


Clinical efficacy and immune regulation with peanut oral

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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 IgG₄ 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* 2009;124:292-300.)

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

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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 labels⁷ 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 asthma¹¹ 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 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

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

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] ≥ 3 mm of negative control), and a peanut CAP FEIA ≥ 15 kU/L (Phadia AB; Pharmacia, Inc, Uppsala, Sweden). Subjects were also included if they had a CAP FEIA ≥ 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 (30,000g 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).

Titred skin prick testing

Titred 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 μ g/mL peanut extract; 1 μ g/mL anti-IgE (polyclonal rabbit antihuman; Bethyl Laboratories, Montgomery, Tx); or 2 μ mol/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-DR⁺ events were acquired. Data were analyzed by using FlowJo software (TreeStar, Ashland, Ore).

Assays for IgE, IgG, and IgG₄

Peanut-specific IgE, IgG, and IgG₄ 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 μ L) of serum obtained from the clinical study and indicator serum were incubated with peanut extract (0.04 μ g/mL in 2.5 μ L) 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 4×10^5 cells/well in triplicate and incubated with crude peanut protein (40 μ g/well), Ara h 2 (20 μ g/well), concanavalin A (8 μ g/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 μ g/mL streptomycin; Mediatech, Manassas, Va). Cells were cultured at 37°C in 5% CO₂ 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 \times months on immunotherapy, and time of culture. The response variable was

$$\log(y+I),$$

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 (2×10^6 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 Microarrays²¹ 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)	

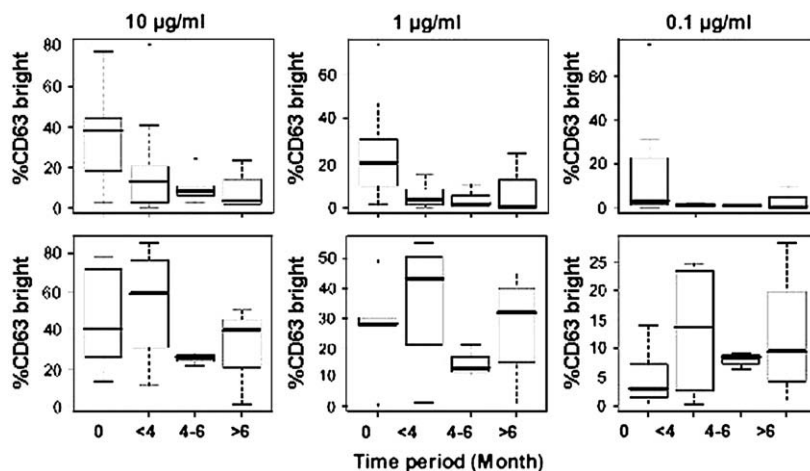


FIG 1. Effect of peanut OIT on basophil activation. *Top row*, Subjects who received peanut OIT. *Bottom row*, Subjects in an observational study of peanut allergy. At a peanut concentration of 10 µg/mL, OIT results in significant initial changes in basophil responsiveness ($*P < .001$).

