | 4322 // ferroxidase activity // inferred from electronic annotation /// 5488 // binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 8199 // ferric iron binding // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 19900 // kinase binding // inferred from sequence or structural similarity /// 19900 // kinase binding // non-traceable author statement /// 46872 // metal ion binding // inferred from electronic annotation /// 5506 // iron ion binding // inferred from electronic annotation /// 3779 // actin binding // inferred from electronic annotation /// 5506 // iron ion binding // traceable author statement |
| 1554786_at | -0.937690667 | 57091 | C20orf32 | chromosome 20 open reading frame 32 | 7165 // signal transduction // inferred from electronic annotation | 16020 // membrane // inferred from electronic annotation | 155 // two-component sensor activity // inferred from electronic annotation |
| 202750_s_at | -0.933455333 | 24144 | TFIP11 | tuftelin interacting protein 11 | 1503 // ossification // inferred from electronic annotation /// 30154 // cell differentiation // inferred from sequence or structural similarity /// 30198 // extracellular matrix organization and biogenesis // inferred from sequence or structural similarity /// 45045 // secretory pathway // inferred from sequence or structural similarity | 5622 // intracellular // inferred from sequence or structural similarity /// 5634 // nucleus // inferred from electronic annotation /// 5622 // intracellular // inferred from electronic annotation | 3676 // nucleic acid binding // inferred from electronic annotation /// 5515 // protein binding // inferred from sequence or structural similarity |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 225768_at | -0.923958167 | 9975 | NR1D2 | nuclear receptor subfamily 1, group D, member 2 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // inferred from electronic annotation /// 3707 // steroid hormone receptor activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4879 // ligand-dependent nuclear receptor activity // inferred from electronic annotation /// 4879 // ligand-dependent nuclear receptor activity // traceable author statement |
| 219357_at | -0.923290333 | 9567 | GTPBP1 | GTP binding protein 1 | 6412 // protein biosynthesis // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement | — | 166 // nucleotide binding // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 5525 // GTP binding // traceable author statement /// 9055 // electron carrier activity // inferred from electronic annotation /// 15035 // protein disulfide oxidoreductase activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 212665_at | -0.922794667 | 25976 | TIPARP | TCDD-inducible poly(ADP-ribose) polymerase | 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 5515 // protein binding // inferred from physical interaction /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3950 // NAD+ ADP-ribosyltransferase activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 1556698_a_at | -0.917641167 | 285513 | GRIN3 | G protein-regulated inducer of neurite outgrowth 3 | — | — | — |
| 201303_at | -0.916190167 | 9775 | DDX48 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 | 6364 // rRNA processing // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation /// 8026 // ATP-dependent helicase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 4386 // helicase activity // inferred from electronic annotation |
| 226811_at | -0.912053833 | 54855 | FAM46C | family with sequence similarity 46, member C | — | — | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 208653_s_at | -0.905639833 | 8763 | CD164 | CD164 molecule, sialomucin | 6955 // immune response // traceable author statement /// 7155 // cell adhesion // inferred from direct assay /// 7157 // heterophilic cell adhesion // inferred from direct assay /// 7162 // negative regulation of cell adhesion // non-traceable author statement /// 7165 // signal transduction // traceable author statement /// 7275 // development // traceable author statement /// 8285 // negative regulation of cell proliferation // non-traceable author statement /// 8285 // negative regulation of cell proliferation // traceable author statement /// 30097 // hemopoiesis // non-traceable author statement /// 7155 // cell adhesion // traceable author statement | 5624 // membrane fraction // not recorded /// 5625 // soluble fraction // not recorded /// 5768 // endosome // non-traceable author statement /// 5886 // plasma membrane // inferred from direct assay /// 5887 // integral to plasma membrane // non-traceabl | — |
| 235615_at | -0.900246833 | 5229 | PGGT1B | Protein geranylgeranyltransferase type I, beta subunit | 18348 // protein amino acid geranylgeranylation // traceable author statement | 5953 // CAAX-protein geranylgeranyltransferase complex // traceable author statement | 4659 // prenyltransferase activity // inferred from electronic annotation /// 4662 // CAAX-protein geranylgeranyltransferase activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation |
| 218033_s_at | -0.899702167 | 8303 | SNN | stannin | 6950 // response to stress // traceable author statement /// 9628 // response to abiotic stimulus // traceable author statement | 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 203936_s_at | -0.8976305 | 4318 | MMP9 | matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) | 270 // peptidoglycan metabolism // inferred from electronic annotation /// 6508 // proteolysis // inferred from direct assay /// 30225 // macrophage differentiation // traceable author statement /// 30574 // collagen catabolism // inferred from electronic annotation /// 6508 // proteolysis // inferred from electronic annotation | 5578 // extracellular matrix (sensu Metazoa) // inferred from electronic annotation /// 5615 // extracellular space // inferred from direct assay | 4229 // gelatinase B activity // inferred from direct assay /// 5509 // calcium ion binding // inferred from electronic annotation /// 5518 // collagen binding // traceable author statement /// 8133 // collagenase activity // inferred from direct assay /// 8270 // zinc ion binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 4222 // metalloendopeptidase activity // inferred from electronic annotation /// 4229 // gelatinase B activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 227368_at | -0.890388833 | 55122 | C6orf166 | Chromosome 6 open reading frame 166 | — | — | — |
| 230129_at | -0.886411833 | 118672 | C10orf89 | chromosome 10 open reading frame 89 | — | — | 287 // magnesium ion binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation |
| 219253_at | -0.886326667 | 79134 | FAM11B | family with sequence similarity 11, member B | — | 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 209211_at | -0.8841455 | 688 | KLF5 | Kruppel-like factor 5 (intestinal) | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // inferred from electronic annotation /// 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |
| 218177_at | -0.871392 | 57132 | CHMP1B | chromatin modifying protein 1B | 15031 // protein transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation | — | — |
| 205281_s_at | -0.870478167 | 5277 | PIGA | phosphatidylinositol glycan anchor biosynthesis, class A (paroxysmal nocturnal hemoglobinuria) /// phosphatidylinositol glycan anchor biosynthesis, class A (paroxysmal nocturnal hemoglobinuria) | 6506 // GPI anchor biosynthesis // traceable author statement /// 9058 // biosynthesis // inferred from electronic annotation /// 9893 // positive regulation of metabolism // traceable author statement /// 6506 // GPI anchor biosynthesis // inferred from electronic annotation | 506 // glycosylphosphatidylinositol-N-acetylglucosaminyltransferase (GPI-GnT) complex // inferred from direct assay /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5789 // endoplasmic reticulum membrane // inferred from direct | 5515 // protein binding // inferred from physical interaction /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 17176 // phosphatidylinositol N-acetylglucosaminyltransferase activity // traceable author statement /// 16740 // transferase activity // inferred from electronic annotation /// 17176 // phosphatidylinositol N-acetylglucosaminyltransferase activity // inferred from electronic annotation |
| 220285_at | -0.86751 | 51104 | C9orf77 | chromosome 9 open reading frame 77 | — | — | — |
| 235230_at | -0.865278333 | 257068 | PLCXD2 | Phosphatidylinositol-specific phospholipase C, X domain containing 2 | 7165 // signal transduction // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation | — | 4629 // phospholipase C activity // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 242832_at | -0.864626 | 5187 | PER1 | period homolog 1 (Drosophila) | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 9649 // entrainment of circadian clock // traceable author statement /// 16481 // negative regulation of transcription // inferred from sequence or structural similarity /// 48511 // rhythmic process // inferred from electronic annotation /// 7623 // circadian rhythm // traceable author statement | 5634 // nucleus // inferred from electronic annotation | 3676 // nucleic acid binding // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 5515 // protein binding // inferred from sequence or structural similarity |
| 204071_s_at | -0.859363167 | 10210 | TOPORS | topoisomerase I binding, arginine/serine-rich | 6512 // ubiquitin cycle // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 16874 // ligase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 200673_at | -0.856153333 | 9741 | LAPTM4A | lysosomal-associated protein transmembrane 4 alpha | 6810 // transport // inferred from electronic annotation | 5794 // Golgi apparatus // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | — |
| 202988_s_at | -0.852217 | 5996 | RGS1 | regulator of G-protein signalling 1 | 6955 // immune response // traceable author statement /// 7165 // signal transduction // non-traceable author statement /// 7193 // G-protein signaling, adenylate cyclase inhibiting pathway // traceable author statement /// 9968 // negative regulation of signal transduction // inferred from electronic annotation | 5886 // plasma membrane // traceable author statement | 4871 // signal transducer activity // inferred from electronic annotation /// 5096 // GTPase activator activity // traceable author statement /// 5516 // calmodulin binding // traceable author statement |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 225140_at | -0.849931333 | 51274 | KLF3 | Kruppel-like factor 3 (basic) | 122 // negative regulation of transcription from RNA polymerase II promoter // not recorded /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7275 // development // traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // non-traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation |
| 226370_at | -0.842846333 | 80311 | KLHL15 | kelch-like 15 (Drosophila) | — | — | 5515 // protein binding // inferred from electronic annotation |
| 1564027_a_at | -0.8388195 | 285966 | FLJ40722 | hypothetical protein FLJ40722 | — | — | — |
| 207735_at | -0.838808167 | 54941 | RNF125 | ring finger protein 125 | 6512 // ubiquitin cycle // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation | 3676 // nucleic acid binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 16874 // ligase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 201181_at | -0.8354975 | 2773 | GNAI3 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 | 6810 // transport // non-traceable author statement /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7194 // negative regulation of adenylate cyclase activity // traceable author statement | — | 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 19001 // guanyl nucleotide binding // inferred from electronic annotation |
| 227337_at | -0.832628667 | 353322 | ANKRD37 | ankyrin repeat domain 37 | — | 5634 // nucleus // inferred from electronic annotation | — |
