

ORIGINAL ARTICLE

STAT3 Mutations in the Hyper-IgE Syndrome

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ABSTRACT

BACKGROUND

The hyper-IgE syndrome (or Job's syndrome) is a rare disorder of immunity and connective tissue characterized by dermatitis, boils, cyst-forming pneumonias, elevated serum IgE levels, retained primary dentition, and bone abnormalities. Inheritance is autosomal dominant; sporadic cases are also found.

METHODS

We collected longitudinal clinical data on patients with the hyper-IgE syndrome and their families and assayed the levels of cytokines secreted by stimulated leukocytes and the gene expression in resting and stimulated cells. These data implicated the signal transducer and activator of transcription 3 gene (*STAT3*) as a candidate gene, which we then sequenced.

RESULTS

We found increased levels of proinflammatory gene transcripts in unstimulated peripheral-blood neutrophils and mononuclear cells from patients with the hyper-IgE syndrome, as compared with levels in control cells. In vitro cultures of mononuclear cells from patients that were stimulated with lipopolysaccharide, with or without interferon- γ , had higher tumor necrosis factor α levels than did identically treated cells from unaffected persons ($P=0.003$). In contrast, the cells from patients with the hyper-IgE syndrome generated lower levels of monocyte chemoattractant protein 1 in response to the presence of interleukin-6 ($P=0.03$), suggesting a defect in interleukin-6 signaling through its downstream mediators, one of which is *STAT3*. We identified missense mutations and single-codon in-frame deletions in *STAT3* in 50 familial and sporadic cases of the hyper-IgE syndrome. Eighteen discrete mutations, five of which were hot spots, were predicted to directly affect the DNA-binding and SRC homology 2 (SH2) domains.

CONCLUSIONS

Mutations in *STAT3* underlie sporadic and dominant forms of the hyper-IgE syndrome, an immunodeficiency syndrome involving increased innate immune response, recurrent infections, and complex somatic features.

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THE SYNDROME DESCRIBED AS JOB'S SYNDROME by Davis et al. in 1966¹ and as hyperimmunoglobulinemia E by Buckley et al. in 1972² was originally characterized by recurrent cold staphylococcal abscesses, pneumonia, eczema, hyperextensibility, and extreme elevation of IgE levels. Since then, additional features of the hyper-IgE syndrome have been recognized, including scoliosis, pathologic fractures, pneumatoceles, delayed dental deciduation,^{3,4} coronary-artery aneurysms,⁵ brain lesions, and Chiari's malformations.⁶ Pneumonia in patients with the hyper-IgE syndrome is typically caused by infections with *Staphylococcus aureus*, *Haemophilus influenzae*, or *Streptococcus pneumoniae* and leads to pneumatoceles,³ providing portals for fatal infections with bacteria and filamentous fungi.⁷

Eosinophilia, eczema, and elevated IgE levels focused attention on the T helper cell Th1/Th2 profile,⁸ but no primary defect was uncovered. Cytogenetic and linkage data suggested the presence of a locus on chromosome 4q, but no disease gene was found there.⁹ Microarray-based approaches have yielded inconsistent results.^{10,11} We therefore aimed to comprehensively describe the phenotypes of affected persons in a large cohort and to assay gene expression and in vitro cytokine production to identify relevant pathways.

METHODS

PATIENTS AND CONTROLS

Patients suspected to have the hyper-IgE syndrome, or their parents, and their relatives gave written informed consent. These patients and relatives were enrolled in studies approved by the institutional review board of the National Institute of Allergy and Infectious Diseases. We collected blood samples while patients were clinically well and were not receiving corticosteroids or nonsteroidal antiinflammatory drugs. An empirical scoring system was used to calculate the risk of carrying the hyper-IgE syndrome trait on the basis of an aggregation of diagnostic features.⁹ We arbitrarily categorized hyper-IgE syndrome scores of 0 to 15 as unaffected, 16 to 39 as possibly affected, 40 to 59 as probably affected, and 60 or more as definitely affected.⁹ We analyzed by microarray blood samples obtained from probands who were definitely affected (had scores of 60 or more) and were over the age of 16 years. We also performed cyto-

kine phenotyping on these samples, in addition to those from persons with familial and sporadic hyper-IgE syndrome (which included possibly and probably affected persons). Samples from 50 patients and 48 family members were available for sequence analysis. The race or ethnic group of patients was determined by a physician author and by self report (for details, see the Supplementary Appendix, available with the full text of this article at www.nejm.org). Control DNA was collected according to several approved protocols from unaffected persons: 125 whites, 15 Hispanics, 4 blacks, 2 Asians, 1 white Hispanic, 1 black Hispanic, and 10 persons of unknown ancestry. Race or ethnic group of these control subjects was self-reported.

MICROARRAY ANALYSIS

We isolated polymorphonuclear leukocytes and peripheral-blood mononuclear cells from venous blood samples and carried out phagocytosis and microarray assays as previously described.^{12,13} We labeled samples, allowed for hybridization of complementary RNA to microarrays (HU133 Plus 2.0, Affymetrix), and scanned the microarrays according to standard Affymetrix protocols. For each time point, we analyzed cells from 9 control donors of peripheral-blood mononuclear cells or 10 control donors of polymorphonuclear leukocytes and 7 patients with the hyper-IgE syndrome, using a separate oligonucleotide array for each donor. One sample of stimulated control polymorphonuclear leukocytes for the 360-minute time point was lost owing to technical error.

We analyzed the gene-expression data by using Microarray Suite software, version 5.0 (Affymetrix), and GeneSpring software, version 5.0 (Silicon Genetics), as described previously,^{12,13} but with modifications. We defined genes as being differentially expressed when all three of the following criteria were met: the gene was identified as "present" by the Microarray Suite software in 8 of the 9 samples of peripheral-blood mononuclear cells or 9 of the 10 samples of polymorphonuclear leukocytes from control subjects and in 6 of the 7 samples of cells from patients, the difference in gene expression between the samples from control subjects and those from patients was twofold or greater, and the normalized signal intensity was at least 100. We carried out principal-component analysis using software from Partek and compared

the average difference intensity of transcript levels in cells from control subjects and patients with the use of Student's *t*-test. Complete microarray data are provided, with analysis, in Tables 1, 2, 3, 4, and 5 of the Supplementary Appendix. Raw data are available at the Gene Expression Omnibus Web site (www.ncbi.nlm.nih.gov/geo/) under accession number GSE8507. We visualized the implicated biochemical pathways using Ingenuity Pathways Analysis software (Ingenuity Systems).

CYTOKINES

Peripheral-blood mononuclear cells were prepared with the use of density centrifugation from heparinized whole blood, as previously described.¹⁴ Cells were stimulated for 48 hours at 37°C in 5% carbon dioxide with phytohemagglutinin (1:100), phytohemagglutinin with interleukin-12 (10 ng per milliliter), lipopolysaccharide (200 ng per milliliter), lipopolysaccharide with interferon- γ (1000 IU per milliliter), or interleukin-6 (40 ng per milliliter). The supernatants were harvested and stored at -20°C until cytokine levels could be measured with the use of plate-based methods (Meso Scale Discovery) or bead-based methods (BioRad Luminex), according to the manufacturers' recommendations. The cytokine levels were compared with the use of a Mann-Whitney U test (GraphPad Software), with *P* values of less than 0.05 considered to indicate statistical significance.

SEQUENCING

Complementary DNA (cDNA) was prepared from peripheral-blood mononuclear cells and neutrophils of unrelated probands and control subjects and was sequenced for the signal transducer and activator of transcription 3 gene (*STAT3*) (for a list of primers, see the Methods in the Supplementary Appendix). Sequencing was performed on an Applied Biosystems 3100 sequencer and analyzed using Sequencher software (Gene Codes). We also sequenced cDNA from peripheral-blood leukocytes or transformed lymphoblastoid cell lines or genomic DNA of relatives. For sequencing of genomic DNA, polymerase-chain-reaction primers (available in the Supplementary Appendix) were chosen according to the proband's mutation. GenBank recognizes three human isoforms of *STAT3*: NP_644805.1, NP_003141.2, and NP_998827.1. The amino acid positions reported here are for the isoform NP_644805.1.

FLOW CYTOMETRY FOR DETECTION OF PHOSPHORYLATED STAT3

Peripheral-blood mononuclear cells from healthy adults or from patients with the hyper-IgE syndrome were isolated with the use of a Ficoll gradient. Peripheral-blood mononuclear cells (1×10^6) were incubated in 100 μ l of phosphate-buffered saline with 2% fetal-calf serum, either without stimuli or with interleukin-6 (10 ng per milliliter) (R&D Systems), for 25 or 60 minutes. Cells were fixed, permeabilized, and stained, as previously described.¹⁵ An Alexa Fluor 647 conjugated phospho-STAT3 antibody against phospho-S727 (BD Biosciences) was used to identify intracellular or intranuclear phospho-STAT3. Mouse IgG1 (BD Biosciences) was used as isotype control. Analysis was carried out on a FACSCalibur flow cytometer (BD Biosciences) with Cell Quest software (BD Biosciences).

BIOINFORMATICS ANALYSIS OF MISSENSE CHANGES IN STAT3

For the missense changes detected, we used bioinformatics methods encoded in the programs Sorting Intolerant from Tolerant (SIFT)¹⁶ and PolyPhen.¹⁷ SIFT reports the probability that the substitution is deleterious by predicting whether the substitution is or is not probably damaging. PolyPhen reports a score, with putatively benign changes scored from 0.00 to 1.50, possibly damaging changes scored from 1.51 to 2.00, and probably damaging changes scored as 2.01 or greater.

RESULTS

GENE-EXPRESSION PROFILING OF LEUKOCYTES

We found greater levels of expression of proinflammatory molecules in unstimulated and phagocytosis-stimulated leukocytes of patients with the hyper-IgE syndrome than in those of controls (Fig. 1 in the Supplementary Appendix and Tables 1, 2, 3, and 4 in the Supplementary Appendix). Thirty transcripts encoding proteins related to interferon signal transduction or typically induced by interferon showed elevated levels of expression in polymorphonuclear leukocytes from patients with the hyper-IgE syndrome (Table 1 in the Supplementary Appendix). Known or putative genes involved in host defense were up-regulated in polymorphonuclear leukocytes and peripheral-blood mononuclear cells from the patients (Fig. 1C in

Table 1. Stimulated Cytokine Production in Leukocytes from Patients with the Hyper-IgE Syndrome and in Those from Controls.*

Analyte and Stimulus	Patient <i>pg/ml</i>	Control	P Value
TNF- α			
Unstimulated (LPS)	17.9 $\pm$ 6.6 (N=38)	54.3 $\pm$ 20.8 (N=32)	0.23
LPS	1368.0 $\pm$ 192.3 (N=38)	597.3 $\pm$ 86.8 (N=32)	0.003
LPS + interferon- γ	4244.0 $\pm$ 382.5 (N=38)	3044.0 $\pm$ 311.9 (N=32)	0.02
Unstimulated (SAC)	19.7 $\pm$ 8.0 (N=31)	68.1 $\pm$ 27.3 (N=24)	0.22
SAC	5651.0 $\pm$ 519.9 (N=31)	2404.0 $\pm$ 397.3 (N=24)	<0.001
HKLM	2807.0 $\pm$ 364.8 (N=30)	862.4 $\pm$ 101.7 (N=12)	<0.001
Interleukin-12p70			
Unstimulated	5.8 $\pm$ 0.7 (N=31)	10.3 $\pm$ 3.4 (N=24)	0.77
LPS	36.5 $\pm$ 6.3 (N=30)	12.9 $\pm$ 2.7 (N=23)	0.001
LPS + interferon- γ	837.1 $\pm$ 132.2 (N=31)	385.3 $\pm$ 93.0 (N=24)	0.003
Interferon- γ			
Unstimulated	36.4 $\pm$ 4.5 (N=31)	43.7 $\pm$ 7.4 (N=25)	0.75
PHA	127,610.0 $\pm$ 17,956.0 (N=27)	71,238.0 $\pm$ 11,382.0 (N=24)	0.03
PHA + interleukin-12	158,823.0 $\pm$ 14,900.0 (N=29)	102,820.0 $\pm$ 20,715.0 (N=23)	0.03
MCP-1			
Unstimulated	346.4 $\pm$ 263.3 (N=10)	252.5 $\pm$ 145.6 (N=6)	0.07
Interleukin-6	1761.0 $\pm$ 878.7 (N=10)	4494.0 $\pm$ 649.3 (N=6)	0.03

* Plus-minus values are means $\pm$ SD. TNF- α denotes tumor necrosis factor α , LPS lipopolysaccharide, SAC *Staphylococcus aureus* Cowan strain, HKLM heat-killed *Listeria monocytogenes*, and MCP-1 monocyte chemoattractant protein 1.

the Supplementary Appendix and Tables 1, 2, and 3 in the Supplementary Appendix). After phagocytosis, 15 genes encoding proteins related to interferon signal transduction or induced by interferon showed elevated levels of expression in

polymorphonuclear leukocytes from patients, as compared with those from controls (Fig. 2 in the Supplementary Appendix and Table 4 in the Supplementary Appendix). Taken together, these data suggest that cytokine-related signal transduction,

Table 2. Results of STAT3 DNA Sequencing of Selected Probands and Family Members.*

Member	Race or Ethnic Group†	Hyper-IgE Syndrome Score‡	Mutation		
			Nucleotide and Amino Acid	Domain	Type
Family J001					
Proband	White	68	1144C→T, R382W	DNA binding	Sporadic
Daughter	White	55	1144C→T, R382W	DNA binding	Transmitted
Daughter	White	25	None		
Husband	White	1	None		
Family J002					
Proband	White	90	1865C→T, T622I	SH2	De novo
Daughter	White	80	1865C→T, T622I	SH2	Transmitted
Daughter	White	6	None		
Sister	White	16	None		
Sister	White	25	None		
Mother	White	4	None		
Father	White	33	None		
Wife	White	16	None		
Family J004					
Proband	White	87	1144C→T, R382W	DNA binding	Sporadic
Grandfather	White	Not scored	None		
Father	White	3	None		
Family J005					
Proband	White–Black	54	1144C→T, R382W	DNA binding	De novo
Father	Black	Not scored	None		
Mother	White	Not scored	None		
Family J006					
Proband	White	90	1151T→C, F384S	DNA binding	Sporadic
Family J007					
Proband	White	82	1268G→A, R423Q	DNA binding	Sporadic
Brother	White	4	None		
Sister	White	3	None		
Daughter	White	82	1268G→A, R423Q	DNA binding	Transmitted
Sister	White	24	None		
Niece	White	9	None		
Mother	White	6	None		
Family J008					
Proband	White	79	1145G→A, R382Q	DNA binding	De novo
Father	White	4	None		
Mother	White	3	None		
Family J009					
Proband	White	82	1832G→A, S611N	SH2	Sporadic

Table 2. (Continued.)

Member	Race or Ethnic Group†	Hyper-IgE Syndrome Score‡	Mutation		
			Nucleotide and Amino Acid	Domain	Type
Family J010					
Proband	White	85	1144C→T, R382W	DNA binding	De novo
Father	White	9	None		
Brother	White	1	None		
Sister	White	4	None		
Cousin	White	5	None		
Mother	White	0	None		
Family J011					
Proband	White	69	1909G→A, V637M	SH2	Transmitted
Sister	White	86	1909G→A, V637M	SH2	Transmitted
Mother	White	19	None		
Family J012					
Proband	White	84	1387delGTG, V463del	DNA binding	Sporadic
Family J013					
Proband	White	66	1150T→C, F384L	DNA binding	Sporadic
Family J014					
Proband	White	96	1909G→A, V637M	SH2	De novo
Father	White	14	None		
Mother	White	16	None		
Sister	White	38	None		
Sister	White	5	None		
Family J015					
Proband	White	96	1861T→G, F621V	SH2	Sporadic
Family J016					
Proband	Asian	65	1268G→A, R423Q	DNA binding	De novo
Son	Asian	34	1268G→A, R423Q	DNA binding	Transmitted
Daughter	Asian	10	None		
Daughter	Asian	34	1268G→A, R423Q	DNA binding	Transmitted
Wife	Asian	1	None		
Father	Asian	0	None		
Mother	Asian	1	None		
Family J017					
Proband	White	82	1145G→A, R382Q	DNA binding	Transmitted
Brother	White	3	None		
Father	White	48	1145A→G, R382Q mosaic	DNA binding	Sporadic
Mother	White	1	None		
Sister	White	6	None		
Brother	White	67	1145G→A, R382Q	DNA binding	Transmitted

Table 2. (Continued.)

Member	Race or Ethnic Group†	Hyper-IgE Syndrome Score‡	Mutation		
			Nucleotide and Amino Acid	Domain	Type
Family J020					
Proband	Black	100	1144C→T, R382W	DNA binding	Sporadic
Mother	Black	Not scored	None		
Family J021					
Proband	Black	71	1145G→A, R382Q	DNA binding	Sporadic
Family J022					
Proband	White	93	1909G→A, V637M	SH2	Sporadic
Family J029					
Proband	White	62	1939A→G, N647D	SH2	Transmitted
Mother	White	4	None		
Sister	White	52	None		
Sister	White	69	1939A→G, N647D	SH2	Transmitted
Niece	White	29	None		
Niece	White	56	1939A→G, N647D	SH2	Transmitted
Family J030					
Proband	Black	65	1145G→A, R382Q	DNA binding	De novo
Father	Black	4	None		
Mother	Black	10	None		
Family J035					
Proband	White	77	1909G→A, V637M	SH2	Sporadic
Daughter	White	76	1909G→A, V637M	SH2	Transmitted
Daughter	White	27	None		
Wife	White	1	None		
Family J045					
Proband	Hispanic	64	1144C→T, R382W	DNA binding	Sporadic
Family J053					
Proband	White	87	1915C→G, P639A	SH2	Sporadic
Family J054					
Proband	White	78	1393T→G, S465A	DNA binding	Sporadic
Family J068					
Proband	White	73	1144C→T, R382W	DNA binding	Sporadic
Family J074					
Proband	White	69	1954G→A, E652K	SH2	Sporadic
Husband	White	1	None		
Daughter	White	64	1954G→A, E652K	SH2	Transmitted
Daughter	White	54	1954G→A, E652K	SH2	Transmitted
Family J083					
Proband	White	84	1909G→A, V637M	SH2	Sporadic
Sister	White	36	None		
Mother	White	4	None		

Table 2. (Continued.)

Member	Race or Ethnic Group†	Hyper-IgE Syndrome Score‡	Mutation		
			Nucleotide and Amino Acid	Domain	Type
Family J087					
Proband	White	69	1387delGTG; V463del	DNA binding	Sporadic
Daughter	White	82	1387delGTG; V463del	DNA binding	Transmitted
Family J088					
Proband	White–Hispanic	76	1145G→T, R382L	DNA binding	Sporadic
Family J098					
Proband	White	65	1909G→T, V637L	SH2	Sporadic
Family J100					
Proband	Hispanic	81	1909G→A, V637M	SH2	Sporadic
Family J112					
Proband	White	52	1970A→G, Y657C	SH2	Sporadic
Son	White	31	1970A→G, Y657C	SH2	Transmitted
Family J113					
Proband	White	58	1145G→A, R382Q	DNA binding	Sporadic
Mother	White	Not scored	None		
Family J121					
Proband	White	65	1930delCAG; Q644del	SH2	Sporadic

* Probands and family members are included if DNA samples were obtained for sequencing. SH2 denotes SRC homology 2.

[†] Race or ethnic group was determined by a physician author or was self-reported.

[‡] The hyper-IgE syndrome scores were arbitrarily categorized as follows: 0 to 15, unaffected; 16 to 39, possibly affected; 40 to 59, probably affected; and 60 or more, definitely affected.

such as that involving the interferons and STATs, is altered in patients with the hyper-IgE syndrome (Fig. 1D in the Supplementary Appendix).

CYTOKINE EXPRESSION IN LEUKOCYTES

Consistent with the microarray data, cytokine protein levels were elevated in the supernatants of leukocytes from patients with the hyper-IgE syndrome as compared with those of controls, depending on the stimulus (Table 1). For example, tumor necrosis factor α (TNF- α) levels were higher in the supernatants of leukocytes from patients with the hyper-IgE syndrome than in those from controls, after the leukocytes were stimulated by the toll-like receptor 4 agonist lipopolysaccharide alone ($P=0.003$) or by lipopolysaccharide and interferon- γ ($P=0.03$). TNF- α levels were also elevated in the supernatants from leukocytes of patients after exposure to the toll-like receptor 2 agonist heat-killed *Listeria monocytogenes* ($P<0.001$)

or to *S. aureus* Cowan strain ($P=0.001$). Similarly, stimulation with lipopolysaccharide or lipopolysaccharide and interferon- γ resulted in elevated interleukin-12p70 production in patients with the hyper-IgE syndrome, as compared with controls ($P=0.001$ and $P=0.003$, respectively). In response to the nonspecific T-cell mitogen phytohemagglutinin or phytohemagglutinin and interleukin-12, interferon- γ levels were also elevated in the patients ($P=0.03$ for both comparisons). In contrast, we found diminished production of monocyte chemoattractant protein 1 in leukocytes from patients, as compared with control leukocytes, after exposure to interleukin-6 ($P=0.03$) (Table 1).

In aggregate, these data indicated a defect leading to elevated cytokine production in response to certain stimuli but impaired signaling through the interleukin-6 receptor. Since the production of monocyte chemoattractant protein 1 after stimulus with interleukin-6 was impaired in the leu-

kocytes of patients with the hyper-IgE syndrome, we decided to investigate components of the interleukin-6 signal-transduction pathway.

STAT3 MUTATIONS IN THE HYPER-IgE SYNDROME

Expression levels of the interleukin-6 receptor (IL6R or CD126) and the interleukin-6 signal transducer (IL6ST, CD130, or gp130) were normal on cells from patients with the hyper-IgE syndrome (data not shown). We inferred that Janus kinase 1 was intact in cells from patients, because it mediates TNF- α production in response to interferon- γ . STAT3 is physically associated with gp130, and its deletion in animal models and inhibition in tumor-cell lines is associated with increased production of interferon- γ and TNF- α .¹⁸ We therefore sequenced STAT3 in DNA samples obtained from 50 persons affected with the hyper-IgE syndrome and 48 unaffected relatives from 35 independent and unrelated white, Asian, Hispanic, or black families (Table 2). Seven patients had de novo STAT3 mutations, 17 had familial transmission of STAT3 mutations, and 26 had sporadic STAT3 mutations (defined as those for which the parents were reported to be clinically unaffected and, in cases in which DNA was available for analysis, did not carry a STAT3 mutation), 1 of whom had chimerism for the STAT3 mutation. All STAT3 mutations localized to regions encoding the DNA-binding or SH2 domains; several mutational “hot spots” were apparent (Fig. 1). For example, 13 mutations from unrelated patients affected the arginine (R) residue at position 382 in the DNA-binding domain. Several other residues in the DNA-binding domain — phenylalanine (F) at position 384, arginine (R) at position 423, and valine (V) at position 463 — were each affected by at least two de novo mutations. The SH2 domain has a hot spot at position 637; we found seven mutations from unrelated patients that involved the valine (V) residue normally found at this position. All mutations are missense or in-frame deletions, consistent with protein expression, and affect residues included in all splice variants of STAT3.¹⁹ We did not find any of the mutations in the 158 unaffected control subjects of various ancestral origins.

The hyper-IgE syndrome scores⁹ generally correlated well with the STAT3 genotypes. Parents of probands with sporadic mutations from whom DNA samples could be obtained did not have the STAT3 mutation, indicating a substantial incidence

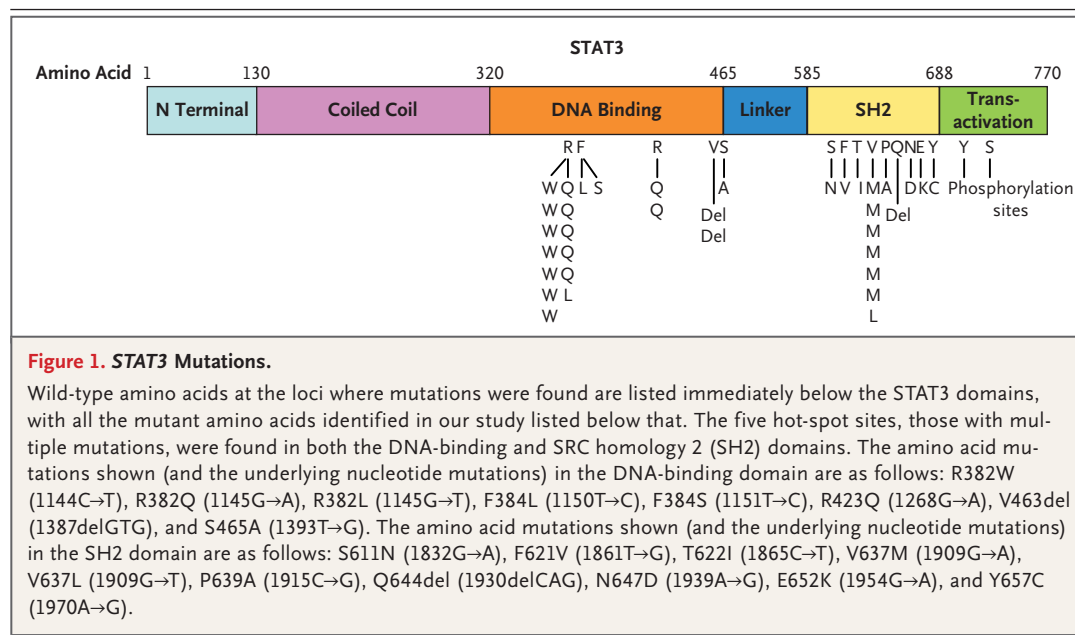
of new mutations (Fig. 2). In Families J002, J014, and J016, the mutation in the proband was de novo and was associated with a high hyper-IgE syndrome score in the proband and offspring (if present), as well as with clinical disease. We could not collect DNA from both parents of every proband, but even in families in which DNA from one parent was available (such as Family J007), if a STAT3 mutation occurred in a definitely affected individual, it was transmitted with disease as a stable autosomal dominant trait. Relatives of the proband who were possibly or probably affected (hyper-IgE syndrome scores of 16 to 59) did not necessarily have mutations, such as the father of the proband in Family J002 who had a hyper-IgE syndrome score of 33 and the sister in Family J014 who had a score of 31. Because the scoring system is tied to medical complications that accumulate over time, the scores of 34 in the children with a STAT3 mutation in Family J016 are consistent with being affected with the hyper-IgE syndrome, since they were only 11 and 14 years old at the time of testing.

BIOINFORMATICS ANALYSIS WITH SIFT AND POLYPHEN

Thirteen of the 16 missense mutations identified are predicted to be possibly or probably damaging to STAT3 function according to at least one of the two methods (Table 6 in the Supplementary Appendix). R423Q, a recurrent mutation, is not predicted to be damaging but is clearly associated with disease in Families J007 and J016.

FUNCTIONAL STUDIES

Phosphorylation and expression of STAT3, as determined with the use of flow cytometry, was equivalent in the leukocytes from patients and those from controls (Fig. 3 in the Supplementary Appendix). The trafficking of STAT3 from the cytoplasm into the nucleus of leukocytes from patients was grossly normal (data not shown). Unlike in mouse models of STAT3 mutation,²⁰ superoxide production by neutrophils from patients in response to opsonized zymosan and N-formyl-methionyl-leucyl-phenylalanine and phorbol myristate acetate was normal, as was killing of staphylococci by neutrophils in vitro (data not shown). Although interferon- γ and related proinflammatory cytokines prolong neutrophil survival, and our microarray suggested that this should be the case,²¹ the rates of spontaneous and phagocytosis-induced apoptosis did not differ between poly-



morphonuclear leukocytes from patients with the hyper-IgE syndrome and those from controls (data not shown). This is consistent with an inability of mutant STAT3 to promote cytokine-mediated delay of neutrophil apoptosis.²²

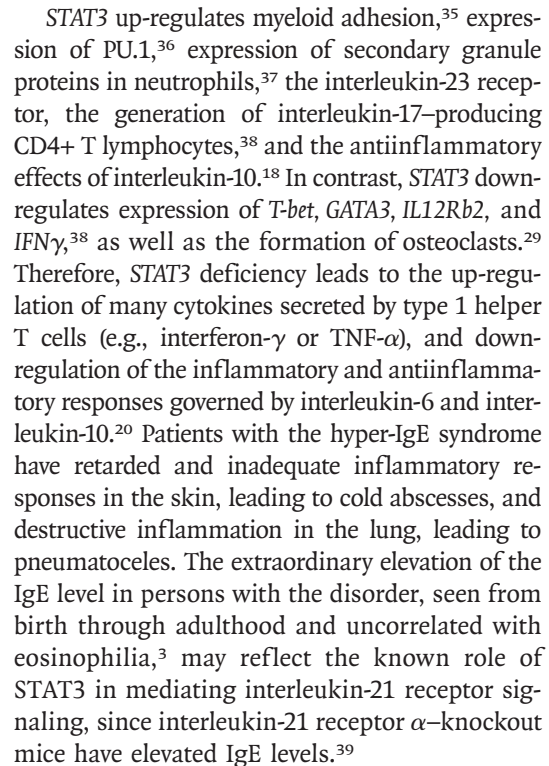
DISCUSSION

STAT3 mutation is the predominant cause of sporadic and familial hyper-IgE syndrome, although other genomic loci may also be involved. Within the gene encoding STAT3, we found mutational hot spots, indicated by independent mutations that affect the same codons, in the evolutionarily conserved SH2 and DNA-binding domains of STAT3. These mutations are predicted not to affect protein levels of STAT3 and are consistent with the survival of those carrying the mutations. In support of STAT3 as the cause of the hyper-IgE syndrome, Minegishi et al. found STAT3 mutations affecting the DNA-binding domain in 8 of 15 patients examined.²³ Therefore, all mutations associated with the hyper-IgE syndrome identified to date are restricted to the DNA-binding or SH2 regions of STAT3. These mutations are likely to preserve protein levels, phosphorylation, and nuclear localization. Mice with half the normal dose of Stat3 seem unaffected, suggesting that haploinsufficiency is an unlikely pathogenic mechanism.²⁴

A patient with a newly discovered primary immunodeficiency with mild IgE elevation due to

homozygous recessive tyrosine kinase 2 deficiency has also been reported,²⁵ but this patient differs from our patients with classic hyper-IgE syndrome in the pattern of inheritance, susceptibility to viral infection, the degree of IgE elevation, and the absence of nonimmune features. Patients with the syndrome reported as autosomal recessive hyper-IgE syndrome also differ from those with the classic hyper-IgE syndrome described here in that they have fewer pulmonary infections and pneumatoceles, more viral infections, and vasculitis.²⁶ In keeping with these clinical differences, an index patient with autosomal recessive hyper-IgE syndrome from our original report²⁶ had no STAT3 mutations (data not shown).

STAT3 mutations in the hyper-IgE syndrome clarify many disparate aspects of the syndrome that have puzzled investigators. Targeted mutations in mice show specific roles of Stat3 in organogenesis, organ preservation, and organ-specific inflammation, distinct from hematopoiesis. Stat3 deficiency specific to the pulmonary epithelium in mice exposed to hyperoxia causes excessive lung inflammation and airspace enlargement,²⁷ and lung expression of Stat3 is critical for repression of the inflammatory response to lipopolysaccharide²⁰; these observations are consistent with the development of pneumatoceles after infection in patients with the hyper-IgE syndrome. Myeloid-specific Stat3 deficiency causes increased myelopoiesis and eosinophilia in mice,²⁸



In conclusion, the newly recognized genetic cause of the hyper-IgE syndrome — *STAT3* mutation — affects complex, compartmentalized somatic and immune regulation. The discovery of this genetic cause opens new doors to understanding organ-specific infection, inflammation, and therapy.

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Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to: Holland SM, DeLeo FR, Elloumi HZ, et al. *STAT3* mutations in the hyper-IgE syndrome. *N Engl J Med* 2007;357:1608-19.

Supplemental Methods

Apoptosis. To measure constitutive neutrophil apoptosis, unstimulated PMNs were cultured for the desired times as described (13), transferred to a microscope slide by Cytospin (ThermoShandon, Pittsburgh, PA), and stained with a modified Wright-Giemsa. Approximately 500 neutrophils from each subject (2 slides and 5 separate fields of view each) were scored for apoptosis using a standard microscope-based method (15). Alternatively, phagocytosis-induced PMN apoptosis was determined as described (12, 13). Statistics were performed using one-way ANOVA and Bonferroni's posttest for multiple comparisons.

Nuclear Localization. STAT3 intracellular localization was determined using phospho-specific and unphosphorylated anti-STAT3 antibodies (Santa Cruz Biotechnology, Santa Cruz, CA) before and after stimulation with IL-6 and other agonists. PBMCs (2×10^6 cells/well) were grown on glass cover slips. After cell adherence, media were replaced and cells were stimulated for the indicated time points. The cells were then washed with PBS and fixed with 3.7% paraformaldehyde for 15 min, washed with PBS and permeabilized with PBS-0.5% triton X-100 for 15 min. Nonspecific binding was blocked by incubating the cover slips in PBS-10% BSA for 30 min at room temperature. Following 1h incubation with a rabbit anti-STAT3 antibody (Santa Cruz Biotechnology), cells were washed three times, then incubated with secondary antibody FITC-conjugated. The nucleus was stained with DAPI. Images were acquired on a Leica fluorescence microscope.

Sequencing. Primers used for sequencing cDNA were:

54F- 5'-CGCCCGTCCCCGGCACACG-3' and
2764R- 5'-AGGAGGGCAGGGGAACAAAACAACAAGA-3' were used to amplify cDNA.

The remaining primers were used for sequencing.

222F- 5'-GCGGCAGTTTCTGGCCCCTTGGATTG-3',
511F- 5'-GGCCAGGCCAACCACCCACAGC-3',
1170R- 5'-AGTGAAGTGGACGCCGGTCTTGATGACGAG-3',
958F- 5'-CAGACCCGTCAACAAATTAAGAACTGGAG-3',
1391F- 5'-ATGGGGGCGGAGCCAATTGTGATGCT-3',
2199R- 5'-TGGCCGACAATACTTTCCGAATGCCTCCTC-3',
1900F- 5'-AGTAAGGAGCGGGAGCGGGCCATCTTG-3',
2232F- 5'-TAGCGCTGCCCCATACCTGAAGACCAAGTT-3'.

For genomic DNA amplification and sequencing, the following primer sets were used.
Exons 12 - 14 amplification yields a 632 bp genomic fragment that contains nucleotides 1144, 1145, 1150, 1151, 1268.
Primer 13F is used for sequencing.

12F amp- 5'-TAGTTTAAAGAAATGCCAGGAGCACAGAGGTTTT-3'
14R amp- 5'-TTTGGCCTGAAGTGACTTTTTGGAATAACTACAGC-3'
13F seq- 5'-CTGGGGACGTTGCAGCTCTCAGAGGGTAAGT-3'

Exons 15-17 amplification yields a 3750 bp genomic fragment that contains nucleotides 1387 and 1393.

Primer 16F is used for sequencing.

15F amp- 5'-CCAAAAGAATTCATTGGAGTCCATAAGTGTAAGGT-3'

17R amp- 5'-AAGAGTCAAGTAGTACATTTTCAGCTTGGGGTCAA-3'

16F seq- 5'-CTCGCCTAGAGTTGGCAGCAGGTGTGGTT-3'

Exons 18-21 amplification yields a 2488 bp genomic fragment that contains nucleotides 1832, 1861, 1865, 1909, 1915, 1930, 1939, 1954, 1970.

Primer 19F is used for sequencing nucleotides 1832, 1861, and 1865.

Primer sgEX21R is used for sequencing nucleotides 1909, 1915, 1930, 1939, 1954, and 1970.

18F amp- 5'-AGGTGGCACTAAAGGCTTGACATTCCCTGTCCATT-3'

21R amp- 5'-TCCTCCCACCTCAGCCTCCCAAGTAGCTACGACTA-3'

19F seq- 5'-AAGGTAGACGGGCCTGAGGATTTGGGTGATG-3'

sgEX21R- 5'-TAAGGAGAAATAATTATCCCCCAGGTTA-3'

Authorship. The natural history study was designed by SMH, JMP, BG, and AAS. Data were gathered by SMH, FRD, HZE, APH, GU, BG, CW. Data were analyzed by SMH, AAS, APH, BG. SMH, JMP, AAS, and BG vouch for the data and the analysis. The initial draft of the paper was written by SMH with extensive contribution from FRD, JMP, BG, and AAS. SMH, FRD, JMP, AAS, and BG decided to publish the paper. There were no confidentiality agreements between the authors and the NIH, the sponsor of the study. No editorial assistance was provided other than the authors.

Supplemental Table 1. IFN-regulated or host defense-related transcripts increased constitutively in PMNs from patients with hyper-IgE recurrent infection (Job's) syndrome.

Entrez Gene	Encoded protein	Fold change	P value
<i>BIRC4BP</i> ³	XIAP associated factor-1	3.1	0.04
<i>CCL23</i> ²	chemokine (C-C motif) ligand 23	4.8	0.002
<i>CD24</i> ⁶	CD24	4.1	0.04
<i>CD244</i>	CD244, natural killer cell receptor 2B4	2.2	0.01
<i>CD274</i> ²	CD274	4.0	0.06
<i>CD2AP</i>	CD2-associated protein	2.5	0.02
<i>CD52</i> ²	CD52	2.4	0.02
<i>CD69</i>	CD69	3.0	0.04
<i>CEACAM1</i> ⁴	CEA-related cell adhesion molecule 1	2.7	0.004
<i>CLEC12A</i>	C-type lectin domain family 12A	5.2	0.003
<i>CSF1</i>	colony stimulating factor 1 (macrophage)	2.3	0.03
<i>CYBB</i> ²	cytochrome b-245, beta polypeptide	2.1	0.05
<i>FCGR1A</i> ²	CD64	2.7	0.07
<i>GIP2</i>	IFN, alpha-inducible protein	2.0	0.09
<i>GBP1</i> ⁴	guanylate binding protein 1	2.4	0.03
<i>GBP3</i>	guanylate binding protein 3	3.7	0.02
<i>GBP4</i> ²	guanylate binding protein 4	2.9	0.04
<i>GPR34</i> ²	G protein-coupled receptor 34	3.0	0.01
<i>HLA-DRA</i>	MHC, class II, DR alpha	2.1	0.04
<i>HLA-DRB1</i>	MHC, class II, DR beta 1	2.2	0.12
<i>IFI35</i>	IFN-induced protein 35	2.1	0.07
<i>IFI44</i> ²	IFN-induced protein 44	4.0	0.06
<i>IFI44L</i>	IFN-induced protein 44-like	4.5	0.06
<i>IFIH1</i>	IFN-induced with helicase C domain 1	2.0	0.09
<i>IFIT5</i>	IFN-induced protein with TPRs 5	2.2	0.06
<i>IL18R1</i>	interleukin 18 receptor 1	2.7	0.25
<i>INDO</i>	indoleamine-pyrrole 2,3 dioxygenase	2.6	0.01
<i>LRAP</i> ³	leukocyte-derived arginine aminopeptidase	2.2	0.08
<i>LY6E</i>	lymphocyte antigen 6 complex, locus E	5.1	0.08
<i>OAS1</i> ²	2',5'-oligoadenylate synthetase 1	7.9	0.09
<i>OAS2</i>	2'-5'-oligoadenylate synthetase 2	4.1	0.13
<i>OAS3</i>	2'-5'-oligoadenylate synthetase 3	2.7	0.11

<i>OASL</i>	2'-5'-oligoadenylate synthetase-like	2.2	0.09
<i>PLSCR1</i>	phospholipid scramblase 1	2.0	0.02
<i>RSAD2</i> ²	radical S-adenosyl methionine domain containing 2	3.0	0.06
<i>S100A10</i>	S100 calcium binding protein A10	2.5	0.01
<i>SOCS1</i>	suppressor of cytokine signaling 1	2.4	0.01
<i>SOCS2</i>	suppressor of cytokine signaling 2	2.3	0.21
<i>STAT2</i>	signal transducer & activator of transcription 2	2.2	0.04

Transcripts constitutively increased in patient PMNs compared with control cells were identified by expression microarray analysis. Results are the average fold-increase in selected patient transcripts. Superscript indicates number of probe sets that support the data for that gene, in which case a representative was used in the Table.

Supplemental Table 2. Transcripts increased or decreased constitutively in PMNs from patients with hyper-IgE recurrent infection (Job's) syndrome.