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 IgG₄

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

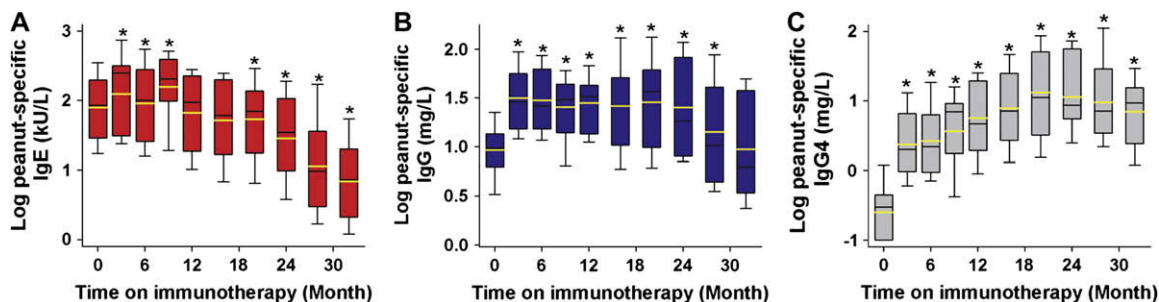


FIG 2. Serum levels of peanut-specific immunoglobulins during peanut OIT. In the serum of 28 subjects undergoing immunotherapy, peanut-specific IgE (A), IgG (B), and IgG₄ (C) were measured by using the ImmunoCAP instrument. Values are log-transformed, and median and mean values are represented by black and yellow horizontal lines, respectively. A mixed model, repeated-measures ANOVA was used to determine the statistical significance between baseline and treatment time points (* $P < .0005$).

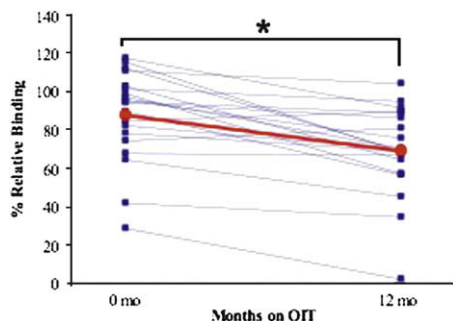


FIG 3. Peanut OIT leads to FAB inhibition. Blue lines represent individual data points, red line the mean. Statistical differences between pre-OIT and 12-month-post-OIT serum were determined by Wilcoxon signed-rank test (* $P < .001$).

(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 IgG₄ 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 IgG₄ 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 study¹⁶ 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% \pm 23.4% at baseline to 69.3% \pm 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-1 β , IL-6, IL-8, macrophage inflammatory protein [MIP] 1 β , 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-1 β , IL-5, TNF- α , and MIP-1 β , 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 chemoattractant 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