| 220368_s_at | -0.827011833 | 55671 | KIAA2010 | KIAA2010 | — | — | 5488 // binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 223209_s_at | -0.8263325 | 55829 | SELS | selenoprotein S | 6980 // redox signal response // inferred from direct assay /// 9749 // response to glucose stimulus // inferred from expression pattern /// 30433 // ER-associated protein catabolism // inferred from direct assay /// 30503 // regulation of cell redox homeostasis // inferred from direct assay /// 30968 // unfolded protein response // inferred from direct assay /// 30970 // retrograde protein transport, ER to cytosol // inferred from direct assay /// 45184 // establishment of protein localization // traceable author statement /// 6886 // intracellular protein transport // inferred from electronic annotation /// 6412 // protein biosynthesis // inferred from electronic annotation | 5783 // endoplasmic reticulum // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 30176 // integral to endoplasmic reticulum membr | 4872 // receptor activity // non-traceable author statement /// 8430 // selenium binding // inferred from electronic annotation /// 16209 // antioxidant activity // inferred from direct assay /// 19899 // enzyme binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 3735 // structural constituent of ribosome // inferred from electronic annotation |
| 225237_s_at | -0.824858833 | 124540 | MSI2 | musashi homolog 2 (Drosophila) | — | — | 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 207445_s_at | -0.820649 | 10803 | CCR9 | chemokine (C-C motif) receptor 9 | 6935 // chemotaxis // traceable author statement /// 6968 // cellular defense response // traceable author statement /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 7204 // elevation of cytosolic calcium ion concentration // traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation | 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotati | 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 16493 // C-C chemokine receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation |
| 212430_at | -0.819566 | 55544 | RBM38 | RNA binding motif protein 38 /// RNA binding motif protein 38 | — | — | 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation |
| 204335_at | -0.8186395 | 55702 | CCDC94 | coiled-coil domain containing 94 | — | — | — |
| 1555274_a_at | -0.805795 | 85465 | SELI | selenoprotein I | 8654 // phospholipid biosynthesis // inferred from electronic annotation | 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | 8430 // selenium binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation |
| 208093_s_at | -0.804331833 | 81565 | NDEL1 | nudE nuclear distribution gene E homolog like 1 (A. nidulans) /// nudE nuclear distribution gene E homolog like 1 (A. nidulans) | 6810 // transport // inferred from electronic annotation /// 7399 // nervous system development // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation | 5856 // cytoskeleton // inferred from electronic annotation /// 5874 // microtubule // inferred from electronic annotation | 5515 // protein binding // inferred from physical interaction |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 208581_x_at | -0.8033455 | 4501 | MT1X | metallothionein 1X | 10038 // response to metal ion // traceable author statement /// 6118 // electron transport // inferred from electronic annotation | — | 5507 // copper ion binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46870 // cadmium ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 46872 // metal ion binding // traceable author statement /// 5506 // iron ion binding // inferred from electronic annotation /// 9055 // electron carrier activity // inferred from electronic annotation |
| 226328_at | -0.801374333 | 83855 | KLF16 | Kruppel-like factor 16 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |
| 225282_at | -0.800108 | 64744 | SMAP1L | stromal membrane-associated protein 1-like | 43087 // regulation of GTPase activity // inferred from electronic annotation | — | 5096 // GTPase activator activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 202236_s_at | -0.795418167 | 6566 | SLC16A1 | solute carrier family 16, member 1 (monocarboxylic acid transporter 1) | 6810 // transport // inferred from electronic annotation /// 15711 // organic anion transport // inferred from electronic annotation /// 15728 // mevalonate transport // traceable author statement /// 15718 // monocarboxylic acid transport // traceable author statement | 5624 // membrane fraction // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement | 5215 // transporter activity // inferred from electronic annotation /// 15130 // mevalonate transporter activity // traceable author statement /// 15293 // symporter activity // inferred from electronic annotation /// 15355 // monocarboxylate porter activity // inferred from electronic annotation /// 8028 // monocarboxylic acid transporter activity // traceable author statement |
| 221596_s_at | -0.793717167 | 84060 | DKFZP564O0523 | hypothetical protein DKFZp564O0523 | — | — | 166 // nucleotide binding // inferred from electronic annotation |
| 224206_x_at | -0.791450833 | 55892 | MYNN | myoneurin | 6351 // transcription, DNA-dependent // traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 5515 // protein binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3700 // transcription factor activity // traceable author statement /// 8270 // zinc ion binding // traceable author statement |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 212185_x_at | -0.790314 | 4502 | MT2A | metallothionein 2A | 6878 // copper ion homeostasis // traceable author statement | 5737 // cytoplasm // non-traceable author statement | 5507 // copper ion binding // not recorded /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 5507 // copper ion binding // inferred from electronic annotation /// 46870 // cadmium ion binding // inferred from electronic annotation /// 5507 // copper ion binding // non-traceable author statement /// 8270 // zinc ion binding // non-traceable author statement /// 46870 // cadmium ion binding // non-traceable author statement |
| 225493_at | -0.789475333 | 144438 | LOC144438 | hypothetical protein LOC144438 | — | — | — |
| 218193_s_at | -0.789208167 | 51026 | GOLT1B | golgi transport 1 homolog B (S. cerevisiae) | 15031 // protein transport // inferred from electronic annotation /// 16192 // vesicle-mediated transport // inferred from electronic annotation /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from mutant phenotype /// 6810 // transport // inferred from electronic annotation | 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | 4871 // signal transducer activity // inferred from mutant phenotype |
| 221020_s_at | -0.774771333 | 81034 | SLC25A32 | solute carrier family 25, member 32 /// solute carrier family 25, member 32 | 6810 // transport // inferred from electronic annotation /// 15884 // folic acid transport // non-traceable author statement | 5739 // mitochondrion // inferred from electronic annotation /// 5743 // mitochondrial inner membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electro | 5215 // transporter activity // inferred from electronic annotation /// 5488 // binding // inferred from electronic annotation /// 8517 // folic acid transporter activity // non-traceable author statement |
| 225607_at | -0.771569167 | 124808 | CCDC43 | coiled-coil domain containing 43 | — | — | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 208290_s_at | -0.7705815 | 1983 | EIF5 | eukaryotic translation initiation factor 5 | 6412 // protein biosynthesis // inferred from electronic annotation /// 6446 // regulation of translational initiation // traceable author statement /// 6413 // translational initiation // inferred from electronic annotation /// 6446 // regulation of translational initiation // inferred from electronic annotation /// 6413 // translational initiation // non-traceable author statement | 5737 // cytoplasm // traceable author statement /// 5829 // cytosol // non-traceable author statement | 166 // nucleotide binding // inferred from electronic annotation /// 3743 // translation initiation factor activity // non-traceable author statement /// 3924 // GTPase activity // traceable author statement /// 5525 // GTP binding // inferred from electronic annotation /// 3743 // translation initiation factor activity // inferred from electronic annotation /// 8135 // translation factor activity, nucleic acid binding // traceable author statement |

*(Continued)*



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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 209878_s_at | -0.767165 | 5970 | RELA | v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian) | 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6916 // anti-apoptosis // inferred from direct assay /// 6954 // inflammatory response // inferred from direct assay /// 6968 // cellular defense response // non-traceable author statement /// 10033 // response to organic substance // inferred from direct assay /// 10224 // response to UV-B // inferred from direct assay /// 19221 // cytokine and chemokine mediated signaling pathway // inferred from direct assay /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from expression pattern /// 51092 // activation of NF-kappaB transcription factor // inferred from direct assay /// 51607 // defense response to virus // non-traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation | 5634 // nucleus // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation /// 5667 // transcription factor complex // inferred from direct assay /// 5737 // cytoplasm // inferred from direct assay | 3700 // transcription factor activity // inferred from electronic annotation /// 3705 // RNA polymerase II transcription factor activity, enhancer binding // inferred from direct assay /// 4871 // signal transducer activity // inferred from expression pattern /// 19901 // protein kinase binding // inferred from physical interaction /// 42301 // phosphate binding // inferred from direct assay /// 42802 // identical protein binding // inferred from direct assay /// 47485 // protein N-terminus binding // inferred from physical interaction /// 51059 // NF-kappaB binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 8134 // transcription factor binding // inferred from physical interaction /// 42802 // identical protein binding // inferred from physical interaction /// 3677 // DNA binding // inferred from direct assay /// 3700 // transcription factor activity // inferred from direct assay /// 5515 // protein binding // inferred from direct assay /// 367 |
| 216902_s_at | -0.765497 | 54700 | RRN3 | RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6360 // transcription from RNA polymerase I promoter // traceable author statement | 5634 // nucleus // inferred from electronic annotation | 3701 // RNA polymerase I transcription factor activity // traceable author statement |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 206689_x_at | -0.764248 | 10524 | HTATIP | HIV-1 Tat interacting protein, 60kDa | 1558 // regulation of cell growth // inferred from electronic annotation /// 6302 // double-strand break repair // inferred from mutant phenotype /// 6333 // chromatin assembly or disassembly // inferred from electronic annotation /// 6350 // transcription // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // traceable author statement /// 16568 // chromatin modification // inferred from electronic annotation /// 16573 // histone acetylation // inferred from direct assay /// 30521 // androgen receptor signaling pathway // non-traceable author statement /// 45893 // positive regulation of transcription, DNA-dependent // non-traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 785 // chromatin // inferred from electronic annotation /// 5634 // nucleus // traceable author statement /// 35267 // TIP60 histone acetyltransferase complex // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation | 3682 // chromatin binding // inferred from electronic annotation /// 3713 // transcription coactivator activity // non-traceable author statement /// 4402 // histone acetyltransferase activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 8415 // acyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 50681 // androgen receptor binding // non-traceable author statement /// 3713 // transcription coactivator activity // traceable author statement |