<i>Entrez Gene</i>	Encoded protein	UniGene#	Chromosome	FC	P
Up-Regulated (141)					
<i>ABHD10</i>	abhydrolase domain containing 10	Hs.477115	3q13.2	2.2	0.001
<i>ABP1</i>	amiloride binding protein 1	Hs.521296	7q34-q36	2.1	0.01
<i>ADFP</i>	adipose differentiation-related protein	Hs.3416	9p22.1	3.4	0.02
<i>AGPAT5</i>	lysophosphatidic acid acyltransferase, ϵ	Hs.490899	8p23.1	2.3	0.005
<i>AHR</i>	aryl hydrocarbon receptor	Hs.171189	7p15	2.1	0.04
<i>AIM2</i>	absent in melanoma 2	Hs.281898	1q22	2.4	0.03
<i>ALDH6A1</i> ²	aldehyde dehydrogenase 6A1	Hs.293970	14q24.3	2.5	0.004
<i>ANKRD22</i> ²	ankyrin repeat domain 22	Hs.217484	10q23.31	3.2	0.2
<i>ANKRD28</i>	ankyrin repeat domain 28	Hs.547037	3p25.1	2.3	0.09
<i>ANXA2</i>	annexin A2	Hs.511605	15q21-q22	2.0	0.01
<i>ARG1</i>	arginase, liver	Hs.440934	6q23	2.1	0.2
<i>ASPH</i> ²	aspartate beta-hydroxylase	Hs.332422	8q12.1	2.3	0.1
<i>BANK1</i>	B-cell scaffold protein with ankyrin repeats 1	Hs.480400	4q24	2.3	0.02
<i>BCOR</i>	BCL6 co-repressor	Hs.186424	Xp11.4	2.0	0.08
<i>BIRC4BP</i> ³	XIAP associated factor-1	Hs.441975	17p13.1	3.1	0.04
<i>BST2</i>	bone marrow stromal cell antigen 2	Hs.118110	19p13.2	2.5	0.03
<i>CAPN2</i>	calpain 2, (m/II) large subunit	Hs.350899	1q41-q42	2.0	0.01
<i>CCL23</i> ²	chemokine (C-C motif) ligand 23	Hs.169191	17q12	4.8	0.002
<i>CD24</i> ⁶	CD24 antigen	Hs.375108	6q21	4.1	0.04
<i>CD244</i>	CD244 natural killer cell receptor 2B4	Hs.157872	1q23.3	2.2	0.01
<i>CD274</i> ²	CD274 antigen	Hs.521989	9p24	4.0	0.06
<i>CD2AP</i>	CD2-associated protein	Hs.485518	6p12	2.5	0.02
<i>CD52</i> ²	CD52 antigen (CAMPATH-1 antigen)	Hs.276770	1p36	2.4	0.02
<i>CD69</i>	CD69 antigen	Hs.208854	12p13-p12	3.0	0.04

<i>CEACAM1</i> ⁴	carcinoembryonic antigen-related cell adhesion molecule 1	Hs.512682	19q13.2	2.7	0.005
<i>CEACAM6</i>	carcinoembryonic antigen-related cell adhesion molecule 6	Hs.466814	19q13.2	2.3	0.1
<i>CEACAM8</i>	carcinoembryonic antigen-related cell adhesion molecule 8	Hs.41	19q13.2	2.3	0.2
<i>CLEC12A</i>	C-type lectin domain family 12A	Hs.190519	12p13.31	5.2	0.003
<i>CRIP1</i>	cysteine-rich protein 1 (intestinal)	Hs.70327	14q32.33	2.8	0.005
<i>CSF1</i>	colony stimulating factor 1 (macrophage)	Hs.173894	1p21-p13	2.3	0.03
<i>CYBB</i> ²	cytochrome b-245, beta polypeptide	Hs.292356	Xp21.1	2.4	0.09
<i>CYP1B1</i>	cytochrome P450, family 1, B1	Hs.154654	2p21	5.7	0.24
<i>DACH1</i> ²	dachshund homolog 1 (Drosophila)	Hs.129452	13q22	2.3	0.0001
<i>DDX58</i>	DEAD box polypeptide 58	Hs.190622	9p12	2.2	0.1
<i>DEFA4</i>	defensin, alpha 4	Hs.2582	8p23	2.1	0.14
<i>DKFZP586-A0522</i>	DKFZP586A0522 protein	Hs.288771	12q13.12	2.1	0.01
<i>DUT</i>	dUTP pyrophosphatase	Hs.527980	15q15-q21.1	2.0	0.05
<i>ECHDC3</i>	enoyl CoA hydrat. domain containing 3	Hs.22242	10p14	2.1	0.3
<i>EMR1</i>	EGF-like module containing, mucin-like, hormone receptor-like 1	Hs.2375	19p13.3	2.9	0.01
<i>ENC1</i>	ectodermal-neural cortex	Hs.104925	5q12-q13.3	2.0	0.05
<i>EPSTI1</i>	epithelial stromal interaction 1 (breast)	Hs.546467	13q13.3	4.4	0.05
<i>ETS1</i>	v-ets oncogene homolog 1 (avian)	Hs.369438	11q23.3	2.0	0.01
<i>ETV7</i> ²	ets variant gene 7	Hs.272398	6p21	2.5	0.03
<i>EXOSC9</i>	exosome component 9	Hs.91728	4q27	3.1	0.01
<i>FADD</i>	Fas-associated via death domain	Hs.86131	11q13.3	2.0	0.002
<i>FAM62A</i>	family with sequence similarity 62A	Hs.8309	12q13.2	2.1	0.01
<i>FCGR1A</i> ²	CD64	Hs.77424	1q21.2-q21.3	2.7	0.07
<i>FRMD3</i>	FERM domain containing 3	Hs.127535	9q21.32	3.8	0.04
<i>G1P2</i>	IFN, alpha-inducible protein	Hs.458485	1p36.33	2.0	0.09
<i>GBP1</i> ⁴	guanylate binding protein 1, IFN-induc.	Hs.62661	1p22.2	2.4	0.03
<i>GBP3</i>	guanylate binding protein 3	Hs.534284	1p22.2	3.7	0.02
<i>GBP4</i> ²	guanylate binding protein 4	Hs.409925	1p22.2	2.9	0.04
<i>GCH1</i>	GTP cyclohydrolase 1	Hs.86724	14q22.1-q22.2	2.3	0.04
<i>GIMAP2</i>	GTPase, IMAP family member 2	Hs.255008	7q36.1	2.2	0.06
<i>GOLPH4</i>	golgi phosphoprotein 4	Hs.143600	3q26.2	2.4	0.01
<i>GPR34</i> ²	G protein-coupled receptor 34	Hs.495989	Xp11.4-p11.3	3.0	0.01
<i>GPR44</i>	G protein-coupled receptor 44	Hs.299567	11q12-q13.3	2.1	0.005
<i>GRB10</i> ²	growth factor receptor-bound protein 10	Hs.164060	7p12-p11.2	2.7	0.08
<i>HERC2</i>	hect domain and RLD 2	Hs.434890	15q13	2.8	0.05
<i>HERC5</i>	hect domain and RLD 5	Hs.26663	4q22.1-q23	2.0	0.1
<i>HLA-DRA</i>	MHC, class II, DR alpha	Hs.520048	6p21.3	2.1	0.04
<i>HLA-DRB1</i>	MHC, class II, DR beta 1	Hs.520049	6p21.3	2.2	0.1
<i>HMOX1</i>	heme oxygenase (decycling) 1	Hs.517581	22q12 22q13.1	2.1	0.2
<i>HRH4</i>	histamine receptor H4	Hs.287388	18q11.2	2.2	0.01
<i>HSZFP36</i>	ZFP-36 for a zinc finger protein	Hs.142167	19p13.2	3.0	0.01
<i>IFI35</i>	interferon-induced protein 35	Hs.50842	17q21	2.1	0.07
<i>IFI44</i> ²	interferon-induced protein 44	Hs.82316	1p31.1	4.0	0.06

<i>IFI44L</i>	interferon-induced protein 44-like	Hs.389724	1p31.1	4.5	0.06
<i>IFIH1</i>	IFN-induced with helicase C domain 1	Hs.163173	2p24.3-q24.3	2.0	0.09
<i>IFIT5</i>	IFN-induced protein with TPR 5	Hs.252839	10q23.31	2.2	0.06
<i>IL18R1</i>	interleukin 18 receptor 1	Hs.469521	2q12	2.7	0.3
<i>INDO</i>	indoleamine-pyrrole 2,3 dioxygenase	Hs.840	8p12-p11	2.6	0.01
<i>INSR</i>	Insulin receptor	Hs.465744	19p13.3-p13.2	2.2	0.03
<i>ITGA6</i>	integrin, alpha 6	Hs.133397	2q31.1	2.3	0.01
<i>KLF9</i>	Kruppel-like factor 9	Hs.150557	9q13	4.1	0.2
<i>KNTC2</i>	kinetochore associated 2	Hs.414407	18p11.32	2.1	0.04
<i>LCN2</i>	lipocalin 2 (oncogene 24p3)	Hs.204238	9q34	2.5	0.2
<i>LRAP</i> ³	leukocyte-derived Arg aminopeptidase	Hs.482910	5q15	2.2	0.08
<i>LTF</i>	lactotransferrin	Hs.529517	3q21-q23	2.2	0.2
<i>LY6E</i>	lymphocyte antigen 6 complex, locus E	Hs.521903	8q24.3	5.1	0.08
<i>MS4A3</i> ²	membrane-spanning 4-domains, A 3	Hs.99960	11q12	2.6	0.2
<i>OAS1</i> ²	2',5'-oligoadenylate synthetase 1	Hs.524760	12q24.1	7.9	0.09
<i>OAS2</i>	2'-5'-oligoadenylate synthetase 2	Hs.414332	12q24.2	4.1	0.1
<i>OAS3</i>	2'-5'-oligoadenylate synthetase 3	Hs.528634	12q24.2	2.7	0.1
<i>OASL</i>	2'-5'-oligoadenylate synthetase-like	Hs.118633	12q24.2	2.2	0.09
<i>OLIG2</i>	oligodendrocyte lineage transcription factor 2	Hs.176977	21q22.11	2.8	0.04
<i>P2RY14</i>	purinergic receptor P2Y14	Hs.2465	3q21-q25	2.0	0.02
<i>PARP14</i>	poly (ADP-ribose) polymerase family, member 14	Hs.518203	3q21.1	2.4	0.06
<i>PCGF5</i>	polycomb group ring finger 5	Hs.500512	10q23.32	2.1	0.03
<i>PDK4</i> ²	pyruvate dehydrogenase kinase 4	Hs.8364	7q21.3-q22.1	3.6	0.01
<i>PLSCR1</i>	phospholipid scramblase 1	Hs.130759	3q23	2.0	0.02
<i>PMP22</i>	peripheral myelin protein 22	Hs.372031	17p12-p11.2	2.5	0.07
<i>PPM1K</i>	protein phosphatase 1K	Hs.291000	4q22.1	2.2	0.08
<i>PRSS33</i>	protease, serine, 33	Hs.280658	16p13.3	2.1	0.03
<i>PSTPIP2</i>	proline-serine-threonine phosphatase interacting protein 2	Hs.368623	18q12	2.3	0.04
<i>PTGER2</i>	prostaglandin E receptor 2, 53kDa	Hs.2090	14q22	2.1	0.03
<i>RARRES3</i>	retinoic acid receptor responder 3	Hs.17466	11q23	2.2	0.02
<i>RHOBTB3</i>	Rho-related BTB domain containing 3	Hs.445030	5q15	2.0	0.02
<i>RNASE3</i>	ribonuclease, RNase A family, 3 (eosinophil cationic protein)	Hs.73839	14q24-q31	2.3	0.09
<i>RSAD2</i> ²	radical S-adenosyl methionine domain containing 2	Hs.17518	2p25.2	3.0	0.06
<i>S100A10</i>	S100 calcium binding protein A10	Hs.143873	1q21	2.5	0.01
<i>SAMD9L</i> ²	sterile alpha motif domain containing 9-like	Hs.489118	7q21.3	2.1	0.05
<i>SAP30</i>	sin3-associated polypeptide, 30kDa	Hs.413835	4q34.1	3.6	0.3
<i>SERPING1</i>	serine (or cysteine) proteinase inhibitor	Hs.384598	11q12-q13.1	2.6	0.07
<i>SIGLEC8</i>	sialic acid binding Ig-like lectin 8	Hs.447899	19q13.33-q13.41	2.0	0.04
<i>SLC29A1</i>	nucleoside transporter	Hs.25450	6p21.1-p21.2	2.2	0.01
<i>SNX5</i>	sorting nexin 5	Hs.316890	20p11	2.2	0.01

<i>SOCS1</i>	suppressor of cytokine signaling 1	Hs.50640	16p13.13	2.4	0.01
<i>SOCS2</i>	suppressor of cytokine signaling 2	Hs.485572	12q	2.3	0.2
<i>STAT2</i>	signal transducer and activator of transcription 2, 113kDa	Hs.530595	12q13.3	2.2	0.04
<i>THEDC1²</i>	thioesterase domain containing 1	Hs.24309	10p13	6.6	0.3
<i>TIFA</i>	TRAF-interacting protein with a forkhead-associated domain	Hs.310640	4q25	2.1	0.07
<i>TIMM10</i>	translocase of inner mitochondrial membrane 10 homolog (yeast)	Hs.235750	11q12.1-q12.3	3.2	0.02
<i>TNFSF14</i>	tumor necrosis factor (ligand) superfamily, member 14	Hs.129708	19p13.3	2.1	0.05
<i>TRIM5</i>	tripartite motif-containing 5	Hs.370515	11p15	2.1	0.03
<i>UNQ3033</i>	LAIR homolog	Hs.444431	19q13.42	2.3	0.02
<i>VLDLR</i>	very low density lipoprotein receptor	Hs.370422	9p24	2.0	<0.0001
<i>YIPF5</i>	Yip1 domain family, member 5	Hs.372050	5q31.3	2.0	0.03
<i>ZBP1²</i>	Z-DNA binding protein 1	Hs.302123	20q13.32	2.5	0.02
<i>ZCCHC2</i>	zinc finger, CCHC domain containing 2	Hs.114191	18q21.33	2.2	0.03
<i>C10orf58</i>	chromosome 10 open reading frame 58	Hs.500333	10q22.3	2.2	0.002
<i>FLJ11000</i>	hypothetical protein FLJ11000	Hs.521215	7q33	2.3	0.07
<i>FLJ13955</i>	Hypothetical protein FLJ13955	Hs.309489	8q22.2	2.1	0.004
<i>FLJ20035</i>	hypothetical protein FLJ20035	Hs.481141	4q32.3	2.7	0.05
<i>FLJ31265</i>	Nudix-type motif 16	Hs.282050	3q21.3	2.6	0.2
<i>KIAA0564</i>	KIAA0564 protein	Hs.368282	13q14.11	2.1	0.2
<i>LOC129607</i>	hypothetical protein LOC129607	Hs.7155	2p25.2	2.4	0.05
<i>LOC90355</i>	hypothetical protein	Hs.482976	5q21.1	2.8	0.1
<i>MGC20410</i>	hypothetical protein BC012330	Hs.124840	11q13.1	2.6	0.04
	FLJ39947	Hs.550177		2.1	0.04
		Hs.349076	22q12.3	3.1	0.02
	FLJ31513	Hs.30977	2q31.2	2.1	0.01
	Transcribed locus	Hs.20255	2q23.3	2.1	0.03
	Transcribed locus	Hs.550853	11q22.2	3.5	0.2
	FLJ23098	Hs.306876	12q12	2.6	0.01
		Hs.122587	13q14.11	3.5	0.04
	similar to NP_775735.1 l(3)mbt-like 4	Hs.133020	7q34	3.1	0.01
	FLJ46881	Hs.551636	1p11.2/5q11.1	2.0	0.0006
	transcribed locus	Hs.169979	19p13.3	2.3	0.003
Down-Regulated (18)					
<i>APOBEC3B</i>	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	Hs.226307	22q13.1-q13.2	-14.0	0.3
<i>CCL5</i>	chemokine (C-C motif) ligand 5	Hs.514821	17q11.2-q12	-2.0	0.05
<i>CHI3L1²</i>	chitinase 3-like 1 (cartilage glycoprotein-39)	Hs.382202	1q32.1	-2.9	0.001
<i>CREM</i>	cAMP responsive element modulator	Hs.200250	10p11.21	-2.2	0.06
<i>DUSP2</i>	dual specificity phosphatase 2	Hs.1183	2q11	-2.4	0.02
<i>FLJ25467</i>	Coiled-coil domain containing 13	Hs.191036	3p22.1	-2.1	0.004
<i>FOSB</i>	FBJ murine osteosarcoma viral oncogene	Hs.75678	19q13.32	-2.1	0.04

	homolog B				
<i>GPX3</i> ²	glutathione peroxidase 3 (plasma)	Hs.386793	5q23	-3.2	0.0003
<i>HOXA5</i>	homeo box A5	Hs.37034	7p15-p14	-3.5	0.1
<i>KIAA0999</i>	KIAA0999 protein	Hs.167451	11q23.3	-2.4	0.0003
<i>MLLT4</i>	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 4	Hs.549055	6q27	-2.4	0.07
<i>NR4A2</i>	nuclear receptor subfamily 4, group A, member 2	Hs.165258	2q22-q23	-2.1	0.0003
<i>SLC35F5</i>	solute carrier family 35, member F5	Hs.292509	2q14.1	-2.1	0.01
<i>SNAPC1</i>	small nuclear RNA activating complex, polypeptide 1, 43kDa	Hs.179312	14q22	-2.2	0.03
<i>SYAP1</i>	synapse associated protein 1, SAP47 homolog (Drosophila)	Hs.489336	Xp22.2	-2.0	0.02
<i>THBS1</i>	thrombospondin 1	Hs.164226	15q15	-2.1	0.3
<i>TSPAN13</i>	tetraspanin 13	Hs.364544	7p21.1	-3.4	0.002
	Clone IMAGE:110218 mRNA sequence	Hs.283884		-2.1	0.004

Baseline transcript levels in 10 healthy control donors were compared with that in 7 patients with hyper-IgE recurrent infection (Job's) syndrome using Affymetrix HU133plus2 microarrays as described in Methods. Results are the average fold-change compared with healthy control donors. *P*, Statistics were performed with a Student's *t* test. FC, fold-change. Superscript indicates the number of probe sets that support the data for that gene, in which case a representative probe set was used in the Table.

Supplemental Table 3. Transcripts increased or decreased constitutively in PBMCs from patients with hyper-IgE recurrent infection (Job's) syndrome.

<i>Entrez Gene</i>	Encoded protein	UniGene#	Chr	FC	P
Up-Regulated (39)					
<i>ANKRD22</i>	ankyrin repeat domain 22	Hs.217484	10q23.31	3.5	0.08
<i>ANXA3</i>	annexin A3	Hs.480042	4q13-q22	5.4	0.2
<i>ARG1</i>	arginase, liver	Hs.440934	6q23	5.4	0.08
<i>C3AR1</i>	complement component 3a receptor 1	Hs.551500	12p13.31	2.7	0.03
<i>CD151</i>	CD151 antigen	Hs.512857	11p15.5	2.0	0.01
<i>CD24</i> ⁵	CD24 antigen	Hs.375108	6q21	2.8	0.05
<i>CEACAM6</i>	carcinoembryonic antigen-related cell adhesion molecule 6	Hs.466814	19q13.2	4.0	0.1
<i>CEACAM8</i>	carcinoembryonic antigen-related cell adhesion molecule 8	Hs.41	19q13.2	4.6	0.2
<i>CH25H</i>	cholesterol 25-hydroxylase	Hs.47357	10q23	2.5	0.3
<i>CLEC12A</i>	C-type lectin domain family 12A	Hs.190519	12p13.31	2.2	<0.0001
<i>DACT1</i>	dapper homolog 1, antagonist of beta-catenin	Hs.48950	14q23.1	2.9	0.02
<i>DEFA1</i>	defensin, alpha 1, myeloid-related sequence	Hs.294176	8p23.1	2.6	0.06

<i>DEFA4</i>	defensin, alpha 4, corticostatin	Hs.2582	8p23	2.9	0.08
<i>FAM20C</i>	family with sequence similarity 20, member C	Hs.134742	7p22.3	2.6	0.002
<i>FCGR1A</i>	CD64 antigen	Hs.77424	1q21.2-q21.3	2.1	0.01
<i>FER1L3</i> ²	fer-1-like 3, myoferlin (<i>C. elegans</i>)	Hs.500572	10q24	2.2	0.001
<i>HBA1</i> ⁴	hemoglobin, alpha 1	Hs.449630	16p13.3	3.5	0.004
<i>HBA2</i> ²	hemoglobin, alpha 2	Hs.398636	16p13.3	3.2	0.01
<i>HBB</i> ³	hemoglobin, beta	Hs.523443	11p15.5	3.3	0.01
<i>HBG1</i> ²	hemoglobin, gamma A	Hs.530049	11p15.5	3.6	0.1
<i>HP</i>	haptoglobin	Hs.513711	16q22.1	2.2	0.2
<i>IFI44L</i>	interferon-induced protein 44-like	Hs.389724	1p31.1	2.2	0.1
<i>IFIT3</i>	IFN-induced protein with TPR repeats 3	Hs.549041	10q24	2.1	0.09
<i>IL1R2</i>	interleukin 1 receptor, type II	Hs.25333	2q12-q22	6.0	0.3
<i>LCN2</i>	lipocalin 2 (oncogene 24p3)	Hs.204238	9q34	4.8	0.10
<i>LILRA3</i>	leukocyte Ig-like receptor, subfamily A3	Hs.113277	19q13.4	2.4	0.02
<i>LTF</i>	lactotransferrin	Hs.529517	3q21-q23	4.1	0.05
<i>MLSTD1</i> ²	male sterility domain containing 1	Hs.298851	12p11.22	2.1	0.001
<i>MMP9</i>	matrix metalloproteinase 9 (gelatinase B)	Hs.297413	20q11.2-q13.1	2.4	0.09
<i>OAS1</i>	2',5'-oligoadenylate synthetase 1, 40/46kDa	Hs.524760	12q24.1	2.2	0.1
<i>OLR1</i>	oxidised LDL (lectin-like) receptor 1	Hs.412484	12p13.2-p12.3	3.9	0.2
<i>PDK4</i> ²	pyruvate dehydrogenase kinase, isoenzyme 4	Hs.8364	7q21.3-q22.1	2.7	0.01
<i>RETN</i>	resistin	Hs.283091	19p13.2	3.1	0.1
<i>RPL23AP7</i>	ribosomal protein L23a pseudogene 7	Hs.247828	2q14	2.1	0.06
<i>S100P</i>	S100 calcium binding protein P	Hs.2962	4p16	2.6	0.01
<i>TAP2</i>	transporter 2, ATP-binding cassette, B	Hs.502	6p21.3	2.4	0.0009
<i>TCN1</i>	transcobalamin I	Hs.2012	11q11-q12	2.1	0.2
<i>VSIG4</i>	V-set and immunoglobulin domain containing 4	Hs.8904	Xq12-q13.3	4.9	0.2
	transcribed locus	Hs.550853	11q22.2	7.6	0.1
Down-Regulated (26)					
<i>APOBEC3B</i>	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	Hs.226307	22q13.1-q13.2	-2.3	0.4
<i>COL6A2</i>	collagen, type VI, alpha 2	Hs.420269	21q22.3	-2.0	0.0006
<i>CREM</i> ³	cAMP responsive element modulator	Hs.200250	10p11.21	-2.8	0.003
<i>DDX17</i> ²	DEAD box polypeptide 17	Hs.528305	22q13.1	-2.0	0.03
<i>DUSP2</i>	dual specificity phosphatase 2	Hs.1183	2q11	-2.2	<0.0001
<i>EDG8</i>	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	Hs.501561	19p13.2	-2.2	0.01
<i>EREG</i>	epiregulin	Hs.115263	4q13.3	-2.2	0.01
<i>HELB</i>	helicase (DNA) B	Hs.505941	12q14.3	-2.1	0.0003
<i>IGHA1/2</i>	Ig heavy constant alpha 1 or 2	Hs.497723	14q32.33	-2.2	0.01
<i>KIR3DL2</i>	killer cell Ig-like receptor, three domains, long cytoplasmic tail, 2	Hs.546263	19q13.4	-2.0	0.02
<i>MT1F</i>	metallothionein 1F (functional)	Hs.513626	16q13	-2.1	0.3

<i>MYBL1</i>	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	Hs.445898	8q22	-2.1	0.0006
<i>PIK3R1</i>	PI-3-kinase, regulatory subunit 1 (p85 alpha)	Hs.132225	5q13.1	-2.1	0.01
<i>PLK2</i>	polo-like kinase 2 (Drosophila)	Hs.398157	5q12.1-q13.2	-2.3	0.002
<i>PTGDS</i> ²	prostaglandin D2 synthase 21kDa (brain)	Hs.446429	9q34.2-q34.3	-3.3	0.02
<i>RANBP2L1</i>	RAN binding protein 2-like 1	Hs.469630	2q13	-2.0	0.01
<i>RORA</i> ²	RAR-related orphan receptor A	Hs.511626	15q21-q22	-2.2	0.0001
<i>SFXN1</i>	sideroflexin 1	Hs.369440	---	-2.0	0.02
<i>TGFBR3</i>	Transforming growth factor, beta receptor III	Hs.482390	1p33-p32	-2.1	0.002
<i>TNFRSF21</i>	TNF receptor superfamily, member 21	Hs.443577	6p21.1-12.2	-2.2	0.08
<i>XCL1/2</i>	chemokine (C motif) ligand 1 or 2	Hs.546295	1q23, 1q23-q25	-2.0	0.0009
<i>YES1</i>	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	Hs.194148	18p11.31-p11.21	-2.2	0.003
<i>ZNF331</i> ²	zinc finger protein 331	Hs.185674	19q13.3-q13.4	-2.4	0.0004
<i>ZNF447</i>	zinc finger protein 447	Hs.235390	19q13.43	-2.0	0.0007
<i>MGC27165</i>	hypothetical protein MGC27165	Hs.497723	14q32.33	-3.0	0.002
<i>FLJ31407</i> ²	FLJ31407	Hs.37648	15q22.2	-2.9	0.0007

Baseline transcript levels in 9 healthy control donors were compared with that in 7 patients with hyper-IgE recurrent infection (Job's) syndrome using Affymetrix HU133plus2 microarrays as described in Methods. Results are the average fold-change compared with healthy control donors. P, Statistics were performed with a Student's t test. FC, fold-change. Superscript indicates the number of probe sets that support the data for that gene, in which case a representative probe set was used in the Table.

Supplemental Table 4. Transcripts up- and down-regulated in PMNs from healthy subjects and patients with hyper-IgE recurrent infection (Job's) syndrome following exposure to phagocytic stimuli.

ProbeSet	Public ID	UniGene#	Entrez Gene	Chromosome	Healthy 180min	Job's 180up	Healthy 360min	Job's 360min
Up-Regulated								
1553605_a_at	NM_152701	Hs.226568	<i>ABCA13</i>	7p12.3	4.2	3.1	4.4	3.2
221641_s_at	AF241787	Hs.298885	<i>ACATE2</i>	Xp22.11	1.2	1.4	1.6	2.7
218795_at	NM_016361	Hs.528084	<i>ACP6</i>	1q21	2.6	2.2	2.6	2.5
222592_s_at	AW173691	Hs.11638	<i>ACSL5</i>	10q25.1-q25.2	1.9	2.1	3.1	3.2
1555326_a_at	AF495383	Hs.2442	<i>ADAM9</i>	8p11.23	1.5	1.4	2.2	2.4
202381_at	NM_003816	Hs.2442	<i>ADAM9</i>	8p11.23	1.4	1.3	2.0	2.1
209122_at	BC005127	Hs.3416	<i>ADFP</i>	9p22.1	11.8	11.3	14.0	10.8
205013_s_at	NM_000675	Hs.197029	<i>ADORA2A</i>	22q11.23	3.0	5.1	4.3	4.7
1555436_a_at	BC025700	Hs.519313	<i>AF5Q31</i>	5q31	1.9	2.3	2.0	1.9
225229_at	AL044396	Hs.519313	<i>AFF4</i>	5q31	2.4	2.4	2.2	2.3
232865_at	N59653	Hs.519313	<i>AFF4</i>	5q31	2.6	2.6	2.2	2.0
239439_at	BF963382	Hs.519313	<i>AFF4</i>	5q31	2.5	2.6	2.6	2.2

201900_s_at	NM_006066	Hs.474584	<i>AKR1A1</i>	1p33-p32	1.8	1.8	2.3	1.8
226025_at	AV740426	Hs.547037	<i>ANKRD28</i>	3p25.1	3.5	3.0	3.4	2.7
229307_at	N32051	Hs.335239	<i>ANKRD28</i>	3p25.1	6.8	6.9	11.0	5.5
242209_at	BF590315	Hs.433492	<i>ANKRD33</i>	12q13.13	5.4	9.1	14.1	4.3
230972_at	AW194999	Hs.432945	<i>ANKRD9</i>	14q32.32	2.6	2.5	5.6	6.5
206632_s_at	NM_004900	Hs.226307	<i>APOBEC3B</i>	22q13.1-q13.2	1.3	3.7	0.6	2.0
218098_at	AL121903	Hs.62578	<i>ARFGEF2</i>	20q13.13	1.9	1.9	3.5	2.8
222518_at	BF525399	Hs.62578	<i>ARFGEF2</i>	20q13.13	2.3	2.1	3.5	2.6
207606_s_at	NM_018287	Hs.499264	<i>ARHGAP12</i>	10p11.22	2.2	2.6	2.0	2.0
244548_at	AI189587	Hs.293593	<i>ARHGAP26</i>	5q31	1.8	2.0	1.6	1.4
213606_s_at	AI571798	Hs.159161	<i>ARHGDI1</i>	17q25.3	2.3	2.7	1.4	1.1
225347_at	AL520984	Hs.497399	<i>ARL10B</i>	1q32.1	2.2	2.0	2.4	1.9
217852_s_at	NM_018184	Hs.250009	<i>ARL10C</i>	3p26.1	4.3	3.3	2.6	2.7
222442_s_at	AW055237	Hs.250009	<i>ARL10C</i>	3p26.1	4.8	3.7	2.9	3.1
242727_at	BG032269	Hs.25362	<i>ARL8</i>	10p12.31	1.9	2.2	2.1	2.5
226055_at	AK000689	Hs.515249	<i>ARRDC2</i>	19p13.11	1.7	1.7	1.7	2.1
225283_at	AV701177	Hs.6093	<i>ARRDC4</i>	15q26.3	1.7	2.0	2.0	2.1
1555419_a_at	BC016828	Hs.527412	<i>ASAH1</i>	8p22-p21.3	1.5	1.5	1.8	2.3
213902_at	AI379338	Hs.527412	<i>ASAH1</i>	8p22-p21.3	1.8	1.9	2.4	2.7
204244_s_at	NM_006716	Hs.489037	<i>ASK</i>	7q21.3	2.3	1.9	6.3	6.8
202024_at	NM_004317	Hs.465985	<i>ASNA1</i>	19q13.3	2.0	1.9	2.1	1.8
207809_s_at	NM_001183	Hs.6551	<i>ATP6AP1</i>	Xq28	4.1	3.8	4.0	3.7
200954_at	NM_001694	Hs.389107	<i>ATP6V0C</i>	16p13.3	2.4	2.4	2.5	2.6
202872_at	AW024925	Hs.86905	<i>ATP6V1C1</i>	8q22.3	2.0	2.5	2.7	3.0
202873_at	BF034973	Hs.86905	<i>ATP6V1C1</i>	8q22.3	1.9	2.3	2.2	2.3
202874_s_at	NM_001695	Hs.86905	<i>ATP6V1C1</i>	8q22.3	2.4	2.8	2.9	3.9
226463_at	AW241758	Hs.86905	<i>ATP6V1C1</i>	8q22.3	2.3	2.7	2.8	2.8
208898_at	AF077614	Hs.272630	<i>ATP6V1D</i>	14q23-q24.2	5.6	4.2	3.5	3.0
208899_x_at	AF100741	Hs.272630	<i>ATP6V1D</i>	14q23-q24.2	5.5	4.5	3.1	2.9
201527_at	NM_004231	Hs.78089	<i>ATP6V1F</i>	7q32	4.8	4.0	6.9	5.4
221504_s_at	AF112204	Hs.491737	<i>ATP6V1H</i>	8p22-q22.3	2.6	2.1	2.3	2.2
225557_at	AI091372	Hs.370950	<i>AXUD1</i>	3p22	2.1	2.5	2.1	2.7
237338_at	AI760623	Hs.441681	<i>B3GALT7</i>	19q13.2	2.0	1.7	1.4	0.9
1559391_s_at	AI084451	Hs.370487	<i>B4GALT5</i>	20q13.1-q13.2	1.3	1.5	2.0	1.7
201169_s_at	BG326045	Hs.171825	<i>BHLHB2</i>	3p26	3.4	2.8	2.1	2.4
201170_s_at	NM_003670	Hs.171825	<i>BHLHB2</i>	3p26	2.3	1.9	1.7	2.0
228244_at	BF062383	Hs.103902	<i>BLOC1S3</i>	19q13.32	2.0	1.8	1.5	1.4
1568768_s_at	AW080339	Hs.258314	<i>BRE</i>	2p23.2	2.4	4.3	1.9	2.9
223376_s_at	AB055977	Hs.410497	<i>BRI3</i>	7q21.3	2.0	1.9	2.0	1.6
227775_at	BE467313	Hs.348342	<i>BRUNOL6</i>	15q24	3.4	3.8	5.8	4.4
1561890_at	BC037922	Hs.385493	<i>C10orf128</i>	10q11.23	2.1	1.8	2.0	1.7
228372_at	AW204712	Hs.385493	<i>C10orf128</i>	10q11.23	2.5	2.0	1.7	1.8
212500_at	AL049319	Hs.99821	<i>C10orf22</i>	10q21.3	2.1	2.2	1.5	1.6
212502_at	AV713053	Hs.99821	<i>C10orf22</i>	10q21.3	2.1	2.5	1.2	1.6
213246_at	AI346504	Hs.275352	<i>C14orf109</i>	14q32.13	5.2	4.5	3.2	2.7
212460_at	BE738425	Hs.269909	<i>C14orf147</i>	14q13.1	1.6	1.5	3.9	3.0
218493_at	NM_024571	Hs.15277	<i>C16orf33</i>	16p13.3	2.2	1.8	3.8	2.2

235022_at	BE326738	Hs.13034	<i>C18orf19</i>	18p11.21	5.5	6.1	6.3	3.7
220193_at	NM_024676	Hs.524496	<i>C1orf113</i>	1p34.3	4.0	5.1	4.8	4.3
1555225_at	BC008306	Hs.287471	<i>C1orf43</i>	1q21.2	2.7	2.6	2.5	2.1
1555226_s_at	BC008306	Hs.287471	<i>C1orf43</i>	1q21.2	2.4	2.2	1.7	1.9
233248_at	AK022028	Hs.287471	<i>C1orf43</i>	1q21.2	2.1	2.0	1.6	1.1
225551_at	AW291187	Hs.368353	<i>C1orf71</i>	1q44	2.1	1.9	1.5	1.6
221710_x_at	BC006241	Hs.87016	<i>C1orf78</i>	1p34.3	1.6	2.1	1.6	1.3
225401_at	BF977145	Hs.202522	<i>C1orf85</i>	1q22	5.9	5.3	6.1	4.5
231835_at	AL359575	Hs.462033	<i>C1orf93</i>	1p36.32	14.1	13.8	24.2	23.8
219633_at	NM_024331	Hs.283869	<i>C20orf121</i>	20q13.12	3.2	3.9	4.5	4.7
228031_at	AW444778	Hs.283869	<i>C20orf121</i>	20q13.12	4.0	4.5	6.5	6.6
225890_at	AI678096	Hs.320823	<i>C20orf72</i>	20p11.23	2.6	2.1	1.6	1.7
223039_at	BC004144	Hs.9850	<i>C22orf13</i>	22q11.2	2.1	1.7	1.6	1.2
212421_at	AB023147	Hs.369682	<i>C22orf9</i>	22q13.31	2.2	1.9	3.6	2.8
217118_s_at	AK025608	Hs.369682	<i>C22orf9</i>	22q13.31	1.6	1.6	3.7	2.9
219023_at	NM_018569	Hs.435991	<i>C4orf16</i>	4q25	12.4	10.2	22.3	18.1
205457_at	NM_024294	Hs.485162	<i>C6orf106</i>	6p21.31	1.7	1.8	2.0	1.6
217924_at	AL523965	Hs.485162	<i>C6orf106</i>	6p21.31	1.9	2.1	2.0	2.3
217925_s_at	NM_022758	Hs.485162	<i>C6orf106</i>	6p21.31	2.0	1.9	2.1	2.0
1554486_a_at	BC009205	Hs.551569	<i>C6orf114</i>	6p23	2.6	3.0	1.9	1.8
223361_at	AF116682	Hs.238205	<i>C6orf115</i>	6q24.1	2.3	1.5	2.0	1.3
212923_s_at	AK024828	Hs.484500	<i>C6orf145</i>	6p25.2	2.6	2.7	3.1	2.6
244669_at	T16443	Hs.292457	<i>C6orf160</i>	6q14.3	1.1	1.3	3.0	2.1
213810_s_at	AW007137	Hs.485915	<i>C6orf166</i>	6q15	2.7	2.8	2.1	2.1
223143_s_at	AI742378	Hs.485915	<i>C6orf166</i>	6q15	3.2	3.3	2.0	2.5
223144_s_at	BC000764	Hs.485915	<i>C6orf166</i>	6q15	2.2	2.2	1.9	1.8
223145_s_at	BC000764	Hs.485915	<i>C6orf166</i>	6q15	2.6	2.6	2.0	2.0
227368_at	AW009630	Hs.485915	<i>C6orf166</i>	6q15	3.7	4.2	2.5	2.6
226536_at	AL562908	Hs.388297	<i>C8orf36</i>	8q24.13	2.8	3.3	5.2	4.1
218904_s_at	NM_017998	Hs.532296	<i>C9orf40</i>	9q21.13	2.9	2.6	1.6	1.5
222781_s_at	BF590861	Hs.532296	<i>C9orf40</i>	9q21.13	3.6	2.7	1.9	1.8
209301_at	M36532	Hs.155097	<i>CA2</i>	8q22	3.6	3.0	3.7	4.0
238435_at	AA521288	Hs.532326	<i>CA5BL</i>	Xp22.2	2.0	2.2	1.4	1.1
225914_s_at	AW242839	Hs.87159	<i>CAB39L</i>	13q14.2	2.8	2.6	5.9	4.3
212252_at	AA181179	Hs.297343	<i>CAMKK2</i>	12q24.2	2.3	1.9	2.5	2.0
213812_s_at	AK024748	Hs.297343	<i>CAMKK2</i>	12q24.2	1.9	1.8	2.4	2.0
201850_at	NM_001747	Hs.516155	<i>CAPG</i>	2p11.2	1.2	1.2	2.5	1.9
240392_at	BF752351	Hs.550529	<i>CARD14</i>	17q25	5.7	4.7	5.8	4.4
1564010_at	AK026822	Hs.440961	<i>CAST</i>	5q15-q21	1.8	2.4	2.0	2.0
207467_x_at	NM_001750	Hs.440961	<i>CAST</i>	5q15-q21	2.2	1.9	3.1	2.2
208908_s_at	AF327443	Hs.440961	<i>CAST</i>	5q15-q21	3.0	2.3	4.9	3.0
212586_at	AA195244	Hs.440961	<i>CAST</i>	5q15-q21	2.1	1.8	2.4	2.0
238549_at	AI420611	Hs.153934	<i>CBFA2T2</i>	20q11	2.5	1.8	2.9	1.8
225323_at	AW514783	Hs.318773	<i>CC2D1B</i>	1p32.3	2.5	2.1	2.1	1.6
205114_s_at	NM_002983	Hs.514107	<i>CCL3, CCL3L1, CCL3L3</i>	17q11-q21, 17q21.1	6.1	6.8	4.0	7.1
204103_at	NM_002984	Hs.75703	<i>CCL4</i>	17q12	2.1	2.5	1.6	2.3
205098_at	AI421071	Hs.301921	<i>CCR1</i>	3p21	2.4	2.6	1.9	2.3

205099_s_at	NM_001295	Hs.301921	<i>CCR1</i>	3p21	2.4	2.8	2.0	2.0
211434_s_at	AF015524	Hs.458436	<i>CCRL2</i>	3p21	15.3	15.1	9.7	12.8
203645_s_at	NM_004244	Hs.504641	<i>CD163</i>	12p13.3	4.9	4.4	9.0	11.7
215049_x_at	Z22969	Hs.504641	<i>CD163</i>	12p13.3	4.7	5.7	7.2	10.6
208653_s_at	AF263279	Hs.520313	<i>CD164</i>	6q21	2.5	2.1	2.2	2.2
220307_at	NM_016382	Hs.157872	<i>CD244</i>	1q23.3	2.7	1.9	3.8	2.7
209933_s_at	AF020314	Hs.9688	<i>CD300A</i>	17q25.1	2.1	1.8	1.7	1.5
217078_s_at	AJ010102	Hs.9688	<i>CD300A</i>	17q25.1	2.8	2.3	1.6	1.7
204118_at	NM_001778	Hs.243564	<i>CD48</i>	1q21.3-q22	3.8	3.5	3.7	4.0
237759_at	AI378026	Hs.243564	<i>CD48</i>	1q21.3-q22	4.0	4.4	3.7	4.4
200663_at	NM_001780	Hs.445570	<i>CD63</i>	12q12-q13	1.9	1.7	2.1	1.8
203507_at	NM_001251	Hs.246381	<i>CD68</i>	17p13	3.6	5.1	8.4	5.5
204440_at	NM_004233	Hs.484703	<i>CD83</i>	6p23	7.4	7.4	5.7	7.1
201005_at	NM_001769	Hs.114286	<i>CD9</i>	12p13.3	2.8	2.4	2.9	3.4
209286_at	AI754416	Hs.369574	<i>CDC42EP3</i>	2p21	2.8	2.6	2.2	1.8
209287_s_at	AF104857	Hs.369574	<i>CDC42EP3</i>	2p21	3.0	2.6	2.1	2.1
209288_s_at	AL136842	Hs.369574	<i>CDC42EP3</i>	2p21	2.3	2.4	2.0	1.9
225685_at	AI801777	Hs.369574	<i>CDC42EP3</i>	2p21	2.5	2.4	2.3	1.9
202246_s_at	NM_000075	Hs.95577	<i>CDK4</i>	12q14	5.1	3.2	4.4	3.0
202284_s_at	NM_000389	Hs.370771	<i>CDKN1A</i>	6p21.2	2.7	3.1	3.4	4.2
206576_s_at	NM_001712	Hs.512682	<i>CEACAM1</i>	19q13.2	1.9	2.3	2.0	2.3
209498_at	X16354	Hs.512682	<i>CEACAM1</i>	19q13.2	3.1	2.4	2.2	2.4
211883_x_at	M76742	Hs.512682	<i>CEACAM1</i>	19q13.2	2.1	1.8	1.8	2.2
211889_x_at	D12502	Hs.512682	<i>CEACAM1</i>	19q13.2	2.5	2.5	2.6	2.4
225789_at	BE876194	Hs.195048	<i>CENTG3</i>	7q36.1	2.7	2.7	3.6	3.0
219375_at	NM_006090	Hs.363572	<i>CEPT1</i>	1p13.3	1.9	1.8	2.3	2.1
219082_at	NM_015944	Hs.433499	<i>CGI-14</i>	16p13.3	7.6	6.6	8.1	10.0
227841_at	BG260181	Hs.433499	<i>CGI-14</i>	16p13.3	9.0	7.7	6.5	5.8
204233_s_at	AI991328	Hs.77221	<i>CHKA</i>	11q13.2	6.3	4.4	19.6	12.5
204266_s_at	NM_001277	Hs.77221	<i>CHKA</i>	11q13.2	6.6	5.3	10.7	6.6
202536_at	AK002165	Hs.476930	<i>CHMP2B</i>	3p12.1	2.7	2.4	2.2	2.2
202537_s_at	AF151842	Hs.476930	<i>CHMP2B</i>	3p12.1	2.8	2.5	2.5	2.5
202538_s_at	NM_014043	Hs.476930	<i>CHMP2B</i>	3p12.1	2.8	2.5	2.2	2.5
64900_at	AA401703	Hs.420796	<i>CHST5</i> , <i>MGC15429</i>	16q22.3, 3p21.2	5.7	7.7	9.3	10.7
206756_at	NM_019886	Hs.138155	<i>CHST7</i>	Xp11.23	2.3	2.8	2.0	2.7
203950_s_at	NM_001286	Hs.193043	<i>CLCN6</i>	1p36	3.5	4.3	2.8	4.5
209235_at	AL031600	Hs.459649	<i>CLCN7</i>	16p13	4.8	8.0	6.4	10.6
38069_at	Z67743	Hs.459649	<i>CLCN7</i>	16p13	4.1	4.0	7.7	5.4
209275_s_at	AF015593	Hs.446747	<i>CLN3</i>	16p12.1	2.3	2.1	3.1	3.0
210859_x_at	AF077973	Hs.446747	<i>CLN3</i>	16p12.1	2.3	2.3	2.8	3.0
219340_s_at	AF123759	Hs.127675	<i>CLN8</i>	8p23	2.3	1.6	2.1	1.8
200960_x_at	NM_007096	Hs.522114	<i>CLTA</i>	9p13	3.4	3.0	1.8	1.7
204050_s_at	NM_001833	Hs.522114	<i>CLTA</i>	9p13	2.4	2.6	1.8	1.5
216295_s_at	X81636	Hs.522114	<i>CLTA</i>	9p13	3.2	2.9	1.7	1.8
238646_at	AA747756	Hs.491351	<i>CLTC</i>	17q11-qter	2.7	4.2	2.4	2.1
223198_x_at	BC002672	Hs.2076	<i>COMMD5</i>	8q24-qter	2.5	2.5	2.1	1.9
223819_x_at	BC003055	Hs.2076	<i>COMMD5</i>	8q24-qter	2.6	2.6	2.5	1.8