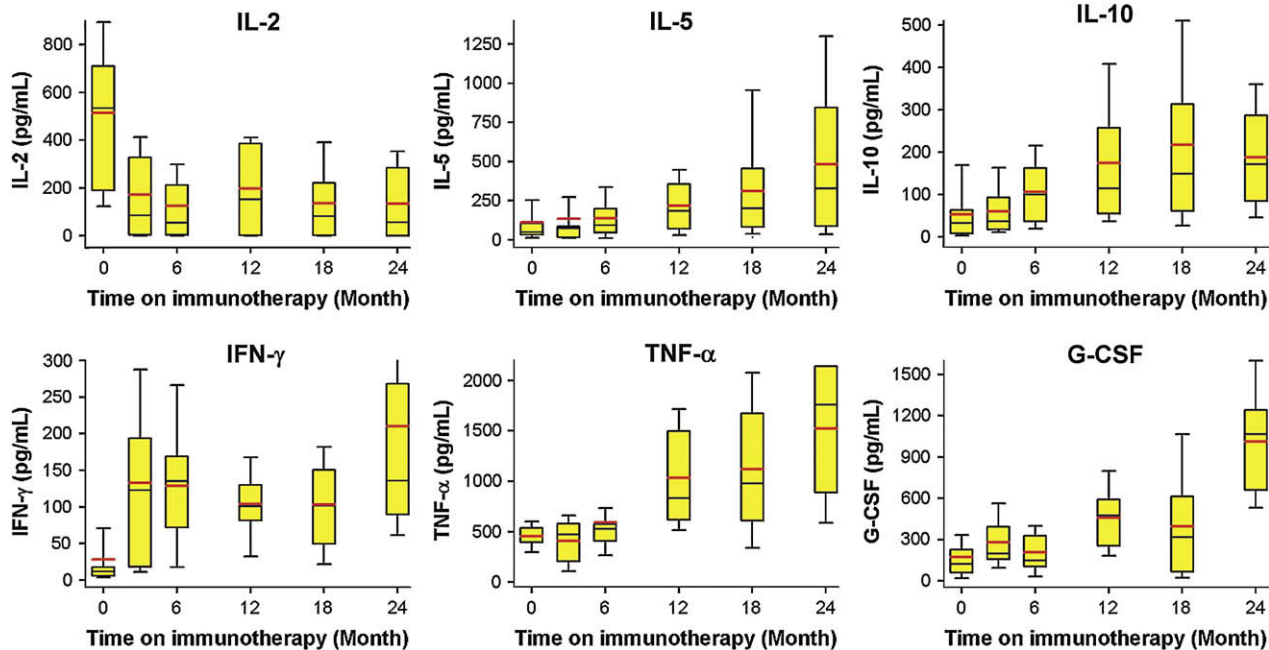


FIG 4. Cytokines secreted from PBMCs after ConA stimulation. The plotted 6 cytokines/chemokines all had statistically significant changes versus medium alone ($P < .05$). *Black lines* are median values; *red lines* are means.

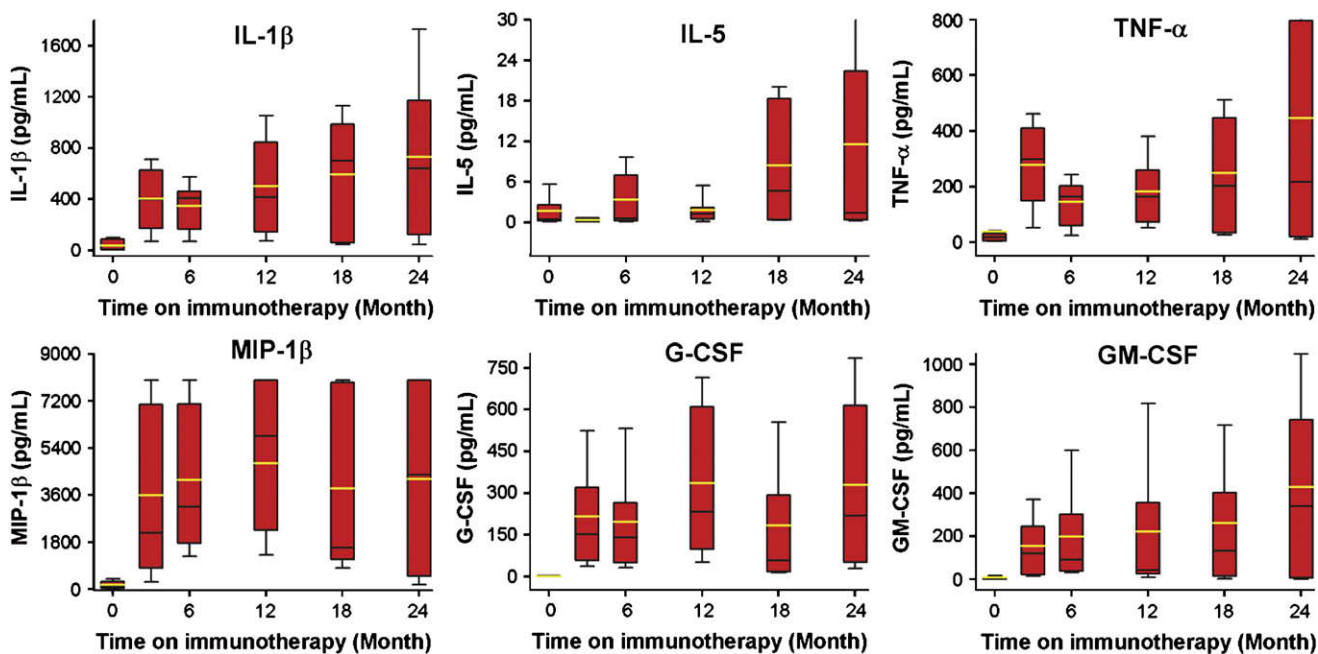


FIG 5. Cytokines secreted from PBMCs stimulated with crude peanut extract. The plotted 6 cytokines/chemokines all had statistically significant changes versus medium alone ($P < .05$). *Black lines* are median values; *yellow lines* are means.