| 226008_at | -0.762606 | 56160 | NDNL2 | necdin-like 2 | 1558 // regulation of cell growth // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | — |
| 232048_at | -0.761400167 | 143684 | FAM76B | family with sequence similarity 76, member B | — | — | — |
| 209149_s_at | -0.757001833 | 10548 | TM9SF1 | transmembrane 9 superfamily member 1 | 6810 // transport // inferred from electronic annotation | 5624 // membrane fraction // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement | 5215 // transporter activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 229043_at | -0.755587 | 64282 | PAPD5 | PAP associated domain containing 5 | 6260 // DNA replication // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7067 // mitosis // inferred from electronic annotation /// 51301 // cell division // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // inferred from electronic annotation /// 3887 // DNA-directed DNA polymerase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16779 // nucleotidyltransferase activity // inferred from electronic annotation |
| 208673_s_at | -0.755549667 | 6428 | SFRS3 | splicing factor, arginine/serine-rich 3 | 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 6397 // mRNA processing // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement /// 3676 // nucleic acid binding // inferred from electronic annotation |
| 222706_at | -0.753962333 | 54883 | CCDC49 | coiled-coil domain containing 49 | — | — | — |
| 202879_s_at | -0.750898 | 9267 | PSCD1 | pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1) | 16192 // vesicle-mediated transport // traceable author statement /// 30155 // regulation of cell adhesion // inferred from direct assay /// 32012 // regulation of ARF protein signal transduction // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5737 // cytoplasm // inferred from direct assay /// 5886 // plasma membrane // inferred from direct assay | 5086 // ARF guanyl-nucleotide exchange factor activity // traceable author statement /// 5515 // protein binding // inferred from direct assay /// 5085 // guanyl-nucleotide exchange factor activity // inferred from electronic annotation /// 5086 // ARF guanyl-nucleotide exchange factor activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 203079_s_at | -0.750733833 | 8453 | CUL2 | cullin 2 | 82 // G1/S transition of mitotic cell cycle // traceable author statement /// 6512 // ubiquitin cycle // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7050 // cell cycle arrest // traceable author statement /// 8285 // negative regulation of cell proliferation // traceable author statement /// 8629 // induction of apoptosis by intracellular signals // traceable author statement | — | 5515 // protein binding // inferred from physical interaction |
| 211797_s_at | -0.7486355 | 4802 | NFYC | nuclear transcription factor Y, gamma | 74 // regulation of progression through cell cycle // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement /// 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6457 // protein folding // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from direct assay /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from expression pattern /// 5634 // nucleus // non-traceable author statement /// 16602 // CCAAT-binding factor complex // inferred from direct assay /// 5634 // | 3700 // transcription factor activity // traceable author statement /// 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 3713 // transcription coactivator activity // traceable author statement /// 3887 // DNA-directed DNA polymerase activity // inferred from electronic annotation /// 5515 // protein binding // inferred from direct assay /// 16740 // transferase activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from direct assay /// 3677 // DNA binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 224654_at | -0.7481835 | 9188 | DDX21 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation /// 5730 // nucleolus // traceable author statement /// 5622 // intracellular // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 4004 // ATP-dependent RNA helicase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4386 // helicase activity // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 8026 // ATP-dependent helicase activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 206126_at | -0.745837 | 643 | BLR1 | Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C-X-C motif) receptor 5) | 6928 // cell motility // traceable author statement /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 42113 // B cell activation // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation | 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4945 // angiotensin type II receptor activity // inferred from electronic annotation /// 16494 // C-X-C chemokine receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // traceable author statement |
| 202543_s_at | -0.7452865 | 2764 | GMFB | glia maturation factor, beta | — | 5622 // intracellular // inferred from electronic annotation | 3779 // actin binding // inferred from electronic annotation /// 8083 // growth factor activity // inferred from electronic annotation |
| 244828_x_at | -0.743475833 | 92345 | LOC92345 | hypothetical protein BC008207 | — | — | — |
| 231771_at | -0.7422205 | 10804 | GJB6 | gap junction protein, beta 6 (connexin 30) | 6955 // immune response // non-traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 7605 // sensory perception of sound // traceable author statement /// 7605 // sensory perception of sound // inferred from electronic annotation | 5576 // extracellular region // non-traceable author statement /// 5922 // connexon complex // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic a | 3823 // antigen binding // non-traceable author statement /// 15285 // connexon channel activity // inferred from electronic annotation |
| 1553947_at | -0.7418275 | 118460 | EXOSC6 | exosome component 6 | 6396 // RNA processing // inferred from electronic annotation | — | 175 // 3'-5'-exoribonuclease activity // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 218738_s_at | -0.741725 | 51444 | RNF138 | ring finger protein 138 | 6512 // ubiquitin cycle // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation | 3676 // nucleic acid binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 232612_s_at | -0.740365167 | 55054 | ATG16L1 | ATG16 autophagy related 16-like 1 (S. cerevisiae) | 6914 // autophagy // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation | 16020 // membrane // inferred from electronic annotation | — |
| 208841_s_at | -0.739521833 | 9908 | G3BP2 | Ras-GTPase activating protein SH3 domain-binding protein 2 | 6397 // mRNA processing // inferred from electronic annotation /// 6406 // mRNA export from nucleus // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 7253 // cytoplasmic sequestering of NF-kappaB // non-traceable author statement /// 7265 // Ras protein signal transduction // non-traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5737 // cytoplasm // non-traceable author statement | 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // non-traceable author statement /// 30159 // receptor signaling complex scaffold activity // non-traceable author statement /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation |
| 203622_s_at | -0.7391365 | 56902 | LOC56902 | putatative 28 kDa protein | — | — | 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation |
| 223787_s_at | -0.734289 | 51244 | C3orf19 | chromosome 3 open reading frame 19 | — | — | — |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 224330_s_at | -0.732788167 | 51264 | MRPL27 | mitochondrial ribosomal protein L27 /// mitochondrial ribosomal protein L27 | 6412 // protein biosynthesis // inferred from electronic annotation /// 6412 // protein biosynthesis // non-traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5739 // mitochondrion // inferred from electronic annotation /// 5762 // mitochondrial large ribosomal subunit // non-traceable author statement /// 5840 // ribosome // inferred from electro | 3735 // structural constituent of ribosome // inferred from electronic annotation /// 3735 // structural constituent of ribosome // non-traceable author statement |
| 201083_s_at | -0.7325775 | 9774 | BCLAF1 | BCL2-associated transcription factor 1 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 16481 // negative regulation of transcription // inferred from direct assay /// 43065 // positive regulation of apoptosis // inferred from direct assay | 5634 // nucleus // non-traceable author statement /// 5634 // nucleus // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // inferred from direct assay /// 5515 // protein binding // inferred from physical interaction /// 16564 // transcriptional repressor activity // traceable author statement /// 16564 // transcriptional repressor activity // inferred from direct assay /// 3677 // DNA binding // inferred from electronic annotation |
| 220703_at | -0.729714333 | 55853 | C10orf110 | chromosome 10 open reading frame 110 | — | — | — |
| 206360_s_at | -0.727941333 | 9021 | SOCS3 | suppressor of cytokine signaling 3 | 1558 // regulation of cell growth // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7259 // JAK-STAT cascade // traceable author statement /// 9968 // negative regulation of signal transduction // inferred from electronic annotation | — | 4860 // protein kinase inhibitor activity // traceable author statement |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 218172_s_at | -0.725955833 | 79139 | DERL1 | Der1-like domain family, member 1 | 15031 // protein transport // inferred from electronic annotation /// 19060 // intracellular transport of viral proteins in host cell // traceable author statement /// 30433 // ER-associated protein catabolism // inferred from direct assay /// 30968 // unfolded protein response // inferred from direct assay /// 30970 // retrograde protein transport, ER to cytosol // inferred from direct assay /// 6810 // transport // inferred from electronic annotation /// 45184 // establishment of protein localization // traceable author statement | 5783 // endoplasmic reticulum // inferred from direct assay /// 5783 // endoplasmic reticulum // inferred from mutant phenotype /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic anno | 4872 // receptor activity // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 42288 // MHC class I protein binding // inferred from direct assay |
| 213899_at | -0.725638333 | 10988 | METAP2 | methionyl aminopeptidase 2 | 6445 // regulation of translation // traceable author statement /// 6464 // protein modification // traceable author statement /// 6508 // proteolysis // inferred from electronic annotation /// 18206 // peptidyl-methionine modification // traceable author statement /// 31365 // N-terminal protein amino acid modification // traceable author statement /// 6417 // regulation of protein biosynthesis // traceable author statement | 5737 // cytoplasm // traceable author statement | 4239 // methionyl aminopeptidase activity // inferred from electronic annotation /// 4239 // methionyl aminopeptidase activity // traceable author statement /// 8233 // peptidase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 50897 // cobalt ion binding // inferred from electronic annotation /// 4177 // aminopeptidase activity // inferred from electronic annotation /// 8235 // metalloexopeptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation |
| 224642_at | -0.724945833 | 84248 | FYTTD1 | forty-two-three domain containing 1 | — | — | — |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 207164_s_at | -0.723781 | 10472 | ZNF238 | zinc finger protein 238 | 122 // negative regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6810 // transport // traceable author statement /// 7001 // chromosome organization and biogenesis (sensu Eukaryota) // not recorded | 228 // nuclear chromosome // traceable author statement /// 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 3676 // nucleic acid binding // inferred from electronic annotation /// 3700 // transcription factor activity // traceable author statement /// 3704 // specific RNA polymerase II transcription factor activity // not recorded /// 5515 // protein binding // inferred from electronic annotation /// 5515 // protein binding // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3677 // DNA binding // traceable author statement |