224387_at	AF290195	Hs.2076	COMMD5	8q24-qter	2.3	2.8	2.0	2.2
1554744_at	BC033638	Hs.348365	COPI	---	2.5	3.1	2.3	1.9
1569703_a_at	BC014583	Hs.330384	CORO1C	12q24.1	1.9	2.0	1.6	1.3
221676_s_at	BC002342	Hs.330384	CORO1C	12q24.1	2.4	2.2	2.0	1.9
222409_at	AL162070	Hs.330384	CORO1C	12q24.1	2.3	2.0	1.7	1.5
201940_at	AA897514	Hs.446079	CPD	17p11.1-q11.2	1.9	1.8	1.7	2.0
201942_s_at	D85390	Hs.446079	CPD	17p11.1-q11.2	2.4	2.1	2.1	2.5
201943_s_at	NM_001304	Hs.446079	CPD	17p11.1-q11.2	2.2	1.9	1.7	2.4
242280_x_at	N53564	Hs.127126	CPEB4	5q21	1.6	1.7	2.1	1.4
201200_at	NM_003851	Hs.5710	CREG1	1q24	2.9	2.3	2.4	2.5
209674_at	D83702	Hs.151573	CRY1	12q23-q24.1	2.0	2.0	4.4	3.5
209716_at	M37435	Hs.173894	CSF1	1p21-p13	4.9	5.5	2.1	2.8
201201_at	NM_000100	Hs.695	CSTB	21q22.3	3.5	3.1	3.0	2.8
204925_at	NM_004937	Hs.187667	CTNS	17p13	2.5	2.6	1.9	1.9
36566_at	AJ222967	Hs.187667	CTNS	17p13	2.8	2.3	2.1	2.0
200766_at	NM_001909	Hs.546248	CTSD	11p15.5	8.9	7.0	6.2	4.4
204470_at	NM_001511	Hs.789	CXCL1	4q21	1.8	2.1	2.0	2.2
209774_x_at	M57731	Hs.75765	CXCL2	4q21	12.9	17.3	19.2	20.5
207850_at	NM_002090	Hs.89690	CXCL3	4q21	2.8	3.8	4.5	2.9
202435_s_at	AU154504	Hs.154654	CYP1B1	2p21	1.1	1.4	2.0	2.8
202436_s_at	AU144855	Hs.154654	CYP1B1	2p21	1.1	1.3	2.0	2.9
202437_s_at	NM_000104	Hs.154654	CYP1B1	2p21	1.2	1.2	1.8	3.1
201623_s_at	BC000629	Hs.503787	DARS	2q21.3	2.7	2.1	2.3	2.0
201624_at	NM_001349	Hs.503787	DARS	2q21.3	2.4	2.0	2.1	2.0
224827_at	AK022894	Hs.179852	DC-Ubp	5q35.1	3.0	1.8	2.2	1.9
225965_at	H16810	Hs.513260	DDHD1	14q21	1.7	1.8	2.3	2.0
225970_at	AA029818	Hs.513260	DDHD1	14q21	3.4	2.5	7.7	4.2
225971_at	A1741411	Hs.513260	DDHD1	14q21	2.9	2.2	5.3	3.6
231165_at	BE857355	Hs.513260	DDHD1	14q21	4.8	4.2	4.2	3.8
244154_at	A1751130	Hs.513260	DDHD1	14q21	1.6	1.7	2.5	2.1
209383_at	BC003637	Hs.505777	DDIT3	12q13.1-q13.2	3.6	3.7	2.1	2.2
203785_s_at	NM_018380	Hs.458313	DDX28	16q22.1	3.8	1.9	1.8	1.3
40255_at	AC004531	Hs.458313	DDX28	16q22.1	2.0	1.8	1.4	1.2
201584_s_at	NM_005804	Hs.311609	DDX39	19p13.12	7.4	6.1	2.2	2.3
231896_s_at	AF103800	Hs.22393	DENR	12q24.31	2.2	1.6	1.3	1.3
234915_s_at	BC000925	Hs.22393	DENR	12q24.31	2.0	1.6	1.4	1.3
215468_at	AK001442	Hs.191518	DHX9	1q25	2.1	2.5	1.9	1.5
221311_x_at	NM_020466	Hs.483841	DJ122O8.2	6q14.2-q16.1	2.8	2.3	2.5	1.9
227712_at	AV682940	Hs.483841	DJ122O8.2	6q14.2-q16.1	2.0	2.9	2.1	2.1
227170_at	BF338409	Hs.112668	DKFZp547K054	7p22.1	2.3	2.3	2.5	2.6
224952_at	BF115054	Hs.410889	DKFZp564D166	17q23.3	1.1	1.0	3.1	3.4
226657_at	H27948	Hs.14478	DKFZp762H185	17p11.1	3.7	3.0	2.6	2.2
203810_at	BG252490	Hs.380282	DNAJB4	1p31.1	1.7	2.0	1.8	2.7
1554462_a_at	AF115512	Hs.6790	DNAJB9	7q31, 14q24.2-q24.3	2.5	2.3	1.7	1.9
202842_s_at	AL080081	Hs.6790	DNAJB9	7q31, 14q24.2-q24.3	2.6	2.5	1.9	2.0
202843_at	NM_012328	Hs.6790	DNAJB9	7q31,	2.5	2.5	1.8	1.8

				14q24.2-q24.3				
208499_s_at	NM_006260	Hs.59214	<i>DNAJC3</i>	13q32	1.4	1.3	2.1	1.6
240574_at	BE501239	Hs.59214	<i>DNAJC3</i>	13q32	1.9	1.4	2.1	1.9
205545_x_at	NM_014280	Hs.433540	<i>DNAJC8</i>	1p35.3	2.0	2.1	1.7	2.0
212491_s_at	AA843895	Hs.433540	<i>DNAJC8</i>	1p35.3	2.3	2.1	2.0	2.1
214992_s_at	AD000092	Hs.118243	<i>DNASE2</i>	19p13.2	3.1	2.0	2.2	1.6
235236_at	AI991459	Hs.325528	<i>DOCK2</i>	5q35.1	2.2	2.4	2.3	2.2
221985_at	AW006750	Hs.407709	<i>DRE1</i>	3q27.1	2.7	2.2	2.1	2.1
221986_s_at	AW006750	Hs.407709	<i>DRE1</i>	3q27.1	2.8	2.3	2.2	2.1
226158_at	AL120021	Hs.4094	<i>DRE1</i>	3q27.3	2.1	1.8	1.7	1.7
242088_at	AI961401	Hs.407709	<i>DRE1</i>	3q27.1	2.2	2.3	1.8	1.8
243918_at	AI459554	Hs.407709	<i>DRE1</i>	3q27.1	5.0	5.5	4.3	5.1
203635_at	NM_006052	Hs.369488	<i>DSCR3</i>	21q22.2	2.7	2.5	1.4	1.4
217309_s_at	AJ001867	Hs.369488	<i>DSCR3</i>	21q22.2	2.1	2.3	1.4	1.3
223445_at	AF061734	Hs.519583	<i>DTNBP1</i>	6p22.3	6.2	4.6	5.9	4.3
223446_s_at	AF061734	Hs.519583	<i>DTNBP1</i>	6p22.3	15.0	6.9	10.9	9.0
223763_at	AL136637	Hs.519583	<i>DTNBP1</i>	6p22.3	4.8	4.3	3.0	2.7
237890_at	AW026356	Hs.519583	<i>DTNBP1</i>	6p22.3	24.7	15.0	28.7	18.1
215501_s_at	AK022513	Hs.497822	<i>DUSP10</i>	1q41	3.3	2.9	4.6	3.8
221563_at	N36770	Hs.497822	<i>DUSP10</i>	1q41	3.3	2.5	3.7	3.7
201536_at	AL048503	Hs.181046	<i>DUSP3</i>	17q21	4.4	3.7	3.8	3.4
201537_s_at	BC002682	Hs.181046	<i>DUSP3</i>	17q21	5.8	4.6	5.1	3.9
201538_s_at	NM_004090	Hs.181046	<i>DUSP3</i>	17q21	3.4	3.1	3.5	2.3
57532_at	AW016304	Hs.118640	<i>DVL2</i>	17p13.2	4.0	2.7	3.3	2.2
203957_at	NM_001952	Hs.135465	<i>E2F6</i>	2p25.1	2.0	2.0	1.6	2.0
222802_at	J05008	Hs.511899	<i>EDN1</i>	6p24.1	3.1	3.5	1.7	2.3
201693_s_at	AV733950	Hs.326035	<i>EGR1</i>	5q31.1	1.0	1.7	2.0	1.9
205249_at	NM_000399	Hs.1395	<i>EGR2</i>	10q21.1	5.3	7.2	3.6	6.8
206115_at	NM_004430	Hs.534313	<i>EGR3</i>	8p23-p21	3.3	3.7	2.8	3.4
231292_at	AI964053	Hs.170337	<i>EID3</i>	12q23-q24.1	2.7	2.8	3.0	2.4
218696_at	NM_004836	Hs.434326	<i>EIF2AK3</i>	2p12	3.4	2.3	2.1	1.4
201530_x_at	NM_001416	Hs.129673	<i>EIF4A1</i>	17p13	1.7	1.8	2.0	2.4
211787_s_at	BC006210	Hs.129673	<i>EIF4A1</i>	17p13	2.0	2.0	2.4	2.5
214805_at	U79273	Hs.129673	<i>EIF4A1</i>	17p13	2.0	2.2	2.0	2.0
220386_s_at	NM_019063	Hs.432438	<i>EML4</i>	2p22-p21	2.4	2.2	1.9	2.0
223068_at	AV707345	Hs.432438	<i>EML4</i>	2p22-p21	2.5	2.4	2.0	2.4
223069_s_at	AF177377	Hs.432438	<i>EML4</i>	2p22-p21	1.9	2.2	2.2	2.3
228674_s_at	AA524507	Hs.432438	<i>EML4</i>	2p22-p21	2.8	2.9	3.6	3.5
231926_at	AK023744	Hs.292072	<i>EPS15L1</i>	19p13.11	1.8	1.8	2.4	2.2
217941_s_at	NM_018695	Hs.519346	<i>ERBB2IP</i>	5q12.3	2.1	1.8	1.6	1.7
222473_s_at	AI807103	Hs.519346	<i>ERBB2IP</i>	5q12.3	2.4	2.0	1.8	2.0
202776_at	NM_014597	Hs.85769	<i>ERBP</i>	1p22.1	1.7	2.1	2.0	2.3
235745_at	AV704183	Hs.133982	<i>ERN1</i>	17q24.2	2.0	2.5	1.5	1.7
226866_at	BF211488	Hs.464733	<i>ESCO1</i>	18q11.2	2.2	1.9	1.7	1.5
235216_at	BG532121	Hs.464733	<i>ESCO1</i>	18q11.2	2.0	2.0	1.6	1.3
223242_s_at	AF015186	Hs.464166	<i>ET</i>	17q25	1.9	2.1	1.6	1.5
201573_s_at	M75715	Hs.483494	<i>ETF1</i>	5q31.1	1.8	1.9	1.9	2.1

236554_x_at	AI370364	Hs.15284	EVER2	17q25.3	2.7	2.0	2.1	1.7
202862_at	NM_000137	Hs.73875	FAH	15q23-q25	1.5	1.6	3.0	2.3
221601_s_at	AI084226	Hs.58831	FAIM3	1q32.1	2.2	1.9	2.2	2.1
212929_s_at	W68158	Hs.365286	FAM21B, FAM21C, LOC387680	10q11.22, 10q11.1, 10q11.23	6.6	4.1	4.6	3.5
214946_x_at	AV728658	Hs.365286	FAM21B, FAM21C, LOC387680	10q11.22, 10q11.1, 10q11.23	7.6	5.1	5.1	4.1
212370_x_at	AL080183	Hs.375174	FAM21B, LOC387680	10q11.22, 10q11.23	5.7	4.3	4.4	3.4
211068_x_at	BC006456	Hs.365286	FAM21C	10q11.1	5.9	4.0	4.4	3.4
203262_s_at	NM_004699	Hs.54277	FAM50A	Xq28	3.1	3.0	3.6	3.1
229344_x_at	AW135012	Hs.504670	FAM80B	12p13.31	1.6	1.9	1.9	2.3
203620_s_at	NM_014824	Hs.445748	FCHSD2	11q13.4	1.4	1.2	2.5	2.8
241917_at	AA875908	Hs.445748	FCHSD2	11q13.4	2.5	2.2	2.7	2.1
242563_at	AI535736	Hs.445748	FCHSD2	11q13.4	3.6	3.6	3.7	2.9
1552664_at	NM_144997	Hs.513975	FLCN	17p11.2	2.4	2.2	1.6	1.3
215645_at	AF090883	Hs.513975	FLCN	17p11.2	4.5	3.2	2.4	1.6
209688_s_at	BC005078	Hs.107845	FLJ10996	2q14.1	2.2	2.5	2.8	2.9
209689_at	BC005078	Hs.107845	FLJ10996	2q14.1	2.5	2.8	3.2	3.7
219774_at	NM_019044	Hs.107845	FLJ10996	2q14.1	2.2	2.5	3.2	3.3
244648_at	AA007283	Hs.107845	FLJ10996	2q14.1	2.2	2.3	2.3	2.0
228745_at	AI376997	Hs.482301	FLJ13611	5q12.3	4.9	4.1	4.2	3.9
218532_s_at	NM_019000	Hs.481704	FLJ20152	5p15.1	1.9	1.5	2.2	1.7
218035_s_at	NM_019027	Hs.518727	FLJ20273	4p13-p12	2.2	1.9	1.4	1.4
222496_s_at	AW241742	Hs.518727	FLJ20273	4p13-p12	2.2	2.0	1.4	1.6
229439_s_at	AI830823	Hs.518727	FLJ20273	4p13-p12	2.9	2.5	1.6	1.6
221685_s_at	AF269167	Hs.368710	FLJ20364	5q35.1	5.1	4.6	5.7	4.2
219449_s_at	NM_017866	Hs.106650	FLJ20533	8q21.11	3.1	2.6	2.0	1.8
221081_s_at	NM_024901	Hs.552603	FLJ22457	1p13.3	6.9	4.6	8.4	6.8
236327_at	AA767373	Hs.363572	FLJ22457	1p13.3	2.6	2.8	2.3	2.1
219690_at	NM_024660	Hs.352548	FLJ22573	19q13.12	1.1	1.6	1.4	2.1
225607_at	AI948491	Hs.349758	FLJ31795	17q21.31	3.9	3.4	6.6	5.0
226738_at	BE675297	Hs.234572	FLJ33817	17p13.3	11.1	8.8	6.0	4.1
1553449_at	NM_173617	Hs.375664	FLJ36701	16q24.3	15.0	7.8	6.9	5.0
225466_at	BG291961	Hs.523698	FLJ36874	11q12.1	2.8	2.2	2.1	2.2
225468_at	AI761804	Hs.523698	FLJ36874	11q12.1	3.2	2.5	2.1	2.4
235234_at	AA359612	Hs.523698	FLJ36874	11q12.1	3.3	2.8	2.3	2.8
235235_s_at	AA359612	Hs.523698	FLJ36874	11q12.1	2.8	2.4	2.2	2.1
213294_at	AV755522	Hs.546523	FLJ38348	2p22.2	1.5	1.4	1.6	2.1
226589_at	BE964222	Hs.369632	FLJ38482	4q32.3	2.4	2.3	2.6	2.4
228937_at	AI659800	Hs.210586	FLJ38725	13q14.11	1.3	1.4	2.0	2.1
226497_s_at	AA149648	Hs.507621	FLT1	13q12	1.9	2.1	0.9	1.1
202304_at	NM_014923	Hs.508010	FND3A	13q14.2	2.7	2.2	2.9	3.1
215910_s_at	AL137000	Hs.508010	FND3A	13q14.2	2.8	2.1	3.7	3.5
231343_at	AW300131	Hs.508010	FND3A	13q14.2	4.4	3.5	3.1	2.2
241611_s_at	BE675600	Hs.508010	FND3A	13q14.2	2.0	1.8	2.4	2.3
222693_at	BF444916	Hs.159430	FND3B	3q26.31	1.6	1.7	1.5	2.1

205409_at	NM_005253	Hs.220971	<i>FOSL2</i>	2p23.3	2.1	2.1	1.2	1.2
218880_at	N36408	Hs.220971	<i>FOSL2</i>	2p23.3	2.1	2.4	1.4	1.4
218881_s_at	NM_024530	Hs.220971	<i>FOSL2</i>	2p23.3	2.0	2.6	1.4	1.2
202838_at	NM_000147	Hs.370858	<i>FUCA1</i>	1p34	1.4	1.3	2.4	2.3
223042_s_at	BC000255	Hs.356050	<i>FUNDC2</i>	Xq28	2.0	2.6	1.4	2.1
202419_at	NM_002035	Hs.74050	<i>FVT1</i>	18q21.3	2.9	2.7	3.2	2.9
213524_s_at	NM_015714	Hs.432132	<i>G0S2</i>	1q32.2-q41	3.8	4.3	4.2	4.7
205483_s_at	NM_005101	Hs.458485	<i>G1P2</i>	1p36.33	1.8	1.4	2.1	2.8
238405_at	AI792896	Hs.429434	<i>GAB2</i>	11q14.1	5.9	5.1	7.9	4.0
207574_s_at	NM_015675	Hs.110571	<i>GADD45B</i>	19p13.3	6.3	4.8	4.4	4.3
209304_x_at	AF087853	Hs.110571	<i>GADD45B</i>	19p13.3	6.9	5.9	4.4	4.4
209305_s_at	AF078077	Hs.110571	<i>GADD45B</i>	19p13.3	6.9	5.5	4.1	4.0
213560_at	AV658684	Hs.110571	<i>GADD45B</i>	19p13.3	2.5	2.0	2.1	1.8
222235_s_at	AL139812	Hs.180758	<i>GALNACT-2</i>	10q11.21	1.8	1.8	2.0	1.9
239077_at	W81648	Hs.180758	<i>GALNACT-2</i>	10q11.21	2.1	2.2	2.2	1.8
208693_s_at	D30658	Hs.404321	<i>GARS</i>	7p15	2.3	1.9	2.3	1.7
202191_s_at	BE439987	Hs.462214	<i>GAS7</i>	17p13.1	1.6	1.5	5.7	3.5
202192_s_at	NM_005890	Hs.462214	<i>GAS7</i>	17p13.1	1.5	1.3	3.8	3.2
207704_s_at	NM_003644	Hs.462214	<i>GAS7</i>	17p13.1	1.6	1.7	4.3	3.4
210872_x_at	BC001152	Hs.462214	<i>GAS7</i>	17p13.1	1.2	1.5	2.7	2.7
211067_s_at	BC006454	Hs.462214	<i>GAS7</i>	17p13.1	1.8	1.9	6.3	4.6
209093_s_at	K02920	Hs.511984	<i>GBA, GBAP</i>	1q21	7.1	5.6	4.4	3.3
210589_s_at	D13287	Hs.511984	<i>GBA, GBAP</i>	1q21	16.3	7.8	5.2	3.1
203282_at	NM_000158	Hs.436062	<i>GBE1</i>	3p12.3	1.5	1.5	4.0	3.7
202922_at	BF676980	Hs.271264	<i>GCLC</i>	6p12	2.8	2.1	2.8	2.6
202923_s_at	NM_001498	Hs.271264	<i>GCLC</i>	6p12	3.9	2.6	3.7	3.1
203925_at	NM_002061	Hs.315562	<i>GCLM</i>	1p22.1	1.9	2.1	2.9	3.6
234986_at	AA630626	Hs.315562	<i>GCLM</i>	1p22.1	1.8	1.7	2.7	2.9
236140_at	AI753488	Hs.315562	<i>GCLM</i>	1p22.1	2.0	2.0	2.6	2.7
219821_s_at	NM_018988	Hs.484686	<i>GFOD1</i>	6pter-p22.1	2.6	1.9	1.7	1.8
207131_x_at	NM_013430	Hs.287505	<i>GGT1</i>	22q11.23	1.8	2.2	2.4	1.8
208284_x_at	NM_013421	Hs.287505	<i>GGT1</i>	22q11.23	2.0	2.2	2.7	2.0
209919_x_at	L20490	Hs.287505	<i>GGT1</i>	22q11.23	1.7	2.1	2.4	2.0
211417_x_at	L20493	Hs.287505	<i>GGT1</i>	22q11.23	1.7	1.9	2.3	1.9
223278_at	M86849	Hs.524894	<i>GJB2</i>	13q11-q12	5.5	5.8	12.1	7.6
231771_at	AI694073	Hs.511757	<i>GJB6</i>	13q11-q12.1, 13q12	1.9	2.3	7.3	9.0
214430_at	NM_000169	Hs.69089	<i>GLA</i>	Xq22	2.9	3.4	4.4	4.9
219267_at	NM_016433	Hs.381256	<i>GLTP</i>	12q24.11	1.4	1.6	3.3	2.6
226177_at	AI052020	Hs.381256	<i>GLTP</i>	12q24.11	1.6	1.5	2.9	2.9
202382_s_at	NM_005471	Hs.278500	<i>GNPDA1</i>	5q21	15.0	10.0	4.3	4.0
224887_at	AF302786	Hs.241575	<i>GNPTG</i>	16p13.3	2.0	1.9	2.6	2.1
210007_s_at	U36310	Hs.148266	<i>GPD2</i>	2q24.1	6.8	4.8	3.6	3.5
225447_at	AA613031	Hs.148266	<i>GPD2</i>	2q24.1	6.5	3.6	3.2	2.7
243598_at	AI393727	Hs.148266	<i>GPD2</i>	2q24.1	4.1	3.1	3.0	2.0
201141_at	NM_002510	Hs.190495	<i>GPNMB</i>	7p15	2.4	1.7	8.6	3.8
205220_at	NM_006018	Hs.458425	<i>GPR109B</i>	12q24.31	2.6	2.2	2.6	2.3
218855_at	NM_016372	Hs.6418	<i>GPR175</i>	3q21.2	3.4	2.7	4.2	3.4

200736_s_at	NM_000581	Hs.76686	<i>GPX1</i>	3p21.3	3.0	2.4	2.4	2.2
212090_at	AL571424	Hs.339697	<i>GRINA</i>	8q24.3	1.1	1.3	2.1	1.5
200678_x_at	NM_002087	Hs.514220	<i>GRN</i>	17q21.32	2.2	1.7	2.7	2.1
211284_s_at	BC000324	Hs.514220	<i>GRN</i>	17q21.32	2.4	1.8	3.3	2.4
216041_x_at	AK023348	Hs.514220	<i>GRN</i>	17q21.32	2.3	1.7	2.9	2.1
205770_at	NM_000637	Hs.271510	<i>GSR</i>	8p21.1	1.5	1.6	2.5	2.3
225609_at	AI888037	Hs.271510	<i>GSR</i>	8p21.1	1.8	1.9	2.7	2.4
1557915_s_at	U56250	Hs.190028	<i>GSTO1</i>	10q25.1	3.1	2.4	3.0	2.3
201470_at	NM_004832	Hs.190028	<i>GSTO1</i>	10q25.1	3.3	2.5	3.4	2.3
1559009_at	BC040628	Hs.510068	<i>GTF2A1</i>	14q31.1	2.1	2.5	2.9	2.6
206521_s_at	NM_015859	Hs.510068	<i>GTF2A1</i>	14q31.1	2.3	2.2	1.7	1.1
225433_at	AU144104	Hs.547415	<i>GTF2A1</i>	14q31.1	2.6	2.5	1.6	1.7
202451_at	BC000365	Hs.523510	<i>GTF2H1</i>	11p15.1-p14	4.5	4.0	2.6	2.2
202453_s_at	NM_005316	Hs.523510	<i>GTF2H1</i>	11p15.1-p14	5.2	4.2	2.4	2.6
207168_s_at	NM_004893	Hs.420272	<i>H2AFY</i>	5q31.3-q32	1.5	1.4	2.2	1.9
214500_at	AF044286	Hs.420272	<i>H2AFY</i>	5q31.3-q32	1.9	1.7	2.3	2.0
214501_s_at	AF044286	Hs.420272	<i>H2AFY</i>	5q31.3-q32	1.9	1.7	2.3	1.9
226840_at	AW291297	Hs.420272	<i>H2AFY</i>	5q31.3-q32	2.9	2.4	1.7	1.3
229593_at	BE503981	Hs.420272	<i>H2AFY</i>	5q31.3-q32	2.0	2.0	1.4	1.1
218450_at	NM_015987	Hs.294133	<i>HEBP1</i>	12p13.1	2.3	1.7	3.5	2.3
219863_at	NM_016323	Hs.26663	<i>HERC5</i>	4q22.1-q23	1.4	1.5	1.7	2.2
203394_s_at	BE973687	Hs.250666	<i>HES1</i>	3q28-q29	2.3	3.7	3.8	6.2
203395_s_at	NM_005524	Hs.250666	<i>HES1</i>	3q28-q29	1.6	2.5	1.9	3.1
227347_x_at	NM_021170	Hs.154029	<i>HES4</i>	1p36.33	2.5	2.7	4.2	5.1
201765_s_at	AL523158	Hs.513008	<i>HEXA</i>	15q23-q24	7.3	4.5	7.4	5.3
215155_at	J04178	Hs.513008	<i>HEXA</i>	15q23-q24	12.2	9.3	8.9	7.6
201944_at	NM_000521	Hs.69293	<i>HEXB</i>	5q13	2.8	2.4	2.2	2.1
226533_at	BF694956	Hs.72325	<i>HINT3</i>	6q22.32	3.9	3.7	3.4	2.4
226537_at	AW418666	Hs.72325	<i>HINT3</i>	6q22.32	6.7	5.4	3.6	3.7
225097_at	BF594155	Hs.397465	<i>HIPK2</i>	7q32-q34	1.3	1.2	2.0	2.3
225115_at	BF529628	Hs.397465	<i>HIPK2</i>	7q32-q34	1.5	1.0	2.2	2.3
225116_at	AW300045	Hs.397465	<i>HIPK2</i>	7q32-q34	1.1	1.1	2.1	2.2
225368_at	BF218115	Hs.397465	<i>HIPK2</i>	7q32-q34	1.2	1.1	2.3	2.5
203932_at	NM_002118	Hs.1162	<i>HLA-DMB</i>	6p21.3	1.2	1.1	2.5	1.6
1560297_at	BG928538	Hs.373741	<i>HM13</i>	20q11.21	2.7	2.5	1.9	1.7
224615_x_at	AL110115	Hs.373741	<i>HM13</i>	20q11.21	1.7	1.8	2.8	2.0
212596_s_at	AJ010070	Hs.197086	<i>HMG2L1</i>	22q13.1	2.4	1.9	1.8	1.6
212597_s_at	AL079310	Hs.197086	<i>HMG2L1</i>	22q13.1	2.3	1.8	1.5	1.6
206074_s_at	NM_002131	Hs.518805	<i>HMGA1</i>	6p21	1.7	2.5	2.4	2.5
203665_at	NM_002133	Hs.517581	<i>HMOX1</i>	22q12, 22q13.1	8.1	7.6	4.8	5.5
206809_s_at	NM_005758	Hs.524276	<i>HNRPA3P1</i> , <i>HNRPA3</i>	10q11.21, 2q31.2	1.6	2.1	1.8	2.1
201376_s_at	AI591354	Hs.808	<i>HNRPF</i>	10q11.21- q11.22	6.1	5.2	4.3	4.2
204647_at	NM_004838	Hs.410683	<i>HOMER3</i>	19p13.11	2.4	1.7	1.8	1.2
207117_at	NM_015852	---	<i>H-plk</i>	7q11.21	2.2	2.1	1.6	1.2
203309_s_at	NM_000195	Hs.404568	<i>HPS1</i>	10q23.1-q23.3	2.1	1.6	1.6	1.7

210112_at	U96721	Hs.404568	<i>HPS1</i>	10q23.1-q23.3	2.3	1.6	2.3	1.7
204544_at	NM_007216	Hs.437599	<i>HPS5</i>	11p14	2.5	2.5	2.7	3.3
219020_at	NM_022460	Hs.531785	<i>HS1BP3</i>	2p24.1	3.3	2.8	1.5	1.3
201413_at	NM_000414	Hs.406861	<i>HSD17B4</i>	5q21	7.3	4.5	7.3	4.9
202581_at	NM_005346	Hs.274402	<i>HSPA1B</i>	6p21.3	2.0	2.3	3.3	2.7
218971_s_at	NM_014149	Hs.371722	<i>HSPC049</i>	7q33	2.6	2.5	2.3	1.9
222799_at	AK001606	Hs.371722	<i>HSPC049</i>	7q33	3.4	3.4	2.7	3.1
230888_at	AW300278	Hs.371722	<i>HSPC049</i>	7q33	2.3	2.2	1.9	2.1
219998_at	NM_014181	Hs.372208	<i>HSPC159</i>	2p14	4.5	2.7	2.9	2.1
226188_at	AK025603	Hs.372208	<i>HSPC159</i>	2p14	3.1	2.3	2.0	2.3
211969_at	BG420237	Hs.523560	<i>HSPCA</i>	14q32.33	1.7	1.7	1.9	2.0
200064_at	AF275719	Hs.509736	<i>HSPCB</i>	6p12	1.6	1.7	1.7	2.1
214359_s_at	AI218219	Hs.509736	<i>HSPCB</i>	6p12	1.4	1.6	1.8	2.4
206976_s_at	NM_006644	Hs.36927	<i>HSPH1</i>	13q12.3	4.3	3.6	2.5	4.4
221622_s_at	AF246240	Hs.525063	<i>HT007</i>	11q14.1	2.9	2.0	1.8	1.8
209192_x_at	BC000166	Hs.528299	<i>HTATIP</i>	11q13	2.0	1.9	1.8	1.8
1555464_at	BC046208	Hs.163173	<i>IFIH1</i>	2p24.3-q24.3	1.4	1.7	1.3	2.5
203595_s_at	N47725	Hs.252839	<i>IFIT5</i>	10q23.31	1.8	1.6	1.4	2.0
203596_s_at	NM_012420	Hs.252839	<i>IFIT5</i>	10q23.31	1.6	1.7	1.4	2.1
222868_s_at	AI521549	Hs.325978	<i>IL18BP</i>	11q13	1.7	1.6	2.3	2.4
202948_at	NM_000877	Hs.516249	<i>IL1R1</i>	2q12	1.6	1.6	2.0	3.0
215561_s_at	AK026803	Hs.516249	<i>IL1R1</i>	2q12	1.7	1.6	1.9	2.2
208930_s_at	BG032366	Hs.465885	<i>ILF3</i>	19p13.2	1.5	2.1	3.7	3.3
208931_s_at	AF147209	Hs.465885	<i>ILF3</i>	19p13.2	1.2	1.2	2.1	2.2
211375_s_at	AF141870	Hs.465885	<i>ILF3</i>	19p13.2	2.0	1.9	2.7	2.4
217805_at	NM_004516	Hs.465885	<i>ILF3</i>	19p13.2	1.9	1.9	2.4	2.0
201625_s_at	BE300521	Hs.520819	<i>INSIG1</i>	7q36	2.1	2.0	1.9	1.7
201627_s_at	NM_005542	Hs.520819	<i>INSIG1</i>	7q36	2.0	2.1	1.6	1.8
223309_x_at	BG025248	Hs.418133	<i>IPLA2(GAMMA)</i>	7q31	2.1	1.6	1.0	0.9
234304_s_at	AL162083	Hs.482269	<i>IPO11</i>	5q12.1	5.0	4.7	5.9	6.1
201587_s_at	NM_001569	Hs.522819	<i>IRAK1</i>	Xq28	3.8	3.4	4.7	3.5
231779_at	AI246590	Hs.449207	<i>IRAK2</i>	3p25.3	2.3	2.4	4.1	4.5
224572_s_at	BG485163	Hs.350268	<i>IRF2BP2</i>	1q42.3	2.8	2.3	1.1	1.3
203710_at	NM_002222	Hs.374613	<i>ITPR1</i>	3p26-p25	4.1	3.2	3.0	3.1
211323_s_at	L38019	Hs.374613	<i>ITPR1</i>	3p26-p25	4.5	3.5	3.4	3.1
216944_s_at	U23850	Hs.374613	<i>ITPR1</i>	3p26-p25	3.7	2.9	2.6	2.8
224933_s_at	AA425650	Hs.413416	<i>JMJD1C</i>	10q21.3	2.2	2.0	1.5	1.5
228793_at	BF002296	Hs.413416	<i>JMJD1C</i>	10q21.3	2.1	2.0	1.5	1.5
241661_at	AA001021	Hs.413416	<i>JMJD1C</i>	10q21.3	2.2	2.1	1.4	1.6
226352_at	BF447037	Hs.482605	<i>JMY</i>	5q14.1	3.7	3.4	3.1	2.6
241985_at	AI814405	Hs.482605	<i>JMY</i>	5q14.1	2.9	2.9	3.9	2.4
203402_at	AL520102	Hs.440497	<i>KCNAB2</i>	1p36.3	2.9	2.7	3.8	2.5
211791_s_at	AF044253	Hs.440497	<i>KCNAB2</i>	1p36.3	2.6	2.2	3.3	2.5
216782_at	AK026679	Hs.411299	<i>KCNJ15</i>	21q22.2	2.4	2.3	1.9	1.4
238428_at	BG542347	Hs.411299	<i>KCNJ15</i>	21q22.2	2.1	1.2	1.3	1.4
34221_at	D83778	Hs.549664	<i>KIAA0194</i>	5q33.1	1.8	2.3	2.2	2.5
201985_at	NM_014846	Hs.270043	<i>KIAA0196</i>	8p22	5.9	4.3	3.4	2.7

212621_at	AB006624	Hs.533787	KIAA0286	12q13.3	4.0	3.1	2.0	2.2
209912_s_at	AI373854	Hs.520634	KIAA0415	7p22.2	2.7	2.1	2.2	1.7
202860_at	NM_014856	Hs.6684	KIAA0476	1p36.13-q31.3	2.0	1.5	1.3	1.3
205888_s_at	AI962693	Hs.533025	KIAA0555	5q32	7.3	5.0	12.4	9.1
212663_at	AB014574	Hs.522351	KIAA0674	9q32	3.1	2.4	2.1	2.1
31826_at	AB014574	Hs.522351	KIAA0674	9q32	2.8	2.5	2.1	1.8
203321_s_at	AK022688	Hs.131915	KIAA0863	18q23	1.9	1.9	2.1	2.0
203322_at	AU145934	Hs.131915	KIAA0863	18q23	1.8	1.8	2.2	1.9
226164_x_at	AI760919	Hs.504670	KIAA1238	12p13.31	2.0	1.9	2.0	2.1
227504_s_at	N64630	Hs.18861	KIAA1276	4p16	2.2	1.9	1.6	1.4
235288_at	AI627532	Hs.18861	KIAA1276	4p16	2.4	2.2	1.9	1.9
229001_at	BE259127	Hs.39911	KIAA1443	14q11.2	4.3	3.1	1.6	1.2
1569352_at	BC030251	Hs.377588	KIAA1450	4q32.1	25.4	7.6	19.7	7.5
225922_at	BE501838	Hs.377588	KIAA1450	4q32.1	8.8	9.5	26.4	25.7
225924_at	AI478634	Hs.377588	KIAA1450	4q32.1	7.9	9.0	22.9	25.3
226460_at	AB040883	Hs.377588	KIAA1450	4q32.1	9.5	9.1	24.0	19.6
227638_at	AI393091	Hs.546416	KIAA1632	18q12.3	2.0	1.6	3.0	2.6
232030_at	AK023817	Hs.546416	KIAA1632	18q12.3	2.5	2.1	3.3	2.6
225623_at	AI621225	Hs.22452	KIAA1737	14q24.3	2.1	1.7	1.5	1.5
1559060_a_at	BF677986	Hs.483329	KIAA1961	5q23.3	3.0	3.9	3.2	3.1
223997_at	BC001956	Hs.483329	KIAA1961	5q23.3	2.3	2.4	1.5	1.1
228250_at	AW263086	Hs.483329	KIAA1961	5q23.3	2.2	2.2	1.3	1.4
202393_s_at	NM_005655	Hs.435001	KLF10	8q22.2	7.2	9.6	9.5	10.6
244447_at	AW292830	Hs.435001	KLF10	8q22.2	8.9	11.8	5.8	3.3
218486_at	AA149594	Hs.12229	KLF11	2p25	5.3	4.4	2.9	2.3
221841_s_at	BF514079	Hs.376206	KLF4	9q31	4.6	4.3	2.9	3.2
203068_at	NM_014851	Hs.7764	KLHL21	1p36.31	2.2	2.2	1.7	1.4
1555275_a_at	BC032348	Hs.333181	KLHL6	3q27.1	3.1	2.5	2.6	2.8
1560396_at	AK097976	Hs.333181	KLHL6	3q27.1	2.5	2.3	3.2	2.7
1560397_s_at	AK097976	Hs.333181	KLHL6	3q27.1	3.0	2.2	3.4	2.5
228167_at	AW574798	Hs.333181	KLHL6	3q27.1	2.8	2.0	2.8	2.5
218701_at	NM_016027	Hs.118554	LACTB2	8p22-q22.3	3.7	2.5	2.5	1.8
222714_s_at	BC000878	Hs.118554	LACTB2	8p22-q22.3	3.3	2.4	2.3	2.2
201551_s_at	J03263	Hs.494419	LAMP1	13q34	2.5	2.7	3.5	3.4
201552_at	NM_005561	Hs.494419	LAMP1	13q34	2.5	2.3	3.4	3.3
201553_s_at	NM_005561	Hs.494419	LAMP1	13q34	1.9	1.8	2.9	2.6
205569_at	NM_014398	Hs.518448	LAMP3	3q26.3-q27	1.3	1.2	1.2	2.3
217933_s_at	NM_015907	Hs.479264	LAP3	4p15.32	1.3	1.2	1.3	2.8
207092_at	NM_000230	Hs.194236	LEP	7q31.3	12.1	5.7	16.1	5.6
1557197_a_at	AW085690	Hs.531081	LGALS3	14q21-q22	15.8	18.6	16.1	11.8
208949_s_at	BC001120	Hs.531081	LGALS3, GALIG	14q21-q22	6.4	5.9	4.4	4.4
208933_s_at	AI659005	Hs.4082	LGALS8	1q42-q43	1.7	1.9	2.0	2.0
208934_s_at	AF342815	Hs.4082	LGALS8	1q42-q43	1.8	1.9	2.3	2.4
208935_s_at	L78132	Hs.4082	LGALS8	1q42-q43	2.2	2.0	2.1	1.7
208936_x_at	AF074000	Hs.4082	LGALS8	1q42-q43	1.7	1.8	2.3	2.2
210732_s_at	AF342816	Hs.4082	LGALS8	1q42-q43	2.0	2.1	2.0	2.7
207198_s_at	NM_004987	Hs.469593	LIMS1	2q12.3-q13	1.7	2.1	1.7	2.0