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 *BCL2L1*, *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,

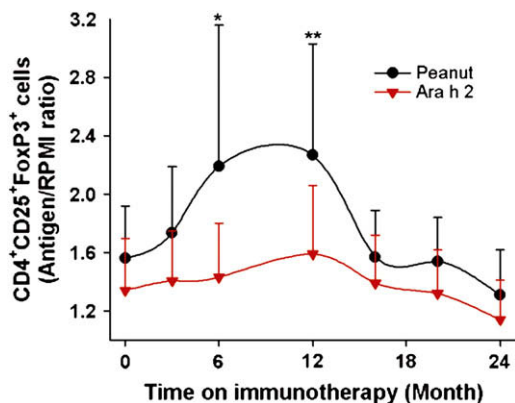


FIG 6. Changes of FoxP3⁺ Treg cells during peanut oral immunotherapy. PBMCs from 10 subjects were cultured in presence of peanut proteins, Ara h 2, or medium alone (RPMI). Paired *t* tests were used to determine statistical differences between baseline and later time points (*P* < .05, 6 months; *P*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

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 IgG₄ increased by approximately 3 months, and then the IgE declined by 18 months. IgG began to decrease by the end of the study, whereas IgG₄ remained elevated. Increased levels of specific IgG₄ 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

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

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

§Log₂ (expression after 6 months OIT/expression before OIT), calculated from microarray data.

exposure.^{28,29} Previous reports have demonstrated that fractionated IgG₄ antibodies from serum of patients who received grass pollen immunotherapy inhibit IgE-FAB binding to B cells,³⁰⁻³³ suggesting a functional role of IgG₄ 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 IgG₄ 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 IgG₄ 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.