| 206108_s_at | -0.717038667 | 6431 | SFRS6 | splicing factor, arginine/serine-rich 6 | 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 6376 // mRNA splice site selection // traceable author statement /// 6397 // mRNA processing // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // not recorded | 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 212218_s_at | -0.7161915 | 2194 | FASN | fatty acid synthase | 6633 // fatty acid biosynthesis // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic annotation /// 8610 // lipid biosynthesis // inferred from electronic annotation /// 9058 // biosynthesis // inferred from electronic annotation /// 6631 // fatty acid metabolism // traceable author statement | — | 3824 // catalytic activity // inferred from electronic annotation /// 4313 // [acyl-carrier protein] S-acetyltransferase activity // inferred from electronic annotation /// 4314 // [acyl-carrier protein] S-malonyltransferase activity // inferred from electronic annotation /// 4315 // 3-oxoacyl-[acyl-carrier protein] synthase activity // inferred from electronic annotation /// 4316 // 3-oxoacyl-[acyl-carrier protein] reductase activity // inferred from electronic annotation /// 4317 // 3-hydroxypalmitoyl-[acyl-carrier protein] dehydratase activity // inferred from electronic annotation /// 4319 // enoyl-[acyl-carrier protein] reductase (NADPH, B-specific) activity // inferred from electronic annotation /// 4320 // oleoyl-[acyl-carrier protein] hydrolase activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotatio |
| 202887_s_at | -0.714806667 | 54541 | DDIT4 | DNA-damage-inducible transcript 4 | — | — | — |
| 202776_at | -0.713180333 | 30836 | DNTTIP2 | deoxynucleotidyltransferase, terminal, interacting protein 2 | — | — | 4872 // receptor activity // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 208114_s_at | -0.7129725 | 81875 | ISG20L2 | interferon stimulated exonuclease gene 20kDa-like 2 /// interferon stimulated exonuclease gene 20kDa-like 2 | — | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 4527 // exonuclease activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4518 // nuclease activity // inferred from electronic annotation |
| 221766_s_at | -0.708867667 | 55603 | FAM46A | family with sequence similarity 46, member A | — | — | — |
| 244868_at | -0.708648333 | 22882 | ZHX2 | Zinc fingers and homeoboxes 2 | 45892 // negative regulation of transcription, DNA-dependent // inferred from direct assay /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // inferred from direct assay /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation |
| 219798_s_at | -0.7066985 | 56257 | BCDIN3 | bin3, bicoid-interacting 3, homolog (Drosophila) | — | — | 8168 // methyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 201096_s_at | -0.706202167 | 378 | ARF4 | ADP-ribosylation factor 4 | 6364 // rRNA processing // inferred from electronic annotation /// 6888 // ER to Golgi vesicle-mediated transport // inferred from electronic annotation /// 7264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 7046 // ribosome biogenesis // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 5525 // GTP binding // inferred from electronic annotation /// 8047 // enzyme activator activity // not recorded |
| 229958_at | -0.705591333 | 619435 | C8orf61 | chromosome 8 open reading frame 61 | — | — | — |
| 230764_at | -0.7044995 | 23731 | C9orf5 | Chromosome 9 open reading frame 5 | — | 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation | — |
| 203013_at | -0.704272333 | 11319 | ECD | ecdysoneless homolog (Drosophila) | 6110 // regulation of glycolysis // traceable author statement /// 6366 // transcription from RNA polymerase II promoter // traceable author statement | — | 3713 // transcription coactivator activity // traceable author statement |
| 225699_at | -0.703454167 | 285958 | C7orf40 | chromosome 7 open reading frame 40 | — | — | — |
| 204833_at | -0.703122667 | 9140 | ATG12 | ATG12 autophagy related 12 homolog (S. cerevisiae) | 45 // autophagic vacuole formation // inferred from electronic annotation /// 6512 // ubiquitin cycle // inferred from electronic annotation /// 6914 // autophagy // traceable author statement /// 6915 // apoptosis // traceable author statement /// 6914 // autophagy // inferred from electronic annotation /// 6464 // protein modification // traceable author statement | 5737 // cytoplasm // traceable author statement /// 5737 // cytoplasm // inferred from electronic annotation | 5515 // protein binding // inferred from physical interaction |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 222443_s_at | -0.702617833 | 9939 | RBM8A | RNA binding motif protein 8A | 184 // mRNA catabolism, nonsense-mediated decay // inferred from electronic annotation /// 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 6406 // mRNA export from nucleus // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6396 // RNA processing // inferred from electronic annotation /// 6397 // mRNA processing // inferred from electronic annotation | 5634 // nucleus // non-traceable author statement /// 5737 // cytoplasm // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation /// 5737 // cytoplasm // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3729 // mRNA binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3723 // RNA binding // non-traceable author statement |
| 227018_at | -0.701506667 | 54878 | DPP8 | dipeptidyl-peptidase 8 | 6508 // proteolysis // non-traceable author statement /// 6955 // immune response // traceable author statement /// 6508 // proteolysis // inferred from electronic annotation | 5737 // cytoplasm // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation | 4177 // aminopeptidase activity // inferred from electronic annotation /// 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 4274 // dipeptidyl-peptidase IV activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8236 // serine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 8239 // dipeptidyl-peptidase activity // non-traceable author statement |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 200753_x_at | -0.701344833 | 6427 | SFRS2 | splicing factor, arginine/serine-rich 2 | 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 8380 // RNA splicing // traceable author statement /// 86 // G2/M transition of mitotic cell cycle // inferred from direct assay /// 6916 // anti-apoptosis // inferred from direct assay /// 6915 // apoptosis // inferred from electronic annotation /// 6916 // anti-apoptosis // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7067 // mitosis // inferred from electronic annotation /// 51301 // cell division // inferred from electronic annotation /// 6397 // mRNA processing // inferred from electronic annotation /// 6397 // mRNA processing // traceable author statement | 5634 // nucleus // inferred from direct assay /// 16605 // PML body // inferred from direct assay /// 775 // chromosome, pericentric region // inferred from direct assay /// 30496 // midbody // inferred from direct assay /// 775 // chromosome, pericentric | 166 // nucleotide binding // inferred from electronic annotation /// 3714 // transcription corepressor activity // non-traceable author statement /// 3723 // RNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 43027 // caspase inhibitor activity // inferred from mutant phenotype /// 8017 // microtubule binding // inferred from direct assay /// 4866 // endopeptidase inhibitor activity // inferred from electronic annotation /// 4869 // cysteine protease inhibitor activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // non-traceable author statement /// 30414 // protease inhibitor activity // non-traceable author statement |
| 210285_x_at | -0.7002035 | 9589 | WTAP | Wilms tumor 1 associated protein | — | 5634 // nucleus // inferred from direct assay /// 31965 // nuclear membrane // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation | — |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 1552612_at | -0.698609 | 56990 | CDC42SE2 | CDC42 small effector 2 | 7165 // signal transduction // traceable author statement | 5886 // plasma membrane // traceable author statement | 16301 // kinase activity // inferred from electronic annotation /// 5198 // structural molecule activity // traceable author statement /// 5515 // protein binding // traceable author statement |
| 224336_s_at | -0.695251667 | 80824 | DUSP16 | dual specificity phosphatase 16 /// dual specificity phosphatase 16 | 188 // inactivation of MAPK activity // traceable author statement /// 6470 // protein amino acid dephosphorylation // inferred from electronic annotation /// 45204 // MAPK export from nucleus // traceable author statement /// 45209 // MAPK phosphatase export from nucleus, leptomycin B sensitive // traceable author statement /// 16311 // dephosphorylation // traceable author statement | 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 4725 // protein tyrosine phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 17017 // MAP kinase phosphatase activity // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation /// 8138 // protein tyrosine/serine/ threonine phosphatase activity // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // traceable author statement |
| 213376_at | -0.694042833 | 22890 | ZBTB1 | zinc finger and BTB domain containing 1 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 3676 // nucleic acid binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 202703_at | -0.693309833 | 8446 | DUSP11 | dual specificity phosphatase 11 (RNA/RNP complex 1-interacting) | 6396 // RNA processing // traceable author statement /// 6470 // protein amino acid dephosphorylation // inferred from electronic annotation | 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 3723 // RNA binding // traceable author statement /// 4725 // protein tyrosine phosphatase activity // traceable author statement /// 8138 // protein tyrosine/serine/threonine phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation |
| 202523_s_at | -0.688867167 | 9806 | SPOCK2 | sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2 | 7416 // synaptogenesis // non-traceable author statement /// 30198 // extracellular matrix organization and biogenesis // non-traceable author statement /// 45595 // regulation of cell differentiation // non-traceable author statement | 5578 // extracellular matrix (sensu Metazoa) // non-traceable author statement /// 5578 // extracellular matrix (sensu Metazoa) // inferred from electronic annotation | 5509 // calcium ion binding // inferred from direct assay /// 5509 // calcium ion binding // inferred from electronic annotation |
| 228263_at | -0.676218167 | 160622 | GRASP | GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein | — | 5634 // nucleus // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation | 5515 // protein binding // inferred from electronic annotation |
| 203203_s_at | -0.676017 | 11103 | KRR1 | KRR1, small subunit (SSU) processome component, homolog (yeast) | 6364 // rRNA processing // inferred from sequence or structural similarity | 5634 // nucleus // inferred from electronic annotation /// 5732 // small nucleolar ribonucleoprotein complex // inferred from sequence or structural similarity | 5515 // protein binding // inferred from sequence or structural similarity /// 30515 // snoRNA binding // inferred from sequence or structural similarity /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation |
| 230493_at | -0.672263 | 387914 | TMEM46 | transmembrane protein 46 | — | 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | — |
| 223511_at | -0.672153667 | 83932 | C1orf124 | chromosome 1 open reading frame 124 | 6281 // DNA repair // inferred from electronic annotation | — | 3677 // DNA binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 231983_at | -0.671169 | 200205 | C1orf69 | chromosome 1 open reading frame 69 | 6546 // glycine catabolism // inferred from electronic annotation | 5737 // cytoplasm // inferred from electronic annotation | 4047 // aminomethyltransferase activity // inferred from electronic annotation |