212687_at	AL110164	Hs.469593	<i>LIMS1</i>	2q12.3-q13	1.7	2.0	2.0	2.2
223800_s_at	AF288404	Hs.469633	<i>LIMS3</i>	2q14-q21	2.0	2.3	1.7	1.7
204249_s_at	NM_005574	Hs.34560	<i>LMO2</i>	11p13	4.2	3.6	2.2	1.8
225479_at	AL524175	Hs.518084	<i>LOC116064</i>	3q13.33	2.0	1.5	1.6	1.4
226702_at	AI742057	Hs.7155	<i>LOC129607</i>	2p25.2	1.5	1.4	1.8	2.8
228658_at	R54042	---	<i>LOC150271</i>	22q12.1	1.4	1.3	2.1	1.3
1554229_at	AY174896	Hs.484195	<i>LOC153222</i>	5q35.1	2.2	1.8	1.6	1.5
238476_at	AA481560	Hs.484195	<i>LOC153222</i>	5q35.1	2.5	2.1	1.5	1.7
1556750_at	AI701480	Hs.438905	<i>LOC153577</i>	5q35.3	7.4	4.8	3.3	2.4
236717_at	AI632621	Hs.47647	<i>LOC165186</i>	2p23.2	2.6	2.7	5.5	3.1
227037_at	AA029500	Hs.31652	<i>LOC201164</i>	17p11.2	6.9	5.3	2.9	2.7
1560007_at	BG337478	Hs.128037	<i>LOC220929</i>	10p11.23	3.6	3.3	4.9	4.5
229743_at	AI886666	Hs.128037	<i>LOC220929</i>	10p11.23	3.3	3.0	3.9	3.7
244752_at	AI563915	Hs.128037	<i>LOC220929</i>	10p11.23	3.2	3.0	3.2	3.0
229090_at	AK026657	Hs.372654	<i>LOC220930</i>	10p11.23	2.2	2.0	1.6	1.3
211996_s_at	BG256504	Hs.528462	<i>LOC23117</i>	16p12.3	1.4	1.3	2.9	1.6
1556180_at	BE646146	Hs.348292	<i>LOC255458</i>	5q35.3	5.4	3.5	3.1	2.5
226146_at	BE503186	Hs.348292	<i>LOC255458</i>	5q35.3	3.2	2.5	2.2	2.4
228453_at	AW004076	Hs.514843	<i>LOC284267</i>	18q21.1	1.7	1.4	2.0	1.8
1562019_at	AK092780	Hs.434250	<i>LOC284958</i>	2q13	2.3	2.9	8.4	6.1
226159_at	N31982	Hs.29899	<i>LOC285636</i>	5p13.1	4.0	2.8	1.9	2.0
230179_at	N52572	Hs.435694	<i>LOC285812</i>	6p23	3.9	3.3	2.3	2.3
238893_at	AI377324	Hs.136888	<i>LOC338758</i>	12q21.33	2.2	2.7	1.9	1.8
215123_at	AL049250	Hs.528464	<i>LOC348162</i>	16p11.2	1.3	1.5	2.1	1.3
225567_at	BE207755	Hs.530791	<i>LOC388114</i>	15q15.1	3.9	3.2	2.5	3.5
231431_s_at	AI125670	Hs.530791	<i>LOC388114</i>	15q15.1	3.0	2.8	2.3	3.0
226608_at	AW157311	Hs.406551	<i>LOC388272</i>	16q11.2	1.7	1.7	2.0	2.0
226249_at	AI674625	Hs.522350	<i>LOC401548</i>	9q32	2.5	2.3	2.7	2.7
229951_x_at	H24473	Hs.549433	<i>LOC440667</i>	1q21.1	2.0	1.4	2.5	2.1
236453_at	AW243154	Hs.99081	<i>LOC441422</i>	9p11.2	1.0	1.6	4.6	5.4
216908_x_at	AF001549	Hs.546468	<i>LOC94431</i>	16p12.1	7.2	6.1	6.5	5.5
201186_at	NM_002337	Hs.533136	<i>LRPAP1</i>	4p16.3	1.6	1.6	3.2	2.3
200900_s_at	AI583537	Hs.134084	<i>M6PR</i>	12p13	6.3	5.7	5.6	5.6
200901_s_at	NM_002355	Hs.134084	<i>M6PR</i>	12p13	4.3	3.6	4.8	3.8
208634_s_at	AB029290	Hs.472475	<i>MACF1</i>	1p32-p31	0.8	0.8	2.2	1.6
218559_s_at	NM_005461	Hs.169487	<i>MAFB</i>	20q11.2-q13.1	10.3	8.5	3.5	4.3
222670_s_at	AW135013	Hs.169487	<i>MAFB</i>	20q11.2-q13.1	5.2	4.8	2.2	2.2
205193_at	NM_012323	Hs.517617	<i>MAFF</i>	22q13.1	6.5	7.9	10.1	13.9
36711_at	AL021977	Hs.517617	<i>MAFF</i>	22q13.1	7.9	9.1	7.6	10.6
204970_s_at	NM_002359	Hs.252229	<i>MAFG</i>	17q25.3	4.5	3.9	3.6	3.3
224466_s_at	BC006143	Hs.252229	<i>MAFG</i>	17q25.3	26.7	13.2	21.6	17.7
38521_at	X59350	Hs.262150	<i>MAG</i>	19q13.1	2.6	1.5	4.8	3.1
227562_at	AI335267	Hs.433332	<i>MAP2K1IP1</i>	4q23	2.1	2.0	1.5	1.4
205448_s_at	NM_006301	Hs.211601	<i>MAP3K12</i>	12q13	1.3	1.5	2.0	1.8
206571_s_at	NM_004834	Hs.431550	<i>MAP4K4</i>	2q11.2-q12	1.9	1.9	3.7	3.8
218181_s_at	NM_017792	Hs.431550	<i>MAP4K4</i>	2q11.2-q12	1.9	1.9	2.7	3.0
222547_at	AL561281	Hs.431550	<i>MAP4K4</i>	2q11.2-q12	2.0	2.1	3.1	3.5

222548_s_at	AL561281	Hs.431550	MAP4K4	2q11.2-q12	2.0	2.2	3.4	3.7
238769_at	AW450572	Hs.431550	MAP4K4	2q11.2-q12	4.3	5.0	4.7	3.4
244846_at	AI953395	Hs.431550	MAP4K4	2q11.2-q12	3.2	3.6	3.3	2.4
207121_s_at	NM_002748	Hs.411847	MAPK6	15q21	4.5	4.9	4.2	4.5
205716_at	NM_018843	Hs.208414	MCFP	7q21.12	1.2	1.1	2.4	2.1
202107_s_at	NM_004526	Hs.477481	MCM2	3q21	4.6	2.8	2.9	3.6
201930_at	NM_005915	Hs.444118	MCM6	2q21	7.9	5.6	7.9	8.2
219952_s_at	NM_020533	Hs.546413	MCOLN1	19p13.3-p13.2	3.9	4.5	2.3	4.3
241924_at	BE897518	Hs.200716	MECP2	Xq28	2.2	1.8	2.1	2.2
218438_s_at	NM_025205	Hs.33032	MED28	4p16	1.9	2.0	1.8	2.0
224416_s_at	AF358829	Hs.33032	MED28	4p16	2.1	2.0	2.1	2.2
228992_at	BF064162	Hs.434075	MED28	4p16	2.1	1.9	1.9	1.9
1556538_at	AK096182	Hs.184727	MFI2	3q28-q29	2.2	1.4	2.1	1.5
218109_s_at	NM_022736	Hs.58663	MFSD1	3q25.32	2.2	1.9	2.2	2.0
212945_s_at	BE502432	Hs.187569	MGA	15q14	14.8	10.2	12.5	8.0
235409_at	AU149225	Hs.187569	MGA	15q14	6.8	6.1	7.0	5.6
201126_s_at	NM_002406	Hs.519818	MGAT1	5q35	7.1	5.1	4.1	3.0
223469_at	BC004942	Hs.4188	MGC10812	19p13.11	3.5	2.6	2.0	1.9
223455_at	BG493862	Hs.410924	MGC10854	12q24.11	3.1	2.1	4.0	2.8
224132_at	BC005072	Hs.326732	MGC13008	17p11.2	1.8	2.1	1.5	1.3
221864_at	AW517464	Hs.460617	MGC13024	16p11.2	2.4	1.9	2.0	1.4
224660_at	AL570697	Hs.26136	MGC14156	4q22.1	1.2	1.5	1.1	2.1
214696_at	AF070569	Hs.417157	MGC14376	17p13.3	2.1	2.4	2.4	2.9
221756_at	AL540260	Hs.26670	MGC17330	22q12.2	2.6	2.2	2.4	1.9
221757_at	BE042976	Hs.26670	MGC17330	22q12.2	2.8	2.1	2.7	2.0
214754_at	AB007861	Hs.516107	MGC22014	2p13.1	2.1	1.9	1.4	1.5
1555789_s_at	AY099328	Hs.534483	MGC2941	17p13.1	2.5	2.4	2.4	2.3
223081_at	BC002509	Hs.534483	MGC2941	17p13.1	2.4	2.3	2.5	2.3
1558692_at	AW090182	Hs.202522	MGC31963	1q22	19.4	10.7	10.5	9.7
1558693_s_at	AW090182	Hs.202522	MGC31963	1q22	17.2	15.2	9.9	6.8
225755_at	AI160540	Hs.13781	MGC35097	3p21.31	3.4	3.3	2.8	2.8
227563_at	AI950007	Hs.31240	MGC42630	9q12	4.5	3.4	4.9	3.8
223296_at	BC004991	Hs.443826	MGC4399	1p36.22	7.4	6.0	7.1	5.6
211026_s_at	BC006230	Hs.277035	MGLL	3q21.3	2.2	2.3	8.8	6.2
225102_at	BG168471	Hs.277035	MGLL	3q21.3	7.3	4.4	26.7	10.6
239914_at	H17941	Hs.277035	MGLL	3q21.3	5.5	5.3	8.5	10.3
204168_at	NM_002413	Hs.81874	MGST2	4q28.3	2.2	2.0	1.8	2.1
235970_at	AI807408	Hs.446201	MLR1	4p15.32	2.2	1.9	2.4	2.2
240592_at	AI939336	Hs.446201	MLR1	4p15.32	2.1	1.7	2.6	1.9
201994_at	NM_012286	Hs.326387	MORF4L2	Xq22	1.5	1.7	2.0	2.2
243683_at	H43976	Hs.326387	MORF4L2	Xq22	1.9	2.5	2.5	2.0
243857_at	AI700608	Hs.326387	MORF4L2	Xq22	2.2	2.6	2.3	2.3
1557455_s_at	AF086333	Hs.378505	MOSPD1	Xq26.3	2.5	2.1	2.3	1.9
218853_s_at	NM_019556	Hs.378505	MOSPD1	Xq26.3	2.4	2.2	2.7	2.3
235864_at	AW449078	Hs.509699	MPP5	14q23.3	11.2	6.8	2.7	2.2
217772_s_at	NM_014342	Hs.269944	MTCH2	11p11.2	2.4	2.1	2.2	2.1
226929_at	AA524272	Hs.214142	MTHFR	1p36.3	2.9	3.0	2.3	2.2

239035_at	AL138431	Hs.214142	<i>MTHFR</i>	1p36.3	3.9	3.6	2.9	2.6
213448_at	AI693193	Hs.490874	<i>MTX1</i>	1q21	2.7	2.8	2.1	1.9
202086_at	NM_002462	Hs.517307	<i>MX1</i>	21q22.3	1.6	1.6	1.9	2.5
206491_s_at	NM_003827	Hs.126938	<i>NAPA</i>	19q13.32	1.7	1.6	2.8	2.9
208751_at	BC001165	Hs.126938	<i>NAPA</i>	19q13.32	1.7	1.7	2.8	3.0
200027_at	NM_004539	Hs.465224	<i>NARS</i>	18q21.2-q21.3	5.0	3.8	3.6	3.3
217800_s_at	NM_030571	Hs.9788	<i>NDFIP1</i>	5q31.3	2.2	2.2	3.2	2.7
222422_s_at	AW167859	Hs.9788	<i>NDFIP1</i>	5q31.3	2.9	2.5	3.6	3.1
222423_at	H05010	Hs.9788	<i>NDFIP1</i>	5q31.3	1.8	1.6	2.5	2.2
223158_s_at	BE616825	Hs.197071	<i>NEK6</i>	9q33.3-q34.11	1.3	1.0	2.3	1.7
208926_at	U84246	Hs.520037	<i>NEU1</i>	6p21.3	5.9	5.6	3.4	3.2
229235_at	AI983432	Hs.513470	<i>NFATC2IP</i>	16p11.2	1.8	1.7	2.8	2.1
212808_at	AI884627	Hs.513470	<i>NFATC2IP</i>	16p11.2	1.9	1.5	2.6	1.8
217526_at	AI478300	Hs.513470	<i>NFATC2IP</i>	16p11.2	1.6	1.7	2.4	1.7
217527_s_at	AI478300	Hs.513470	<i>NFATC2IP</i>	16p11.2	1.6	1.9	2.7	1.9
1567013_at	AF323119	Hs.155396	<i>NFE2L2</i>	2q31	2.1	1.8	2.0	1.6
1553103_at	NM_147134	Hs.413074	<i>NFX1</i>	9p13.3	2.9	2.7	2.2	1.9
225943_at	BF222737	Hs.247460	<i>NLN</i>	5q12.3	7.3	6.1	7.4	5.8
225944_at	AW006938	Hs.247460	<i>NLN</i>	5q12.3	5.9	3.9	4.4	4.9
223484_at	AF228422	Hs.112242	<i>NMES1</i>	15q21.1	1.6	2.4	1.9	2.7
214321_at	BF440025	Hs.235935	<i>NOV</i>	8q24.1	1.8	1.4	2.0	1.7
201695_s_at	NM_000270	Hs.75514	<i>NP</i>	14q13.1	2.2	2.6	2.2	2.0
202679_at	NM_000271	Hs.464779	<i>NPC1</i>	18q11-q12	3.3	2.9	3.1	3.1
200701_at	NM_006432	Hs.433222	<i>NPC2</i>	14q24.3	2.9	2.4	3.0	2.6
221210_s_at	NM_030769	Hs.496969	<i>NPL</i>	1q25	2.2	2.2	1.9	1.8
240440_at	AI368358	Hs.496969	<i>NPL</i>	1q25	2.6	2.5	1.9	1.6
243066_at	AW119018	Hs.496969	<i>NPL</i>	1q25	2.2	2.5	1.6	1.5
200063_s_at	BC002398	Hs.519452	<i>NPM1</i>	5q35	2.1	2.3	2.0	1.9
221691_x_at	AB042278	Hs.519452	<i>NPM1</i>	5q35	1.7	1.8	1.7	2.2
221923_s_at	AA191576	Hs.519452	<i>NPM1</i>	5q35	2.1	2.1	2.0	2.4
209750_at	N32859	Hs.37288	<i>NR1D2</i>	3p24.2	4.9	3.4	3.8	3.1
225768_at	AI761621	Hs.37288	<i>NR1D2</i>	3p24.2	4.8	3.2	3.9	3.1
207978_s_at	NM_006981	Hs.279522	<i>NR4A3</i>	9q22	2.2	2.3	1.3	1.3
209959_at	U12767	Hs.279522	<i>NR4A3</i>	9q22	2.4	2.3	1.5	1.5
219557_s_at	NM_020645	Hs.523467	<i>NRIP3</i>	11p15.3	4.1	4.6	3.5	2.5
222900_at	AJ400877	Hs.523467	<i>NRIP3</i>	11p15.3	3.3	4.1	2.6	1.6
232148_at	BF056507	Hs.372000	<i>NSMAF</i>	8q12-q13	2.8	2.6	2.0	2.0
232149_s_at	BF056507	Hs.372000	<i>NSMAF</i>	8q12-q13	2.7	2.6	2.2	2.5
218039_at	NM_016359	Hs.511093	<i>NUSAP1</i>	15q15.1	1.7	1.5	3.4	1.9
219978_s_at	NM_018454	Hs.511093	<i>NUSAP1</i>	15q15.1	2.2	1.4	3.6	1.6
204972_at	NM_016817	Hs.414332	<i>OAS2</i>	12q24.2	1.0	1.0	0.9	2.3
228170_at	AL355743	Hs.56663	<i>OLIG1</i>	21q22.11	3.2	2.5	2.4	2.2
213825_at	AA757419	Hs.176977	<i>OLIG2</i>	21q22.11	4.8	2.9	5.0	2.9
205041_s_at	NM_000607	Hs.494894	<i>ORM1, ORM2</i>	9q31-q32, 9q32	3.2	1.9	5.2	3.0
214637_at	BG437034	Hs.248156	<i>OSM</i>	22q12.2	3.2	3.0	2.3	3.2
230170_at	AI079327	Hs.248156	<i>OSM</i>	22q12.2	2.7	2.6	2.3	2.6
218196_at	NM_014028	Hs.226780	<i>OSTM1</i>	6q21	2.1	2.0	1.8	1.8

235197_s_at	AV713913	Hs.226780	<i>OSTM1</i>	6q21	2.0	1.8	1.7	1.6
1553432_s_at	NM_170664	Hs.408336	<i>OTOA</i>	16p12.2	2.5	2.9	4.9	3.5
204088_at	NM_002560	Hs.321709	<i>P2RX4</i>	12q24.32	2.3	2.2	2.2	2.3
225622_at	AI860212	Hs.266175	<i>PAG1</i>	8q21.13	3.3	2.9	2.5	2.7
225626_at	AK000680	Hs.266175	<i>PAG1</i>	8q21.13	3.3	2.6	2.5	2.5
227354_at	BF589359	Hs.492106	<i>PAG1</i>	8q21.13	2.7	2.1	2.2	2.4
209700_x_at	AB042555	Hs.381235	<i>PDE4DIP</i>	1q12	1.8	1.1	3.1	2.4
244859_at	R44149	Hs.487925	<i>PDE4DIP</i>	1q12	2.8	2.8	3.8	3.1
204524_at	NM_002613	Hs.459691	<i>PDPK1</i>	16p13.3	2.7	2.8	2.0	1.7
224986_s_at	AL040394	Hs.459691	<i>PDPK1</i>	16p13.3	2.8	2.5	1.5	1.6
32029_at	AC005591	Hs.459691	<i>PDPK1</i>	16p13.3	2.1	1.9	1.7	1.3
224902_at	BE644918	Hs.461183	<i>PDPR</i>	16q22.1	2.2	1.9	2.1	1.7
218018_at	AW449022	Hs.284491	<i>PDXK</i>	21q22.3	1.5	1.4	2.3	1.4
202464_s_at	NM_004566	Hs.195471	<i>PFKFB3</i>	10p14-p15	1.6	2.0	1.7	2.0
219891_at	NM_017712	Hs.131776	<i>PGPEP1</i>	19p13.11	2.7	2.4	1.8	1.6
213638_at	AW054711	Hs.436996	<i>PHACTR1</i>	6p24.1	7.5	6.6	5.5	5.9
232045_at	AW468218	Hs.436996	<i>PHACTR1</i>	6p24.1	21.8	15.7	9.0	6.1
218338_at	NM_004426	Hs.305985	<i>PHC1</i>	12p13	6.3	5.3	4.0	3.3
225958_at	AI554106	Hs.305985	<i>PHC1</i>	12p13	2.5	2.2	2.6	2.0
225005_at	AL039384	Hs.516079	<i>PHF13</i>	1p36.31	2.3	2.1	1.7	1.8
209803_s_at	AF001294	Hs.154036	<i>PHLDA2</i>	11p15.5	2.6	4.1	4.4	3.1
204484_at	NM_002646	Hs.497487	<i>PIK3C2B</i>	1q32	24.5	12.4	6.7	3.8
209193_at	M24779	Hs.81170	<i>PIM1</i>	6p21.2	1.8	1.7	2.0	2.1
218942_at	NM_024779	Hs.144502	<i>PIP5K2C</i>	12q13.3	2.1	1.7	1.3	1.3
213700_s_at	AA554945	Hs.198281	<i>PKM2</i>	15q22	1.6	1.5	2.0	1.0
206214_at	NM_005084	Hs.93304	<i>PLA2G7</i>	6p21.2-p12	2.7	1.9	5.2	7.9
205479_s_at	NM_002658	Hs.77274	<i>PLAU</i>	10q24	5.1	5.7	7.3	7.9
211668_s_at	K03226	Hs.77274	<i>PLAU</i>	10q24	8.1	7.9	8.2	10.4
222826_at	BC004819	Hs.7037	<i>PLDN</i>	15q21.1	1.6	1.7	2.7	2.6
224883_at	AI344311	Hs.7037	<i>PLDN</i>	15q21.1	1.6	1.5	2.1	2.4
224892_at	BF680495	Hs.7037	<i>PLDN</i>	15q21.1	1.5	1.5	2.3	2.5
217677_at	BF542055	Hs.369123	<i>PLEKHA2</i>	8p11.23	2.2	1.9	3.1	2.5
225136_at	BF968578	Hs.369123	<i>PLEKHA2</i>	8p11.23	2.0	1.7	2.5	2.1
238013_at	BF347859	Hs.369123	<i>PLEKHA2</i>	8p11.23	2.5	2.0	3.9	2.7
238082_at	AA777270	Hs.369123	<i>PLEKHA2</i>	8p11.23	2.9	1.9	2.4	1.9
201410_at	AI983043	Hs.469944	<i>PLEKHB2</i>	2q21.1	1.7	1.8	2.4	2.6
201411_s_at	NM_017958	Hs.469944	<i>PLEKHB2</i>	2q21.1	2.3	2.3	3.1	3.0
212146_at	AB020649	Hs.145049	<i>PLEKHM2</i>	1p36.13	3.1	2.9	2.1	2.4
241916_at	AI984040	Hs.130759	<i>PLSCR1</i>	3q23	1.3	1.8	1.2	2.3
204285_s_at	AI857639	Hs.96	<i>PMAIP1</i>	18q21.32	1.8	2.0	1.5	2.0
204286_s_at	NM_021127	Hs.96	<i>PMAIP1</i>	18q21.32	2.0	2.4	1.4	2.1
225291_at	AI967971	Hs.388733	<i>PNPT1</i>	2p15	1.3	1.6	1.6	2.3
218866_s_at	NM_016310	Hs.437186	<i>POLR3K</i>	16p13.3	2.0	1.4	2.0	1.6
226707_at	AI925574	Hs.493164	<i>PP3856</i>	8q24.3	2.4	2.6	1.8	1.8
209355_s_at	AB000889	Hs.405156	<i>PPAP2B</i>	1pter-p22.1	80.7	62.2	121.9	42.7
212226_s_at	AA628586	Hs.405156	<i>PPAP2B</i>	1pter-p22.1	22.2	17.0	30.9	20.0
212230_at	AV725664	Hs.405156	<i>PPAP2B</i>	1pter-p22.1	18.4	16.3	25.4	19.0

232324_x_at	AK001092	Hs.405156	<i>PPAP2B</i>	1pter-p22.1	2.1	2.6	4.0	3.5
212841_s_at	AI692180	Hs.16019	<i>PPFIBP2</i>	11p15.4	3.8	2.1	3.0	2.1
200661_at	NM_000308	Hs.517076	<i>PPGB</i>	20q13.1	5.8	3.8	8.8	6.0
201489_at	BC005020	Hs.381072	<i>PPIF</i>	10q22-q23	1.7	1.8	1.9	2.3
201490_s_at	NM_005729	Hs.381072	<i>PPIF</i>	10q22-q23	2.3	2.8	2.2	3.0
235061_at	AV706522	Hs.291000	<i>PPM1K</i>	4q22.1	1.2	1.6	1.4	2.2
201702_s_at	AI492873	Hs.106019	<i>PPP1R10</i>	6p21.3	2.9	3.1	1.6	1.8
201703_s_at	NM_002714	Hs.106019	<i>PPP1R10</i>	6p21.3	2.0	2.1	1.4	1.4
202014_at	NM_014330	Hs.76556	<i>PPP1R15A</i>	19q13.2	3.6	4.5	2.6	3.2
37028_at	U83981	Hs.76556	<i>PPP1R15A</i>	19q13.2	3.2	3.7	2.6	3.0
227412_at	AK024489	Hs.39911	<i>PPP1R3E</i>	14q11.2	3.1	2.2	1.3	1.3
1555781_at	BC015324	Hs.523036	<i>PQLC2</i>	1p36.13	2.6	2.4	2.9	1.4
209323_at	AF081567	Hs.503315	<i>PRKRIR</i>	11q13.5	2.1	1.7	1.9	1.9
200866_s_at	M32221	Hs.523004	<i>PSAP</i>	10q21-q22	1.5	1.4	2.1	2.2
206631_at	NM_000956	Hs.2090	<i>PTGER2</i>	14q22	2.0	2.6	2.4	2.0
204897_at	AA897516	Hs.199248	<i>PTGER4</i>	5p13.1	2.3	2.3	1.5	1.5
223150_s_at	AF290614	Hs.25524	<i>PTPN23</i>	3p21.3	2.1	1.9	1.7	1.1
202895_s_at	D86043	Hs.128846	<i>PTPNS1</i>	20p13	1.6	1.5	2.1	1.4
202896_s_at	NM_004648	Hs.128846	<i>PTPNS1</i>	20p13	1.7	1.5	2.0	1.7
207791_s_at	NM_004161	Hs.310645	<i>RAB1A</i>	2p14	2.8	3.0	2.1	2.6
213440_at	AL530264	Hs.310645	<i>RAB1A</i>	2p14	2.1	2.0	1.8	1.7
219622_at	NM_017817	Hs.508720	<i>RAB20</i>	13q34	6.2	5.2	4.6	5.0
204214_s_at	NM_006834	Hs.287714	<i>RAB32</i>	6q24.3	2.6	2.4	2.3	1.9
228161_at	N21210	Hs.287714	<i>RAB32</i>	6q24.3	2.6	2.1	2.1	2.2
204828_at	NM_004584	Hs.240457	<i>RAD9A</i>	11q13.1-q13.2	3.1	2.8	2.0	1.6
209050_s_at	AI421559	Hs.106185	<i>RALGDS</i>	9q34.3	7.8	7.7	6.3	5.4
209051_s_at	AF295773	Hs.106185	<i>RALGDS</i>	9q34.3	10.3	8.8	6.9	5.3
230563_at	BF446578	Hs.125293	<i>RASGEF1A</i>	10q11.21	2.1	2.1	1.8	1.8
230233_at	BF110534	Hs.480068	<i>RASGEF1B</i>	4q21.3	20.5	19.9	22.1	26.2
218593_at	NM_018077	Hs.274263	<i>RBM28</i>	7q32.2	4.4	3.4	4.1	3.0
218352_at	NM_018191	Hs.508021	<i>RCBTB1</i>	13q14	5.4	3.6	4.5	3.3
236291_at	AI887702	Hs.172914	<i>RDH5</i>	12q13-q14	2.3	1.7	1.6	1.2
206617_s_at	NM_002910	Hs.158331	<i>RENBP</i>	Xq28	17.9	11.1	4.7	3.7
219041_s_at	NM_014374	Hs.521289	<i>REPIN1</i>	7q36.1	5.9	3.8	3.5	2.4
238736_at	AA805939	Hs.232021	<i>REV3L</i>	6q21	2.0	2.4	1.5	1.5
226060_at	BF475369	Hs.444899	<i>RFT1</i>	3p21.1	3.0	2.5	5.5	4.8
209568_s_at	AF186779	Hs.497148	<i>RGL1</i>	1q25.3	1.1	1.2	1.8	2.1
1555780_a_at	AF493921	Hs.283521	<i>RHEB</i>	7q36	2.6	2.5	2.7	2.6
201453_x_at	NM_005614	Hs.283521	<i>RHEB</i>	7q36	2.5	2.4	2.6	2.7
213404_s_at	BF033683	Hs.283521	<i>RHEB</i>	7q36	2.4	2.3	2.7	2.6
213409_s_at	BF593727	Hs.283521	<i>RHEB</i>	7q36	2.2	2.0	2.3	2.4
220009_at	NM_024778	Hs.144266	<i>RNF127</i>	Xq24	3.2	2.8	2.6	3.1
237264_at	R38642	Hs.12333	<i>RNF13</i>	3q25.1	1.8	2.0	1.8	1.5
239554_at	AI634646	Hs.12333	<i>RNF13</i>	3q25.1	1.9	2.3	2.1	2.6
201823_s_at	NM_004290	Hs.508993	<i>RNF14</i>	5q23.3-q31.1	3.1	2.9	2.0	2.0
201824_at	AB022663	Hs.508993	<i>RNF14</i>	5q23.3-q31.1	2.5	2.4	1.7	1.5
224750_at	AK027035	Hs.517553	<i>RNF185</i>	22q12.2	2.2	1.7	1.6	1.3

202683_s_at	NM_003799	Hs.8086	<i>RNMT</i>	18p11.22-p11.23	2.4	2.3	1.8	1.7
202684_s_at	AB020966	Hs.8086	<i>RNMT</i>	18p11.22-p11.23	2.6	3.6	2.3	2.7
208904_s_at	BC000354	Hs.153177	<i>RPS28</i>	19p13.2	1.6	1.8	2.2	2.0
218088_s_at	NM_022157	Hs.532461	<i>RRAGC</i>	1p34	5.4	4.3	2.4	2.3
222514_at	AK023373	Hs.532461	<i>RRAGC</i>	1p34	5.3	4.5	2.2	2.2
242531_at	H56010	Hs.532461	<i>RRAGC</i>	1p34	2.4	2.6	1.8	1.6
221523_s_at	AL138717	Hs.485938	<i>RRAGD</i>	6q15-q16	5.2	3.9	2.7	2.1
221524_s_at	AF272036	Hs.485938	<i>RRAGD</i>	6q15-q16	5.9	4.2	3.2	2.9
203704_s_at	AW118862	Hs.298248	<i>RREB1</i>	6p25	2.2	1.8	2.1	1.8
242297_at	BF904033	Hs.298248	<i>RREB1</i>	6p25	2.1	1.8	1.9	1.3
216902_s_at	AF001549	Hs.460078	<i>RRN3</i>	16p12	6.9	5.3	5.9	4.9
230328_at	BF057656	Hs.460078	<i>RRN3</i>	16p12	3.6	3.4	3.1	2.5
213797_at	AI337069	Hs.17518	<i>RSAD2</i>	2p25.2	1.9	1.6	1.7	2.8
242625_at	AW189843	Hs.17518	<i>RSAD2</i>	2p25.2	1.8	1.5	2.0	2.4
225780_at	AL565415	Hs.239459	<i>RSC1A1</i>	1p36.1	2.1	1.7	1.3	1.5
226425_at	AU144247	Hs.122927	<i>RSNL2</i>	2p23.2	2.4	2.0	12.9	4.9
225272_at	AA128261	Hs.10846	<i>SAT2</i>	17p13.1	2.5	2.8	3.5	3.6
241331_at	BE671499	Hs.200770	<i>SCAP2</i>	7p21-p15	2.0	2.4	1.7	1.6
220232_at	NM_024906	Hs.379191	<i>SCD5</i>	4q21.3	1.1	0.9	2.3	0.7
218793_s_at	NM_006746	Hs.109655	<i>SCML1</i>	Xp22.2-p22.1	2.9	2.8	2.7	2.5
222747_s_at	BF001786	Hs.109655	<i>SCML1</i>	Xp22.2-p22.1	2.1	2.0	2.2	1.8
222849_s_at	AI306487	Hs.470679	<i>SCRN3</i>	2q31.1	2.8	2.3	2.0	2.0
223282_at	W60810	Hs.284217	<i>SDCCAG33</i>	18q22.3	4.9	4.2	11.3	8.9
223283_s_at	AF039698	Hs.284217	<i>SDCCAG33</i>	18q22.3	5.3	4.2	10.9	7.3
242279_at	R11494	Hs.187866	<i>SDFR1</i>	15q22	1.9	1.9	2.4	2.0
242865_at	AI332638	Hs.187866	<i>SDFR1</i>	15q22	2.4	2.4	2.2	2.1
209206_at	AV701283	Hs.534212	<i>SEC22L1</i>	1q21.2-q21.3	1.9	2.1	2.3	2.6
209207_s_at	BC001364	Hs.534212	<i>SEC22L1</i>	1q21.2-q21.3	2.1	2.4	3.1	3.3
233020_at	AU154125	Hs.534212	<i>SEC22L1</i>	1q21.2-q21.3	2.6	2.8	3.3	2.9
206442_at	NM_003007	Hs.1968	<i>SEMG1</i>	20q12-q13.2	1.9	2.1	2.4	2.0
200961_at	NM_012248	Hs.118725	<i>SEPHS2</i>	16p11.2	3.2	2.4	1.9	1.8
1564970_at	AF277186	Hs.446217	<i>SETDB2</i>	13q14	23.3	19.5	31.4	18.6
1564972_x_at	AF277186	Hs.446217	<i>SETDB2</i>	13q14	9.9	10.3	24.4	20.6
235338_s_at	W65369	Hs.446217	<i>SETDB2</i>	13q14	6.0	5.9	12.4	9.1
235339_at	W65369	Hs.446217	<i>SETDB2</i>	13q14	28.3	10.8	19.8	14.0
238731_at	AW977837	Hs.446217	<i>SETDB2</i>	13q14	6.1	5.5	6.5	6.5
227210_at	T65020	Hs.407983	<i>SFMBT2</i>	10p14	2.8	2.2	2.6	2.8
220038_at	NM_013257	Hs.380877	<i>SGKL</i>	8q12.3-8q13.1	2.4	1.8	3.3	3.0
227627_at	AV690866	Hs.380877	<i>SGKL</i>	8q12.3-8q13.1	2.4	1.8	3.0	2.3
221268_s_at	NM_030791	Hs.24678	<i>SGPP1</i>	14q23.2	2.2	1.9	1.8	2.0
223391_at	BE880703	Hs.24678	<i>SGPP1</i>	14q23.2	2.4	2.1	2.2	1.8
226560_at	AA576959	Hs.210043	<i>SGPP2</i>	2q36.1	1.3	1.9	3.4	2.5
204293_at	NM_000199	Hs.31074	<i>SGSH</i>	17q25.3	5.7	5.2	6.7	9.2
35626_at	U30894	Hs.31074	<i>SGSH</i>	17q25.3	6.2	5.2	8.0	5.6
232084_at	BE671098	Hs.287971	<i>SGTB</i>	5q12.3	4.7	4.0	4.6	4.1
201810_s_at	AL562152	Hs.257761	<i>SH3BP5</i>	3p24.3	2.0	1.9	3.1	2.1

201811_x_at	NM_004844	Hs.257761	SH3BP5	3p24.3	1.5	1.5	2.3	1.9
225589_at	AB040927	Hs.301804	SH3MD2	4q32.3-q33	14.3	13.6	12.7	11.0
227304_at	N25727	Hs.513987	SHMT1	17p11.2	2.3	2.0	2.1	2.1
227305_s_at	N25727	Hs.513987	SHMT1	17p11.2	2.4	2.0	2.1	1.9
224601_at	BE891646	Hs.281434, Hs.288215	SIAT7B	17q25.1	2.4	2.1	3.1	3.1
224603_at	AL519192	Hs.281434	SIAT7B	17q25.1	2.9	2.3	3.7	3.2
225056_at	AB037810	Hs.268774	SIPA1L2	1q42.2	2.8	2.3	1.8	1.6
233587_s_at	AK022852	Hs.268774	SIPA1L2	1q42.2	2.4	2.0	1.8	1.4
219159_s_at	NM_021181	Hs.517265	SLAMF7	1q23.1-q24.1	56.8	33.1	54.1	25.5
222838_at	AL121985	Hs.517265	SLAMF7	1q23.1-q24.1	41.4	26.1	43.5	27.0
234306_s_at	AJ271869	Hs.517265	SLAMF7	1q23.1-q24.1	30.0	30.7	57.8	27.8
203124_s_at	NM_000617	Hs.505545	SLC11A2	12q13	1.3	1.2	2.8	2.4
206599_at	NM_004695	Hs.369554	SLC16A5	17q25.1	2.0	1.6	1.7	1.3
206600_s_at	NM_004695	Hs.369554	SLC16A5	17q25.1	2.5	1.7	1.9	1.6
213590_at	AA705628	Hs.369554	SLC16A5	17q25.1	2.3	1.7	1.8	1.5
221041_s_at	NM_012434	Hs.485760	SLC17A5	6q14-q15	2.4	3.3	2.0	2.2
223441_at	AK026921	Hs.485760	SLC17A5	6q14-q15	3.8	3.6	2.2	3.0
201920_at	NM_005415	Hs.187946	SLC20A1	2q11-q14	5.4	4.8	4.1	4.1
207201_s_at	NM_003057	Hs.117367	SLC22A1	6q26	1.5	1.5	2.1	1.8
204981_at	NM_002555	Hs.50868	SLC22A18	11p15.5	1.8	1.9	2.8	2.5
206097_at	NM_007105	Hs.300076	SLC22A1LS	11p15.5	5.4	6.2	3.7	4.2
203775_at	NM_014251	Hs.489190	SLC25A13	7q21.3	6.9	7.1	9.2	7.9
229061_s_at	AW268880	Hs.489190	SLC25A13	7q21.3	6.8	6.8	8.0	7.7
229081_at	AW268880	Hs.489190	SLC25A13	7q21.3	2.9	2.8	4.3	2.6
214140_at	AI827990	Hs.180408	SLC25A16	10q21.3	1.8	2.1	1.4	1.5
226679_at	BE964598	Hs.4866	SLC26A11	17q25.3	12.7	7.4	11.2	9.1
212907_at	AI972416	Hs.519469	SLC30A1	1q32-q41	2.5	2.6	1.3	1.2
228181_at	AI553933	Hs.519469	SLC30A1	1q32-q41	2.1	2.5	1.3	1.2
200924_s_at	NM_002394	Hs.502769	SLC3A2	11q13	12.9	10.5	7.0	7.1
210692_s_at	BC003163	Hs.99962	SLC43A3	11q11	3.8	4.8	4.1	4.5
213113_s_at	AI630178	Hs.99962	SLC43A3	11q11	4.5	4.5	4.9	4.4
1565595_at	AU144979	Hs.130949	SLC6A16	19q13.1-q13.4	6.4	3.9	9.0	4.4
1569940_at	BC039336	Hs.130949	SLC6A16	19q13.1-q13.4	4.0	3.4	4.6	3.3
207528_s_at	NM_014331	Hs.6682	SLC7A11	4q28-q32	1.5	1.6	3.0	2.9
209921_at	AB040875	Hs.6682	SLC7A11	4q28-q32	1.8	1.9	3.0	3.4
217678_at	AA488687	Hs.6682	SLC7A11	4q28-q32	1.6	2.0	2.6	3.1
238488_at	BF511602	Hs.482268	SLRN	5q12.1	8.6	8.1	5.9	6.3
205443_at	NM_003082	Hs.179312	SNAPC1	14q22	8.0	8.6	17.8	15.9
224684_at	AL559283	Hs.260750	SNX12	Xq13.1	2.3	2.3	2.0	2.0
219793_at	NM_022133	Hs.492121	SNX16	8q21.13	2.2	2.2	1.8	1.8
229618_at	AW150236	Hs.492121	SNX16	8q21.13	2.1	1.8	1.5	1.7
202113_s_at	AF043453	Hs.134822	SNX2	5q23	2.1	1.8	1.6	1.7
221006_s_at	NM_030918	Hs.192326	SNX27	1q21.3	2.4	2.1	1.7	1.6
221498_at	BF939727	Hs.192326	SNX27	1q21.3	2.7	2.1	1.7	1.5
223241_at	AF121858	Hs.551538	SNX8	7p22.3	26.8	28.5	19.8	19.3
203373_at	NM_003877	Hs.485572	SOCS2	12q	1.2	2.0	1.3	1.8
206359_at	BG035761	Hs.527973	SOCS3	17q25.3	2.5	3.9	2.3	2.4

227697_at	AI244908	Hs.527973	SOCS3	17q25.3	2.1	2.7	2.2	2.6
1554543_at	BC007524	Hs.463439	SPAG9	17q21.33	1.8	2.0	1.6	1.3
206748_s_at	NM_003971	Hs.463439	SPAG9	17q21.33	2.2	2.4	1.9	2.5
212470_at	AB011088	Hs.463439	SPAG9	17q21.33	1.8	2.0	1.7	2.1
221542_s_at	T90773	Hs.125849	SPFH2	8p11.2	2.3	2.0	1.3	1.2
221543_s_at	AL442077	Hs.125849	SPFH2	8p11.2	2.4	2.2	1.4	1.5
212526_at	AK002207	Hs.440414	SPG20	13q13.3	2.7	2.6	2.0	2.5
236600_at	AI651603	Hs.440414	SPG20	13q13.3	2.4	2.3	1.6	1.5
219257_s_at	NM_021972	Hs.68061	SPHK1	17q25.2	5.6	5.5	5.7	4.5
223173_at	AF212371	Hs.498992	SPIN1	16p11.2	11.2	8.9	15.0	11.2
206239_s_at	NM_003122	Hs.407856	SPINK1	5q32	3.4	4.4	15.2	7.6
224995_at	AJ277587	Hs.515283	SPIRE1	18p11.21	1.7	1.2	3.0	2.8
224639_at	AI928466	Hs.507087	SPPL3	12q24.31	2.3	2.0	2.0	1.8
200672_x_at	NM_003128	Hs.503178	SPTBN1	2p21	3.1	3.1	6.3	4.7
212071_s_at	BE968833	Hs.503178	SPTBN1	2p21	4.2	3.7	9.6	7.8
226765_at	AA971514	Hs.503178	SPTBN1	---	4.1	3.0	9.1	8.7
213112_s_at	N30649	Hs.529892	SQSTM1	5q35	5.1	5.8	4.4	5.9
239004_at	AI041019	Hs.529892	SQSTM1	5q35	2.0	1.5	2.2	1.6
244804_at	AW293441	Hs.529892	SQSTM1	5q35	3.4	3.9	3.3	2.4
202199_s_at	AW082913	Hs.443861	SRPK1	6p21.3-p21.2	1.5	1.6	2.6	2.9
202200_s_at	NM_003137	Hs.443861	SRPK1	6p21.3-p21.2	1.3	1.4	2.8	3.0
202591_s_at	NM_003143	Hs.490394	SSBP1	7q34	1.7	1.7	2.3	1.9
204963_at	AL136756	Hs.183428	SSPN	12p11.2	2.9	2.3	6.1	3.9
203217_s_at	NM_003896	Hs.415117	ST3GAL5	2p11.2	1.7	1.6	2.4	2.5
200887_s_at	NM_007315	Hs.470943	STAT1	2q32.2	1.2	1.2	1.5	2.1
209969_s_at	BC002704	Hs.470943	STAT1	2q32.2	1.2	1.4	1.6	2.4
225636_at	H98105	Hs.530595	STAT2	12q13.3	1.2	1.2	1.5	2.1
231969_at	AB037813	Hs.21958	STOX2	4q35.1	6.1	4.0	17.4	4.1
228353_x_at	AA233308	Hs.444075	STS-1	11q24.1	5.9	4.6	2.8	2.9
228359_at	AA037664	Hs.444075	STS-1	11q24.1	7.8	5.9	3.7	3.9
238462_at	AI418293	Hs.444075	STS-1	11q24.1	3.9	2.9	2.3	2.1
238587_at	AI927919	Hs.444075	STS-1	11q24.1	4.7	3.5	2.5	2.9
229395_at	BF939292	Hs.83734	STX4A	16p11.2	2.0	2.1	2.2	2.1
203530_s_at	NM_004604	Hs.83734	STX4A	16p11.2	2.5	2.7	3.4	3.1
223939_at	AF348078	Hs.279575	SUCNR1	3q24-3q25.1	12.0	9.5	18.4	16.8
202168_at	NM_003187	Hs.248941	TAF9	5q11.2-q13.1	3.2	2.7	2.1	2.0
203893_at	NM_016283	Hs.248941	TAF9	5q11.2-q13.1	3.2	3.2	2.0	1.8
224622_at	AB037743	Hs.518611	TBC1D14	4p16.1	1.9	2.0	2.0	1.9
230072_at	BF062875	Hs.284630	TBC1D15	12q21.1	2.6	1.8	2.1	1.8
218268_at	NM_022771	Hs.284630	TBC1D15	12q21.1	2.6	2.8	2.9	3.0
222173_s_at	AK026105	Hs.371016	TBC1D2	9q22.33	35.7	20.5	15.5	13.3
223461_at	AF151073	Hs.484678	TBC1D7	6p24.1	5.0	4.5	3.4	2.6
228285_at	AI989706	Hs.21454	TDRD9	14q32.33	3.3	3.6	3.5	2.7
218104_at	NM_017746	Hs.494648	TEX10	9q31.1	3.2	2.9	2.2	1.7
207332_s_at	NM_003234	Hs.529618	TFRC	3q29	4.3	3.1	6.4	4.3
208691_at	BC001188	Hs.529618	TFRC	3q29	3.6	2.9	7.0	5.2
206943_at	NM_004612	Hs.494622	TGFBF1	9q22	3.5	3.2	2.4	2.8