REFERENCES

1. Sicherer SH, Munoz-Furlong A, Sampson HA. Prevalence of peanut and tree nut allergy in the United States determined by means of a random digit dial telephone survey: a 5-year follow-up study. *J Allergy Clin Immunol* 2003;112:1203-7.
2. Emmett SE, Angus FJ, Fry JS, Lee PN. Perceived prevalence of peanut allergy in Great Britain and its association with other atopic conditions and with peanut allergy in other household members. *Allergy* 1999;54:380-5.
3. Kanny G, Moneret-Vautrin DA, Flabbee J, Beaudouin E, Morisset M, Thevenin F. Population study of food allergy in France. *J Allergy Clin Immunol* 2001;108:133-40.
4. Bock SA, Munoz-Furlong A, Sampson HA. Fatalities due to anaphylactic reactions to foods. *J Allergy Clin Immunol* 2001;107:191-3.
5. Bock SA, Munoz-Furlong A, Sampson HA. Further fatalities caused by anaphylactic reactions to food, 2001-2006. *J Allergy Clin Immunol* 2007;119:1016-8.
6. Sampson HA. Update on food allergy. *J Allergy Clin Immunol* 2004;113:805-19.
7. Joshi P, Mofidi S, Sicherer SH. Interpretation of commercial food ingredient labels by parents of food-allergic children. *J Allergy Clin Immunol* 2002;109:1019-21.
8. Vierk K, Falci K, Wolyniak C, Klontz KC. Recalls of foods containing undeclared allergens reported to the US Food and Drug Administration, fiscal year 1999. *J Allergy Clin Immunol* 2002;109:1022-6.
9. Altschul AS, Scherrer DL, Munoz-Furlong A, Sicherer SH. Manufacturing and labeling issues for commercial products: relevance to food allergy. *J Allergy Clin Immunol* 2001;108:468.
10. Sicherer SH, Burks AW, Sampson HA. Clinical features of acute allergic reactions to peanut and tree nuts in children. *Pediatrics* 1998;102:e6.
11. Till SJ, Francis JN, Nouri-Aria K, Durham SR. Mechanisms of immunotherapy. *J Allergy Clin Immunol* 2004;113:1025-34.
12. Oppenheimer JJ, Nelson HS, Bock SA, Christensen F, Leung DY. Treatment of peanut allergy with rush immunotherapy. *J Allergy Clin Immunol* 1992;90:256-62.
13. Nelson HS, Lahr J, Rule R, Bock A, Leung D. Treatment of anaphylactic sensitivity to peanuts by immunotherapy with injections of aqueous peanut extract. *J Allergy Clin Immunol* 1997;99:744-51.
14. Patriarca G, Nucera E, Roncallo C, Pollastrini E, Bartolozzi F, De Pasquale T, et al. Oral desensitizing treatment in food allergy: clinical and immunological results. *Aliment Pharmacol Ther* 2003;17:459-65.
15. Meglio P, Bartone E, Plantamura M, Arabito E, Giampietro PG. A protocol for oral desensitization in children with IgE-mediated cow's milk allergy. *Allergy* 2004;59:980-7.
16. Buchanan AD, Green TD, Jones SM, Scurlock AM, Christie L, Althage KA, et al. Egg oral immunotherapy in nonanaphylactic children with egg allergy. *J Allergy Clin Immunol* 2007;119:199-205.
17. United States Department of Agriculture. USDA National Nutrient Database for Standard Reference, release 21 (2002). Available at: <http://ars.usda.gov/Services/docs.htm?docid=17477>. Accessed January 20, 2009.
18. McDermott RA, Porterfield HS, El Mezayen R, Burks AW, Pons L, Schlichting DG, et al. Contribution of Ara h 2 to peanut-specific, immunoglobulin E-mediated, cell activation. *Clin Exp Allergy* 2007;37:752-63.
19. Wanich N, Nowak-Wegrzyn A, Sampson HA, Shreffler WG. Allergen-specific basophil activation associated with clinical tolerance in patients with milk allergy. *J Allergy Clin Immunol* 2009;123:789-94.
20. Wilcock LK, Francis JN, Durham SR. IgE-facilitated antigen presentation: role in allergy and the influence of allergen immunotherapy. *Immunol Allergy Clin North Am* 2006;26:333-9.
21. Tusher VG, Tibshirani R, Chu G. Significance analysis of microarrays applied to the ionizing radiation response. *Proc Natl Acad Sci U S A* 2001;98:5116-21.
22. Longo G, Barbi E, Berti I, Meneghetti R, Pittalis A, Ronfani L, et al. Specific oral tolerance induction in children with very severe cow's milk-induced reactions. *J Allergy Clin Immunol* 2008;121:343-7.
23. Sullivan TJ. Antigen-specific desensitization of patients allergic to penicillin. *J Allergy Clin Immunol* 1982;69:500-8.
24. MacGlashan D, Miura K. Loss of syk kinase during IgE-mediated stimulation of human basophils. *J Allergy Clin Immunol* 2004;114:1317-24.
25. Clements JL, Yang B, Ross-Barta SE, Eliason SL, Hrstka RF, Williamson RA, et al. Requirement for the leukocyte-specific adapter protein SLP-76 for normal T cell development. *Science* 1998;281:416-9.
26. Yazdanbakhsh M, van den Biggelaar A, Maizels RM. Th2 responses without atopy: immunoregulation in chronic helminth infections and reduced allergic disease. *Trends Immunol* 2001;22:372-7.