| 223819_x_at | -0.665328667 | 28991 | COMMD5 | COMM domain containing 5 | — | 5634 // nucleus // inferred from electronic annotation | — |
| 238476_at | -0.663777833 | 153222 | LOC153222 | adult retina protein | 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation |
| 230023_at | -0.662249833 | 387338 | NSUN4 | NOL1/NOP2/Sun domain family, member 4 | — | — | — |
| 226612_at | -0.662115 | 134111 | FLJ25076 | similar to CG4502-PA | 6512 // ubiquitin cycle // inferred from electronic annotation | — | 4842 // ubiquitin-protein ligase activity // inferred from electronic annotation |
| 207515_s_at | -0.661354333 | 9533 | POLR1C | polymerase (RNA) I polypeptide C, 30kDa | 6350 // transcription // inferred from electronic annotation /// 6360 // transcription from RNA polymerase I promoter // traceable author statement | 5634 // nucleus // inferred from electronic annotation /// 5736 // DNA-directed RNA polymerase I complex // traceable author statement | 3677 // DNA binding // inferred from electronic annotation /// 3899 // DNA-directed RNA polymerase activity // inferred from electronic annotation /// 3899 // DNA-directed RNA polymerase activity // traceable author statement /// 16740 // transferase activity // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 16779 // nucleotidyltransferase activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 217821_s_at | -0.657838167 | 51729 | WBP11 | WW domain binding protein 11 | 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 6364 // rRNA processing // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6811 // ion transport // inferred from electronic annotation /// 15986 // ATP synthesis coupled proton transport // inferred from electronic annotation /// 15992 // proton transport // inferred from electronic annotation /// 6397 // mRNA processing // inferred from electronic annotation /// 6091 // generation of precursor metabolites and energy // not recorded | 5634 // nucleus // traceable author statement /// 5739 // mitochondrion // inferred from electronic annotation /// 16469 // proton-transporting two-sector ATPase complex // inferred from electronic annotation /// 45263 // proton-transporting ATP synthase | 3697 // single-stranded DNA binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 15078 // hydrogen ion transporter activity // inferred from electronic annotation /// 46933 // hydrogen-transporting ATP synthase activity, rotational mechanism // inferred from electronic annotation /// 46961 // hydrogen-transporting ATPase activity, rotational mechanism // inferred from electronic annotation /// 5215 // transporter activity // non-traceable author statement |
| 209339_at | -0.655213333 | 6478 | SIAH2 | seven in absentia homolog 2 (Drosophila) /// seven in absentia homolog 2 (Drosophila) | 6511 // ubiquitin-dependent protein catabolism // traceable author statement /// 6915 // apoptosis // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7264 // small GTPase mediated signal transduction // traceable author statement /// 7275 // development // inferred from electronic annotation /// 6511 // ubiquitin-dependent protein catabolism // inferred from electronic annotation /// 6512 // ubiquitin cycle // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation /// 5737 // cytoplasm // traceable author statement | 3714 // transcription corepressor activity // traceable author statement /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 16874 // ligase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 200706_s_at | -0.654586667 | 9516 | LITAF | lipopolysaccharide-induced TNF factor | 6350 // transcription // inferred from electronic annotation /// 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6915 // apoptosis // inferred from electronic annotation /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from mutant phenotype /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | — | 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 4871 // signal transducer activity // inferred from mutant phenotype |
| 204448_s_at | -0.653306 | 5082 | PDCL | phosducin-like | 7165 // signal transduction // non-traceable author statement /// 7601 // visual perception // inferred from electronic annotation /// 50896 // response to stimulus // inferred from electronic annotation | — | 16299 // regulator of G-protein signaling activity // non-traceable author statement |
| 226308_at | -0.652660667 | 93323 | NY-SAR-48 | sarcoma antigen NY-SAR-48 | — | — | — |
| 202010_s_at | -0.649903833 | 57862 | ZNF410 | zinc finger protein 410 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |
| 224717_s_at | -0.649120167 | 79086 | C19orf42 | chromosome 19 open reading frame 42 | — | — | — |
| 207332_s_at | -0.646887667 | 7037 | TFRC | transferrin receptor (p90, CD71) | 6508 // proteolysis // inferred from electronic annotation /// 6826 // iron ion transport // not recorded /// 6879 // iron ion homeostasis // non-traceable author statement /// 6897 // endocytosis // inferred from electronic annotation /// 6879 // iron ion homeostasis // traceable author statement | 5576 // extracellular region // inferred from direct assay /// 5768 // endosome // inferred from direct assay /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // non-traceable author statement /// 16023 // cytopl | 4872 // receptor activity // inferred from electronic annotation /// 4998 // transferrin receptor activity // non-traceable author statement /// 8233 // peptidase activity // inferred from electronic annotation /// 4998 // transferrin receptor activity // traceable author statement |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 229428_at | -0.644320167 | 8505 | PARG | Poly (ADP-ribose) glycohydrolase | — | 5634 // nucleus // inferred from electronic annotation /// 5737 // cytoplasm // traceable author statement | 4649 // poly(ADP-ribose) glycohydrolase activity // inferred from direct assay /// 16787 // hydrolase activity // inferred from electronic annotation /// 4649 // poly(ADP-ribose) glycohydrolase activity // inferred from electronic annotation /// 4649 // poly(ADP-ribose) glycohydrolase activity // traceable author statement |
| 222510_s_at | -0.644074 | 23609 | MKRN2 | makorin, ring finger protein, 2 | — | 5622 // intracellular // inferred from expression pattern | 3676 // nucleic acid binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 201242_s_at | -0.641335833 | 481 | ATP1B1 | ATPase, Na+/K+ transporting, beta 1 polypeptide | 6811 // ion transport // inferred from electronic annotation /// 6813 // potassium ion transport // inferred from electronic annotation /// 6814 // sodium ion transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6810 // transport // traceable author statement | 5890 // sodium:potassium-exchanging ATPase complex // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | 5391 // sodium:potassium-exchanging ATPase activity // inferred from electronic annotation /// 5391 // sodium:potassium-exchanging ATPase activity // traceable author statement /// 30955 // potassium ion binding // inferred from electronic annotation /// 31402 // sodium ion binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 214141_x_at | -0.640103333 | 6432 | SFRS7 | splicing factor, arginine/serine-rich 7, 35kDa | 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 8380 // RNA splicing // inferred from direct assay /// 6397 // mRNA processing // inferred from electronic annotation /// 6397 // mRNA processing // traceable author statement | 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |
| 200071_at | -0.639138 | 10285 | SMNDC1 | survival motor neuron domain containing 1 /// survival motor neuron domain containing 1 | 245 // spliceosome assembly // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 8380 // RNA splicing // traceable author statement /// 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 6397 // mRNA processing // inferred from electronic annotation /// 6397 // mRNA processing // traceable author statement | 5634 // nucleus // traceable author statement /// 5681 // spliceosome complex // traceable author statement /// 5737 // cytoplasm // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation /// 5681 // spliceosome com | 5515 // protein binding // inferred from physical interaction /// 31202 // RNA splicing factor activity, transesterification mechanism // traceable author statement /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation |
| 222748_s_at | -0.638796333 | 54957 | TXNL4B | thioredoxin-like 4B | 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7067 // mitosis // inferred from electronic annotation /// 6397 // mRNA processing // inferred from electronic annotation /// 51301 // cell division // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation /// 5681 // spliceosome complex // inferred from electronic annotation | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 233458_at | -0.637089667 | 55718 | POLR3E | polymerase (RNA) III (DNA directed) polypeptide E (80kD) | 6350 // transcription // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 3899 // DNA-directed RNA polymerase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16779 // nucleotidyltransferase activity // inferred from electronic annotation |
| 210275_s_at | -0.633341667 | 7763 | ZFAND5 | zinc finger, AN1-type domain 5 | — | — | 3677 // DNA binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 202643_s_at | -0.623726667 | 7128 | TNFAIP3 | tumor necrosis factor, alpha-induced protein 3 | 6512 // ubiquitin cycle // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation /// 6916 // anti-apoptosis // non-traceable author statement /// 43124 // negative regulation of I-kappaB kinase/NF-kappaB cascade // inferred from direct assay | 5634 // nucleus // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 206404_at | -0.622537167 | 2254 | FGF9 | fibroblast growth factor 9 (glia-activating factor) | 74 // regulation of progression through cell cycle // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 8283 // cell proliferation // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation | 5615 // extracellular space // traceable author statement | 8083 // growth factor activity // traceable author statement /// 8201 // heparin binding // inferred from electronic annotation /// 8083 // growth factor activity // inferred from electronic annotation |
| 212240_s_at | -0.615695 | 5295 | PIK3R1 | phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) | 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7242 // intracellular signaling cascade // non-traceable author statement /// 8286 // insulin receptor signaling pathway // inferred from physical interaction /// 46854 // phosphoinositide phosphorylation // inferred from sequence or structural similarity /// 48009 // insulin-like growth factor receptor signaling pathway // inferred from physical interaction /// 7165 // signal transduction // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5942 // phosphoinositide 3-kinase complex // inferred from electronic annotation /// 35030 // phosphoinositide 3-kinase complex, class IA // inferred from sequence or structural similarity | 5158 // insulin receptor binding // inferred from physical interaction /// 5159 // insulin-like growth factor receptor binding // inferred from physical interaction /// 5545 // phosphatidylinositol binding // non-traceable author statement /// 16301 // kinase activity // inferred from electronic annotation /// 19903 // protein phosphatase binding // inferred from physical interaction /// 35014 // phosphoinositide 3-kinase regulator activity // inferred from electronic annotation /// 35014 // phosphoinositide 3-kinase regulator activity // inferred from sequence or structural similarity /// 43125 // ErbB-3 class receptor binding // inferred from direct assay /// 43559 // insulin binding // inferred from direct assay /// 43560 // insulin receptor substrate binding // inferred from sequence or structural similarity /// 5515 // protein binding // inferred from physical interaction |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 241756_at | -0.607308333 | 6595 | SMARCA2 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 | 6350 // transcription // inferred from electronic annotation /// 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement | 5634 // nucleus // inferred from electronic annotation /// 5654 // nucleoplasm // traceable author statement | 166 // nucleotide binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3713 // transcription coactivator activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation /// 8026 // ATP-dependent helicase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 4386 // helicase activity // inferred from electronic annotation /// 4386 // helicase activity // traceable author statement |