224793_s_at	AA604375	Hs.494622	<i>TGFBR1</i>	9q22	2.7	2.3	2.6	2.1
236561_at	AV700621	Hs.494622	<i>TGFBR1</i>	9q22	4.0	3.7	3.1	2.3
239605_x_at	AI743727	Hs.494622	<i>TGFBR1</i>	9q22	4.1	3.0	2.4	1.7
1566901_at	AL832409	Hs.373550	<i>TGIF</i>	18p11.3	2.8	2.3	1.7	1.5
203313_s_at	NM_003244	Hs.373550	<i>TGIF</i>	18p11.3	3.0	2.7	1.8	1.9
206004_at	NM_003245	Hs.2022	<i>TGM3</i>	20q11.2	6.4	5.3	4.3	3.8
1316_at	X55005	Hs.724	<i>THRA</i>	17q11.2	2.6	2.5	2.9	1.7
31637_s_at	X72631	Hs.724	<i>THRA, NR1D1</i>	17q11.2	6.5	6.0	6.9	5.7
223804_s_at	BC001622	Hs.443081	<i>THUMPD3</i>	3p25.3	3.1	2.3	3.4	2.5
225730_s_at	AI921788	Hs.443081	<i>THUMPD3</i>	3p25.3	3.3	2.8	3.5	2.6
225741_at	AU154401	Hs.443081	<i>THUMPD3</i>	3p25.3	2.9	2.4	3.3	3.3
214183_s_at	X91817	Hs.102866	<i>TKTL1</i>	Xq28	3.2	3.3	4.6	6.3
216370_s_at	Z49258	Hs.102866	<i>TKTL1</i>	Xq28	3.4	3.1	3.3	4.1
202606_s_at	NM_012290	Hs.470586	<i>TLK1</i>	2q31.1	1.4	1.3	2.1	2.0
210379_s_at	AF162666	Hs.470586	<i>TLK1</i>	2q31.1	1.4	1.5	2.8	2.4
211077_s_at	Z25421	Hs.470586	<i>TLK1</i>	2q31.1	1.3	1.6	2.3	2.1
225287_s_at	AI992151	Hs.7001	<i>TMEM55B</i>	14q11.2	4.6	4.1	2.5	2.3
223396_at	AF260336	Hs.19025	<i>TMEM60</i>	7q11.23	2.8	2.4	1.9	1.8
214657_s_at	AU134977	Hs.523789	<i>TncRNA</i>	11q13.1	2.1	2.7	2.1	2.2
224566_at	AI042152	Hs.523789	<i>TncRNA</i>	11q13.1	1.4	1.7	1.4	2.0
207113_s_at	NM_000594	Hs.241570	<i>TNF</i>	6p21.3	1.9	2.3	1.4	1.7
209354_at	BC002794	Hs.512898	<i>TNFRSF14</i>	1p36.3-p36.2	2.3	2.1	2.5	2.2
221085_at	NM_005118	Hs.241382	<i>TNFSF15</i>	9q32	44.8	28.9	51.4	25.8
206393_at	NM_003282	Hs.523403	<i>TNNI2</i>	11p15.5	2.1	1.9	2.1	1.5
217930_s_at	NM_019009	Hs.368527	<i>TOLLIP</i>	11p	2.4	2.3	1.8	1.6
222469_s_at	AL136835	Hs.368527	<i>TOLLIP</i>	11p	3.3	2.7	1.9	1.5
233881_s_at	AK022871	Hs.368527	<i>TOLLIP</i>	11p	2.9	2.5	1.7	1.8
202807_s_at	NM_005488	Hs.474705	<i>TOM1</i>	22q13.1	2.3	2.5	2.9	2.7
226059_at	AK022832	Hs.321653	<i>TOMM40L</i>	1q23.3	3.3	3.3	5.2	4.5
200742_s_at	BG231932	Hs.523454	<i>TPP1</i>	11p15	3.8	3.0	3.1	3.2
200743_s_at	NM_000391	Hs.523454	<i>TPP1</i>	11p15	3.1	2.6	2.9	3.0
214195_at	AA602532	Hs.523454	<i>TPP1</i>	11p15	3.4	3.8	2.0	2.6
214196_s_at	AA602532	Hs.523454	<i>TPP1</i>	11p15	4.0	3.5	2.9	2.4
235761_at	BG111808	Hs.167167	<i>TPST2</i>	22q12.1	2.1	2.8	1.7	1.6
204079_at	NM_003595	Hs.474441	<i>TPST2</i>	22q12.1	4.0	3.9	2.6	2.3
221571_at	AI721219	Hs.510528	<i>TRAF3</i>	14q32.32	1.2	1.2	2.3	2.3
203511_s_at	AF041432	Hs.523131	<i>TRAPPC3</i>	1p34.3	2.0	2.0	1.6	1.6
239818_x_at	AA576947	Hs.444947	<i>TRIB1</i>	8q24.13	2.4	2.5	1.9	2.1
218145_at	NM_021158	Hs.516826	<i>TRIB3</i>	20p13-p12.2	5.5	4.6	2.0	2.2
203148_s_at	NM_014788	Hs.549094	<i>TRIM14</i>	9q22.33	1.8	1.6	2.8	2.7
224806_at	BE563152	Hs.528952	<i>TRIM25</i>	17q23.2	1.9	1.9	2.0	2.5
210266_s_at	AF220137	Hs.26837	<i>TRIM33</i>	1p13.1	1.9	1.5	2.5	2.0
239716_at	AA908970	Hs.26837	<i>TRIM33</i>	1p13.1	1.5	1.2	2.2	1.2
205708_s_at	AI051254	Hs.369759	<i>TRPM2</i>	21q22.3	4.7	5.1	6.1	3.9
1565886_at	W04694	Hs.512894	<i>TRPM7</i>	15q21	6.0	6.5	4.7	2.8
223324_s_at	AF346629	Hs.512894	<i>TRPM7</i>	15q21	5.5	4.9	6.7	5.0
209390_at	AF013168	Hs.370854	<i>TSC1</i>	9q34	2.5	2.0	1.7	1.5

221002_s_at	NM_030927	Hs.310453	<i>TSPAN14</i>	10q22.3	1.8	1.7	2.1	1.8
208864_s_at	AF313911	Hs.435136	<i>TXN</i>	9q31	1.6	1.6	2.4	1.9
201266_at	NM_003330	Hs.434367	<i>TXNRD1</i>	12q23-q24.1	1.3	1.3	1.7	2.1
219192_at	NM_018449	Hs.493739	<i>UBAP2</i>	9p13.3	2.0	2.0	2.9	2.2
201377_at	NM_014847	Hs.490551	<i>UBAP2L</i>	1q21.3	5.3	4.4	5.0	4.4
201378_s_at	NM_014847	Hs.490551	<i>UBAP2L</i>	1q21.3	3.1	3.1	2.7	2.8
209947_at	BC003170	Hs.490551	<i>UBAP2L</i>	1q21.3	2.3	1.9	2.1	1.5
214695_at	AW051361	Hs.490551	<i>UBAP2L</i>	1q21.3	2.5	2.5	2.9	2.1
221765_at	AI378044	Hs.304249	<i>UGCG</i>	9q31	4.8	5.4	4.2	3.9
204881_s_at	NM_003358	Hs.304249	<i>UGCG</i>	9q31	5.4	5.3	3.6	4.2
224967_at	W72338	Hs.304249	<i>UGCG</i>	9q31	5.3	5.2	3.3	4.1
200883_at	NM_003366	Hs.528803	<i>UQCRC2</i>	16p12	1.9	2.1	2.9	3.3
212600_s_at	AV727381	Hs.528803	<i>UQCRC2</i>	16p12	2.1	2.1	2.6	2.7
239465_at	AA355403	Hs.528803	<i>UQCRC2</i>	16p12	3.0	2.7	2.8	2.3
241755_at	AI961429	Hs.528803	<i>UQCRC2</i>	16p12	4.0	4.4	3.5	3.3
208970_s_at	M14016	Hs.78601	<i>UROD</i>	1p34	2.2	1.5	2.2	1.7
220370_s_at	NM_025090	Hs.464243	<i>USP36</i>	17q25.3	2.2	2.8	4.0	2.6
224978_s_at	BF430981	Hs.464243	<i>USP36</i>	17q25.3	1.5	1.9	2.5	2.0
227093_at	AU152298	Hs.464243	<i>USP36</i>	17q25.3	1.7	1.4	2.0	1.6
203241_at	NM_003369	Hs.202470	<i>UVRAG</i>	11q13.5	1.2	1.1	5.6	4.2
208626_s_at	BC001913	Hs.514199	<i>VAT1</i>	17q21	2.2	2.1	2.5	2.6
210512_s_at	AF022375	Hs.73793	<i>VEGF</i>	6p12	9.9	10.0	7.9	7.4
210513_s_at	AF091352	Hs.73793	<i>VEGF</i>	6p12	7.0	8.3	5.6	4.6
211527_x_at	M27281	Hs.73793	<i>VEGF</i>	6p12	24.5	21.5	13.8	13.0
212171_x_at	H95344	Hs.73793	<i>VEGF</i>	6p12	12.2	10.9	6.3	6.4
223346_at	AF308802	Hs.23876	<i>VPS18</i>	15q14-q15	7.7	6.0	3.8	3.5
240957_at	AI620726	Hs.499925	<i>VPS26</i>	10q21.1	2.7	3.0	2.3	1.6
201807_at	NM_004896	Hs.499925	<i>VPS26</i>	10q21.1	3.0	2.7	1.9	1.9
243316_x_at	AA004710	Hs.499925	<i>VPS26</i>	10q21.1	3.1	2.5	2.3	1.9
233559_s_at	AK023415	Hs.368359	<i>WDFY1</i>	2q36.1	1.8	1.2	2.1	1.3
203721_s_at	NM_016001	Hs.463465	<i>WDR50</i>	17q21.33	3.1	2.7	1.9	2.0
226668_at	W80623	Hs.20848	<i>WDSUB1</i>	2q24.2	4.5	3.2	5.0	3.3
201294_s_at	N24643	Hs.446017	<i>WSB1</i>	17q11.1	2.0	2.3	2.5	2.3
201295_s_at	BF111821	Hs.446017	<i>WSB1</i>	17q11.1	2.2	1.9	2.3	2.0
210561_s_at	AL110243	Hs.446017	<i>WSB1</i>	17q11.1	2.0	1.8	2.0	2.0
227501_at	AI377135	Hs.446017	<i>WSB1</i>	17q11.1	2.3	2.2	2.3	1.9
201760_s_at	NM_018639	Hs.506985	<i>WSB2</i>	12q24.23	5.1	3.2	4.9	3.5
213734_at	BG260658	Hs.506985	<i>WSB2</i>	12q24.23	5.0	2.8	4.1	3.2
1554239_s_at	BC033780	Hs.465433	<i>ZADH2</i>	18q22.3	20.3	11.3	18.6	10.6
227049_at	N21127	Hs.465433	<i>ZADH2</i>	18q22.3	5.8	3.6	4.8	3.7
227977_at	BF591611	Hs.465433	<i>ZADH2</i>	18q22.3	6.2	4.1	4.7	4.1
227978_s_at	BF591611	Hs.465433	<i>ZADH2</i>	18q22.3	8.8	5.8	6.4	4.2
234977_at	BG168924	Hs.465433	<i>ZADH2</i>	18q22.3	4.0	3.8	3.9	3.3
1557036_at	BU950380	Hs.400802	<i>ZBTB1</i>	14q23.3	1.7	2.0	1.8	1.4
213376_at	AI656706	Hs.400802	<i>ZBTB1</i>	14q23.3	1.9	1.8	1.7	2.1
231899_at	AB051513	Hs.376289	<i>ZC3H12C</i>	11q22.3	4.3	3.7	8.7	7.8
1557797_a_at	AW611486	Hs.34871	<i>ZFH1B</i>	2q22	2.7	2.4	2.2	1.5

203603_s_at	NM_014795	Hs.34871	ZFHX1B	2q22	2.2	1.8	1.8	1.7
239296_at	AI623184	Hs.34871	ZFHX1B	2q22	2.2	2.1	1.7	1.2
227796_at	AW157773	Hs.509227	ZFP62	5p15.33	2.9	1.8	2.1	1.4
1555790_a_at	BC036301	Hs.369632	ZFPL, FLJ38482	19q13.41, 4q32.3	3.4	3.2	2.9	2.5
240859_at	N20928	Hs.482660	ZFYVE16	5p15.2-q14.3	3.6	4.1	3.7	3.3
1554638_at	BC032227	Hs.482660	ZFYVE16	5p15.2-q14.3	3.5	4.0	4.0	3.2
203651_at	NM_014733	Hs.482660	ZFYVE16	5p15.2-q14.3	2.7	2.6	2.6	2.6
213073_at	AB002319	Hs.98041	ZFYVE26	14q24.1	8.0	5.1	8.2	7.3
37943_at	AB002319	Hs.98041	ZFYVE26	14q24.1	7.9	6.4	8.2	6.9
235408_x_at	AW058673	Hs.250693	ZNF117	7q11.2	2.9	2.2	2.3	1.7
235564_at	BF107006	Hs.250693	ZNF117	7q11.2	3.1	2.5	2.7	2.0
206683_at	NM_003447	Hs.55481	ZNF165	6p21.3	7.5	10.2	5.0	6.5
206862_at	NM_004876	Hs.434406	ZNF254, ZNF539	19p13.12- p13.11,19p12	3.4	2.2	4.7	3.8
212366_at	BF223237	Hs.485892	ZNF292	6q15	1.9	1.8	2.1	2.2
212368_at	AA972711	Hs.485892	ZNF292	6q15	1.9	1.9	2.1	2.0
236435_at	BE219036	Hs.485892	ZNF292	6q15	2.1	1.6	1.6	1.5
227991_x_at	BF516567	Hs.355581	ZNF297B	9p24.1-q22.33	2.1	1.9	1.3	1.4
227768_at	AB051490	Hs.536490	ZNF407	18q23	3.7	2.8	3.0	3.1
1558754_at	AA484731	Hs.398022	ZNF440L	19p13.2	3.7	3.0	1.6	1.3
1558755_x_at	AA484731	Hs.398022	ZNF440L	19p13.2	3.3	2.5	1.4	1.3
236133_x_at	AI983886	Hs.434406	ZNF539	19p12	2.4	3.0	3.7	2.5
205739_x_at	NM_016220	Hs.50216	ZNF588	7q11.2	2.1	2.0	2.6	2.7
227918_s_at	N21008	Hs.476280	ZYG11B	1p32.3	2.2	1.3	1.3	1.0
212893_at	AL080063	Hs.480506	ZZZ3	1p31.1	2.3	1.9	1.7	1.7
1555982_at	BU078629	Hs.463022	---	5q14.1	2.1	1.8	2.2	2.9
1558732_at	AK074900	---	---	2q11.2	3.3	3.7	3.5	2.4
1559455_at	BG430958	Hs.304130	---	---	20.6	11.9	15.5	12.1
1560869_a_at	AF085902	Hs.481068	---	4q32.1	10.4	12.7	23.9	16.2
1561017_at	AF087983	Hs.384565	---	13q14.2	4.2	3.6	6.3	4.6
1562777_at	AK097499	Hs.553142	---	7q11.21	3.1	2.5	2.3	1.7
1565852_at	BC035098	Hs.551982	---	18q23	2.0	2.0	1.9	1.6
1568838_at	AI015847	Hs.498519	---	16p13.3	1.6	1.2	2.7	1.6
1569746_s_at	BC036500	Hs.351485	---	20q13.12	2.1	1.9	1.3	1.6
1570061_at	BC014200	Hs.372904	---	3q21.3	2.6	2.3	2.2	1.4
209446_s_at	BC001743	---	---	15q23	1.8	1.6	2.1	1.4
217490_at	AL049301	---	---	11p11.2	2.3	2.5	2.0	1.5
217606_at	AI653960	Hs.196555	---	2q14.1	10.6	12.0	11.3	11.1
217649_at	AV702306	Hs.448937	---	19q13.2	1.8	2.1	1.6	1.8
220702_at	NM_018616	---	---	2q31.1	2.0	1.9	1.9	1.3
226397_s_at	BG502771	Hs.6083	---	6p24.1	5.7	5.2	3.6	4.5
226550_at	AI672159	Hs.91389	---	Xp11.3	2.1	2.2	1.2	1.4
227124_at	AI870473	Hs.21177	---	6p24.2	2.1	1.8	2.4	2.0
228333_at	AI912571	Hs.293676	---	2q22.3	2.6	2.1	1.4	1.2
228697_at	AW731710	Hs.175417	---	6q22.32	4.8	4.1	3.2	2.5
229242_at	BF439063	Hs.23349	---	9q32	25.8	21.0	35.6	22.8
230267_at	AI673025	Hs.246593	---	17q11.1	1.9	1.9	2.1	2.5

230304_at	AW005298	Hs.143408	---	19p13.13	4.3	3.9	2.4	2.3
230494_at	AI671885	Hs.110855	---	2q13	7.8	6.8	4.7	3.9
231367_s_at	AW300131	---	---	13q14.2	5.5	7.3	4.1	3.2
231470_at	BE138486	Hs.557480	---	19p12	2.9	4.1	3.1	3.8
231597_x_at	AI371550	---	---	---	1.2	0.9	3.2	0.8
231890_at	AK022804	Hs.273830	---	1q21.1	2.5	2.4	2.7	2.2
231972_at	AK024681	Hs.6083	---	6p24.1	7.5	7.1	3.7	4.0
232665_x_at	AL137424	---	---	7q22.1	2.0	1.0	1.8	1.4
234983_at	BE893995	Hs.120170	---	12q24.22	2.5	2.1	3.5	2.7
235174_s_at	AW952781	Hs.302631	---	7q36.1	2.1	1.9	1.5	1.5
235539_at	AW964431	---	---	11q13.4	3.1	2.9	2.9	2.8
235579_at	AA679858	---	---	12q13.11	2.0	2.0	1.7	1.6
235901_at	BE671060	Hs.127279	---	17p13.1	2.0	1.9	1.8	1.4
236198_at	AW292872	Hs.124554	---	3q13.12	2.2	2.1	2.4	2.1
236232_at	BF509528	Hs.145038	---	16p11.2	3.1	2.8	4.0	3.4
236423_at	AI022821	Hs.539431	---	---	3.6	3.2	2.7	2.4
236660_at	N25555	Hs.31712	---	6q15	4.3	3.1	2.9	2.3
238178_at	BF110268	Hs.559668	---	1p32.2	22.7	12.0	38.3	26.9
238412_at	AI344253	Hs.548005	---	16p12.1	3.6	4.1	3.4	4.6
238524_at	BE897147	---	---	1p13.3	7.4	5.7	6.8	6.3
238684_at	AI300909	Hs.433547	---	13q14.2	4.7	3.6	4.6	4.5
239129_at	AA521218	---	---	9q22.33	4.0	3.6	2.8	1.9
239287_at	AA769410	Hs.443475	---	2q33.3	4.6	2.1	7.9	5.0
239302_s_at	AA931539	Hs.516367	---	2q14.3	2.5	2.3	1.4	1.3
240013_at	AI949912	Hs.126963	---	16p11.2	1.9	2.1	1.5	1.7
240439_at	AW276240	---	---	19p12	2.9	2.8	3.9	3.9
241501_at	BE218228	Hs.253450	---	2p13.3	1.8	1.6	2.1	1.4
241853_at	AA760878	Hs.192268	---	---	6.0	4.7	5.1	3.4
241877_at	AW444451	Hs.134812	---	5q33.3	2.4	2.8	2.2	2.0
242058_at	AA206363	---	---	4q32.1	6.4	4.4	8.9	6.7
242270_at	AA017536	Hs.550790	---	1q21.1	4.2	2.9	2.6	2.0
242476_at	AI436356	Hs.130729	---	9p11.2	2.5	2.4	3.3	1.7
242582_at	AA621549	Hs.156918	---	10p11.23	2.1	2.3	2.6	2.9
242931_at	AI218358	Hs.175048	---	Xq24	3.2	3.4	2.7	2.6
243252_at	AA173465	---	---	1p21.2	1.9	1.8	1.5	2.0
243417_at	AA704162	Hs.442736	---	18q22.3	4.7	3.7	4.5	2.8
243511_at	AI652277	Hs.343015	---	15q24.1	8.2	7.3	5.1	4.7
243675_at	BF512500	Hs.445342	---	4q32.1	15.0	27.2	72.4	32.8
244600_at	AA868653	Hs.444114	---	1p36.32	5.8	5.2	4.9	3.4
Down-Regulated								
ProbeSet	Public ID	UniGene#	Entrez Gene	Chromosome	Healthy 180min	Job's 180up	Healthy 360min	Job's 360min
1557418_at	W95007	Hs.268785	ACSL4	Xq22.3-q23	-2.1	-1.7	-1.8	-1.5
1559663_at	AF090916	Hs.268785	ACSL4	Xq22.3-q23	-2.1	-2.5	-1.4	-1.6
202422_s_at	NM_022977	Hs.268785	ACSL4	Xq22.3-q23	-1.8	-1.6	-2.1	-1.5
206513_at	NM_004833	Hs.281898	AIM2	1q22	-2.0	-1.9	1.1	-1.1
212172_at	AW277253	Hs.470907	AK2	1p34	-2.6	-2.4	-1.2	-1.9

235380_at	AA768919	Hs.89499	<i>ALOX5</i>	10q11.2	-2.4	-2.2	-1.4	-2.1
226431_at	AK025007	Hs.471130	<i>ALS2CR13</i>	2q33.2	-1.5	-1.6	-2.2	-2.2
209424_s_at	AI796120	Hs.508343	<i>AMACR</i>	5p13.2-q11.1	-2.2	-2.1	-2.4	-2.4
201196_s_at	M21154	Hs.159118	<i>AMD1</i>	6q21-q22	-2.0	-1.9	-1.9	-1.8
201197_at	NM_001634	Hs.159118	<i>AMD1</i>	6q21-q22	-2.0	-1.9	-1.8	-1.7
205609_at	NM_001146	Hs.369675	<i>ANGPT1</i>	8q22.3-q23	-1.5	-1.6	-2.9	-2.9
238851_at	BF516252	Hs.528703	<i>ANKRD13</i>	12q24.11	-2.3	-2.4	-1.8	-2.2
238439_at	AI925518	Hs.217484	<i>ANKRD22</i>	10q23.31	-2.0	-2.2	-1.9	-1.4
155536_at	AY040326	Hs.162963	<i>ANTXR2</i>	4q21.21	-1.3	-1.4	-2.2	-1.9
205639_at	NM_001637	Hs.488007	<i>AOAH</i>	7p14-p12	-1.7	-1.4	-1.8	-2.1
204894_s_at	NM_003734	Hs.198241	<i>AOC3</i>	17q21	-1.6	-1.8	-2.2	-2.4
227057_at	AI814329	Hs.463165	<i>ARHGAP27</i>	17q21.31	-1.8	-1.7	-1.6	-2.0
215684_s_at	AL096741	Hs.517438	<i>ASCC2</i>	22q12.1	-2.2	-3.0	-2.4	-1.7
223338_s_at	BC001867	Hs.241336	<i>ATPIF1</i>	1p35.3	-2.1	-1.8	-1.9	-1.6
205539_at	NM_006576	Hs.333257	<i>AVIL</i>	12q14.1	-1.3	-1.4	-1.7	-2.1
209203_s_at	BC002327	Hs.436939	<i>BICD2</i>	9q22.31	-2.2	-2.4	-1.8	-1.7
213154_s_at	AI934125	Hs.436939	<i>BICD2</i>	9q22.31	-2.2	-2.1	-1.8	-1.9
219191_s_at	NM_016293	Hs.14770	<i>BIN2</i>	12q13	-1.2	-1.6	-1.8	-2.1
243431_at	BF000597	Hs.112895	<i>BTBD14A</i>	9q34.3	-2.0	-1.8	-1.9	-1.9
225372_at	AK024449	Hs.552663	<i>C10orf54</i>	10q22.3	-1.7	-2.0	-1.5	-1.6
224649_x_at	AI765014	Hs.14745	<i>C10orf9</i>	10p11.21	-1.6	-1.5	-2.1	-1.9
224651_at	AI921096	Hs.14745	<i>C10orf9</i>	10p11.21	-1.3	-1.5	-1.9	-2.0
224652_at	AV701987	Hs.14745	<i>C10orf9</i>	10p11.21	-1.3	-1.5	-2.1	-2.2
218298_s_at	NM_024952	Hs.309849	<i>C14orf159</i>	14q32.12	-1.7	-1.7	-2.1	-2.2
221958_s_at	AA775681	Hs.479491	<i>C1orf139</i>	1p31.2	-1.4	-1.5	-1.6	-2.0
202877_s_at	W72082	Hs.97199	<i>C1QR1</i>	20p11.21	-2.0	-2.3	-2.0	-3.2
202878_s_at	NM_012072	Hs.97199	<i>C1QR1</i>	20p11.21	-1.3	-1.4	-1.7	-2.1
225224_at	AL034550	Hs.516977	<i>C20orf112</i>	20q11.1-q11.23	-1.9	-2.1	-1.5	-1.8
225313_at	AI627538	Hs.504920	<i>C20orf177</i>	20q13.2-q13.33	-1.9	-2.0	-1.7	-1.7
1554786_at	BC027951	Hs.473144	<i>C20orf32</i>	20q13.31	-2.1	-2.3	-2.1	-2.0
220888_s_at	NM_020356	Hs.473144	<i>C20orf32</i>	20q13.31	-2.7	-2.1	-2.5	-2.5
212406_s_at	AB028973	Hs.473317	<i>C20orf36</i>	20q13.33	-1.6	-1.6	-2.0	-1.7
238469_at	BE620374	Hs.368337	<i>C6orf155</i>	6q13	-1.7	-1.7	-2.8	-2.3
206707_x_at	NM_015864	Hs.484915	<i>C6orf32</i>	6p22.3-p21.32	-1.7	-1.6	-2.2	-2.3
1555945_s_at	AK091785	Hs.372003	<i>C9orf10</i>	9q22.31	-2.0	-2.0	-2.0	-2.2
1555948_s_at	AU116818	Hs.372003	<i>C9orf10</i>	9q22.31	-1.9	-1.9	-2.1	-1.8
241242_at	BE503118	Hs.372003	<i>C9orf10</i>	9q22.31	-3.2	-1.9	-1.5	-2.1
218168_s_at	NM_020247	Hs.118241	<i>CABC1</i>	1q42.13	-1.8	-1.8	-1.7	-2.1
212757_s_at	BF111268	Hs.523045	<i>CAMK2G</i>	10q22	-1.8	-2.0	-1.7	-1.9
238556_at	AW295338	Hs.523045	<i>CAMK2G</i>	10q22	-1.5	-1.9	-1.2	-2.2
239179_at	AU155612	Hs.523045	<i>CAMK2G</i>	10q22	-2.7	-2.3	-1.8	-2.1
1552553_a_at	NM_021209	Hs.23248	<i>CARD12</i>	2p22-p21	-2.3	-2.3	-1.4	-2.1
240718_at	AW303384	Hs.407771	<i>CASC1</i>	12p12.1	-2.2	-2.0	-1.8	-2.1
209850_s_at	BC005406	Hs.343380	<i>CDC42EP2</i>	11q13	-2.3	-1.9	1.4	-0.7
234260_at	AL122039	Hs.508829	<i>CDC42SE2</i>	5q23.3	-2.8	-2.1	-1.6	-2.1
204995_at	AL567411	Hs.500015	<i>CDK5R1</i>	17q11.2	-2.5	-2.3	-2.0	-2.2

207205_at	NM_001817	Hs.12	<i>CEACAM4</i>	19q13.2	-1.7	-1.7	-1.3	-2.0
204039_at	NM_004364	Hs.76171	<i>CEBPA</i>	19q13.1	-1.9	-2.2	-1.6	-1.7
207075_at	NM_004895	Hs.159483	<i>CIAS1</i>	1q44	-3.1	-3.5	-3.0	-2.7
216015_s_at	AK027194	Hs.159483	<i>CIAS1</i>	1q44	-3.0	-3.1	-3.4	-2.0
218223_s_at	NM_016274	Hs.438824	<i>CKIP-1</i>	1q21.2	-2.7	-2.8	-2.1	-2.6
221724_s_at	AF200738	Hs.504657	<i>CLEC4A</i>	12p13	-1.9	-1.9	-2.1	-1.7
201560_at	NM_013943	Hs.440544	<i>CLIC4</i>	1p36.11	-2.0	-2.0	-1.2	-1.3
1568732_at	BC013148	Hs.517356	<i>COL18A1</i>	21q22.3	-2.6	-2.9	-1.9	-3.2
209082_s_at	AF018081	Hs.517356	<i>COL18A1</i>	21q22.3	-1.3	-1.4	-1.4	-2.7
202078_at	NM_003653	Hs.6076	<i>COPS3</i>	17p11.2	-1.6	-1.5	-2.1	-1.4
205931_s_at	NM_004904	Hs.437075	<i>CREB5</i>	7p15.1	-1.4	-1.7	-1.5	-2.6
229228_at	AI819043	Hs.437075	<i>CREB5</i>	7p15.1	-1.3	-1.5	-1.6	-2.2
232555_at	AI689210	Hs.437075	<i>CREB5</i>	7p15	-1.5	-1.7	-1.6	-2.4
221541_at	AL136861	Hs.513779	<i>CRISPLD2</i>	16q24.1	-1.7	-1.6	-1.8	-2.2
221731_x_at	BF218922	Hs.443681	<i>CSPG2</i>	5q14.3	-1.5	-1.6	-2.4	-1.6
32723_at	L02547	Hs.172865	<i>CSTF1</i>	20q13.31	-2.1	-1.5	-1.1	1.1
202295_s_at	NM_004390	Hs.148641	<i>CTSH</i>	15q24-q25	-2.4	-2.1	-1.6	-1.7
222453_at	AL136693	Hs.221941	<i>CYBRD1</i>	2q31.1	-1.5	-1.7	-2.2	-1.9
215184_at	AK026801	Hs.237886	<i>DAPK2</i>	15q22.31	-2.3	-1.9	-1.1	-1.5
222858_s_at	AI632216	Hs.436271	<i>DAPP1</i>	4q25-q27	-2.2	-2.1	-1.8	-1.9
222859_s_at	AA150186	Hs.436271	<i>DAPP1</i>	4q25-q27	-2.1	-1.9	-1.8	-1.7
236707_at	AA521016	Hs.436271	<i>DAPP1</i>	4q25-q27	-2.1	-1.6	-1.4	-1.6
230999_at	AI743903	Hs.549346	<i>DCPS</i>	11q24.2	-1.7	-1.6	-1.2	-2.7
214198_s_at	AU150824	Hs.517357	<i>DGCR2</i>	22q11.21	-2.2	-2.2	-1.6	-2.0
219799_s_at	NM_005771	Hs.179608	<i>DHRS9</i>	2q31.1	1.0	-1.3	-2.0	-2.5
223952_x_at	AF240698	Hs.179608	<i>DHRS9</i>	2q31.1	1.1	-1.3	-1.8	-2.5
224009_x_at	AF240697	Hs.179608	<i>DHRS9</i>	2q31.1	1.1	-1.3	-1.7	-2.3
218218_at	NM_018171	Hs.506603	<i>DIP13B</i>	12q24.1	-1.8	-2.1	-1.7	-1.7
201580_s_at	AL544094	Hs.169358	<i>DJ971N18.2</i>	20p12	-1.4	-1.5	-2.0	-2.1
219313_at	NM_017577	Hs.24583	<i>DKFZp434C0328</i>	3q13.31	-1.7	-2.0	-2.8	-3.0
201681_s_at	AB011155	Hs.500245	<i>DLG5</i>	10q23	-1.7	-1.6	-2.5	-1.8
232843_s_at	AL161725	Hs.132599	<i>DOCK8</i>	9p24.3	-1.2	-1.2	-2.0	-1.7
239027_at	AV760561	Hs.132599	<i>DOCK8</i>	9p24.3	-1.7	-1.6	-2.1	-2.5
241891_at	T92908	Hs.132599	<i>DOCK8</i>	9p24.3	-2.3	-2.0	-2.3	-2.4
212611_at	AV728526	Hs.523696	<i>DTX4</i>	11q12.1	-2.2	-2.4	-1.9	-2.1
208891_at	BC003143	Hs.298654	<i>DUSP6</i>	12q22-q23	-2.5	-2.7	-2.2	-2.0
208893_s_at	BC005047	Hs.298654	<i>DUSP6</i>	12q22-q23	-2.8	-3.0	-2.4	-2.1
212830_at	W68084	Hs.494977	<i>EGFL5</i>	9q32-q33.3	-2.5	-2.2	-2.1	-2.1
212831_at	BF110421	Hs.494977	<i>EGFL5</i>	9q32-q33.3	-2.8	-2.6	-1.9	-3.0
221497_x_at	BC005369	Hs.444450	<i>EGLN1</i>	1q42.1	-1.3	-1.4	-1.9	-2.1
223046_at	AL117352	Hs.444450	<i>EGLN1</i>	1q42.1	-1.4	-1.4	-2.2	-2.4
224314_s_at	AF277174	Hs.444450	<i>EGLN1</i>	1q42.1	-1.5	-1.4	-1.9	-2.3
208112_x_at	NM_006795	Hs.523774	<i>EHD1</i>	11q13	-1.9	-2.3	1.0	-1.3
209038_s_at	AL579035	Hs.523774	<i>EHD1</i>	11q13	-2.0	-2.0	1.1	-1.3
222221_x_at	AY007161	Hs.523774	<i>EHD1</i>	11q13	-1.9	-2.6	1.1	-1.6
221773_at	AW575374	Hs.46523	<i>ELK3</i>	12q23	-1.6	-1.9	-2.3	-2.1
201340_s_at	AF010314	Hs.104925	<i>ENC1</i>	5q12-q13.3	-2.2	-2.2	-2.0	-2.0

201341_at	NM_003633	Hs.104925	<i>ENC1</i>	5q12-q13.3	-2.1	-2.3	-2.0	-1.7
239740_at	BF436898	Hs.504765	<i>ETV6</i>	12p13	-2.1	-1.6	-1.5	-1.9
203780_at	AF275945	Hs.116651	<i>EVA1</i>	11q24	-2.2	-2.1	-2.2	-1.8
206429_at	NM_005242	Hs.154299	<i>F2RL1</i>	5q13	-2.3	-2.5	-2.4	-2.7
213506_at	BE965369	Hs.154299	<i>F2RL1</i>	5q13	-2.9	-2.8	-2.6	-2.5
235009_at	AI049791	Hs.444517	<i>FAM44A</i>	4p16.1	-1.6	-1.7	-1.5	-2.1
209683_at	AA243659	Hs.467769	<i>FAM49A</i>	2p24.3-p24.2	-2.1	-2.2	-1.8	-1.7
210889_s_at	M31933	Hs.492655	<i>FCGR2B</i>	1q23	-1.2	-1.3	-2.1	-1.5
204834_at	NM_006682	Hs.520989	<i>FGL2</i>	7q11.23	-1.7	-1.8	-2.1	-2.1
218530_at	NM_013241	Hs.95231	<i>FHOD1</i>	16q22	-2.1	-2.3	-1.7	-2.1
206497_at	NM_018224	Hs.289007	<i>FLJ10803</i>	7p13	-2.9	-3.2	-2.6	-3.5
209445_x_at	AI765280	Hs.289007	<i>FLJ10803</i>	7p13	-2.0	-2.1	-2.2	-2.3
232330_at	AK024861	Hs.289007	<i>FLJ10803</i>	7p13	-2.3	-2.1	-1.7	-2.0
219694_at	NM_019018	Hs.528644	<i>FLJ11127</i>	5p15.2	-1.4	-1.2	-2.1	-1.8
218610_s_at	NM_018340	Hs.460002	<i>FLJ11151</i>	16p13.12	-1.4	-1.5	-2.0	-2.0
222686_s_at	AL572407	Hs.460002	<i>FLJ11151</i>	16p13.12	-1.5	-1.6	-2.3	-2.1
239135_at	AI675054	Hs.460002	<i>FLJ11151</i>	16p13.12	-1.5	-1.7	-2.2	-2.2
219227_at	NM_024565	Hs.14070	<i>FLJ14166</i>	5q33.3	-1.7	-2.4	-1.1	-1.2
1555486_a_at	BC008922	Hs.19987	<i>FLJ14213</i>	11p13-p12	-2.0	-1.9	-1.8	-1.4
233757_x_at	AK026906	Hs.5111	<i>FLJ20729</i>	1p22.3	1.1	1.1	1.3	-3.2
218454_at	NM_024829	Hs.131933	<i>FLJ22662</i>	12p13.1	-1.3	-1.5	-1.8	-2.1
230012_at	AW574774	Hs.121692	<i>FLJ34790</i>	17p13.1	-2.5	-2.1	-1.9	-1.6
235699_at	H19232	Hs.444911	<i>FLJ38964</i>	14q11.2	-1.3	-1.4	-1.9	-2.4
211299_s_at	BC003683	Hs.514038	<i>FLOT2</i>	17q11-q12	-2.2	-1.8	-2.1	-1.7
213056_at	AU145019	Hs.371681	<i>FRMD4B</i>	3p14.1	-2.1	-2.0	-1.5	-1.8
218373_at	NM_022476	Hs.380897	<i>FTS</i>	16q12.2	-2.3	-2.3	-1.8	-2.1
235346_at	BF033615	Hs.7549	<i>FUNDC1</i>	Xp11.3	-2.8	-2.0	-2.3	-1.8
210506_at	U11282	Hs.457	<i>FUT7</i>	9q34.3	-3.0	-3.6	-1.7	-2.9
234974_at	AI769923	Hs.435012	<i>GALM</i>	2p22.1	-1.2	-1.4	-1.7	-2.2
223434_at	AL136680	Hs.534284	<i>GBP3</i>	1p22.2	-2.2	-2.0	-1.6	-1.5
235574_at	AW392952	Hs.409925	<i>GBP4</i>	1p22.2	-2.4	-2.3	-2.1	-1.8
238581_at	BG271923	Hs.513726	<i>GBP5</i>	1p22.2	-1.7	-1.6	-2.0	-1.5
232024_at	AI431931	Hs.255008	<i>GIMAP2</i>	7q36.1	-1.8	-2.1	-1.7	-1.8
219243_at	NM_018326	Hs.30822	<i>GIMAP4</i>	7q36.1	-1.9	-1.9	-2.0	-2.0
235306_at	AI611648	Hs.95834	<i>GIMAP8</i>	7q36.1	-2.0	-2.9	-1.9	-2.2
209876_at	AF124491	Hs.434996	<i>GIT2</i>	12q24.1	-1.6	-2.1	-1.6	-1.5
204221_x_at	U16307	Hs.205558	<i>GLIPR1</i>	12q21.1	-1.9	-2.1	-2.6	-2.5
204222_s_at	NM_006851	Hs.205558	<i>GLIPR1</i>	12q21.1	-2.1	-2.3	-2.5	-2.2
214085_x_at	AI912583	Hs.205558	<i>GLIPR1</i>	12q21.1	-1.8	-2.0	-2.2	-2.4
226142_at	AV682252	Hs.205558	<i>GLIPR1</i>	12q21.1	-1.9	-2.1	-2.4	-2.4
231166_at	AI733474	Hs.516604	<i>GPR155</i>	2q31.1	-2.1	-2.3	-2.1	-2.5
239533_at	AI970061	Hs.516604	<i>GPR155</i>	2q31.1	-2.0	-1.9	-1.8	-1.9
242517_at	AI819198	Hs.208229	<i>GPR54</i>	19p13.3	-2.5	-3.0	-2.6	-3.4
205240_at	NM_013296	Hs.489353	<i>GPSM2</i>	1p13.3	-6.7	-2.1	-2.7	-2.7
201348_at	NM_002084	Hs.386793	<i>GPX3</i>	5q23	-2.1	-2.2	-2.2	-1.6
214091_s_at	AW149846	Hs.386793	<i>GPX3</i>	5q23	-2.0	-1.9	-2.2	-1.5
232080_at	AL390186	Hs.314436	<i>HECW2</i>	2q32.3	-2.2	-2.2	-2.3	-2.5