27. James JA, Sampson HA. Immunologic changes associated with the development of tolerance in children with cow milk allergy. *J Pediatr* 1992;121:371-3.
28. Platts-Mills T, Vaughan J, Squillace S, Woodfolk J, Sporik R. Sensitisation, asthma, and a modified Th2 response in children exposed to cat allergen: a population-based cross-sectional study. *Lancet* 2001;357:752-6.
29. Platts-Mills TA, Vaughan JW, Blumenthal K, Pollart SS, Sporik RB. Serum IgG and IgG4 antibodies to Fel d 1 among children exposed to 20 microg Fel d 1 at home: relevance of a nonallergic modified Th2 response. *Int Arch Allergy Immunol* 2001;124:126-9.
30. Francis JN. The facilitated antigen binding (FAB) assay—a protocol to measure allergen-specific inhibitory antibody activity. *Methods Mol Med* 2008;138:255-61.
31. Klunker S, Saggar LR, Seyfert-Margolis V, Asare AL, Casale TB, Durham SR, et al. Combination treatment with omalizumab and rush immunotherapy for ragweed-induced allergic rhinitis: Inhibition of IgE-facilitated allergen binding. *J Allergy Clin Immunol* 2007;120:688-95.
32. Nouri-Aria KT, Wachholz PA, Francis JN, Jacobson MR, Walker SM, Wilcock LK, et al. Grass pollen immunotherapy induces mucosal and peripheral IL-10 responses and blocking IgG activity. *J Immunol* 2004;172:3252-9.
33. Wachholz PA, Soni NK, Till SJ, Durham SR. Inhibition of allergen-IgE binding to B cells by IgG antibodies after grass pollen immunotherapy. *J Allergy Clin Immunol* 2003;112:915-22.
34. Tighe H, Takabayashi K, Schwartz D, Van Nest G, Tuck S, Eiden JJ, et al. Conjugation of immunostimulatory DNA to the short ragweed allergen amb a 1 enhances its immunogenicity and reduces its allergenicity. *J Allergy Clin Immunol* 2000;106:124-34.
35. Karlsson MR, Rugtveit J, Brandtzaeg P. Allergen-responsive CD4+CD25+ regulatory T cells in children who have outgrown cow's milk allergy. *J Exp Med* 2004;199:1679-88.
36. Chatila TA, Blaeser F, Ho N, Lederman HM, Voulgaropoulos C, Helms C, et al. JM2, encoding a fork head-related protein, is mutated in X-linked autoimmunity-allergic dysregulation syndrome. *J Clin Invest* 2000;106:R75-81.
37. Liu Z, Yelverton RW, Kraft B, Tanner SB, Olsen NJ, Aune TM. Highly conserved gene expression profiles in humans with allergic rhinitis altered by immunotherapy. *Clin Exp Allergy* 2005;35:1581-90.
38. Guerra F, Carracedo J, Madueno JA, Sanchez-Guijo P, Ramirez R. Allergens induce apoptosis in lymphocytes from atopic patients. *Hum Immunol* 1999;60:840-7.
39. Guerra F, Carracedo J, Solana-Lara R, Sanchez-Guijo P, Ramirez R. TH2 lymphocytes from atopic patients treated with immunotherapy undergo rapid apoptosis after culture with specific allergens. *J Allergy Clin Immunol* 2001;107:647-53.
40. Tsai YG, Chien JW, Chen WL, Shieh JJ, Lin CY. Induced apoptosis of TH2 lymphocytes in asthmatic children treated with *Dermatophagoides pteronyssinus* immunotherapy. *Pediatr Allergy Immunol* 2005;16:602-8.

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

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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

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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)

Gene Ontology							
Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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 duncce 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

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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)

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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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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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

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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

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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	ID11	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

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				Gene Ontology			
Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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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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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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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	—

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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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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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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	—

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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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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	—

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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	—	—	—

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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 cytidyltransferase 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	—	—	—

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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 (<i>S. cerevisiae</i>)	—	—	—

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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

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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

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					Gene Ontology		
Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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	—	—	—

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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	—

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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 metalloproteinase 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 // metalloproteinase 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	—

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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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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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 annotation	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

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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

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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

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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	—	—	—

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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

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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

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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

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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

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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	putative 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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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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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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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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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-acyltransferase 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 annotation
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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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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	—

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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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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 statement	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

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					Gene Ontology		
Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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	—	—	—

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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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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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 annotation	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

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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

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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	AVP11	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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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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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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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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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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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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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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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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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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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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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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	—	1991 // 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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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	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

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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 annotation	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

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Probe Set ID	Log Ratio	Entrez Gene	Gene Symbol	Gene Descriptor	Biological Process	Cellular Component	Molecular Function
225997_at	-0.3253695	92597	MOBK1A	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	—	—	—

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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	C9orf100S	Chromosome 9 open reading frame 10 opposite strand	—	—	—
220453_at	-0.211763667	54896	PQLC2	PQ loop repeat containing 2	—	—	—