| 213710_s_at | -0.606039333 | 801 | CALM1 | Calmodulin 1 (phosphorylase kinase, delta) | 7186 // G-protein coupled receptor protein signaling pathway // inferred from sequence or structural similarity /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement | 5737 // cytoplasm // inferred from sequence or structural similarity /// 5886 // plasma membrane // inferred from sequence or structural similarity /// 5737 // cytoplasm // traceable author statement /// 5886 // plasma membrane // traceable author stateme | 5515 // protein binding // inferred from physical interaction /// 31997 // N-terminal myristoylation domain binding // inferred from physical interaction /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5515 // protein binding // inferred from sequence or structural similarity /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // traceable author statement /// 5515 // protein binding // traceable author statement /// 5515 // protein binding // non-traceable author statement |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 207079_s_at | -0.602954833 | 10001 | MED6 | mediator of RNA polymerase II transcription, subunit 6 homolog (S. cerevisiae) | 45944 // positive regulation of transcription from RNA polymerase II promoter // inferred from direct assay /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation /// 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement | 119 // mediator complex // inferred from direct assay /// 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation /// 119 // mediator complex // traceable author statement | 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 3713 // transcription coactivator activity // inferred from direct assay /// 4872 // receptor activity // inferred from electronic annotation /// 30528 // transcription regulator activity // inferred from electronic annotation |
| 231863_at | -0.602114333 | 54556 | ING3 | inhibitor of growth family, member 3 | 1558 // regulation of cell growth // inferred from electronic annotation /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 16568 // chromatin modification // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 226095_s_at | -0.600552833 | 146517 | LOC146517 | hypothetical protein LOC146517 | — | — | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 219226_at | -0.595273167 | 51755 | CRKRS | Cdc2-related kinase, arginine/serine-rich | 46777 // protein amino acid autophosphorylation // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation | 5634 // nucleus // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3702 // RNA polymerase II transcription factor activity // non-traceable author statement /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from direct assay /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation |
| 200597_at | -0.594829167 | 8661 | EIF3S10 | eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa | 6412 // protein biosynthesis // inferred from electronic annotation /// 6446 // regulation of translational initiation // traceable author statement | 5852 // eukaryotic translation initiation factor 3 complex // traceable author statement | 3743 // translation initiation factor activity // inferred from electronic annotation /// 8135 // translation factor activity, nucleic acid binding // traceable author statement |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 217370_x_at | -0.594000833 | 2521 | FUS | fusion (involved in t(12;16) in malignant liposarcoma) | 30503 // regulation of cell redox homeostasis // inferred from direct assay /// 42789 // mRNA transcription from RNA polymerase II promoter // inferred from direct assay /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7050 // cell cycle arrest // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement /// 6974 // response to DNA damage stimulus // traceable author statement /// 74 // regulation of progression through cell cycle // non-traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 5634 // nucleus // n | 166 // nucleotide binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from direct assay /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 5164 // tumor necrosis factor receptor binding // inferred from electronic annotation /// 3714 // transcription corepressor activity // traceable author statement /// 3700 // transcription factor acti |
| 211686_s_at | -0.593885667 | 84549 | RBM13 | RNA binding motif protein 13 /// RNA binding motif protein 13 | — | 5634 // nucleus // inferred from electronic annotation | — |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 201646_at | -0.590403667 | 950 | SCARB2 | scavenger receptor class B, member 2 | 7155 // cell adhesion // inferred from electronic annotation | 5624 // membrane fraction // traceable author statement /// 5765 // lysosomal membrane // not recorded /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 5764 // lysosome | 4872 // receptor activity // inferred from electronic annotation |
| 203898_at | -0.589967833 | 27297 | RCP9 | calcitonin gene-related peptide-receptor component protein | 7340 // acrosome reaction // non-traceable author statement | — | 4948 // calcitonin receptor activity // non-traceable author statement |
| 220104_at | -0.585244333 | 56829 | ZC3HAV1 | zinc finger CCCH-type, antiviral 1 | 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 3676 // nucleic acid binding // inferred from electronic annotation /// 3950 // NAD+ ADP-ribosyltransferase activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 207941_s_at | -0.583783333 | 9584 | RBM39 | RNA binding motif protein 39 | 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6397 // mRNA processing // inferred from electronic annotation /// 6396 // RNA processing // traceable author statement | 5634 // nucleus // inferred from electronic annotation /// 5654 // nucleoplasm // traceable author statement | 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation |
| 1552617_a_at | -0.581591167 | 64326 | RFWD2 | ring finger and WD repeat domain 2 | 6512 // ubiquitin cycle // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 16874 // ligase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 225088_at | -0.569844167 | 123811 | C16orf63 | chromosome 16 open reading frame 63 | — | — | — |
| 1555760_a_at | -0.564309 | 64783 | RBM15 | RNA binding motif protein 15 | 45449 // regulation of transcription // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 5488 // binding // inferred from electronic annotation |
| 1569263_at | -0.5610785 | 9123 | SLC16A3 | Solute carrier family 16 (monocarboxylic acid transporters), member 3 | 6810 // transport // inferred from electronic annotation /// 15711 // organic anion transport // inferred from electronic annotation /// 15718 // monocarboxylic acid transport // traceable author statement | 5624 // membrane fraction // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annota | 5215 // transporter activity // inferred from electronic annotation /// 15293 // symporter activity // inferred from electronic annotation /// 15355 // monocarboxylate porter activity // inferred from electronic annotation /// 8028 // monocarboxylic acid transporter activity // traceable author statement |
| 210016_at | -0.559203167 | 23040 | MYT1L | myelin transcription factor 1-like | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7399 // nervous system development // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 223096_at | -0.5571555 | 51602 | NOP5/NOP58 | nucleolar protein NOP5/NOP58 | 6364 // rRNA processing // traceable author statement /// 6608 // snRNP protein import into nucleus // inferred from sequence or structural similarity /// 16049 // cell growth // traceable author statement /// 7046 // ribosome biogenesis // inferred from electronic annotation /// 7046 // ribosome biogenesis // traceable author statement | 5634 // nucleus // inferred from electronic annotation /// 5730 // nucleolus // traceable author statement | 30519 // snoRNP binding // inferred from sequence or structural similarity /// 51082 // unfolded protein binding // inferred from sequence or structural similarity |
| 200711_s_at | -0.548213167 | 6500 | SKP1A | S-phase kinase-associated protein 1A (p19A) | 6512 // ubiquitin cycle // inferred from electronic annotation | — | 5515 // protein binding // inferred from physical interaction |
| 226475_at | -0.546711833 | 55007 | FAM118A | family with sequence similarity 118, member A | — | 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | — |
| 212901_s_at | -0.546478167 | 23283 | CSTF2T | cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant | 6397 // mRNA processing // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 201586_s_at | -0.539741667 | 6421 | SFPQ | splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated) | 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 6281 // DNA repair // inferred from electronic annotation /// 6310 // DNA recombination // inferred from electronic annotation /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 8380 // RNA splicing // traceable author statement /// 6397 // mRNA processing // inferred from electronic annotation /// 6974 // response to DNA damage stimulus // inferred from electronic annotation /// 6397 // mRNA processing // traceable author statement | 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // not recorded | 166 // nucleotide binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 3676 // nucleic acid binding // inferred from electronic annotation |
| 203175_at | -0.536853833 | 391 | RHOG | ras homolog gene family, member G (rho G) | 74 // regulation of progression through cell cycle // traceable author statement /// 7266 // Rho protein signal transduction // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement /// 7264 // small GTPase mediated signal transduction // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5525 // GTP binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 215716_s_at | -0.536092 | 490 | ATP2B1 | ATPase, Ca++ transporting, plasma membrane 1 | 6812 // cation transport // inferred from electronic annotation /// 6816 // calcium ion transport // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6811 // ion transport // inferred from electronic annotation /// 6810 // transport // traceable author statement | 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 5388 // calcium-transporting ATPase activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5516 // calmodulin binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 16820 // hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation /// 5388 // calcium-transporting ATPase activity // inferred from electronic annotation /// 15085 // calcium ion transporter activity // inferred from electronic annotation /// 15662 // ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism // inferred from electronic annotation /// 4 |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 221693_s_at | -0.535728 | 55168 | MRPS18A | mitochondrial ribosomal protein S18A /// mitochondrial ribosomal protein S18A | 6412 // protein biosynthesis // inferred from electronic annotation /// 6412 // protein biosynthesis // non-traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5739 // mitochondrion // inferred from electronic annotation /// 5763 // mitochondrial small ribosomal subunit // inferred from direct assay /// 5840 // ribosome // inferred from electronic | 3735 // structural constituent of ribosome // inferred from electronic annotation /// 3735 // structural constituent of ribosome // non-traceable author statement |