204689_at	NM_001529	Hs.118651	<i>HHEX</i>	10q23.33	-2.4	-2.3	-1.9	-2.1
215933_s_at	Z21533	Hs.118651	<i>HHEX</i>	10q23.33	-2.7	-2.6	-2.1	-2.4
214472_at	NM_003530	Hs.532144	<i>HIST1H3D</i>	6p21.3	-2.0	-1.4	-1.1	-1.4
1557050_at	CA448125	Hs.445239	<i>HOXA2</i>	7p15-p14	-1.7	-1.8	-2.0	-1.9
1559128_at	BM014995	Hs.59486	<i>HSDL2</i>	9q32	-2.6	-2.1	-1.6	-2.1
117_at	X51757	Hs.3268	<i>HSPA6</i>	1q23	-1.9	-2.0	-1.9	-2.5
213418_at	NM_002155	Hs.3268	<i>HSPA6</i>	1q23	-1.7	-1.9	-1.8	-2.3
235549_at	AL575512	Hs.148741	<i>IBRDC2</i>	6p22.3	-2.1	-2.0	-1.5	-1.8
235202_x_at	BG498328	Hs.252543	<i>IKIP</i>	12q23.1	-2.3	-2.5	-2.2	-3.2
236249_at	BF057681	Hs.252543	<i>IKIP</i>	12q23.1	-2.0	-1.9	-1.9	-2.1
201888_s_at	U81379	Hs.496646	<i>IL13RA1</i>	Xq24	-1.4	-1.3	-2.1	-2.0
210904_s_at	U81380	Hs.496646	<i>IL13RA1</i>	Xq24	-1.3	-1.2	-2.2	-1.8
205227_at	NM_002182	Hs.478673	<i>IL1RAP</i>	3q28	1.0	1.1	-2.3	-1.7
203126_at	NM_014214	Hs.367992	<i>IMPA2</i>	18p11.2	-1.3	-1.4	-3.2	-2.9
203331_s_at	U53470	Hs.262886	<i>INPP5D</i>	2q36-q37	-1.3	-1.4	-1.8	-2.0
232352_at	AK001022	Hs.444677	<i>ISL2</i>	15q23	-2.5	-3.2	-1.8	-3.3
226267_at	AA716425	Hs.196482	<i>JDP2</i>	14q24.3	-2.1	-1.9	-1.9	-2.0
206765_at	AF153820	Hs.1547	<i>KCNJ2</i>	17q23.1-q24.2	-2.3	-2.0	-1.7	-1.4
231513_at	BF111326	Hs.1547	<i>KCNJ2</i>	17q23.1-q24.2	-3.1	-2.7	-1.9	-1.5
212188_at	AA551075	Hs.109438	<i>KCTD12</i>	13q22.3	-1.4	-1.6	-1.7	-2.4
212192_at	AI718937	Hs.109438	<i>KCTD12</i>	13q22.3	-1.5	-1.8	-1.8	-2.3
200699_at	BE962456	Hs.520210	<i>KDELR2</i>	7p22.1	-2.2	-1.8	-1.4	-1.3
212683_at	AL526243	Hs.532375	<i>KIAA0446</i>	1q22	-1.9	-2.2	-1.3	-1.6
32091_at	AB007915	Hs.532375	<i>KIAA0446</i>	1q22	-2.1	-2.1	-1.2	-1.7
1560443_at	BC004890	Hs.8118	<i>KIAA0650</i>	18p11.32	-1.7	-1.5	-1.6	-2.0
219520_s_at	NM_018458	Hs.527524	<i>KIAA1280</i>	Xp22.32	-1.6	-1.7	-2.0	-1.9
225273_at	AB033106	Hs.527524	<i>KIAA1280</i>	Xp22.32	-1.6	-1.6	-2.3	-2.3
239780_at	AA468422	Hs.97858	<i>KIF1B</i>	1p36.2	-2.3	-1.6	-1.8	-1.8
232514_at	AL133654	Hs.546403	<i>KIF27</i>	9q21.32	-1.9	-1.9	-3.1	-3.2
219878_s_at	NM_015995	Hs.525752	<i>KLF13</i>	15q12	-2.0	-1.7	-1.5	-1.8
226874_at	BF591270	Hs.106601	<i>KLHL8</i>	4q22.1	-2.1	-2.0	-1.7	-1.9
242648_at	BE858995	Hs.106601	<i>KLHL8</i>	4q22.1	-2.3	-2.1	-1.9	-2.0
217027_x_at	AC004941	Hs.532793	<i>KPNB1</i>	17q21.32	-2.1	-1.9	-1.5	-1.7
218963_s_at	NM_015515	Hs.9029	<i>KRT23</i>	17q21.2	-1.8	-2.1	-1.5	-2.2
211768_at	BC006080	Hs.56607	<i>LAT2</i>	7q11.23	-2.2	-1.4	-1.5	-1.4
213261_at	AA035414	Hs.517761	<i>LBA1</i>	3p22.3	-1.9	-1.9	-2.2	-1.9
1552546_a_at	NM_144652	Hs.264887	<i>LETM2</i>	8p12	-2.2	-2.1	-2.5	-2.5
1557415_s_at	AI023774	Hs.264887	<i>LETM2</i>	8p12	-2.1	-2.0	-2.1	-2.2
210660_at	AF025529	Hs.534393	<i>LILRA1</i>	19q13.4	-1.6	-1.7	-2.1	-2.1
213589_s_at	AW468201	Hs.512029	<i>LOC146712, B3GNTL1</i>	17q25.3	-1.9	-2.2	-2.3	-3.9
229295_at	BF939473	Hs.48353	<i>LOC150166</i>	22q11.21	-2.4	-2.3	-1.3	-2.5
1560679_at	AK055877	Hs.516245	<i>LOC151438</i>	2q12.1	-2.4	-2.3	-2.3	-2.9
1570585_at	BC031223	Hs.15396	<i>LOC196264</i>	11q23.3	-2.5	-2.2	-2.0	-2.3
225832_s_at	BE795104	Hs.487498	<i>LOC221955</i>	7p22.1	-2.1	-1.8	-1.9	-1.6
225833_at	BE795104	Hs.487498	<i>LOC221955</i>	7p22.1	-2.0	-2.0	-2.1	-1.6
226640_at	AA015606	Hs.487498	<i>LOC221955</i>	7p22.1	-2.2	-2.0	-1.9	-1.7
1557113_at	AK095276	Hs.46519	<i>LOC283588</i>	14q32.12	-2.4	-2.6	-2.3	-2.3

1558525_at	AK095480	Hs.546880	LOC283901	16p12.1	-2.3	-2.3	-2.5	-2.6
243954_at	AI149729	Hs.170991	LOC285286	3p14.2	-2.8	-3.0	-2.0	-2.8
227270_at	BF593037	Hs.399980	LOC285550	4p15.33	-1.7	-1.5	-1.7	-2.0
1552670_a_at	NM_024607	---	LOC286044	8p23.1	-2.0	-2.2	-1.8	-1.7
222662_at	W60806	---	LOC286044	8p23.1	-2.0	-2.4	-1.8	-2.1
232320_at	AK026359	Hs.253806	LOC440703	1q25.3	-1.8	-2.3	-1.8	-2.3
229390_at	AV734646	Hs.381220	LOC441168	6q22.1	-2.7	-2.6	-2.3	-2.2
229391_s_at	AV734646	Hs.381220	LOC441168	6q22.1	-3.3	-3.2	-2.9	-2.7
1554447_at	BC029480	Hs.460785	LOC554203	Xq13.2	-2.1	-1.9	-1.7	-2.4
244357_at	T90760	Hs.15200	LOC64744	1p35.3-p34.1	-1.8	-2.1	-1.2	-2.5
213455_at	W87466	Hs.476517	LOC92689	4p14	-1.7	-2.0	-1.8	-1.7
235104_at	BG292389	Hs.482910	LRAP	5q15	-1.8	-1.4	-2.2	-1.2
229584_at	AK026776	Hs.187636	LRRK2	12q12	-2.1	-1.9	-2.0	-2.1
211581_x_at	AF000426	Hs.436066	LST1	6p21.3	-1.3	-1.3	-1.7	-2.0
1562511_at	AL833100	Hs.532411	LYST	1q42.1-q42.2	-2.2	-2.0	-2.0	-1.9
235841_at	AI190306	Hs.372009	MAML3	4q28	-2.7	-2.0	-2.1	-2.2
242794_at	AI569476	Hs.444627	MAML3	4q28	-1.1	-1.2	-2.1	-1.7
202890_at	AW242297	Hs.486548	MAP7	6q23.3	-1.8	-2.2	-2.6	-2.6
1556658_a_at	AA744622	Hs.478000	MBNL1	3q25	-2.2	-1.5	-1.2	-1.4
213761_at	AW664850	Hs.171265	MDM1	12q15	-2.2	-2.0	-1.7	-1.3
207968_s_at	NM_002397	Hs.444409	MEF2C	5q14	-1.9	-2.1	-2.7	-2.2
209199_s_at	N22468	Hs.444409	MEF2C	5q14	-2.0	-2.2	-3.0	-2.2
209200_at	AL536517	Hs.444409	MEF2C	5q14	-2.2	-2.1	-2.5	-2.2
236395_at	AI523245	Hs.444409	MEF2C	5q14	-2.8	-2.9	-2.3	-2.7
224480_s_at	BC006236	Hs.99196	MGC11324	4q21.23	-1.7	-1.7	-1.6	-2.1
224452_s_at	BC006110	Hs.7980	MGC12966	7p22.1	-2.5	-2.3	-2.3	-1.8
1553158_at	AY099509	Hs.334526	MGC14126	3q29	-2.1	-2.1	-1.7	-1.8
226121_at	AI076793	Hs.5163	MGC23280	17q11.2	-2.7	-2.5	-1.7	-2.2
212473_s_at	BE965029	Hs.501928	MICAL2	11p15.3	-1.4	-1.6	-1.8	-2.0
212748_at	AB037859	Hs.474905	MKL1	22q13	-2.1	-1.7	-1.8	-1.2
1556306_at	AA082707	Hs.489556	MLL5	7q22.1	-2.1	-2.3	-2.1	-2.8
203434_s_at	AI433463	Hs.307734	MME	3q25.1-q25.2	-1.4	-1.5	-1.7	-2.2
203435_s_at	NM_007287	Hs.307734	MME	3q25.1-q25.2	-1.4	-1.4	-1.7	-2.1
226818_at	T64884	Hs.549280	MPEG1	11q12.1	-1.2	-1.3	-2.1	-1.7
226841_at	BF590697	Hs.549280	MPEG1	11q12.1	-1.4	-1.5	-2.3	-2.0
209858_x_at	BC002877	Hs.514713	MPPE1	18p11.21	-1.1	-1.3	-2.1	-2.8
201875_s_at	NM_024569	Hs.493919	MPZL1	1q24.2	-1.5	-1.8	-2.0	-2.1
219666_at	NM_022349	Hs.523702	MS4A6A	11q12.1	-2.3	-1.9	-1.3	-2.2
231274_s_at	R92925	Hs.122514	MSCP	8p21.2	-1.3	-1.6	-1.8	-2.2
237568_at	H67156	Hs.122514	MSCP	8p21.2	-2.2	-2.4	-1.8	-2.2
218380_at	NM_021730	Hs.104305	NALP1	17p13.2	-1.4	-1.5	-1.9	-2.1
204961_s_at	NM_000265	Hs.1583	NCF1	7q11.23	-1.6	-1.5	-1.6	-2.1
222625_s_at	BF973292	Hs.460107	NDE1	16p13.11	-1.9	-1.9	-2.1	-1.8
242642_at	AI963104	Hs.372123	NDEL1	17p13.1	-2.2	-2.0	-1.4	-1.6
209930_s_at	L13974	Hs.75643	NFE2	12q13	-2.8	-2.9	-1.5	-2.8
228933_at	BF111819	Hs.201623	NHS	Xp22.13	1.1	1.0	-2.3	-2.5
209706_at	AF247704	Hs.55999	NKX3-1	8p21	-2.3	-1.6	-2.0	1.4

217831_s_at	NM_016143	Hs.12865	<i>NSFL1C</i>	20p13	-1.9	-2.1	-1.7	-1.9
232520_s_at	AK023585	Hs.12865	<i>NSFL1C</i>	20p13	-2.0	-2.1	-1.7	-1.6
236951_at	BE550891	Hs.12865	<i>NSFL1C</i>	20p13	-2.2	-2.3	-1.6	-1.8
230462_at	AU158026	Hs.509909	<i>NUMB</i>	14q24.3	-2.2	-2.0	-1.6	-1.5
219582_at	NM_024576	Hs.549195	<i>OGFRL1</i>	6q13	-1.6	-1.6	-2.1	-2.2
1559201_a_at	BU929456	Hs.494192	<i>OSTF1</i>	9q13-q21.2	-1.5	-2.1	-1.4	-1.9
1553856_s_at	NM_014499	Hs.296433	<i>P2RY10</i>	Xq21.1	-2.0	-1.7	-2.3	-1.5
214615_at	NM_014499	Hs.296433	<i>P2RY10</i>	Xq21.1	-2.0	-1.6	-2.1	-1.4
1554384_at	BC009701	Hs.33455	<i>PADI2</i>	1p35.2-p35.1	-1.5	-2.1	-1.1	-1.5
239067_s_at	AI360417	Hs.440092	<i>PANX2</i>	22q13.33	-1.5	-1.9	-1.6	-2.2
215175_at	AB023212	Hs.158722	<i>PCNX</i>	14q24.2	-1.8	-1.7	-1.3	-2.5
238792_at	BF209668	Hs.158722	<i>PCNX</i>	14q24.2	-1.8	-2.0	-1.8	-2.0
215671_at	AU144792	Hs.198072	<i>PDE4B</i>	1p31	-2.3	-2.1	-1.7	-1.3
222326_at	AW973834	Hs.198072	<i>PDE4B</i>	1p31	-2.0	-2.0	-1.6	-1.8
208981_at	AA702701	Hs.514412	<i>PECAM1</i>	17q23	-1.9	-1.8	-2.1	-2.1
208982_at	AW574504	Hs.514412	<i>PECAM1</i>	17q23	-1.8	-2.1	-2.0	-2.3
208983_s_at	M37780	Hs.514412	<i>PECAM1</i>	17q23	-2.2	-2.3	-2.7	-2.6
207384_at	NM_005091	Hs.137583	<i>PGLYRP1</i>	19q13.2-q13.3	-1.8	-1.4	1.0	-2.1
218517_at	NM_024900	Hs.12420	<i>PHF17</i>	4q26-q27	-2.3	-1.9	-1.4	-1.1
225820_at	AV646599	Hs.12420	<i>PHF17</i>	4q26-q27	-2.6	-2.1	-1.5	-1.2
236218_at	AI016183	Hs.405607	<i>PHOSPHO1</i>	17q21.32	-2.0	-2.1	-2.3	-1.9
242760_x_at	AA808203	Hs.126115	<i>PIGB</i>	15q21-q22	-1.8	-2.1	-2.1	-2.1
206370_at	NM_002649	Hs.32942	<i>PIK3CG</i>	7q22.3	-2.1	-2.0	-1.6	-1.7
210969_at	AF118089	Hs.440833	<i>PKN2</i>	1p22.2	-1.7	-1.4	-2.1	-1.8
212628_at	BG292065	Hs.440833	<i>PKN2</i>	1p22.2	-1.7	-1.7	-2.0	-1.8
213222_at	AL049593	Hs.310537	<i>PLCB1</i>	20p12	-1.1	-1.2	-2.2	-1.5
213309_at	AL117515	Hs.202010	<i>PLCL2</i>	3p24.3	-2.0	-2.1	-1.9	-2.2
216218_s_at	AK023546	Hs.202010	<i>PLCL2</i>	3p24.3	-1.9	-2.0	-1.8	-2.0
216971_s_at	Z54367	Hs.434248	<i>PLEC1</i>	8q24	-2.1	-1.9	-1.6	-2.4
200827_at	NM_000302	Hs.75093	<i>PLOD1</i>	1p36.3-p36.2	-1.8	-1.8	-2.0	-1.7
202996_at	NM_021173	Hs.523829	<i>POLD4</i>	11q13	-2.4	-1.4	-2.3	-2.2
228343_at	AA805754	Hs.515429	<i>POU2F2</i>	19q13.2	-2.4	-1.8	-1.6	-1.8
203063_at	NM_014634	Hs.112728	<i>PPM1F</i>	22q11.22	-1.7	-1.7	-1.6	-2.1
204555_s_at	NM_006242	Hs.42215	<i>PPP1R3D</i>	20q13.3	-1.5	-2.1	-1.3	-1.7
232811_x_at	AU145382	Hs.524348	<i>PRICKLE1</i>	12q12	-1.0	-1.0	-1.0	-2.2
210543_s_at	U34994	Hs.491682	<i>PRKDC</i>	8q11	-1.7	-1.6	-2.4	-2.3
207291_at	NM_024081	Hs.471695	<i>PRRG4</i>	11p13	-2.0	-2.2	-1.6	-3.0
238513_at	BF905445	Hs.471695	<i>PRRG4</i>	11p13	-2.6	-2.7	-2.0	-3.1
205961_s_at	NM_004682	Hs.493516	<i>PSIP1</i>	9p22.3	-1.8	-2.2	-1.9	-1.7
209337_at	AF063020	Hs.493516	<i>PSIP1</i>	9p22.3	-2.1	-1.9	-1.9	-1.5
1559034_at	AK095499	Hs.405994	<i>PTPNS1L3</i>	20p13	-1.9	-2.1	-1.7	-2.0
238695_s_at	AW960289	Hs.24970	<i>RAB39B</i>	Xq28	-1.5	-2.0	-1.1	-2.5
208466_at	NM_004283	Hs.551520	<i>RAB3D</i>	19p13.2	-2.0	-1.6	-1.7	-1.6
225001_at	AI744658	Hs.551520	<i>RAB3D</i>	19p13.2	-2.0	-2.0	-1.7	-1.6
210541_s_at	AF230394	Hs.440382	<i>RFP</i>	6p22	-1.6	-1.7	-2.3	-1.7
212116_at	NM_006510	Hs.440382	<i>RFP</i>	6p22	-1.9	-2.0	-2.1	-1.9
204280_at	NM_006480	Hs.9347	<i>RGS14</i>	5q35.3	-1.9	-2.4	-1.8	-2.0

211021_s_at	AF037194	Hs.9347	<i>RGS14</i>	5q35.3	-2.6	-2.4	-2.3	-4.1
203823_at	NM_021106	Hs.494875	<i>RGS3</i>	9q32	-2.0	-2.6	-1.5	-2.1
213566_at	NM_005615	Hs.23262	<i>RNASE6</i>	14q11.2	-2.3	-1.9	-2.6	-2.5
232722_at	AK001769	Hs.529989	<i>RNASET2</i>	6q27	-2.6	-2.0	-2.0	-1.8
204633_s_at	AF074393	Hs.510225	<i>RPS6KA5</i>	14q31-q32.1	-1.7	-2.0	-2.1	-1.9
204635_at	NM_004755	Hs.510225	<i>RPS6KA5</i>	14q31-q32.1	-1.7	-1.9	-2.1	-2.1
226387_at	AI439157	Hs.72451	<i>RSBN1L</i>	7q11.23	-1.7	-1.8	-1.7	-2.1
227431_at	BF435958	Hs.72451	<i>RSBN1L</i>	7q11.23	-2.0	-1.9	-1.7	-1.9
232231_at	AL353944	Hs.122116	<i>RUNX2</i>	6p21	-1.9	-1.8	-2.4	-2.2
204900_x_at	NM_003864	Hs.413835	<i>SAP30</i>	4q34.1	-2.9	-2.5	-2.0	-2.1
218854_at	NM_013352	Hs.486292	<i>SART2</i>	6q22	-1.4	-1.6	-1.8	-2.0
212154_at	AI380298	Hs.1501	<i>SDC2</i>	8q22-q23	-1.8	-2.2	-2.8	-2.5
212158_at	AL577322	Hs.1501	<i>SDC2</i>	8q22-q23	-1.9	-2.0	-2.5	-2.0
234725_s_at	AK026133	Hs.474935	<i>SEMA4B</i>	15q25	-2.5	-2.5	-2.0	-2.0
1563357_at	AL049245	Hs.104879	<i>SERPINB9</i>	6p25	-2.4	-1.9	-1.5	1.1
235683_at	BF685808	Hs.120633	<i>SESN3</i>	11q21	-1.9	-2.2	-2.0	-2.4
207224_s_at	NM_016543	Hs.274470	<i>SIGLEC7</i>	19q13.3	-2.0	-2.1	-2.1	-1.9
216537_s_at	AJ130713	Hs.274470	<i>SIGLEC7</i>	19q13.3	-1.7	-2.1	-2.1	-2.0
217159_x_at	AJ130712	Hs.274470	<i>SIGLEC7</i>	19q13.3	-2.6	-3.1	-2.8	-2.2
210569_s_at	AF247180	Hs.245828	<i>SIGLEC9</i>	19q13.41	-2.8	-2.6	-2.7	-2.7
207038_at	NM_004694	Hs.42645	<i>SLC16A6</i>	17q24.2	-1.2	-1.2	-1.4	-2.3
209776_s_at	U15939	Hs.84190	<i>SLC19A1</i>	21q22.3	-1.1	-1.4	-1.7	-2.0
218978_s_at	NM_018586	Hs.122514	<i>SLC25A37</i>	8p21.2	-2.0	-2.5	-2.3	-2.1
222528_s_at	BG251467	Hs.122514	<i>SLC25A37</i>	8p21.2	-1.4	-1.6	-1.8	-2.3
242335_at	AA382004	Hs.530157	<i>SLC25A37</i>	---	-1.4	-1.6	-1.6	-2.2
240055_at	AW590925	Hs.210227	<i>SLC2A14</i>	12p13.31	-2.6	-2.6	-2.2	-2.9
223044_at	AL136944	Hs.529285	<i>SLC40A1</i>	2q32	-2.3	-2.3	-1.8	-2.3
239723_at	AA588092	Hs.529285	<i>SLC40A1</i>	2q32	-2.5	-2.0	-1.6	-1.9
225282_at	AL137764	Hs.15200	<i>SMAP1L</i>	1p35.3-p34.1	-1.5	-1.5	-2.1	-1.9
241620_at	AA873021	Hs.8118	<i>SMCHD1</i>	18p11.32	-1.9	-1.5	-1.6	-2.4
207474_at	NM_017719	Hs.476052	<i>SNRK</i>	3p22.1	-2.2	-1.7	-1.6	-1.8
230707_at	AA290609	Hs.368592	<i>SORL1</i>	11q23.2-q24.2	-1.8	-2.1	-2.0	-2.4
210117_at	AF311312	Hs.492373	<i>SPAG1</i>	8q22.2	-2.0	-2.1	-3.2	-2.8
1558254_s_at	BU155802	Hs.285197	<i>SRPK2</i>	7q22-q31.1	-1.2	-1.3	-2.1	-1.8
203181_x_at	AW149364	Hs.285197	<i>SRPK2</i>	7q22-q31.1	1.0	-1.2	-1.8	-2.0
210829_s_at	AF077048	Hs.102735	<i>SSBP2</i>	5q14.1	-1.1	-1.2	-2.1	-1.3
1560306_at	AF086010	Hs.335205	<i>SSH2</i>	17q11.2	-2.1	-2.2	-2.1	-1.5
230970_at	AA975530	Hs.335205	<i>SSH2</i>	17q11.2	-2.1	-2.0	-1.7	-1.8
206925_at	NM_005668	Hs.308628	<i>ST8SIA4</i>	5q21	-2.5	-2.6	-2.5	-2.7
230261_at	AA552969	Hs.308628	<i>ST8SIA4</i>	5q21	-2.1	-2.0	-2.1	-2.1
230836_at	AI422986	Hs.308628	<i>ST8SIA4</i>	5q21	-2.2	-2.1	-2.1	-2.1
242943_at	AA352113	Hs.308628	<i>ST8SIA4</i>	5q21	-2.2	-2.2	-2.2	-2.3
202694_at	AW183478	Hs.268887	<i>STK17A</i>	7p12-p14	-2.2	-2.3	-1.7	-1.8
212625_at	NM_003765	Hs.43812	<i>STX10</i>	19p13.13	-1.7	-1.8	-1.6	-2.1
1552618_at	NM_005819	Hs.518417	<i>STX6</i>	1q25.3	-1.9	-2.2	-1.9	-1.9
244041_at	AI884934	Hs.518417	<i>STX6</i>	1q25.3	-2.1	-2.4	-2.0	-2.6
218308_at	NM_006342	Hs.104019	<i>TACC3</i>	4p16.3	-1.6	-1.8	-1.5	-2.0

228867_at	BE541548	Hs.530538	<i>TATDN3</i>	1q32.3	-2.0	-1.6	-1.7	-1.5
1569566_at	BC028196	Hs.176503	<i>TBC1D1</i>	4p14	-1.7	-1.8	-1.7	-2.5
208944_at	D50683	Hs.82028	<i>TGFBR2</i>	3p22	-2.0	-1.8	-2.0	-1.5
207334_s_at	NM_003242	Hs.82028	<i>TGFBR2</i>	3p22	-2.4	-2.0	-2.4	-1.9
203887_s_at	NM_000361	Hs.2030	<i>THBD</i>	20p12-cen	-2.5	-2.6	-1.8	-1.1
203888_at	NM_000361	Hs.2030	<i>THBD</i>	20p12-cen	-2.7	-2.5	-1.7	-1.0
237252_at	AW119113	Hs.2030	<i>THBD</i>	20p12-cen	-2.4	-1.6	-1.6	-1.5
223750_s_at	AW665250	Hs.120551	<i>TLR10</i>	4p14	-1.9	-1.8	-2.5	-2.4
207446_at	NM_006068	Hs.366986	<i>TLR6</i>	4p14	-1.7	-1.9	-1.9	-2.0
220832_at	NM_016610	Hs.272410	<i>TLR8</i>	Xp22	-1.7	-2.0	-1.8	-2.0
217979_at	NM_014399	Hs.364544	<i>TM4SF13</i>	7p21.1	-1.6	-1.6	-2.6	-3.3
233217_at	AV741679	Hs.283934	<i>TM4SF16</i>	19p13.2	-1.9	-1.9	-2.2	-2.1
224321_at	AB004064	Hs.144513	<i>TMEFF2</i>	2q32.3	1.1	1.1	2.5	-5.9
230323_s_at	AW242836	Hs.504301	<i>TMEM45B</i>	11q24.3	-2.0	-1.9	-1.9	-2.0
214329_x_at	AW474434	Hs.478275	<i>TNFSF10</i>	3q26	-2.1	-1.5	-1.7	-1.3
214964_at	AA554430	Hs.410404	<i>TNRC18</i>	7p22.1	-2.2	-2.3	-1.9	-2.1
1556389_at	AF161347	Hs.414099	<i>TNRC5</i>	6pter-p12.1	-1.5	-1.5	-1.8	-2.2
209344_at	BC002827	Hs.466088	<i>TPM4</i>	19p13.1	-1.2	-1.2	-2.0	-2.4
238044_at	AW002073	Hs.336810	<i>TRIM8</i>	10q24.3	-1.8	-2.2	-1.6	-2.1
221012_s_at	NM_030912	Hs.336810	<i>TRIM8</i>	10q24.3	-2.4	-2.5	-2.0	-2.5
223131_s_at	AI925572	Hs.336810	<i>TRIM8</i>	10q24.3	-2.0	-2.1	-1.8	-2.2
223132_s_at	AF220034	Hs.336810	<i>TRIM8</i>	10q24.3	-2.2	-2.5	-1.8	-2.6
207001_x_at	NM_004089	Hs.522074	<i>TSC22D3</i>	Xq22.3	-1.7	-1.6	-2.3	-1.9
203246_s_at	NM_006545	Hs.437083	<i>TUSC4</i>	3p21.3	-2.5	-2.4	-2.1	-2.0
1556338_at	BM353142	Hs.154320	<i>UBE1C</i>	3p24.3-p13	-2.1	-1.7	-1.3	-1.4
226752_at	AI816071	Hs.356108	<i>UNQ1912</i>	5q21.1	-2.6	-2.8	-2.2	-2.4
231697_s_at	AV660825	Hs.444569	<i>VMP1</i>	17q23.2	-2.1	-2.1	-1.5	-2.1
1553513_at	NM_078625	Hs.183656	<i>VNN3</i>	6q23-q24	-2.0	-1.9	-2.2	-1.9
1553514_a_at	NM_078625	Hs.183656	<i>VNN3</i>	6q23-q24	-1.9	-1.8	-2.5	-2.0
224789_at	AL555107	Hs.493750	<i>WDR40A</i>	9p13.3	-2.1	-1.8	-1.5	-1.4
217781_s_at	NM_022473	Hs.511143	<i>ZFP106</i>	15q15.1	-1.9	-2.0	-1.5	-1.8
201367_s_at	AI356398	Hs.503093	<i>ZFP36L2</i>	2p22.3-p21	-2.0	-1.9	-1.8	-1.9
201369_s_at	NM_006887	Hs.503093	<i>ZFP36L2</i>	2p22.3-p21	-1.8	-2.1	-1.4	-2.1
226787_at	BF966015	Hs.370473	<i>ZNF18</i>	17p11.2	-1.7	-2.1	-1.6	-1.6
233992_x_at	AK026891	Hs.549305	<i>ZNF445</i>	3p21.32	1.1	-1.0	1.2	-2.3
234982_at	BF577193	Hs.379548	<i>ZNF650</i>	2q31.1	-1.4	-1.3	-2.0	-1.3
243495_s_at	AL036450	Hs.463375	<i>ZNF652</i>	17q21.32	-2.1	-2.2	-2.1	-2.3
200808_s_at	NM_003461	Hs.490415	<i>ZYX</i>	7q32	-1.5	-1.6	-1.5	-2.0
1555311_at	AF125104	---	---	20q13.32	-2.4	-1.7	-1.4	-1.2
1556332_at	CA313430	Hs.270479	---	1p35.1	-2.0	-2.0	-1.8	-1.9
1557383_a_at	AI925316	Hs.523897	---	1p35.3	-3.0	-2.5	-1.9	-2.2
1558397_at	BF976693	Hs.376675	---	17q23.3	-3.3	-3.8	-3.0	-3.3
1562289_at	AL834519	---	---	7p14.1	-2.4	-2.2	-1.5	-2.1
1568915_at	BC033528	Hs.506258	---	3p21.31	-2.0	-1.5	1.1	-1.8
1569551_at	BC012936	Hs.561137	---	---	-2.0	-1.8	-1.9	-2.3
212993_at	AA114166	Hs.531457	---	9q34.3	-2.2	-2.2	-2.1	-2.8
215182_x_at	AL050122	Hs.274511	---	22q12.3	-1.3	-1.4	-1.3	-3.2

220711_at	NM_024978	---	---	5q35.3	-2.1	-2.1	-1.5	-1.7
221419_s_at	NM_013307	---	---	16p11.2	1.1	-1.0	1.2	-3.1
226136_at	N32834	---	---	12q21.1	-1.9	-2.0	-2.5	-2.4
227747_at	AA772172	---	---	11q23.3	-2.2	-1.8	-1.9	-1.5
228088_at	AI092265	Hs.30977	---	2q31.2	-1.9	-2.1	-1.6	-2.0
228412_at	AI991451	Hs.549594	---	2q24.2	-2.3	-2.1	-1.8	-2.0
228932_at	BE467383	Hs.527515	---	1p34.3	-1.5	-2.0	-1.6	-1.3
229040_at	AW303397	Hs.549607, Hs.551744	---	21q22.3	-1.6	-1.3	-1.4	-2.1
229287_at	BE326214	Hs.446559	---	14q24.2	-1.8	-1.8	-1.7	-2.0
229543_at	AV734646	---	---	6q22.1	-2.3	-2.0	-2.0	-1.8
229635_at	AW043859	Hs.235795	---	4q21.21	-1.4	-1.5	-1.6	-2.1
229670_at	BF056369	Hs.180284	---	1q24.2	-1.9	-2.2	-1.5	-1.6
229934_at	N39230	Hs.38218	---	Xq12	-3.7	-2.7	-2.3	-2.0
229968_at	AA504245	Hs.264347	---	4p14	-2.0	-2.1	-1.8	-1.9
230444_at	AI697756	Hs.444831	---	8q13.1	-2.0	-2.2	-1.6	-1.7
230913_at	BE674309	Hs.418279	---	21q22.3	-1.6	-1.9	-1.9	-2.2
232569_at	AK024255	Hs.162990	---	7p13	-2.0	-2.3	-1.7	-2.3
232876_at	AK025534	Hs.550197	---	6p21.31	-1.9	-2.1	-1.3	-2.1
233591_at	AK026751	Hs.306876	---	12q12	-2.7	-2.2	-2.3	-2.4
234644_x_at	AK026079	Hs.545497	---	8p21.3	-1.5	-1.8	-1.3	-2.2
235360_at	AW967747	Hs.159188	---	2q33.3	-1.9	-2.1	-1.3	-1.4
236065_at	BF431214	Hs.443967	---	12q12	-2.2	-1.9	-2.0	-2.4
236180_at	W57613	Hs.79856	---	12p13.31	-2.0	-2.2	-1.9	-2.0
236280_at	AI225238	Hs.445500	---	Xq21.1	-2.1	-1.7	-2.0	-1.5
238050_at	R94785	Hs.561326	---	4q21.21	-1.6	-1.7	-2.0	-1.8
238712_at	BF801735	Hs.439558	---	3p13	-2.7	-2.2	-2.0	-2.2
238725_at	AW392551	Hs.180559	---	5q23.3	-2.1	-1.5	-1.5	-1.2
238999_at	AI610347	Hs.550874	---	12q14.1	-1.5	-1.8	-1.7	-2.1
239021_at	BF512068	Hs.552072	---	4p14	-2.3	-2.3	-1.7	-2.1
239294_at	AA810265	Hs.561747	---	7q22.3	-2.0	-1.9	-1.8	-1.7
239307_at	AA781173	---	---	16p13.11	-1.8	-2.2	-2.1	-2.2
240128_at	H94876	Hs.194290	---	7p14.3	-2.7	-2.2	-1.8	-1.9
240948_at	T79640	Hs.494960	---	9q33.1	-1.8	-2.3	-1.4	-2.0
243699_at	BG432887	Hs.442789	---	2p14	-1.6	-1.6	-2.1	-2.4

Transcript levels in 9 (360 min) or 10 (180 min) healthy control donors (Healthy) were compared with those in 7 patients with hyper-IgE recurrent infection (Job's) syndrome using Affymetrix HU133 Plus 2.0 microarrays as described in Methods. Results are the average fold-change compared with healthy control donors.

Supplemental Table 5. Transcripts up- and down-regulated in PBMCs from healthy subjects and patients with hyper-IgE recurrent infection (Job's) syndrome following exposure to phagocytic stimuli.

Probeset	Public ID	UniGene#	Entrez Gene	Chromosome	Healthy	Job's
Up-Regulated						
226893_at	AW173164	Hs.159472	ABL2	1q24-q25	4.7	3.8
231907_at	AK025877	Hs.159472	ABL2	1q24-q25	2.9	2.8
213497_at	AL050374	Hs.23361	ABTB2	11p13	2.1	2.5
201963_at	NM_021122	Hs.406678	ACSL1	4q34-q35	2.1	1.7
207275_s_at	NM_001995	Hs.406678	ACSL1	4q34-q35	3.0	2.5
206134_at	NM_014479	Hs.521459	ADAMDEC1	8p21.2	7.2	5.6
209320_at	AF033861	Hs.467898	ADCY3	2p24-p22	2.0	2.2
209321_s_at	AF033861	Hs.467898	ADCY3	2p24-p22	3.0	3.3
209122_at	BC005127	Hs.3416	ADFP	9p22.1	3.7	1.8
202912_at	NM_001124	Hs.441047	ADM	11p15.4	3.6	2.0
205013_s_at	NM_000675	Hs.197029	ADORA2A	22q11.23	2.3	2.9
205891_at	NM_000676	Hs.167046	ADORA2B	17p12-p11.2	4.0	3.1
239439_at	BF963382	Hs.519313	AFF4	5q31	2.1	1.5
204348_s_at	NM_013410	Hs.10862	AK3L1	1p31.3	2.2	3.2
225342_at	AK026966	Hs.10862	AK3L1	9pter-p13	1.7	2.3
202760_s_at	NM_007203	Hs.259461	AKAP2, PALM2-AKAP2	9q31-q33	2.6	2.1
205633_s_at	NM_000688	Hs.476308	ALAS1	3p21.1	1.9	2.2
207992_s_at	NM_000480	Hs.501890	AMPD3	11p15	1.8	2.0
223251_s_at	BC001727	Hs.525163	ANKRD10	13q34	2.1	2.5
213005_s_at	D79994	Hs.493272	ANKRD15	9p24.3	4.5	3.5
239196_at	AI097229	Hs.217484	ANKRD22	10q23.31	2.2	2.2
213035_at	AI081194	Hs.335239	ANKRD28	3p25.1	2.1	2.0
229307_at	N32051	Hs.335239	ANKRD28	3p25.1	2.1	2.0
205239_at	NM_001657	Hs.270833	AREG	4q13-q21	2.0	1.9
202211_at	BC005122	Hs.13014	ARFGAP3	22q13.2-q13.3	2.1	1.9
222442_s_at	AW055237	Hs.250009	ARL10C	3p26.1	2.3	1.9
205020_s_at	NM_005738	Hs.245540	ARL4	7p21-p15.3	2.3	2.8
226345_at	AW270158	Hs.25362	ARL8	10p12.31	2.0	2.0
242727_at	BG032269	Hs.25362	ARL8	10p12.31	3.2	3.2
218694_at	NM_016608	Hs.9728	ARMCX1	Xq21.33-q22.2	2.9	2.8
225283_at	AV701177	Hs.6093	ARRDC4	15q26.3	4.6	3.7
209135_at	AF289489	Hs.332422	ASPH	8q12.1	3.2	2.7
210896_s_at	AF306765	Hs.332422	ASPH	8q12.1	2.8	2.5
242738_s_at	BG402859	Hs.451353	ATBF1	---	2.9	2.4
1554980_a_at	AB066566	Hs.460	ATF3	1q32.3	10.0	7.0
202672_s_at	NM_001674	Hs.460	ATF3	1q32.3	9.9	5.5
201242_s_at	BC000006	Hs.291196	ATP1B1	1q24	2.6	2.4
201243_s_at	NM_001677	Hs.291196	ATP1B1	1q24	1.9	2.4
1553155_x_at	NM_152565	Hs.436360	ATP6V0D2	---	2.3	2.6
201971_s_at	NM_001690	Hs.477155	ATP6V1A	3q13.2-q13.31	2.1	1.7
221504_s_at	AF112204	Hs.491737	ATP6V1H	8p22-q22.3	2.9	2.6
225557_at	AI091372	Hs.370950	AXUD1	3p22	2.6	2.5
1554835_a_at	BC028058	Hs.208267	B3GNT5	3q28	4.3	3.5
225612_s_at	BE672260	Hs.208267	B3GNT5	3q28	2.5	2.3
1559391_s_at	AI084451	Hs.370487	B4GALT5	20q13.1-q13.2	2.1	2.6
221484_at	BF691447	Hs.370487	B4GALT5	20q13.1-q13.2	2.2	2.3
221485_at	AL035683	Hs.370487	B4GALT5	20q13.1-q13.2	2.7	2.2
219966_x_at	NM_017869	Hs.461705	BANP	16q24	2.2	2.2

228928_x_at	AL157429	Hs.461705	<i>BANP</i>	16q24	2.3	2.3
233186_s_at	AK001039	Hs.461705	<i>BANP</i>	16q24	2.2	2.3
214390_s_at	AI652662	Hs.438993	<i>BCAT1</i>	12pter-q12	2.0	1.6
244035_at	BF003032	Hs.150749	<i>BCL2</i>	18q21.33	1.9	2.3
205681_at	NM_004049	Hs.227817	<i>BCL2A1</i>	15q24.3	2.3	1.8
201169_s_at	BG326045	Hs.171825	<i>BHLHB2</i>	3p26	2.3	2.6
201170_s_at	NM_003670	Hs.171825	<i>BHLHB2</i>	3p26	2.1	2.0
229437_at	BG231961	Hs.388313	<i>BIC</i>	21q21.3	3.8	3.5
206536_s_at	U32974	Hs.356076	<i>BIRC4</i>	Xq25	2.3	2.0
202201_at	NM_000713	Hs.515785	<i>BLVRB</i>	19q13.1-q13.2	2.4	1.9
1561890_at	BC037922	Hs.385493	<i>C10orf128</i>	10q11.23	2.7	2.2
228372_at	AW204712	Hs.385493	<i>C10orf128</i>	10q11.23	2.3	1.8
213246_at	AI346504	Hs.275352	<i>C14orf109</i>	14q32.13	6.4	4.4
224469_s_at	BC006173	Hs.317821	<i>C14orf151</i>	14q32.33	1.6	2.0
219526_at	NM_024644	Hs.509916	<i>C14orf169</i>	14q24.3	2.4	2.4
219496_at	NM_023016	Hs.355455	<i>C2orf26</i>	2q13	2.7	2.2
227034_at	BE669553	Hs.355455	<i>C2orf26</i>	2q13	2.7	2.1
217767_at	NM_000064	Hs.529053	<i>C3</i>	19p13.3-p13.2	2.1	2.0
1554486_a_at	BC009205	Hs.551569	<i>C6orf114</i>	6p23	5.3	3.5
227368_at	AW009630	Hs.485915	<i>C6orf166</i>	6q15	2.5	2.2
1569403_at	BC016631	Hs.199360	<i>C7orf10</i>	7p14.1	7.3	5.4
227534_at	AI655189	Hs.44640	<i>C9orf21</i>	9q22.32	2.3	2.1
216598_s_at	S69738	Hs.303649	<i>CCL2</i>	17q11.2-q21.1	18.7	15.4
205476_at	NM_004591	Hs.75498	<i>CCL20</i>	2q33-q37	6.2	13.3
205114_s_at	NM_002983	Hs.514107	<i>CCL3, CCL3L1, MGC12815</i>	17q11-q21, 17q21.1	3.9	2.7
204103_at	NM_002984	Hs.75703	<i>CCL4</i>	17q12	4.4	3.8
208075_s_at	NM_006273	Hs.251526	<i>CCL7</i>	17q11.2-q12	5.9	5.8
205098_at	AI421071	Hs.301921	<i>CCR1</i>	3p21	2.6	1.7
205099_s_at	NM_001295	Hs.301921	<i>CCR1</i>	3p21	2.7	1.9
205271_s_at	NM_012119	Hs.522274	<i>CCRK</i>	9q22.1	3.6	3.9
211434_s_at	AF015524	Hs.458436	<i>CCRL2</i>	3p21	10.2	6.9
226545_at	AL110152	Hs.399891	<i>CD109</i>	6q13	2.2	2.2
229900_at	AL576908	Hs.399891	<i>CD109</i>	6q13	2.7	2.5
239719_at	BF978262	Hs.399891	<i>CD109</i>	6q13	3.3	2.9
207840_at	NM_007053	Hs.488237	<i>CD160</i>	1q21.1	2.7	2.4
203645_s_at	NM_004244	Hs.504641	<i>CD163</i>	12p13.3	3.0	1.4
215049_x_at	Z22969	Hs.504641	<i>CD163</i>	12p13.3	3.1	1.4
223834_at	AF233516	Hs.521989	<i>CD274</i>	9p24	3.3	2.8
203507_at	NM_001251	Hs.246381	<i>CD68</i>	17p13	2.0	1.6
215925_s_at	AF283777	Hs.116481	<i>CD72</i>	9p13.3	2.0	2.1
203213_at	AL524035	Hs.334562	<i>CDC2</i>	10q21.1	2.0	2.4
210559_s_at	D88357	Hs.334562	<i>CDC2</i>	10q21.1	1.9	2.2
209286_at	AI754416	Hs.369574	<i>CDC42EP3</i>	2p21	5.8	5.3
209287_s_at	AF104857	Hs.369574	<i>CDC42EP3</i>	2p21	6.7	5.3
209288_s_at	AL136842	Hs.369574	<i>CDC42EP3</i>	2p21	4.7	4.2
225685_at	AI801777	Hs.369574	<i>CDC42EP3</i>	2p21	5.6	4.5
202284_s_at	NM_000389	Hs.370771	<i>CDKN1A</i>	6p21.2	2.7	2.1
225789_at	BE876194	Hs.195048	<i>CENTG3</i>	7q36.1	2.0	2.0
209939_x_at	AF005775	Hs.390736	<i>CFLAR</i>	2q33-q34	1.9	2.0
210563_x_at	U97075	Hs.390736	<i>CFLAR</i>	2q33-q34	2.1	2.3
204233_s_at	AI991328	Hs.77221	<i>CHKA</i>	11q13.2	3.2	2.8
206756_at	NM_019886	Hs.138155	<i>CHST7</i>	Xp11.23	4.9	3.9
204170_s_at	NM_001827	Hs.83758	<i>CKS2</i>	9q22	3.2	3.0