| 218122_s_at | -0.535398833 | 59343 | SENP2 | SUMO1/sentrin/SMT3 specific peptidase 2 | 6508 // proteolysis // inferred from electronic annotation /// 6512 // ubiquitin cycle // inferred from electronic annotation /// 30111 // regulation of Wnt receptor signaling pathway // non-traceable author statement /// 16055 // Wnt receptor signaling pathway // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation /// 5643 // nuclear pore // inferred from direct assay | 5515 // protein binding // inferred from physical interaction /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16929 // SUMO-specific protease activity // inferred from direct assay /// 8233 // peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation |
| 220797_at | -0.532919333 | 79066 | METT10D | methyltransferase 10 domain containing | — | — | — |
| 224743_at | -0.531840167 | 54928 | IMPAD1 | inositol monophosphatase domain containing 1 | — | — | — |
| 205333_s_at | -0.530217333 | 9986 | RCE1 | RCE1 homolog, prenyl protein peptidase (S. cerevisiae) | 6508 // proteolysis // traceable author statement | 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from elec | 8487 // prenyl-dependent CAAX protease activity // traceable author statement /// 16787 // hydrolase activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 203984_s_at | -0.529476833 | 842 | CASP9 | caspase 9, apoptosis-related cysteine peptidase | 6508 // proteolysis // inferred from electronic annotation /// 8632 // apoptotic program // traceable author statement /// 8635 // caspase activation via cytochrome c // traceable author statement /// 42981 // regulation of apoptosis // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation | 5515 // protein binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 8047 // enzyme activator activity // traceable author statement /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 30693 // caspase activity // inferred from electronic annotation /// 30693 // caspase activity // traceable author statement /// 16787 // hydrolase activity // inferred from electronic annotation /// 4197 // cysteine-type endopeptidase activity // traceable author statement /// 8233 // peptidase activity // traceable author statement |
| 221214_s_at | -0.5271525 | 26012 | NELF | nasal embryonic LHRH factor | — | — | — |
| 1554472_a_at | -0.526283833 | 51105 | PHF20L1 | PHD finger protein 20-like 1 | 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | — | 3676 // nucleic acid binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 1567013_at | -0.522735 | 4780 | NFE2L2 | nuclear factor (erythroid-derived 2)-like 2 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // traceable author statement | 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 4867 // serine-type endopeptidase inhibitor activity // inferred from electronic annotation |
| 1565254_s_at | -0.519686167 | 8178 | ELL | elongation factor RNA polymerase II | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6368 // RNA elongation from RNA polymerase II promoter // traceable author statement | 5634 // nucleus // inferred from electronic annotation | 8159 // positive transcription elongation factor activity // traceable author statement /// 3746 // translation elongation factor activity // inferred from electronic annotation |
| 218631_at | -0.519465 | 60370 | AVPI1 | arginine vasopressin-induced 1 | — | — | — |
| 202208_s_at | -0.516053333 | 10123 | ARL4C | ADP-ribosylation factor-like 4C | 6364 // rRNA processing // inferred from electronic annotation /// 7264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 7046 // ribosome biogenesis // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 5525 // GTP binding // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 201017_at | -0.514700167 | 1964 | EIF1AX | eukaryotic translation initiation factor 1A, X-linked | 6412 // protein biosynthesis // inferred from electronic annotation /// 6413 // translational initiation // inferred from electronic annotation /// 6413 // translational initiation // traceable author statement | 16281 // eukaryotic translation initiation factor 4F complex // not recorded | 3723 // RNA binding // inferred from electronic annotation /// 3743 // translation initiation factor activity // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 8135 // translation factor activity, nucleic acid binding // traceable author statement |
| 201329_s_at | -0.512355167 | 2114 | ETS2 | v-ets erythroblastosis virus E26 oncogene homolog 2 (avian) | 1501 // skeletal development // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // non-traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 3677 // DNA binding // traceable author statement |
| 213025_at | -0.5109205 | 55623 | THUMPD1 | THUMP domain containing 1 | — | — | — |
| 1554549_a_at | -0.505288 | 91833 | WDR20 | WD repeat domain 20 | — | — | — |
| 222195_s_at | -0.505278667 | 51531 | C9orf156 | chromosome 9 open reading frame 156 | — | — | — |
| 212438_at | -0.5002295 | 11017 | RY1 | putative nucleic acid binding protein RY-1 | 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 6397 // mRNA processing // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | — |
| 227161_at | -0.499864667 | 64434 | NOM1 | nucleolar protein with MIF4G domain 1 | — | — | 3723 // RNA binding // inferred from electronic annotation |
| 228810_at | -0.498836167 | 151195 | FLJ40432 | hypothetical protein FLJ40432 | 74 // regulation of progression through cell cycle // inferred from electronic annotation | — | — |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 213534_s_at | -0.495716 | 23178 | PASK | PAS domain containing serine/threonine kinase | 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation | — | 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation |
| 203003_at | -0.495187833 | 4209 | MEF2D | MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D) | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // not recorded /// 7517 // muscle development // traceable author statement /// 6183 // GTP biosynthesis // inferred from electronic annotation /// 6228 // UTP biosynthesis // inferred from electronic annotation /// 6241 // CTP biosynthesis // inferred from electronic annotation /// 9209 // pyrimidine ribonucleoside triphosphate biosynthesis // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // inferred from electronic annotation /// 3700 // transcription factor activity // non-traceable author statement /// 3713 // transcription coactivator activity // not recorded /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 4550 // nucleoside diphosphate kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 203410_at | -0.4943545 | 10947 | AP3M2 | adaptor-related protein complex 3, mu 2 subunit | 6886 // intracellular protein transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation | 30119 // membrane coat adaptor complex // traceable author statement /// 30125 // clathrin vesicle coat // inferred from electronic annotation /// 30662 // coated vesicle membrane // inferred from electronic annotation | — |
| 217686_at | -0.491685 | 5770 | PTPN1 | protein tyrosine phosphatase, non-receptor type 1 | 6470 // protein amino acid dephosphorylation // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement | 5625 // soluble fraction // not recorded /// 5737 // cytoplasm // not recorded /// 5783 // endoplasmic reticulum // inferred from electronic annotation | 4725 // protein tyrosine phosphatase activity // traceable author statement /// 16787 // hydrolase activity // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation /// 4725 // protein tyrosine phosphatase activity // inferred from electronic annotation |
| 223196_s_at | -0.490453667 | 83667 | SESN2 | sestrin 2 | 7050 // cell cycle arrest // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | — |
| 203728_at | -0.489473 | 578 | BAK1 | BCL2-antagonist/killer 1 | 6917 // induction of apoptosis // traceable author statement /// 8637 // apoptotic mitochondrial changes // traceable author statement /// 42981 // regulation of apoptosis // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation | 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | 42802 // identical protein binding // inferred from physical interaction /// 46982 // protein heterodimerization activity // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction |
| 231072_at | -0.4836875 | 90007 | MIDN | midnolin | 6464 // protein modification // inferred from electronic annotation | — | — |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 206461_x_at | -0.482664333 | 4496 | MT1H | metallothionein 1H | — | — | 5507 // copper ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46870 // cadmium ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 46872 // metal ion binding // not recorded |
| 218379_at | -0.482546 | 10179 | RBM7 | RNA binding motif protein 7 | 7126 // meiosis // inferred from electronic annotation | — | 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation |
| 201269_s_at | -0.479001833 | 23386 | NUDCD3 | NudC domain containing 3 | — | — | — |
| 205021_s_at | -0.476169333 | 1112 | CHES1 | checkpoint suppressor 1 | 77 // DNA damage checkpoint // traceable author statement /// 85 // G2 phase of mitotic cell cycle // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 45892 // negative regulation of transcription, DNA-dependent // inferred from direct assay /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5634 // nucleus // Unknown /// 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 16564 // transcriptional repressor activity // inferred from direct assay /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation |
| 1553736_at | -0.463725333 | 196441 | CCDC131 | coiled-coil domain containing 131 | 6396 // RNA processing // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation | 5488 // binding // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 202113_s_at | -0.463090667 | 6643 | SNX2 | sorting nexin 2 | 6886 // intracellular protein transport // inferred from electronic annotation /// 6897 // endocytosis // traceable author statement /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation | — | 5515 // protein binding // inferred from electronic annotation /// 8565 // protein transporter activity // inferred from electronic annotation /// 35091 // phosphoinositide binding // inferred from electronic annotation |
| 224739_at | -0.456507333 | 415116 | PIM3 | pim-3 oncogene | 6468 // protein amino acid phosphorylation // inferred from electronic annotation | — | 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation |
| 228435_at | -0.451847667 | 55527 | FEM1A | Fem-1 homolog a (C.elegans) | — | — | 5488 // binding // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation |
| 209712_at | -0.451743167 | 23169 | SLC35D1 | solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 | 6810 // transport // inferred from electronic annotation /// 15789 // UDP-N-acetylgalactosamine transport // non-traceable author statement /// 30206 // chondroitin sulfate biosynthesis // non-traceable author statement | 5783 // endoplasmic reticulum // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 30176 // integral to endoplasmic reticulum membr | 5351 // sugar porter activity // inferred from electronic annotation /// 5463 // UDP-N-acetylgalactosamine transporter activity // non-traceable author statement |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 224613_s_at | -0.449256833 | 80331 | DNAJC5 | DnaJ (Hsp40) homolog, subfamily C, member 5 | 6457 // protein folding // inferred from electronic annotation | 16020 // membrane // inferred from electronic annotation | 31072 // heat shock protein binding // inferred from electronic annotation /// 51082 // unfolded protein binding // inferred from electronic annotation |