219340_s_at	AF123759	Hs.127675	CLN8	8p23	3.7	3.2
222874_s_at	AF123757	Hs.127675	CLN8	8p23	3.4	3.5
223912_s_at	AF123758	Hs.127675	CLN8	8p23	3.2	2.8
209833_at	U79115	Hs.38533	CRADD	12q21.33-q23.1	2.2	2.3
201200_at	NM_003851	Hs.5710	CREG1	1q24	2.1	1.6
206914_at	NM_019604	Hs.159523	CRTAM	11q22-q23	7.1	5.2
209716_at	M37435	Hs.173894	CSF1	1p21-p13	3.8	3.3
201201_at	NM_000100	Hs.695	CSTB	21q22.3	2.3	2.0
236449_at	AI885390	Hs.695	CSTB	21q22.3	3.0	2.8
217127_at	AL354872	Hs.19904	CTH	1p31.1	2.1	3.1
202087_s_at	NM_001912	Hs.418123	CTSL	9q21-q22	3.0	2.4
1563445_x_at	L25629	---	CTSLL3	10q22.3-q23.1	4.7	4.0
204533_at	NM_001565	Hs.413924	CXCL10	4q21	5.9	6.2
209774_x_at	M57731	Hs.75765	CXCL2	4q21	2.5	2.0
207850_at	NM_002090	Hs.89690	CXCL3	4q21	2.1	2.0
205749_at	NM_000499	Hs.72912	CYP1A1	15q22-q24	4.1	3.6
202434_s_at	N21019	Hs.154654	CYP1B1	2p21	2.6	1.5
201278_at	N21202	Hs.481980	DAB2	5p13	3.2	2.7
201279_s_at	BC003064	Hs.481980	DAB2	5p13	3.6	3.0
201280_s_at	NM_001343	Hs.481980	DAB2	5p13	2.5	2.1
210757_x_at	AF188298	Hs.481980	DAB2	5p13	2.6	2.1
224827_at	AK022894	Hs.179852	DC-UbP	5q35.1	3.5	3.4
224834_at	BF243404	Hs.179852	DC-UbP	5q35.1	2.3	2.5
209383_at	BC003637	Hs.505777	DDIT3	12q13.1-q13.2	1.9	2.2
203695_s_at	NM_004403	Hs.520708	DFNA5	7p15	3.3	3.4
230380_at	AW235671	Hs.245798	DKFZP564I0422	12q21.1	3.0	3.2
231412_at	H04388	Hs.150298	DKFZp686L14188	8q21.3	1.8	2.0
203810_at	BG252490	Hs.380282	DNAJB4	1p31.1	2.8	2.7
203811_s_at	NM_007034	Hs.380282	DNAJB4	1p31.1	2.4	2.3
243918_at	AI459554	Hs.407709	DRE1	3q27.1	6.7	5.9
241068_at	BF510881	Hs.279583	DREV1	16p13-p12	2.6	2.1
237890_at	AW026356	Hs.519583	DTNBP1	6p22.3	16.9	16.0
225415_at	AA577672	Hs.518201	DTX3L	3q21.1	2.1	1.6
201044_x_at	AA530892	Hs.171695	DUSP1	5q34	4.2	3.5
201536_at	AL048503	Hs.181046	DUSP3	17q21	2.5	2.3
201537_s_at	BC002682	Hs.181046	DUSP3	17q21	3.1	2.5
201538_s_at	NM_004090	Hs.181046	DUSP3	17q21	2.3	2.3
209457_at	U16996	Hs.2128	DUSP5	10q25	3.6	3.5
226952_at	AU149385	Hs.474479	EAF1	3p25.1	2.7	1.8
228176_at	AA534817	---	EDG3	9q22.1-q22.2	2.1	1.7
222802_at	J05008	Hs.511899	EDN1	6p24.1	4.0	4.0
205249_at	NM_000399	Hs.1395	EGR2	10q21.1	3.8	2.5
208112_x_at	NM_006795	Hs.523774	EHD1	11q13	1.4	2.2
209037_s_at	AW182860	Hs.523774	EHD1	11q13	1.4	2.1
222221_x_at	AY007161	Hs.523774	EHD1	11q13	1.5	2.2
218696_at	NM_004836	Hs.434326	EIF2AK3	2p12	2.7	2.5
201436_at	AI742789	Hs.249718	EIF4E	4q21-q25	3.0	3.0
237718_at	AA913840	Hs.249718	EIF4E	4q21-q25	11.8	7.3
214446_at	NM_012081	Hs.192221	ELL2	5q15	1.6	2.3
235592_at	AW960145	Hs.192221	ELL2	5q15	1.3	2.6
240038_at	AW057518	Hs.192221	ELL2	5q15	1.6	2.4
244026_at	BF063657	Hs.192221	ELL2	5q15	1.5	2.3
227180_at	AW138767	Hs.274256	ELOVL7	5q12.1	3.4	3.2

1564796_at	BC017854	Hs.436298	<i>EMP1</i>	12p12.3	2.6	3.5
201324_at	NM_001423	Hs.436298	<i>EMP1</i>	12p12.3	2.2	1.6
201325_s_at	NM_001423	Hs.436298	<i>EMP1</i>	12p12.3	2.2	1.8
213895_at	BF445047	Hs.436298	<i>EMP1</i>	12p12.3	2.6	2.2
238633_at	W93523	Hs.167805	<i>EPC1</i>	10p11	1.8	2.1
202609_at	NM_004447	Hs.26139	<i>EPS8</i>	12q13	2.4	1.6
239979_at	BE645480	Hs.546467	<i>EPSTI1</i>	13q13.3	2.0	1.6
202776_at	NM_014597	Hs.85769	<i>ERBP</i>	1p22.1	2.1	2.0
235745_at	AV704183	Hs.133982	<i>ERN1</i>	17q24.2	2.5	3.3
239045_at	AW194689	Hs.133982	<i>ERN1</i>	17q24.2	1.7	2.1
224454_at	BC006111	Hs.240056	<i>ETNK1</i>	12p12.1	2.6	2.8
201328_at	AL575509	Hs.517296	<i>ETS2</i>	21q22.3 21q22.2	7.0	6.7
201329_s_at	NM_005239	Hs.517296	<i>ETS2</i>	21q22.3 21q22.2	5.0	4.5
204363_at	NM_001993	Hs.62192	<i>F3</i>	1p22-p21	15.6	12.5
218627_at	NM_018370	Hs.525634	<i>FLJ11259</i>	12q23.3	2.6	2.4
201818_at	NM_024830	Hs.368853	<i>FLJ12443</i>	5p15.33	2.1	1.9
228745_at	AI376997	Hs.482301	<i>FLJ13611</i>	5q12.3	2.1	2.5
222496_s_at	AW241742	Hs.518727	<i>FLJ20273</i>	4p13-p12	2.2	1.8
238829_at	AI540253	Hs.550536	<i>FLJ21439</i>	15q14	2.1	1.8
225922_at	BE501838	Hs.377588	<i>FLJ25371</i>	4q32.1	9.6	6.0
225924_at	AI478634	Hs.377588	<i>FLJ25371</i>	4q32.1	10.0	7.2
1552711_a_at	NM_144607	Hs.27475	<i>FLJ32499</i>	17p13.1	2.3	1.5
244322_at	AW362008	Hs.150556	<i>FLJ43663</i>	7q32.3	3.5	3.1
226497_s_at	AA149648	Hs.507621	<i>FLT1</i>	13q12	5.2	3.9
226498_at	AA149648	Hs.507621	<i>FLT1</i>	13q12	7.6	5.8
215910_s_at	AL137000	Hs.508010	<i>FNDC3A</i>	13q14.2	2.1	1.7
202768_at	NM_006732	Hs.75678	<i>FOSB</i>	19q13.32	4.8	5.5
204420_at	BG251266	Hs.283565	<i>FOSL1</i>	11q13	5.7	5.8
213524_s_at	NM_015714	Hs.432132	<i>G0S2</i>	1q32.2-q41	2.3	4.0
203725_at	NM_001924	Hs.80409	<i>GADD45A</i>	1p31.2-p31.1	1.9	2.4
207574_s_at	NM_015675	Hs.110571	<i>GADD45B</i>	19p13.3	5.6	6.5
209304_x_at	AF087853	Hs.110571	<i>GADD45B</i>	19p13.3	6.4	7.0
209305_s_at	AF078077	Hs.110571	<i>GADD45B</i>	19p13.3	7.1	6.8
208693_s_at	D30658	Hs.404321	<i>GARS</i>	7p15	2.1	1.9
238756_at	AI860012	Hs.20575	<i>GAS2L3</i>	12q23.1	4.9	3.4
202269_x_at	BC002666	Hs.62661	<i>GBP1</i>	1p22.2	3.9	3.1
202270_at	NM_002053	Hs.62661	<i>GBP1</i>	1p22.2	3.1	2.3
231577_s_at	AW014593	Hs.62661	<i>GBP1</i>	1p22.2	3.6	2.9
231578_at	AW014593	Hs.62661	<i>GBP1, LOC400759</i>	1p22.2	3.8	4.1
202748_at	NM_004120	Hs.386567	<i>GBP2</i>	1p22.2	2.1	1.8
242907_at	BF509371	Hs.386567	<i>GBP2</i>	1p22.2	2.4	2.4
235175_at	BG260886	Hs.409925	<i>GBP4</i>	1p22.2	2.1	1.5
229625_at	BG545653	Hs.513726	<i>GBP5</i>	1p22.2	1.9	2.1
238581_at	BG271923	Hs.513726	<i>GBP5</i>	1p22.2	2.1	2.2
202922_at	BF676980	Hs.271264	<i>GCLC</i>	6p12	2.1	2.1
202923_s_at	NM_001498	Hs.271264	<i>GCLC</i>	6p12	2.0	1.8
203925_at	NM_002061	Hs.315562	<i>GCLM</i>	1p22.1	3.7	3.3
234986_at	AA630626	Hs.315562	<i>GCLM</i>	1p22.1	3.7	3.2
236140_at	AI753488	Hs.315562	<i>GCLM</i>	1p22.1	3.8	3.7
204472_at	NM_005261	Hs.345139	<i>GEM</i>	8q13-q21	11.3	10.4
219821_s_at	NM_018988	Hs.484686	<i>GFOD1</i>	6pter-p22.1	2.9	2.6
223278_at	M86849	Hs.524894	<i>GJB2</i>	13q11-q12	14.9	15.2
214430_at	NM_000169	Hs.69089	<i>GLA</i>	Xq22	4.2	3.2

202382_s_at	NM_005471	Hs.278500	<i>GNPDA1</i>	5q21	3.2	2.2
225447_at	AA613031	Hs.148266	<i>GPD2</i>	2q24.1	2.1	1.7
1554018_at	BC011595	Hs.190495	<i>GPNMB</i>	7p15	8.2	3.7
201141_at	NM_002510	Hs.190495	<i>GPNMB</i>	7p15	3.9	2.1
205220_at	NM_006018	Hs.458425	<i>GPR109B</i>	12q24.31	5.2	3.4
218855_at	NM_016372	Hs.6418	<i>GPR175</i>	3q21.2	2.3	2.0
223767_at	AF237762	Hs.306199	<i>GPR84</i>	12q13.13	1.9	2.2
235102_x_at	AI684439	Hs.170600	<i>GRAP</i>	17p11.2	2.5	2.7
212090_at	AL571424	Hs.339697	<i>GRINA</i>	8q24.3	1.6	2.5
227262_at	BE348293	Hs.447530	<i>HAPLN3</i>	15q26.1	2.0	1.9
1554285_at	AF450243	Hs.155111	<i>HAVCR2</i>	5q33.3	2.0	1.6
1555628_a_at	BC020843	Hs.155111	<i>HAVCR2</i>	5q33.3	2.3	1.8
203821_at	NM_001945	Hs.799	<i>HBEGF</i>	5q23	2.2	2.5
38037_at	M60278	Hs.799	<i>HBEGF</i>	5q23	1.8	2.2
203394_s_at	BE973687	Hs.250666	<i>HES1</i>	3q28-q29	59.3	35.5
203395_s_at	NM_005524	Hs.250666	<i>HES1</i>	3q28-q29	29.1	17.3
227347_x_at	NM_021170	Hs.154029	<i>HES4</i>	1p36.33	7.5	7.6
44783_s_at	R61374	Hs.234434	<i>HEY1</i>	8q21	1.8	2.4
1560485_at	BC028111	Hs.549037	<i>HIVEP1</i>	6p24-p22.3	1.8	2.1
202934_at	AI761561	Hs.406266	<i>HK2</i>	2p13	3.3	1.6
203665_at	NM_002133	Hs.517581	<i>HMOX1</i>	22q12 22q13.1	2.5	1.3
200799_at	NM_005345	Hs.520028	<i>HSPA1A</i>	6p21.3	2.4	2.5
200800_s_at	NM_005345	Hs.520028	<i>HSPA1A, HSPA1B</i>	6p21.3	3.9	5.3
202581_at	NM_005346	Hs.274402	<i>HSPA1B</i>	6p21.3	3.9	6.0
202637_s_at	AI608725	Hs.515126	<i>ICAM1</i>	19p13.3-p13.2	2.3	2.3
202638_s_at	NM_000201	Hs.515126	<i>ICAM1</i>	19p13.3-p13.2	2.7	2.3
215485_s_at	AA284705	Hs.515126	<i>ICAM1</i>	19p13.3-p13.2	1.9	2.1
201566_x_at	D13891	Hs.180919	<i>ID2 /// ID2B</i>	2p25 /// 3p21.1	2.4	2.1
242255_at	R49102	Hs.283652	<i>IDI1</i>	10p15.3	2.1	2.3
210354_at	M29383	Hs.856	<i>IFNG</i>	12q14	5.6	6.3
201392_s_at	BG031974	Hs.487062	<i>IGF2R</i>	6q26	2.7	2.2
201393_s_at	NM_000876	Hs.487062	<i>IGF2R</i>	6q26	2.4	2.1
206420_at	NM_005849	Hs.530902	<i>IGSF6</i>	16p12-p13	2.6	2.3
207433_at	NM_000572	Hs.193717	<i>IL10</i>	1q31-q32	2.7	4.2
210118_s_at	M15329	Hs.1722	<i>IL1A</i>	2q14	3.7	3.8
212657_s_at	U65590	Hs.81134	<i>IL1RN</i>	2q14.2	2.2	2.2
212659_s_at	AW083357	Hs.81134	<i>IL1RN</i>	2q14.2	4.6	4.2
216243_s_at	BE563442	Hs.81134	<i>IL1RN</i>	2q14.2	4.6	3.9
205207_at	NM_000600	Hs.512234	<i>IL6</i>	7p21	5.5	6.2
205945_at	NM_000565	Hs.135087	<i>IL6R</i>	1q21	2.6	2.1
217489_s_at	S72848	Hs.135087	<i>IL6R</i>	1q21	3.1	2.3
226333_at	AV700030	Hs.135087	<i>IL6R</i>	1q21	2.4	1.7
237464_at	AI241501	Hs.448808	<i>IMAA</i>	16p12	2.0	2.3
210029_at	M34455	Hs.840	<i>INDO</i>	8p12-p11	2.6	1.6
204926_at	NM_002192	Hs.28792	<i>INHBA</i>	7p15-p13	13.7	11.0
210511_s_at	M13436	Hs.28792	<i>INHBA</i>	7p15-p13	36.2	38.3
227140_at	AI343467	Hs.28792	<i>INHBA</i>	7p15-p13	30.9	26.7
201625_s_at	BE300521	Hs.520819	<i>INSIG1</i>	7q36	2.4	2.2
201627_s_at	NM_005542	Hs.520819	<i>INSIG1</i>	7q36	2.0	1.8
223309_x_at	BG025248	Hs.418133	<i>IPLA2(GAMMA)</i>	7q31	2.6	2.3
223310_x_at	AF217519	Hs.418133	<i>IPLA2(GAMMA)</i>	7q31	2.1	1.7
223982_s_at	AB041261	Hs.418133	<i>IPLA2(GAMMA)</i>	7q31	2.2	1.8
1553740_a_at	NM_001570	Hs.449207	<i>IRAK2</i>	3p25.3	2.2	2.0

231779_at	AI246590	Hs.449207	IRAK2	3p25.3	2.4	2.5
202531_at	NM_002198	Hs.436061	IRF1	5q31.1	3.1	3.0
209184_s_at	BF700086	Hs.442344	IRS2	13q34	2.8	2.2
209185_s_at	AF073310	Hs.442344	IRS2	13q34	2.9	2.0
209098_s_at	U61276	Hs.224012	JAG1	20p12.1-p11.23	2.7	2.9
209099_x_at	U73936	Hs.224012	JAG1	20p12.1-p11.23	4.7	3.0
216268_s_at	U77914	Hs.224012	JAG1	20p12.1-p11.23	4.4	3.3
232835_at	AA533080	Hs.269059	JARID2	6p24-p23	1.7	2.2
1556066_at	AI830331	Hs.549119	JMJD3	17p13.1	2.0	2.2
1556067_a_at	AI830331	Hs.549119	JMJD3	17p13.1	2.0	2.1
213146_at	AA521267	Hs.549119	JMJD3	17p13.1	2.0	2.1
241985_at	AI814405	Hs.482605	JMY	5q14.1	1.9	2.1
201465_s_at	BC002646	Hs.525704	JUN	1p32-p31	3.0	2.3
201466_s_at	NM_002228	Hs.525704	JUN	1p32-p31	3.3	2.5
239835_at	AA669114	Hs.116665	KBTBD8	3p14	4.5	3.6
216913_s_at	AK021460	Hs.434251	KIAA0690	10q24.1	2.9	1.8
203321_s_at	AK022688	Hs.131915	KIAA0863	18q23	2.0	1.9
203322_at	AU145934	Hs.131915	KIAA0863	18q23	2.1	1.9
1554131_at	BC030528	Hs.461988	KIAA1128	10q23.1	1.7	2.5
230492_s_at	BE328402	Hs.472040	KIAA1434	20p12.3	2.1	1.9
1569352_at	BC030251	Hs.377588	KIAA1450	4q32.1	18.1	13.2
226460_at	AB040883	Hs.377588	KIAA1450	4q32.1	11.6	7.9
1559060_a_at	BF677986	Hs.483329	KIAA1961	5q23.3	4.7	3.5
202393_s_at	NM_005655	Hs.435001	KLF10	8q22.2	3.1	2.5
244447_at	AW292830	Hs.435001	KLF10	8q22.2	2.0	2.2
220266_s_at	NM_004235	Hs.376206	KLF4	9q31	3.5	2.4
221841_s_at	BF514079	Hs.376206	KLF4	9q31	4.1	2.6
209211_at	AF132818	Hs.508234	KLF5	13q22.1	2.1	1.7
1555832_s_at	BU683415	Hs.4055	KLF6	10p15	2.1	1.8
208960_s_at	BE675435	Hs.285313	KLF6	10p15	2.8	2.3
208961_s_at	AB017493	Hs.285313	KLF6	10p15	2.5	2.1
224606_at	BG250721	Hs.4055	KLF6	10p15	2.1	2.0
203068_at	NM_014851	Hs.7764	KLHL21	1p36.31	5.7	3.9
221985_at	AW006750	Hs.407709	KLHL24	3q27.1	2.0	1.5
221986_s_at	AW006750	Hs.407709	KLHL24	3q27.1	2.0	1.6
1555275_a_at	BC032348	Hs.333181	KLHL6	---	3.0	2.5
1560396_at	AK097976	Hs.333181	KLHL6	---	2.4	2.5
1560397_s_at	AK097976	Hs.333181	KLHL6	---	2.5	2.6
228167_at	AW574798	Hs.333181	KLHL6	---	2.2	2.0
206785_s_at	NM_002260	Hs.512576	KLRC1, KLRC2	12p13	2.4	2.0
205306_x_at	AI074145	Hs.409081	KMO	1q42-q44	4.9	3.4
205307_s_at	NM_003679	Hs.409081	KMO	1q42-q44	2.4	1.8
211138_s_at	BC005297	Hs.409081	KMO	1q42-q44	4.4	3.1
1552485_at	NM_171846	Hs.410388	LACTB	15q22.1	2.4	2.5
205569_at	NM_014398	Hs.518448	LAMP3	3q26.3-q27	2.0	1.6
217933_s_at	NM_015907	Hs.479264	LAP3	4p15.32	2.1	1.6
205269_at	AI123251	Hs.304475	LCP2	5q33.1-qter	2.1	1.8
205270_s_at	NM_005565	Hs.304475	LCP2	5q33.1-qter	2.5	2.2
244251_at	BF363430	Hs.304475	LCP2	5q33.1-qter	2.1	2.1
244556_at	AI824014	Hs.304475	LCP2	5q33.1-qter	2.2	3.3
202067_s_at	AI861942	Hs.213289	LDLR	19p13.3	1.7	2.2
1557197_a_at	AW085690	Hs.531081	LGALS3	14q21-q22	8.0	8.4
212658_at	N66633	Hs.79299	LHFPL2	5q14.1	3.0	2.6

217475_s_at	AC002073	Hs.474596	<i>LIMK2</i>	22q12.2	2.0	2.1
223800_s_at	AF288404	Hs.469633	<i>LIMS3</i>	2q14-q21	1.9	2.3
226702_at	AI742057	Hs.7155	<i>LOC129607</i>	2p25.2	2.7	1.9
235177_at	AI625022	Hs.552610	<i>LOC151194</i>	2q33.3	2.1	2.4
238422_at	T69015	Hs.516124	<i>LOC151534</i>	2p13.1	2.2	1.8
226146_at	BE503186	Hs.348292	<i>LOC255458</i>	5q35.3	2.2	1.9
1563745_a_at	AK098249	Hs.309176	<i>LOC283050</i>	10q22.3	1.8	2.1
1555847_a_at	BU617052	Hs.436426	<i>LOC284454</i>	19p13.13	2.6	2.8
232504_at	AL389942	Hs.406790	<i>LOC285628</i>	5q34	3.0	3.2
230179_at	N52572	Hs.435694	<i>LOC285812</i>	6p23	2.9	2.5
238893_at	AI377324	Hs.136888	<i>LOC338758</i>	12q21.33	2.8	2.3
240287_at	BG236136	Hs.160789	<i>LOC341720</i>	13q22.3	13.1	15.2
227099_s_at	AW276078	Hs.530443	<i>LOC387763</i>	11p11.2	5.6	7.3
1556754_at	BM666787	Hs.441971	<i>LOC399786</i>	10q22.3	5.5	2.6
1568592_at	BM976092	Hs.489254	<i>LOC400368</i>	15q21.1	2.1	1.9
237465_at	BF196943	Hs.534794	<i>LOC401151</i>	4q26	3.8	3.8
229951_x_at	H24473	Hs.549433	<i>LOC440667</i>	1q21.1	3.1	2.6
235911_at	AI885815	Hs.552645	<i>LOC440995</i>	3q29	3.9	2.8
244828_x_at	F09493	Hs.332844	<i>LOC92345</i>	4q32.2	2.4	2.2
216908_x_at	AF001549	Hs.546468	<i>LOC94431</i>	16p12.1	2.2	2.5
210102_at	BC001234	Hs.152944	<i>LOH11CR2A</i>	11q23	2.4	2.4
203548_s_at	BF672975	Hs.180878	<i>LPL</i>	8p22	5.9	4.6
203549_s_at	NM_000237	Hs.180878	<i>LPL</i>	8p22	3.6	3.0
219631_at	NM_024937	Hs.301974	<i>LRP12</i>	8q22.2-q23.1	2.6	2.3
220253_s_at	NM_013437	Hs.301974	<i>LRP12</i>	8q22.2-q23.1	2.7	2.3
231897_at	AL135787	Hs.546348	<i>LTB4DH</i>	9q31.3	2.7	2.9
231124_x_at	AI524095	Hs.403857	<i>LY9</i>	1q21.3-q22	1.4	2.2
239756_at	AA694099	Hs.209128	<i>MAD1L1</i>	7p22	7.6	9.9
205193_at	NM_012323	Hs.517617	<i>MAFF</i>	22q13.1	5.9	5.1
36711_at	AL021977	Hs.517617	<i>MAFF</i>	22q13.1	3.3	3.1
204970_s_at	NM_002359	Hs.252229	<i>MAFG</i>	17q25.3	2.7	2.4
224466_s_at	BC006143	Hs.252229	<i>MAFG</i>	17q25.3	14.5	5.7
205027_s_at	NM_005204	Hs.432453	<i>MAP3K8</i>	10p11.23	2.6	2.6
207121_s_at	NM_002748	Hs.411847	<i>MAPK6</i>	15q21	2.4	2.0
201668_x_at	AW163148	Hs.519909	<i>MARCKS</i>	6q22.2	1.7	2.0
219952_s_at	NM_020533	Hs.546413	<i>MCOLN1</i>	19p13.3-p13.2	2.2	1.7
223264_at	BC001373	Hs.513071	<i>MESDC1</i>	15q13	2.1	2.1
203510_at	BG170541	Hs.132966	<i>MET</i>	7q31	2.6	2.7
211599_x_at	U19348	Hs.132966	<i>MET</i>	7q31	2.2	1.9
213807_x_at	BE870509	Hs.132966	<i>MET</i>	7q31	1.9	2.2
223723_at	BC001875	Hs.184727	<i>MFI2</i>	3q28-q29	3.8	2.9
1552277_a_at	NM_080655	Hs.530272	<i>MGC17337</i>	9q31.1	1.9	2.2
1553736_at	NM_144982	Hs.527874	<i>MGC23401</i>	12q21.1	3.1	3.8
223296_at	BC004991	Hs.443826	<i>MGC4399</i>	1p36.22	2.1	1.7
226639_at	AI304320	Hs.345849	<i>MGC5391</i>	2q14.3	3.3	3.2
226499_at	W72331	Hs.535075	<i>MGC61598</i>	9q34.3	2.3	1.8
226066_at	AL117653	Hs.166017	<i>MITF</i>	3p14.2-p14.1	2.6	1.8
204475_at	NM_002421	Hs.83169	<i>MMP1</i>	11q22.3	11.8	12.0
205680_at	NM_002425	Hs.2258	<i>MMP10</i>	11q22.3	5.1	2.7
204574_s_at	NM_002429	Hs.154057	<i>MMP19</i>	12q14	1.9	3.3
204575_s_at	U38321	Hs.154057	<i>MMP19</i>	12q14	4.7	4.3
203936_s_at	NM_004994	Hs.297413	<i>MMP9</i>	20q11.2-q13.1	2.8	2.5
212508_at	AK024029	Hs.24719	<i>MOAP1</i>	14q32	3.1	2.9

225185_at	BF343625	Hs.527021	MRAS	3q22.3	2.5	1.7
209928_s_at	AF060154	Hs.442619	MSC	8q21	1.2	2.0
220346_at	NM_025001	Hs.479954	MTHFD2L	4q13.3	2.7	2.8
200632_s_at	NM_006096	Hs.372914	NDRG1	8q24.3	2.2	1.7
208926_at	U84246	Hs.520037	NEU1	6p21.3	2.5	2.1
1567013_at	AF323119	Hs.155396	NFE2L2	2q31	2.4	2.0
236213_at	AI809760	Hs.155396	NFE2L2	2q31	5.7	5.2
203045_at	NM_004148	Hs.494457	NINJ1	9q22	2.6	2.1
225943_at	BF222737	Hs.247460	NLN	5q12.3	2.7	3.3
225944_at	AW006938	Hs.247460	NLN	5q12.3	2.8	2.6
201695_s_at	NM_000270	Hs.75514	NP	14q13.1	2.0	1.7
202679_at	NM_000271	Hs.464779	NPC1	18q11-q12	5.4	4.9
217584_at	U55987	Hs.464779	NPC1	18q11-q12	2.6	2.8
201468_s_at	NM_000903	Hs.406515	NQO1	16q22.1	2.0	1.5
210519_s_at	BC000906	Hs.406515	NQO1	16q22.1	2.6	1.8
204621_s_at	AI935096	Hs.165258	NR4A2	2q22-q23	2.4	3.8
204622_x_at	NM_006186	Hs.165258	NR4A2	2q22-q23	1.8	2.5
216248_s_at	S77154	Hs.165258	NR4A2	2q22-q23	2.2	3.0
219557_s_at	NM_020645	Hs.523467	NRIP3	11p15.3	2.9	2.7
222900_at	AJ400877	Hs.523467	NRIP3	11p15.3	3.3	2.9
203269_at	NM_003580	Hs.372000	NSMAF	8q12-q13	2.9	2.2
232148_at	BF056507	Hs.372000	NSMAF	8q12-q13	3.7	3.7
232149_s_at	BF056507	Hs.372000	NSMAF	8q12-q13	5.3	3.8
228231_at	BE221804	Hs.534331	NUDT1	7p22	2.2	1.7
204435_at	NM_014778	Hs.507537	NUPL1	13q12.13	2.0	2.3
228170_at	AL355743	Hs.56663	OLIG1	21q22.11	3.7	3.5
213824_at	AI870776	Hs.176977	OLIG2	21q22.11	10.3	7.9
213825_at	AA757419	Hs.176977	OLIG2	21q22.11	11.1	9.1
214637_at	BG437034	Hs.248156	OSM	22q12.2	2.2	2.2
230170_at	AI079327	Hs.248156	OSM	22q12.2	2.2	2.0
204088_at	NM_002560	Hs.321709	P2RX4	12q24.32	2.2	2.1
207091_at	NM_002562	Hs.507102	P2RX7	12q24	5.5	3.3
202759_s_at	BE879367	Hs.259461	PALM2-AKAP2	9q31-q33	2.3	1.9
226694_at	BG540494	Hs.259461	PALM2-AKAP2	9q31-q33	2.3	1.7
223220_s_at	AF307338	Hs.518200	PARP9	3q13-q21	2.1	1.7
227807_at	AI738416	Hs.518200	PARP9	3q13-q21	2.1	1.7
227458_at	AI608902	Hs.521989	PDCD1LG1	9p24	7.1	4.6
205872_x_at	NM_022359	Hs.381235	PDE4DIP	1q12	5.3	4.0
209700_x_at	AB042555	Hs.381235	PDE4DIP	1q12	5.0	3.7
210305_at	AB042557	Hs.381235	PDE4DIP	1q12	5.9	7.2
212390_at	AB007923	Hs.381235	PDE4DIP	1q12	1.7	2.0
214099_s_at	AK001619	Hs.381235	PDE4DIP	1q12	2.1	2.4
214129_at	AI821791	Hs.487925	PDE4DIP	1q12	1.7	2.0
214130_s_at	AI821791	Hs.381235	PDE4DIP	1q12	2.2	2.6
244511_at	AV700591	Hs.487925	PDE4DIP	1q12	1.4	2.1
244859_at	R44149	Hs.487925	PDE4DIP	1q12	3.6	4.4
218018_at	AW449022	Hs.284491	PDXK	21q22.3	1.8	2.0
213638_at	AW054711	Hs.436996	PHACTR1	6p24.1	10.0	6.2
217996_at	AA576961	Hs.549112	PHLDA1	12q15	1.6	2.0
217997_at	AI795908	Hs.549112	PHLDA1	12q15	1.7	2.4
218000_s_at	NM_007350	Hs.549112	PHLDA1	12q15	1.7	2.8
209803_s_at	AF001294	Hs.154036	PHLDA2	11p15.5	2.9	2.3
209193_at	M24779	Hs.81170	PIM1	6p21.2	1.9	2.1

224739_at	BE778706	Hs.530381	PIM3	22q13	1.7	2.0
202392_s_at	NM_014338	Hs.420559	PISD	22q12.2	2.1	1.3
210145_at	M68874	Hs.497200	PLA2G4A	1q25	2.4	1.4
205479_s_at	NM_002658	Hs.77274	PLAU	10q24	2.4	2.8
211668_s_at	K03226	Hs.77274	PLAU	10q24	2.3	2.9
218951_s_at	NM_018390	Hs.522568	PLCXD1	Xp22.33; Yp11.32	2.2	2.4
232530_at	AA132961	Hs.478230	PLD1	3q26	5.3	3.3
203470_s_at	AI433595	Hs.468840	PLEK	2p13.3	3.7	3.1
203471_s_at	NM_002664	Hs.468840	PLEK	2p13.3	3.4	2.8
201411_s_at	NM_017958	Hs.469944	PLEKHB2	2q21.1	2.1	1.9
204285_s_at	AI857639	Hs.96	PMAIP1	18q21.32	2.0	2.0
204286_s_at	NM_021127	Hs.96	PMAIP1	18q21.32	2.1	2.1
210139_s_at	L03203	Hs.372031	PMP22	17p12-p11.2	5.0	3.0
209355_s_at	AB000889	Hs.405156	PPAP2B	1pter-p22.1	28.7	12.0
212226_s_at	AA628586	Hs.405156	PPAP2B	1pter-p22.1	12.1	6.5
212230_at	AV725664	Hs.405156	PPAP2B	1pter-p22.1	15.9	6.2
208510_s_at	NM_015869	Hs.162646	PPARG	3p25	5.1	4.5
232331_at	AK027107	Hs.162646	PPARG	3p25	3.1	2.7
202065_s_at	BG033593	Hs.530749	PPFIA1	11q13.3	3.4	2.5
202066_at	AA195259	Hs.530749	PPFIA1	11q13.3	2.7	2.1
210235_s_at	U22815	Hs.530749	PPFIA1	11q13.3	2.9	2.2
210236_at	U22815	Hs.530749	PPFIA1	11q13.3	2.3	2.6
242990_at	AL038704	Hs.530749	PPFIA1	11q13.3	1.7	2.0
202014_at	NM_014330	Hs.76556	PPP1R15A	19q13.2	4.2	3.4
37028_at	U83981	Hs.76556	PPP1R15A	19q13.2	3.6	2.9
215231_at	AU144309	Hs.549162	PRKAG2	7q35-q36	4.3	4.9
218292_s_at	NM_016203	Hs.549162	PRKAG2	7q35-q36	3.4	2.7
222582_at	AF087875	Hs.549162	PRKAG2	7q35-q36	2.9	2.6
233748_x_at	AJ249976	Hs.549162	PRKAG2	7q35-q36	3.1	2.4
232629_at	AF182069	Hs.528665	PROK2	3p21.1	3.5	2.1
219938_s_at	NM_024430	Hs.368623	PSTPIP2	18q12	2.5	2.4
213933_at	AW242315	Hs.445000	PTGER3	1p31.2	4.6	3.7
1554997_a_at	AY151286	Hs.196384	PTGS2	1q25.2-q25.3	5.5	5.6
204748_at	NM_000963	Hs.196384	PTGS2	1q25.2-q25.3	3.4	3.6
206157_at	NM_002852	Hs.546280	PTX3	3q25	3.8	2.8
227718_at	BF337790	Hs.349150	PURB	7p13	2.2	2.4
235711_at	AA495775	Hs.349150	PURB	7p13	1.9	2.0
207791_s_at	NM_004161	Hs.310645	RAB1A	2p14	2.3	2.0
219622_at	NM_017817	Hs.508720	RAB20	13q34	6.4	3.2
209050_s_at	AI421559	Hs.106185	RALGDS	9q34.3	3.3	3.0
209051_s_at	AF295773	Hs.106185	RALGDS	9q34.3	2.7	2.9
1553785_at	NM_152545	Hs.480068	RASGEF1B	4q21.3	5.4	4.6
1554999_at	BC036784	Hs.480068	RASGEF1B	4q21.3	5.8	5.3
230233_at	BF110534	Hs.480068	RASGEF1B	4q21.3	3.2	2.3
204969_s_at	NM_002906	Hs.263671	RDX	11q23	2.3	2.1
212397_at	AL137751	Hs.263671	RDX	11q23	2.2	2.2
209568_s_at	AF186779	Hs.497148	RGL1	1q25.3	1.8	2.2
202988_s_at	NM_002922	Hs.75256	RGS1	1q31	2.9	2.7
1568752_s_at	BC036950	Hs.497220	RGS13	1q31.2	2.0	2.5
210258_at	AF030107	Hs.497220	RGS13	1q31.2	2.1	1.9
244887_at	AI419982	Hs.497220	RGS13	1q31.2	2.6	2.3
1555780_a_at	AF493921	Hs.283521	RHEB	7q36	2.3	1.8
201453_x_at	NM_005614	Hs.283521	RHEB	7q36	2.1	1.7

213404_s_at	BF033683	Hs.283521	<i>RHEB</i>	7q36	2.1	1.6
1553962_s_at	BI668074	Hs.502876	<i>RHOB</i>	2p24	2.5	1.5
212099_at	AI263909	Hs.502876	<i>RHOB</i>	2p24	2.4	1.5
223169_s_at	AB051826	Hs.435106	<i>RHOU</i>	1q42.11-q42.3	1.2	2.2
209544_at	AF027706	Hs.103755	<i>RIPK2</i>	8q21	2.3	2.4
209545_s_at	AF064824	Hs.103755	<i>RIPK2</i>	8q21	2.7	2.5
209882_at	AF084462	Hs.491234	<i>RIT1</i>	1q22	2.3	1.7
236223_s_at	AL037450	Hs.530473	<i>RIT1</i>	---	2.3	1.5
236224_at	AL037450	Hs.530473	<i>RIT1</i>	---	2.4	1.5
243463_s_at	AA417878	Hs.530473	<i>RIT1</i>	1q22	2.2	1.5
202684_s_at	AB020966	Hs.8086	<i>RNMT</i>	18p11.22-p11.23	2.4	1.9
207438_s_at	NM_005701	Hs.21577	<i>RNUT1</i>	15q23	2.0	1.7
204802_at	NM_004165	Hs.1027	<i>RRAD</i>	16q22	7.7	2.7
204803_s_at	NM_004165	Hs.1027	<i>RRAD</i>	16q22	6.4	3.7
218088_s_at	NM_022157	Hs.532461	<i>RRAGC</i>	1p34	2.5	2.2
222514_at	AK023373	Hs.532461	<i>RRAGC</i>	1p34	3.0	2.4
221523_s_at	AL138717	Hs.485938	<i>RRAGD</i>	6q15-q16	3.3	2.9
221524_s_at	AF272036	Hs.485938	<i>RRAGD</i>	6q15-q16	5.3	3.6
213797_at	AI337069	Hs.17518	<i>RSAD2</i>	2p25.2	8.8	5.9
242625_at	AW189843	Hs.17518	<i>RSAD2</i>	2p25.2	13.1	7.2
210365_at	D43967	Hs.149261	<i>RUNX1</i>	21q22.3	1.8	2.0
211180_x_at	D89788	Hs.149261	<i>RUNX1</i>	21q22.3	2.2	1.8
201844_s_at	W84482	Hs.7910	<i>RYBP</i>	3p13	2.0	1.7
201846_s_at	NM_012234	Hs.7910	<i>RYBP</i>	3p13	2.1	1.9
238729_x_at	BF983202	Hs.257341	<i>SAV1</i>	14q13-q23	2.9	2.3
1552365_at	NM_033128	Hs.549223	<i>SCIN</i>	7p21.3	5.7	5.1
205695_at	NM_006843	Hs.439023	<i>SDS</i>	12q24.13	6.0	3.4
233020_at	AU154125	Hs.534212	<i>SEC22L1</i>	1q21.2-q21.3	1.8	2.4
244841_at	AI080364	Hs.211612	<i>SEC24A</i>	5q31.1	2.0	2.3
1564972_x_at	AF277186	Hs.446217	<i>SETDB2</i>	13q14	5.1	5.8
235338_s_at	W65369	Hs.446217	<i>SETDB2</i>	13q14	2.4	2.3
235339_at	W65369	Hs.446217	<i>SETDB2</i>	13q14	2.7	2.7
201739_at	NM_005627	Hs.296323	<i>SGK</i>	6q23	2.4	1.7
226560_at	AA576959	Hs.210043	<i>SGPP2</i>	2q36.1	2.1	3.3
232084_at	BE671098	Hs.287971	<i>SGTB</i>	5q12.3	2.2	2.4
201810_s_at	AL562152	Hs.257761	<i>SH3BP5</i>	3p24.3	3.2	2.5
201811_x_at	NM_004844	Hs.257761	<i>SH3BP5</i>	3p24.3	2.1	1.7
225589_at	AB040927	Hs.301804	<i>SH3MD2</i>	4q32.3-q33	2.1	1.9
219159_s_at	NM_021181	Hs.517265	<i>SLAMF7</i>	1q23.1-q24.1	5.0	4.5
222838_at	AL121985	Hs.517265	<i>SLAMF7</i>	1q23.1-q24.1	4.9	4.0
234306_s_at	AJ271869	Hs.517265	<i>SLAMF7</i>	1q23.1-q24.1	5.6	5.4
1555116_s_at	BC041787	Hs.471393	<i>SLC11A1</i>	2q35	1.6	2.0
203123_s_at	AU154469	Hs.505545	<i>SLC11A2</i>	12q13	2.4	3.1
203124_s_at	NM_000617	Hs.505545	<i>SLC11A2</i>	12q13	3.3	3.3
203125_x_at	AF046997	Hs.505545	<i>SLC11A2</i>	12q13	2.2	2.2
221041_s_at	NM_012434	Hs.485760	<i>SLC17A5</i>	6q14-q15	3.0	2.1
223441_at	AK026921	Hs.485760	<i>SLC17A5</i>	6q14-q15	3.4	2.5
209681_at	AF153330	Hs.30246	<i>SLC19A2</i>	1q23.3	3.1	2.7
203775_at	NM_014251	Hs.489190	<i>SLC25A13</i>	7q21.3	2.1	1.6
229061_s_at	AW268880	Hs.489190	<i>SLC25A13</i>	7q21.3	2.9	2.0
205097_at	AI025519	Hs.302738	<i>SLC26A2</i>	5q31-q34	2.5	2.4
224959_at	AI718385	Hs.302738	<i>SLC26A2</i>	5q31-q34	2.3	2.2
224963_at	AK025078	Hs.302738	<i>SLC26A2</i>	5q31-q34	2.8	2.5