| 206220_s_at | -0.446133 | 22821 | RASA3 | RAS p21 protein activator 3 | 7242 // intracellular signaling cascade // inferred from electronic annotation /// 51056 // regulation of small GTPase mediated signal transduction // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5886 // plasma membrane // traceable author statement | 5096 // GTPase activator activity // inferred from electronic annotation /// 5096 // GTPase activator activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 204516_at | -0.445832 | 6314 | ATXN7 | ataxin 7 | 6997 // nuclear organization and biogenesis // traceable author statement /// 7601 // visual perception // traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation | 3676 // nucleic acid binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation |
| 239788_at | -0.44527 | 55234 | SMU1 | Smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans) | — | 5634 // nucleus // inferred from electronic annotation | — |
| 209675_s_at | -0.443053 | 11100 | HNRPUL1 | heterogeneous nuclear ribonucleoprotein U-like 1 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation /// 30529 // ribonucleoprotein complex // inferred from electronic annotation | 3677 // DNA binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation |
| 208319_s_at | -0.440832 | 5935 | RBM3 | RNA binding motif (RNP1, RRM) protein 3 | 6396 // RNA processing // traceable author statement | — | 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement /// 3723 // RNA binding // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 210269_s_at | -0.438297167 | 8227 | RP13-297E16.1 | DNA segment on chromosome X and Y (unique) 155 expressed sequence, isoform 1 | 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 7165 // signal transduction // non-traceable author statement /// 42113 // B cell activation // non-traceable author statement /// 30187 // melatonin biosynthesis // inferred from electronic annotation /// 48511 // rhythmic process // inferred from electronic annotation /// 6412 // protein biosynthesis // traceable author statement | 16020 // membrane // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 5184 // neuropeptide hormone activity // inferred from electronic annotation /// 8168 // methyltransferase activity // inferred from electronic annotation /// 8171 // O-methyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 17096 // acetylserotonin O-methyltransferase activity // inferred from electronic annotation /// 8171 // O-methyltransferase activity // traceable author statement |
| 228634_s_at | -0.434112833 | 8531 | CSDA | Cold shock domain protein A | 122 // negative regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 9409 // response to cold // traceable author statement | 5634 // nucleus // inferred from electronic annotation /// 5737 // cytoplasm // traceable author statement | 3677 // DNA binding // inferred from electronic annotation /// 3690 // double-stranded DNA binding // traceable author statement /// 3700 // transcription factor activity // non-traceable author statement /// 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 3714 // transcription corepressor activity // traceable author statement /// 3676 // nucleic acid binding // inferred from electronic annotation |
| 224570_s_at | -0.433634667 | 359948 | IRF2BP2 | interferon regulatory factor 2 binding protein 2 | — | — | 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 206485_at | -0.431603667 | 921 | CD5 | CD5 molecule | 8037 // cell recognition // non-traceable author statement /// 8283 // cell proliferation // non-traceable author statement | 5886 // plasma membrane // inferred from direct assay /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic anno | 5044 // scavenger receptor activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 4872 // receptor activity // non-traceable author statement /// 4888 // transmembrane receptor activity // non-traceable author statement |
| 217744_s_at | -0.429976833 | 64065 | PERP | PERP, TP53 apoptosis effector | 6915 // apoptosis // inferred from electronic annotation /// 7155 // cell adhesion // inferred from electronic annotation | 5856 // cytoskeleton // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation | 5198 // structural molecule activity // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation |
| 212461_at | -0.422387333 | 51582 | AZIN1 | antizyme inhibitor 1 | 6596 // polyamine biosynthesis // inferred from electronic annotation | — | 3824 // catalytic activity // inferred from electronic annotation /// 4857 // enzyme inhibitor activity // traceable author statement |
| 202574_s_at | -0.416289 | 1455 | CSNK1G2 | casein kinase 1, gamma 2 | 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // traceable author statement /// 7165 // signal transduction // traceable author statement /// 16055 // Wnt receptor signaling pathway // inferred from electronic annotation | — | 166 // nucleotide binding // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4681 // casein kinase I activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 218884_s_at | -0.414758833 | 60558 | GUF1 | GUF1 GTPase homolog (S. cerevisiae) | 6412 // protein biosynthesis // inferred from electronic annotation /// 6413 // translational initiation // inferred from electronic annotation /// 7264 // small GTPase mediated signal transduction // inferred from electronic annotation | 5622 // intracellular // inferred from electronic annotation | 3743 // translation initiation factor activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation |
| 225408_at | -0.393608 | 4155 | MBP | myelin basic protein | 6955 // immune response // traceable author statement /// 7268 // synaptic transmission // traceable author statement /// 7417 // central nervous system development // traceable author statement /// 8366 // nerve ensheathment // traceable author statement | — | 19911 // structural constituent of myelin sheath // inferred from electronic annotation /// 5198 // structural molecule activity // inferred from electronic annotation |
| 211507_s_at | -0.383815333 | 8897 | MTMR3 | myotubularin related protein 3 | 6470 // protein amino acid dephosphorylation // inferred from direct assay /// 46839 // phospholipid dephosphorylation // inferred from electronic annotation /// 6470 // protein amino acid dephosphorylation // inferred from electronic annotation | 5624 // membrane fraction // inferred from direct assay /// 5737 // cytoplasm // inferred from direct assay | 4437 // inositol or phosphatidylinositol phosphatase activity // inferred from electronic annotation /// 4722 // protein serine/threonine phosphatase activity // inferred from direct assay /// 4725 // protein tyrosine phosphatase activity // inferred from direct assay /// 8270 // zinc ion binding // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation /// 4725 // protein tyrosine phosphatase activity // inferred from electronic annotation |

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**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 214787_at | -0.378812 | 10260 | DENND4A | DENN/MADD domain containing 4A | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6306 // DNA methylation // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 3677 // DNA binding // inferred from electronic annotation /// 8170 // N-methyltransferase activity // inferred from electronic annotation |
| 203883_s_at | -0.376042833 | 22841 | RAB11FIP2 | RAB11 family interacting protein 2 (class I) | 15031 // protein transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation | — | — |
| 212892_at | -0.375620167 | 8427 | ZNF282 | zinc finger protein 282 | 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement | 5622 // intracellular // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement | 3676 // nucleic acid binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 8270 // zinc ion binding // non-traceable author statement /// 16564 // transcriptional repressor activity // traceable author statement /// 46872 // metal ion binding // inferred from electronic annotation |
| 227842_at | -0.373573 | 27314 | RAB30 | RAB30, member RAS oncogene family | 7264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation | 5795 // Golgi stack // traceable author statement /// 16020 // membrane // inferred from electronic annotation | 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 5525 // GTP binding // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 227635_at | -0.36197 | 5930 | RBBP6 | Retinoblastoma binding protein 6 | 16567 // protein ubiquitination // inferred from electronic annotation | 151 // ubiquitin ligase complex // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation | 3676 // nucleic acid binding // inferred from electronic annotation /// 4842 // ubiquitin-protein ligase activity // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 239261_s_at | -0.352969667 | 10699 | CORIN | corin, serine peptidase | 6508 // proteolysis // traceable author statement /// 6629 // lipid metabolism // traceable author statement /// 8217 // blood pressure regulation // traceable author statement /// 9653 // morphogenesis // traceable author statement /// 6508 // proteolysis // inferred from electronic annotation | 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotati | 4252 // serine-type endopeptidase activity // traceable author statement /// 5044 // scavenger receptor activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation |
| 201961_s_at | -0.331560333 | 10193 | RNF41 | ring finger protein 41 | — | — | 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation |
| 241546_at | -0.328537333 | 166378 | SPATA5 | spermatogenesis associated 5 | — | — | 166 // nucleotide binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 17111 // nucleoside-triphosphatase activity // inferred from electronic annotation |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 225997_at | -0.3253695 | 92597 | MOBKL1A | MOB1, Mps One Binder kinase activator-like 1A (yeast) | 46777 // protein amino acid autophosphorylation // inferred from direct assay | 5634 // nucleus // inferred from direct assay /// 5737 // cytoplasm // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation | 8270 // zinc ion binding // inferred from electronic annotation /// 19209 // kinase activator activity // inferred from direct assay /// 19900 // kinase binding // inferred from physical interaction /// 46872 // metal ion binding // inferred from electronic annotation |
| 210681_s_at | -0.322542667 | 9958 | USP15 | ubiquitin specific peptidase 15 | 6511 // ubiquitin-dependent protein catabolism // inferred from electronic annotation /// 6512 // ubiquitin cycle // inferred from electronic annotation | — | 4197 // cysteine-type endopeptidase activity // traceable author statement /// 4221 // ubiquitin thiolesterase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4843 // ubiquitin-specific protease activity // traceable author statement |
| 237741_at | -0.316481833 | 55186 | SLC25A36 | Solute carrier family 25, member 36 | 6810 // transport // inferred from electronic annotation /// 6839 // mitochondrial transport // inferred from electronic annotation | 5739 // mitochondrion // inferred from electronic annotation /// 5743 // mitochondrial inner membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from el | 5215 // transporter activity // inferred from electronic annotation /// 5488 // binding // inferred from electronic annotation |
| 1556839_s_at | -0.309602833 | 645022 | LOC645022 | Hypothetical protein LOC645022 | — | — | — |

*(Continued)*

**TABLE E1**. *(Continued)*

| Probe Set ID | Log Ratio | Entrez Gene | Gene Symbol | Gene Descriptor | Gene Ontology | | |
|---|---|---|---|---|---|---|---|
| | | | | | Biological Process | Cellular Component | Molecular Function |
| 1554379_a_at | -0.305492 | 7161 | TP73 | tumor protein p73 | 6298 // mismatch repair // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 8630 // DNA damage response, signal transduction resulting in induction of apoptosis // traceable author statement /// 45786 // negative regulation of progression through cell cycle // inferred from electronic annotation | 5634 // nucleus // inferred from electronic annotation | 3700 // transcription factor activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation |
| 239391_at | -0.301317167 | 158293 | C9orf10OS | Chromosome 9 open reading frame 10 opposite strand | — | — | — |
| 220453_at | -0.211763667 | 54896 | PQLC2 | PQ loop repeat containing 2 | — | — | — |



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