220123_at	NM_025181	Hs.292509	<i>SLC35F5</i>	2q14.1	2.1	2.1
200924_s_at	NM_002394	Hs.502769	<i>SLC3A2</i>	11q13	2.1	2.1
201195_s_at	AB018009	Hs.513797	<i>SLC7A5</i>	16q24.3	2.0	2.0
219911_s_at	NM_016354	Hs.235782	<i>SLCO4A1</i>	20q13.33	2.1	2.6
205443_at	NM_003082	Hs.179312	<i>SNAPC1</i>	14q22	6.5	3.4
223241_at	AF121858	Hs.551538	<i>SNX8</i>	7p22.3	2.8	2.6
223027_at	BF972871	Hs.191213	<i>SNX9</i>	6q25.1-q26	2.4	2.5
223028_s_at	BC005022	Hs.191213	<i>SNX9</i>	6q25.1-q26	2.8	2.7
221561_at	L21934	Hs.496383	<i>SOAT1</i>	1q25	2.4	1.8
210001_s_at	AB005043	Hs.50640	<i>SOCS1</i>	16p13.13	2.6	2.2
203372_s_at	AB004903	Hs.485572	<i>SOCS2</i>	12q	3.3	3.4
203373_at	NM_003877	Hs.485572	<i>SOCS2</i>	12q	3.3	2.9
206359_at	BG035761	Hs.527973	<i>SOCS3</i>	17q25.3	5.2	5.5
206360_s_at	NM_003955	Hs.527973	<i>SOCS3</i>	17q25.3	2.0	2.1
227697_at	AI244908	Hs.527973	<i>SOCS3</i>	17q25.3	4.0	3.5
215078_at	AL050388	Hs.487046	<i>SOD2</i>	6q25.3	5.7	9.4
203145_at	NM_006461	Hs.514033	<i>SPAG5</i>	17q11.2	2.0	1.9
206748_s_at	NM_003971	Hs.463439	<i>SPAG9</i>	17q21.33	2.0	1.6
219257_s_at	NM_021972	Hs.68061	<i>SPHK1</i>	17q25.2	2.2	2.4
206239_s_at	NM_003122	Hs.407856	<i>SPINK1</i>	5q32	15.7	10.1
209875_s_at	M83248	Hs.313	<i>SPP1</i>	4q21-q25	3.8	2.8
204011_at	NM_005842	Hs.18676	<i>SPRY2</i>	13q31.1	7.7	5.1
201471_s_at	NM_003900	Hs.529892	<i>SQSTM1</i>	5q35	2.0	1.6
213112_s_at	N30649	Hs.529892	<i>SQSTM1</i>	5q35	7.1	6.8
244804_at	AW293441	Hs.529892	<i>SQSTM1</i>	5q35	4.1	3.1
225252_at	AL121758	Hs.516830	<i>SRXN1</i>	20p13	3.1	2.4
210942_s_at	AB022918	Hs.148716	<i>ST3GAL6</i>	3q12.1	6.1	3.4
213355_at	AI989567	Hs.148716	<i>ST3GAL6</i>	3q12.1	5.4	3.0
200887_s_at	NM_007315	Hs.470943	<i>STAT1</i>	2q32.2	2.7	1.9
209969_s_at	BC002704	Hs.470943	<i>STAT1</i>	2q32.2	3.8	2.9
232375_at	AI539443	Hs.470943	<i>STAT1</i>	2q32.2	2.5	2.6
243213_at	BF508977	Hs.463059	<i>STAT3</i>	17q21.31	1.9	2.3
228353_x_at	AA233308	Hs.444075	<i>STS-1</i>	11q24.1	3.1	2.7
228359_at	AA037664	Hs.444075	<i>STS-1</i>	11q24.1	3.8	3.0
238587_at	AI927919	Hs.444075	<i>STS-1</i>	11q24.1	2.1	2.3
209238_at	BE966922	Hs.530733	<i>STX3A</i>	11q12.1	2.3	1.7
216985_s_at	AJ002077	Hs.530733	<i>STX3A</i>	11q12.1	2.5	1.5
1552541_at	NM_138810	Hs.529984	<i>TAGAP</i>	6q25.3	2.2	2.0
1552542_s_at	NM_138810	Hs.529984	<i>TAGAP</i>	6q25.3	2.2	2.3
234050_at	AK025272	Hs.529984	<i>TAGAP</i>	6q25.3	2.0	2.1
242388_x_at	AW576600	Hs.529984	<i>TAGAP</i>	6q25.3	2.5	1.9
202307_s_at	NM_000593	Hs.352018	<i>TAP1</i>	6p21.3	2.3	2.0
1565579_at	BC009749	Hs.475401	<i>TATDN2</i>	3p25.3	1.6	2.5
222173_s_at	AK026105	Hs.371016	<i>TBC1D2</i>	9q22.33	8.3	5.0
223461_at	AF151073	Hs.484678	<i>TBC1D7</i>	6p24.1	10.6	6.4
228285_at	AI989706	Hs.21454	<i>TDRD9</i>	14q32.33	5.5	3.5
217853_at	NM_022748	Hs.520814	<i>TENS1</i>	7p13-p12.3	2.7	1.8
207332_s_at	NM_003234	Hs.529618	<i>TFRC</i>	3q29	2.6	3.1
208691_at	BC001188	Hs.529618	<i>TFRC</i>	3q29	2.5	2.8
203887_s_at	NM_000361	Hs.2030	<i>THBD</i>	20p12-cen	1.9	3.7
203888_at	NM_000361	Hs.2030	<i>THBD</i>	20p12-cen	1.5	3.3
237252_at	AW119113	Hs.2030	<i>THBD</i>	20p12-cen	1.4	3.3
226117_at	AA195074	Hs.310640	<i>TIFA</i>	4q25	2.3	1.8

212665_at	AL556438	Hs.12813	TIPARP	3q25.31	2.1	1.9
221266_s_at	NM_030788	Hs.208036	TM7SF4	8q23	4.3	3.5
218772_x_at	NM_018112	Hs.411925	TMEM38B	9q31.2	2.6	2.2
222735_at	AW452608	Hs.411925	TMEM38B	9q31.2	3.0	2.6
222736_s_at	BC000049	Hs.411925	TMEM38B	9q31.2	2.7	2.5
207113_s_at	NM_000594	Hs.241570	TNF	6p21.3	8.9	5.0
202509_s_at	AI862445	Hs.525607	TNFAIP2	14q32	2.1	2.3
202510_s_at	NM_006291	Hs.525607	TNFAIP2	14q32	3.0	2.3
206025_s_at	AW188198	Hs.437322	TNFAIP6	2q23.3	2.0	2.5
206026_s_at	NM_007115	Hs.437322	TNFAIP6	2q23.3	1.8	2.2
207536_s_at	NM_001561	Hs.193418	TNFRSF9	1p36	4.6	4.0
211786_at	BC006196	Hs.193418	TNFRSF9	1p36	4.2	3.4
207907_at	NM_003807	Hs.129708	TNFSF14	19p13.3	14.9	10.8
221085_at	NM_005118	Hs.241382	TNFSF15	9q32	13.0	10.9
203120_at	NM_005426	Hs.523968	TP53BP2	1q42.1	2.3	2.2
220865_s_at	NM_014317	Hs.551530	TPRT	10p12.1	3.2	2.4
202241_at	NM_025195	Hs.444947	TRIB1	8q24.13	2.8	2.2
239818_x_at	AA576947	Hs.444947	TRIB1	8q24.13	3.4	2.7
206911_at	NM_005082	Hs.551516	TRIM25	17q23.1	3.5	3.6
224806_at	BE563152	Hs.528952	TRIM25	17q23.2	2.8	2.7
227653_at	AI168767	Hs.380159	TRMT5	14q23.1	11.5	6.1
223741_s_at	BC004233	Hs.27935	TTYH2	17q24	2.5	2.1
209118_s_at	AF141347	Hs.524395	TUBA3	12q12-12q14.3	2.1	1.6
204141_at	NM_001069	Hs.512712	TUBB2	6p25	3.1	3.4
202154_x_at	NM_006086	Hs.511743	TUBB3	16q24.3	2.5	2.3
209191_at	BC002654	Hs.193491	TUBB6	18p11.21	2.4	1.9
208864_s_at	AF313911	Hs.435136	TXN	9q31	4.0	2.8
216609_at	AF065241	Hs.435136	TXN	9q31	2.5	2.0
201266_at	NM_003330	Hs.434367	TXNRD1	12q23-q24.1	2.8	2.2
214755_at	AK022632	Hs.142076	UAP1L1	9q34.3	4.3	2.8
211764_s_at	BC005980	Hs.129683	UBE2D1	10q11.2-q21	2.1	1.6
214590_s_at	AL545760	Hs.129683	UBE2D1	10q11.2-q21	2.2	1.9
226729_at	BF789968	Hs.166068	USP37	2q35	2.0	1.8
226730_s_at	BF789968	Hs.166068	USP37	2q35	2.1	2.3
232033_at	BE670098	Hs.166068	USP37	2q35	2.1	2.2
221704_s_at	BC005882	Hs.507162	VPS37B	12q24.31	2.2	2.0
200629_at	NM_004184	Hs.497599	WARS	14q32.31	2.0	1.7
217975_at	NM_016303	Hs.533287	WBP5	Xq22.2	3.4	3.2
233559_s_at	AK023415	Hs.368359	WDFY1	2q36.1	2.1	1.8
1558783_at	AK024805	Hs.446091	WTAP	6q25-q27	1.8	2.1
244219_at	AI613089	Hs.446091	WTAP	6q25-q27	1.8	2.1
214567_s_at	NM_003175	Hs.546295	XCL1, XCL2	1q23 /// 1q23-q25	11.1	16.7
206366_x_at	U23772	Hs.458346	XCL2	1q23-q25	10.8	12.4
219836_at	NM_024508	Hs.136912	ZBED2	3q13.13	3.3	1.7
219312_s_at	NM_023929	Hs.205742	ZBTB10	8q13-q21.1	2.2	2.8
228562_at	N29918	Hs.205742	ZBTB10	8q13-q21.1	1.6	2.0
233899_x_at	AK024296	Hs.205742	ZBTB10	8q13-q21.1	2.0	2.5
218810_at	NM_025079	Hs.471918	ZC3H12A	1p34.3	1.6	2.1
231899_at	AB051513	Hs.376289	ZC3H12C	11q22.3	13.0	12.2
1554638_at	BC032227	Hs.482660	ZFYVE16	5p15.2-q14.3	2.1	1.9
203651_at	NM_014733	Hs.482660	ZFYVE16	5p15.2-q14.3	2.6	2.2
240859_at	N20928	Hs.482660	ZFYVE16	5p15.2-q14.3	3.1	4.3
219540_at	AU150728	Hs.460645	ZNF267	16p11.2	2.0	1.7

204180_s_at	AI745225	Hs.355581	ZNF297B	9p24.1-q22.33	2.8	2.8
204181_s_at	T90308	Hs.355581	ZNF297B	9p24.1-q22.33	2.8	2.5
204182_s_at	NM_014007	Hs.355581	ZNF297B	9p24.1-q22.33	2.5	3.0
227991_x_at	BF516567	Hs.355581	ZNF297B	9p24.1-q22.33	2.8	2.7
219228_at	NM_018555	Hs.185674	ZNF331	19q13.3-q13.4	1.7	2.6
227613_at	AW450874	Hs.185674	ZNF331	19q13.3-q13.4	1.9	2.8
225152_at	BF940944	Hs.60300	ZNF622	5p15.1	2.0	1.7
219904_at	NM_024303	Hs.177688	ZSCAN5	19q13.43	4.6	3.7
1553706_at	NM_153692	Hs.322452	---	8p11.23	6.1	4.4
1555982_at	BU078629	Hs.527051	---	5q14.1	2.2	1.8
1556545_at	AK056941	Hs.317080	---	17q21.31	4.0	4.6
1557236_at	BF512806	---	---	22q12.3	2.2	2.2
1559777_at	AK057428	Hs.563188	---	4q35.1	3.7	4.8
1560869_a_at	AF085902	Hs.481068	---	4q32.1	24.6	13.3
1561017_at	AF087983	Hs.384565	---	13q14.2	2.5	2.1
1564121_at	AK026788	Hs.548025	---	17p13.3	2.8	2.8
1569095_at	BC016366	Hs.563839	---	4p35.1	8.3	6.2
1570061_at	BC014200	Hs.372904	---	3q21.3	2.4	1.9
213281_at	BE327172	---	---	1p32.1	2.3	2.0
215009_s_at	U92014	Hs.370024	---	4q21.3	2.1	1.9
217606_at	AI653960	Hs.196555	---	2q14.1	5.6	6.3
217999_s_at	NM_007350	Hs.484885	---	12q21.2	1.8	2.2
222145_at	AK027225	Hs.460278	---	16p12.1	2.8	3.3
222303_at	AV700891	---	---	21q22.2	3.3	3.6
226189_at	BF513121	Hs.367688	---	7p21.1	7.8	12.6
226397_s_at	BG502771	Hs.6083	---	6p24.1	5.6	3.9
227044_at	AV705507	Hs.40696	---	22q13.31	2.2	1.9
227092_at	AI341383	---	---	8p23.3	2.3	2.4
229242_at	BF439063	Hs.23349	---	9q32	15.4	12.8
229715_at	AW006182	Hs.146274	---	11p15.1	2.8	2.8
229972_at	AI096642	---	---	7	3.7	2.8
230127_at	AW044663	Hs.232417	---	Xp11.3	4.0	3.4
230741_at	AI655467	Hs.439682	---	12q24.31	5.7	3.6
231367_s_at	AW300131	---	---	13q14.2	2.2	2.4
231972_at	AK024681	Hs.6083	---	6p24.1	5.6	4.0
233935_at	AK026704	Hs.548037	---	19p13.3	6.1	3.5
235539_at	AW964431	---	---	11q13.4	1.7	2.0
236423_at	AI022821	Hs.539431	---	---	2.4	2.0
236869_at	AI857429	Hs.171171	---	22q12.2	2.3	2.5
238319_at	AI732843	Hs.567569	---	7q36.1	1.7	2.0
238389_s_at	AI458208	---	---	1q42.11	1.8	2.1
238725_at	AW392551	Hs.180559	---	5q23.3	3.3	3.1
238727_at	AA031832	Hs.238964	---	2q36.1	2.7	4.8
239331_at	AW954199	Hs.184721	---	7q32.3	4.3	4.3
239572_at	BF726530	Hs.130313	---	13q12.11	2.0	3.6
240103_at	H22954	Hs.158152	---	8q22.3	2.9	4.0
241418_at	AI819386	Hs.128803	---	3q27.2	2.7	2.5
242058_at	AA206363	---	---	4q32.1	8.5	5.4
243124_at	AI919493	---	---	16p11.2	2.4	2.3
243675_at	BF512500	Hs.445342	---	4q32.1	26.9	15.9
244080_at	AL552727	Hs.527657	---	1q32.3	32.3	15.3
81737_at	AI424872	Hs.460080	---	16p13.11	2.5	3.1
Down-Regulated						

Probeset	Public ID	UniGene#	Entrez Gene	Chromosome	Healthy	Job's
204072_s_at	NM_023037	Hs.507669	13CDNA73	13q13.1	-3.2	-3.1
227962_at	BF435852	Hs.464137	ACOX1	17q24-q25	-1.8	-2.0
204638_at	NM_001611	Hs.1211	ACP5	19p13.3-p13.2	-2.3	-2.5
203741_s_at	NM_001114	Hs.513578	ADCY7	16q12-q13	-1.8	-2.0
204859_s_at	NM_013229	Hs.552567	APAF1	12q23	-2.5	-2.2
225166_at	AU158022	Hs.486458	ARHGAP18	6q22.33	-2.5	-2.6
225171_at	BE644830	Hs.486458	ARHGAP18	6q22.33	-3.0	-2.8
225173_at	BE501862	Hs.486458	ARHGAP18	6q22.33	-2.5	-2.3
226576_at	AI768563	Hs.293593	ARHGAP26	5q31	-2.1	-1.9
217818_s_at	NM_005718	Hs.323342	ARPC4	3p25.3	-2.3	-2.2
203388_at	NM_004313	Hs.435811	ARRB2	17p13	-2.1	-1.7
206743_s_at	NM_001671	Hs.12056	ASGR1	17p13.2	-2.2	-2.8
219624_at	NM_004874	Hs.194726	BAG4	8p12	-1.6	-2.2
204860_s_at	AI817801	Hs.519374	BIRC1	5q13.1	-2.1	-2.7
226853_at	AU145366	Hs.146551	BMP2K	4q21.21	-1.9	-2.1
228532_at	AW662189	Hs.288010	C1orf162	1p13.2	-2.5	-2.2
223243_s_at	BF439488	Hs.523811	C1orf22	1q24-q25	-2.1	-2.0
207571_x_at	NM_004848	Hs.10649	C1orf38	1p35.3	-2.3	-1.9
210785_s_at	AB035482	Hs.10649	C1orf38	1p35.3	-2.1	-1.8
225224_at	AL034550	Hs.516977	C20orf112	20q11.1-q11.23	-1.9	-2.0
64408_s_at	AW025529	Hs.435457	CALML4	15q23	-2.0	-2.3
212765_at	AB029001	Hs.23585	CAMSAP1L1	1q32.1	-1.7	-2.0
217196_s_at	AL110158	Hs.23585	CAMSAP1L1	1q32.1	-2.1	-2.2
1552553_a_at	NM_021209	Hs.23248	CARD12	2p22-p21	-8.4	-4.0
1552554_a_at	AY027790	Hs.23248	CARD12	2p22-p21	-3.2	-2.1
224414_s_at	AF356193	Hs.200242	CARD6	5p13.1	-2.1	-1.8
206978_at	NM_000647	Hs.511794	CCR2	3p21	-5.8	-6.6
207794_at	NM_000648	Hs.511794	CCR2	3p21	-4.4	-8.0
201743_at	NM_000591	Hs.163867	CD14	5q22-q32 5q31.1	-3.1	-1.9
1553043_a_at	NM_139018	Hs.235768	CD300LF	17q25.1	-2.4	-2.5
205686_s_at	NM_006889	Hs.171182	CD86	3q21	-1.9	-2.1
212899_at	AB028951	Hs.193251	CDC2L6	6q21	-2.0	-2.1
204039_at	NM_004364	Hs.76171	CEBPA	19q13.1	-1.6	-2.4
203973_s_at	NM_005195	Hs.440829	CEBPD	8p11.2-p11.1	-5.7	-3.4
213006_at	AV655640	Hs.440829	CEBPD	8p11.2-p11.1	-6.0	-4.5
218950_at	NM_022481	Hs.25277	CENTD3	5q31.3	-2.6	-2.2
204759_at	NM_001268	Hs.25447	CHC1L	13q14.3	-1.7	-2.0
230292_at	AA868809	Hs.25447	CHC1L	13q14.3	-1.8	-2.5
212615_at	AI742305	Hs.530936	CHD9	16q12.2	-1.6	-2.1
219161_s_at	NM_016951	Hs.15159	CKLF	16q22.1	-2.5	-2.5
221058_s_at	NM_016326	Hs.15159	CKLF	16q22.1	-2.9	-2.5
223451_s_at	AF096895	Hs.15159	CKLF	16q22.1	-4.1	-3.6
235286_at	BG533580	Hs.549232	CKLF	16q22.1	-3.5	-3.1
224733_at	AL574900	Hs.298198	CKLFSF3	16q22.1	-2.1	-2.0
219890_at	NM_013252	Hs.546358	CLEC5A	7q33	-3.0	-1.8
212977_at	AI817041	Hs.471751	CMKOR1	2q37.3	-3.3	-1.7
232746_at	BE552368	Hs.471751	CMKOR1	2q37.3	-3.3	-1.6
203104_at	NM_005211	Hs.483829	CSF1R	5q33-q35	-6.1	-3.8
204619_s_at	BF590263	Hs.443681	CSPG2	5q14.3	-2.4	-1.9
211571_s_at	D32039	Hs.443681	CSPG2	5q14.3	-2.6	-2.1
215646_s_at	R94644	Hs.443681	CSPG2	5q14.3	-2.2	-1.8
206595_at	NM_001323	Hs.139389	CST6	11q13	-4.3	-3.6

1557944_s_at	BG248249	Hs.166011	<i>CTNND1</i>	11q11	-2.6	-1.6
208407_s_at	NM_001331	Hs.166011	<i>CTNND1</i>	11q11	-2.2	-1.9
208862_s_at	AW073672	Hs.166011	<i>CTNND1</i>	11q11	-2.3	-2.1
205898_at	U20350	Hs.78913	<i>CX3CR1</i>	3p21 3p21.3	-1.7	-2.1
204923_at	AL023653	Hs.61469	<i>CXorf9</i>	Xq26	-2.1	-1.8
222453_at	AL136693	Hs.221941	<i>CYBRD1</i>	2q31.1	-2.2	-1.8
202262_x_at	NM_013974	Hs.247362	<i>DDAH2</i>	6p21.3	-2.3	-2.0
214909_s_at	AK026191	Hs.247362	<i>DDAH2</i>	6p21.3	-2.2	-1.9
215537_x_at	AJ012008	Hs.247362	<i>DDAH2</i>	6p21.3	-2.2	-2.0
213420_at	AA100250	Hs.468226	<i>DHX57</i>	2p22.1	-2.4	-2.6
226026_at	AI147467	Hs.477346	<i>DIRC2</i>	3q21.1	-2.1	-1.6
204135_at	NM_014890	Hs.104672	<i>DOC1</i>	3q12.1	-2.1	-1.7
230206_at	AI692645	Hs.195403	<i>DOCK5</i>	8p21.2	-2.1	-2.0
230207_s_at	AI692645	Hs.195403	<i>DOCK5</i>	8p21.2	-2.1	-1.9
226817_at	AU154691	Hs.95612	<i>DSC2</i>	18q12.1	-2.1	-1.6
231192_at	AW274018	Hs.527909	<i>EDG7</i>	1p22.3-p31.1	-5.0	-3.3
212830_at	W68084	Hs.494977	<i>EGFL5</i>	9q32-q33.3	-2.0	-2.4
212831_at	BF110421	Hs.494977	<i>EGFL5</i>	9q32-q33.3	-1.9	-2.0
221755_at	BG334196	Hs.502867	<i>EHBP1L1</i>	11q13.1	-2.3	-1.4
201809_s_at	NM_000118	Hs.76753	<i>ENG</i>	9q33-q34.1	-3.8	-2.8
1569583_at	BC035806	Hs.115263	<i>EREG</i>	4q13.3	-2.6	-1.2
209717_at	AF008915	Hs.387251	<i>EVI5</i>	1p22	-1.4	-2.0
221664_s_at	AF154005	Hs.517293	<i>F11R</i>	1q21.2-q21.3	-2.2	-1.8
221565_s_at	BC000039	Hs.241545	<i>FAM26B</i>	10pter-q26.12	-2.2	-2.9
57715_at	W72694	Hs.241545	<i>FAM26B</i>	10pter-q26.12	-2.3	-2.5
227854_at	BE620258	Hs.411433	<i>FANCL</i>	2p16.1	-2.9	-2.0
211305_x_at	U56236	Hs.193122	<i>FCAR</i>	19q13.2-q13.4	-2.4	-1.3
204006_s_at	NM_000570	Hs.372679	<i>FCGR3A, FCGR3B</i>	1q23	-3.9	-3.4
204007_at	J04162	Hs.372679	<i>FCGR3B</i>	1q23	-2.5	-2.2
228220_at	AI627666	Hs.165762	<i>FCHO2</i>	5q13.2	-2.1	-2.0
227948_at	AI949549	Hs.117835	<i>FGD4</i>	12p11.21	-2.1	-1.6
230559_x_at	AI277617	Hs.117835	<i>FGD4</i>	12p11.21	-2.9	-2.2
218818_at	NM_004468	Hs.57687	<i>FHL3</i>	1p34	-2.7	-2.8
218530_at	NM_013241	Hs.95231	<i>FHOD1</i>	16q22	-2.3	-2.2
58780_s_at	R42449	Hs.35125	<i>FLJ10357</i>	14q11.2	-3.8	-3.1
219696_at	NM_019049	Hs.497279	<i>FLJ20054</i>	1q31.3	-2.1	-2.1
1559910_at	AL080280	Hs.409352	<i>FLJ20701</i>	2q36.3	-2.6	-1.7
219093_at	NM_017933	Hs.409352	<i>FLJ20701</i>	2q36.3	-2.4	-2.1
237867_s_at	AI142544	Hs.409352	<i>FLJ20701</i>	2q36.3	-2.9	-2.6
229770_at	AI041543	Hs.12381	<i>FLJ31978</i>	12q24.32	-2.5	-2.5
1552386_at	NM_152687	Hs.44930	<i>FLJ33641</i>	5q11.2	-7.6	-5.3
205119_s_at	NM_002029	Hs.753	<i>FPR1</i>	19q13.4	-2.6	-1.8
210772_at	M88107	Hs.99855	<i>FPRL1</i>	19q13.3-q13.4	-4.7	-2.7
210773_s_at	U81501	Hs.99855	<i>FPRL1</i>	19q13.3-q13.4	-4.0	-2.5
214560_at	NM_002030	Hs.445466	<i>FPRL2</i>	19q13.3-q13.4	-8.7	-5.1
230422_at	AW026543	Hs.445466	<i>FPRL2</i>	19q13.3-q13.4	-9.2	-6.0
229114_at	AW237741	Hs.80720	<i>GAB1</i>	4q31.21	-2.2	-2.2
223423_at	BC000181	Hs.231320	<i>GPR160</i>	3q26.2-q27	-3.2	-2.1
230252_at	AW183080	Hs.155538	<i>GPR92</i>	12p13.31	-2.1	-1.7
201348_at	NM_002084	Hs.386793	<i>GPX3</i>	5q23	-2.4	-2.1
204689_at	NM_001529	Hs.118651	<i>HHEX</i>	10q23.33	-2.3	-2.6
215933_s_at	Z21533	Hs.118651	<i>HHEX</i>	10q23.33	-2.4	-2.7
217427_s_at	X75296	Hs.474206	<i>HIRA</i>	22q11.2 22q11.21	-1.5	-2.7

209721_s_at	BC002857	Hs.15243	<i>HOM-TES-103</i>	12p13.3	-2.0	-1.8
201888_s_at	U81379	Hs.496646	<i>IL13RA1</i>	Xq24	-2.1	-1.6
207008_at	NM_001557	Hs.846	<i>IL8RB</i>	2q35	-2.8	-2.1
205841_at	NM_004972	Hs.434374	<i>JAK2</i>	9p24	-1.5	-2.2
222922_at	AF302494	Hs.523899	<i>KCNE3</i>	11q13-q14	-6.7	-5.2
222923_s_at	AF302494	Hs.523899	<i>KCNE3</i>	11q13-q14	-2.8	-2.7
227647_at	AI692703	Hs.523899	<i>KCNE3</i>	11q13-q14	-4.5	-3.4
210119_at	U73191	Hs.411299	<i>KCNJ15</i>	21q22.2	-2.6	-1.8
211806_s_at	D87291	Hs.411299	<i>KCNJ15</i>	21q22.2	-2.4	-1.6
238428_at	BG542347	Hs.411299	<i>KCNJ15</i>	21q22.2	-2.5	-1.5
228325_at	AI363213	Hs.381058	<i>KIAA0146</i>	8q11.21	-5.5	-4.4
213839_at	AW028110	Hs.525566	<i>KIAA0500</i>	14q32.2	-2.1	-2.4
204546_at	NM_014732	Hs.301658	<i>KIAA0513</i>	16q24.1	-1.7	-2.6
1556423_at	BE220445	Hs.525479	<i>KIAA1036</i>	14q24.3	-3.2	-2.6
223497_at	AL136820	Hs.211700	<i>KIAA1411</i>	6q12-q13	-1.8	-2.0
1557415_s_at	AI023774	Hs.264887	<i>LETM2</i>	8p12	-2.0	-1.7
229937_x_at	AI681260	Hs.149924	<i>LILRB1</i>	19q13.4	-2.7	-2.3
210146_x_at	AF004231	Hs.534386	<i>LILRB2</i>	19q13.4	-2.5	-1.8
204249_s_at	NM_005574	Hs.34560	<i>LMO2</i>	11p13	-2.3	-2.5
225833_at	BE795104	Hs.487498	<i>LOC221955</i>	7p22.1	-1.6	-2.6
226640_at	AA015606	Hs.487498	<i>LOC221955</i>	7p22.1	-1.7	-2.1
1558882_at	BI868572	Hs.441039	<i>LOC401233</i>	6p25.2	-2.1	-1.5
231406_at	AW205664	Hs.534807	<i>LOC402578</i>	---	-2.0	-2.4
213455_at	W87466	Hs.476517	<i>LOC92689</i>	4p14	-2.5	-2.2
229584_at	AK026776	Hs.187636	<i>LRRK2</i>	12q12	-3.0	-4.4
210044_s_at	BC002796	Hs.46446	<i>LYL1</i>	19p13.2	-2.7	-2.5
202122_s_at	NM_005817	Hs.140452	<i>M6PRBP1</i>	19p13.3	-2.2	-1.6
242794_at	AI569476	Hs.444627	<i>MAML3</i>	4q28	-2.9	-2.6
219574_at	NM_017923	Hs.136900	<i>MARCH-I</i>	4q32.2	-2.2	-3.2
229383_at	AI707896	Hs.136900	<i>MARCH-I</i>	4q32.2	-1.9	-2.4
235385_at	AI935334	Hs.136900	<i>MARCH-I</i>	4q32.2	-2.5	-3.4
213045_at	AB011133	Hs.466184	<i>MAST3</i>	19p13.11	-2.4	-2.0
205018_s_at	NM_005757	Hs.125715	<i>MBNL2</i>	13q32.1	-1.6	-2.1
1553993_s_at	BC024312	Hs.467128	<i>MED25</i>	19q13.3	-2.0	-2.0
236395_at	AI523245	Hs.444409	<i>MEF2C</i>	5q14	-2.2	-2.1
206028_s_at	NM_006343	Hs.306178	<i>MERTK</i>	2q14.1	-2.5	-2.2
244716_x_at	AI817976	Hs.263928	<i>MGC23244</i>	19p13.3	-2.0	-1.4
241384_x_at	AI866260	Hs.409960	<i>MGC40579</i>	3q23	-2.1	-1.8
204959_at	NM_002432	Hs.153837	<i>MNDA</i>	1q22	-1.4	-2.1
219607_s_at	NM_024021	Hs.325960	<i>MS4A4A</i>	11q12	-2.1	-1.7
223343_at	AI301935	Hs.530735	<i>MS4A7</i>	11q12	-2.1	-1.5
223344_s_at	AB026043	Hs.530735	<i>MS4A7</i>	11q12	-2.1	-1.3
224358_s_at	AF237916	Hs.530735	<i>MS4A7</i>	11q12	-2.1	-1.6
1556034_s_at	AK097000	Hs.425144	<i>MTMR11</i>	1q12-q21	-2.2	-2.4
205076_s_at	NM_006697	Hs.425144	<i>MTMR11</i>	1q12-q21	-2.4	-2.2
214058_at	M19720	Hs.437922	<i>MYCL1</i>	1p34.2	-1.5	-2.1
213733_at	BF740152	Hs.408451	<i>MYO1F</i>	19p13.3-p13.2	-2.9	-2.2
234574_at	AK024563	Hs.408451	<i>MYO1F</i>	19p13.3-p13.2	-2.0	-1.7
1554952_s_at	AY116207	Hs.367965	<i>NALP12</i>	19q13.42	-3.4	-3.8
223944_at	AF231021	Hs.367965	<i>NALP12</i>	19q13.42	-2.9	-2.6
227220_at	AI743731	Hs.351839	<i>NFXL1</i>	4p12	-1.4	-3.5
212298_at	BE620457	Hs.131704	<i>NRP1</i>	10p12	-1.6	-2.1
229510_at	AL044520	Hs.28514	<i>NYD-SP21</i>	11q12.2	-2.9	-2.4

242397_at	AI694722	Hs.412484	<i>OLR1</i>	12p13.2-p12.3	-2.0	-1.0
229354_at	AB033060	Hs.50823	<i>PDCD6, AHRR</i>	5pter-p15.2 /// 5p15.3	-2.0	-1.7
203370_s_at	NM_005451	Hs.533040	<i>PDLIM7</i>	5q35.3	-2.3	-1.8
214121_x_at	AA086229	Hs.533040	<i>PDLIM7</i>	5q35.3	-2.7	-2.1
214266_s_at	AW206786	Hs.533040	<i>PDLIM7</i>	5q35.3	-2.3	-1.8
208981_at	AA702701	Hs.514412	<i>PECAM1</i>	17q23	-4.2	-2.9
208982_at	AW574504	Hs.514412	<i>PECAM1</i>	17q23	-3.7	-2.9
208983_s_at	M37780	Hs.514412	<i>PECAM1</i>	17q23	-5.5	-3.7
223551_at	AF225513	Hs.486354	<i>PKIB</i>	6q22.31	-1.8	-2.1
218644_at	NM_016445	Hs.170473	<i>PLEK2</i>	14q23.3	-1.9	-2.4
202996_at	NM_021173	Hs.523829	<i>POLD4</i>	11q13	-2.4	-2.1
203063_at	NM_014634	Hs.112728	<i>PPM1F</i>	22q11.22	-2.1	-2.3
241742_at	AW027174	Hs.465812	<i>PRAM1</i>	19p13.2	-1.6	-2.6
1554676_at	BC022313	Hs.1908	<i>PRG1</i>	10q22.1	-2.2	-1.8
238513_at	BF905445	Hs.471695	<i>PRRG4</i>	11p13	-2.0	-2.7
225214_at	AI762915	Hs.213470	<i>PSMB7</i>	9q34.11-q34.12	-2.0	-1.9
202009_at	NM_007284	Hs.436439	<i>PTK9L</i>	3p21.1	-2.1	-2.0
225001_at	AI744658	Hs.551520	<i>RAB3D</i>	19p13.2	-4.3	-3.2
226872_at	AK024288	Hs.465709	<i>RFX2</i>	19p13.3-p13.2	-2.0	-2.2
227823_at	BE348679	Hs.512180	<i>RGAG4</i>	Xq13.1	-2.1	-2.0
204336_s_at	NM_005873	Hs.422336	<i>RGS19</i>	20q13.3	-2.4	-2.6
213397_x_at	AI761728	Hs.283749	<i>RNASE4</i>	14q11.1	-2.3	-3.3
213566_at	NM_005615	Hs.23262	<i>RNASE6</i>	14q11.2	-2.1	-2.1
223591_at	BC005084	Hs.29874	<i>RNF135</i>	17q11.2	-2.0	-2.2
223592_s_at	BC005084	Hs.29874	<i>RNF135</i>	17q11.2	-2.4	-2.4
203379_at	NM_002953	Hs.149957	<i>RPS6KA1</i>	1p	-2.5	-2.1
204900_x_at	NM_003864	Hs.413835	<i>SAP30</i>	4q34.1	-2.3	-2.6
226673_at	AW665063	Hs.306412	<i>SH2D3C</i>	9q34.11	-2.3	-2.0
210569_s_at	AF247180	Hs.245828	<i>SIGLEC9</i>	19q13.41	-2.1	-1.7
202855_s_at	AL513917	Hs.500761	<i>SLC16A3</i>	17q25	-2.2	-1.5
221572_s_at	AF288410	Hs.436194	<i>SLC26A6</i>	3p21.3	-2.4	-1.8
218452_at	NM_014140	Hs.516674	<i>SMARCA1</i>	2q34-q35	-1.3	-2.0
230707_at	AA290609	Hs.368592	<i>SORL1</i>	11q23.2-q24.2	-2.2	-1.7
205312_at	NM_003120	Hs.502511	<i>SPI1</i>	11p11.2	-2.0	-1.5
222482_at	AA102468	Hs.175551	<i>SSBP3</i>	1p32.3	-2.2	-2.0
206925_at	NM_005668	Hs.308628	<i>ST8SIA4</i>	5q21	-3.6	-3.7
230261_at	AA552969	Hs.308628	<i>ST8SIA4</i>	5q21	-3.3	-3.7
230836_at	AI422986	Hs.308628	<i>ST8SIA4</i>	5q21	-3.0	-3.1
242943_at	AA352113	Hs.308628	<i>ST8SIA4</i>	5q21	-3.4	-3.4
1552618_at	NM_005819	Hs.518417	<i>STX6</i>	1q25.3	-3.4	-2.5
212799_at	BE217875	Hs.518417	<i>STX6</i>	1q25.3	-2.9	-2.4
212800_at	AI740832	Hs.518417	<i>STX6</i>	1q25.3	-3.3	-2.6
214441_at	NM_005819	Hs.518417	<i>STX6</i>	1q25.3	-2.3	-1.8
209269_s_at	AW450910	Hs.371720	<i>SYK</i>	9q22	-2.2	-1.8
226068_at	BF593625	Hs.371720	<i>SYK</i>	9q22	-2.0	-1.8
236345_at	AA044825	Hs.520757	<i>TBXAS1</i>	7q34-q35	-2.5	-2.1
201506_at	NM_000358	Hs.369397	<i>TGFBI</i>	5q31	-2.3	-1.7
1554608_at	BC028219	Hs.14894	<i>TGOLN2</i>	2p11.2	-2.2	-1.7
215775_at	BF084105	Hs.164226	<i>THBS1</i>	15q15	-2.9	-1.5
239336_at	BF109732	Hs.164226	<i>THBS1</i>	15q15	-4.6	-1.8
204276_at	BE895437	Hs.512619	<i>TK2</i>	16q22-q23.1	-3.2	-2.8
210176_at	AL050262	Hs.111805	<i>TLR1</i>	4p14	-4.2	-3.8
1552798_a_at	NM_138557	Hs.174312	<i>TLR4</i>	9q32-q33	-2.3	-2.2

221060_s_at	NM_003266	Hs.174312	<i>TLR4</i>	9q32-q33	-2.3	-2.5
224341_x_at	U93091	Hs.174312	<i>TLR4</i>	9q32-q33	-2.6	-2.3
232068_s_at	AF177765	Hs.174312	<i>TLR4</i>	9q32-q33	-2.5	-2.4
229560_at	AW872374	Hs.272410	<i>TLR8</i>	Xp22	-1.9	-2.6
219892_at	NM_023003	Hs.513094	<i>TM6SF1</i>	15q24-q26	-2.9	-2.5
226489_at	BG177562	Hs.370410	<i>TMCC3</i>	12q22	-2.2	-1.6
235146_at	N51717	Hs.370410	<i>TMCC3</i>	12q22	-2.7	-2.7
226226_at	AI282982	Hs.504301	<i>TMEM45B</i>	11q24.3	-1.9	-2.0
230323_s_at	AW242836	Hs.504301	<i>TMEM45B</i>	11q24.3	-2.2	-2.8
227345_at	AI738556	Hs.213467	<i>TNFRSF10D</i>	8p21	-3.1	-2.4
223501_at	AW151360	Hs.525157	<i>TNFSF13B</i>	13q32-34	-1.8	-2.1
223502_s_at	AF134715	Hs.525157	<i>TNFSF13B</i>	13q32-34	-1.8	-2.1
207216_at	NM_001244	Hs.494901	<i>TNFSF8</i>	9q33	-2.4	-1.5
235735_at	AI936516	Hs.494901	<i>TNFSF8</i>	9q33	-2.2	-1.4
221747_at	AL046979	Hs.471381	<i>TNS</i>	2q35-q36	-2.4	-1.5
221748_s_at	AL046979	Hs.471381	<i>TNS</i>	2q35-q36	-2.5	-1.7
221012_s_at	NM_030912	Hs.336810	<i>TRIM8</i>	10q24.3	-2.1	-2.3
223132_s_at	AF220034	Hs.336810	<i>TRIM8</i>	10q24.3	-1.7	-2.1
1552334_at	BG571343	Hs.533030	<i>TRIOBP</i>	22q13.1	-2.1	-1.8
210276_s_at	AF281030	Hs.533030	<i>TRIOBP</i>	22q13.1	-2.5	-2.4
232653_at	AW265514	Hs.253594	<i>TRPS1</i>	8q24.12	-3.4	-2.4
218502_s_at	NM_014112	Hs.253594	<i>TRPS1</i>	8q24.12	-2.2	-2.1
222651_s_at	BF701166	Hs.253594	<i>TRPS1</i>	8q24.12	-2.0	-1.7
244579_at	AI086336	Hs.253594	<i>TRPS1</i>	8q24.12	-2.9	-2.1
203690_at	NM_006322	Hs.224152	<i>TUBGCP3</i>	13q34	-1.6	-2.0
209333_at	AB018265	Hs.47061	<i>ULK1</i>	12q24.3	-2.0	-2.3
203940_s_at	NM_014909	Hs.525479	<i>VASH1</i>	14q24.3	-2.6	-3.1
205922_at	NM_004665	Hs.293130	<i>VNN2</i>	6q23-q24	-1.8	-2.3
205126_at	NM_006296	Hs.468623	<i>VRK2</i>	2p16-p15	-2.5	-1.8
243299_at	AW167087	Hs.468623	<i>VRK2</i>	2p16-p15	-2.2	-1.6
212606_at	AL536319	Hs.480116	<i>WDFY3</i>	4q21.23	-2.1	-1.7
228788_at	AA425358	Hs.517436	<i>YPEL1</i>	22q11.2	-2.0	-1.6
235916_at	BE673815	Hs.135978	<i>YPEL4</i>	11q12.1	-2.0	-2.9
214746_s_at	BE549732	Hs.112158	<i>ZNF467</i>	7q36.1	-2.3	-1.8
227195_at	AA603467	Hs.195710	<i>ZNF503</i>	10q22.2	-3.0	-1.7
215706_x_at	BC002323	Hs.490415	<i>ZYX</i>	7q32	-2.0	-1.4
1558397_at	BF976693	Hs.376675	---	17q23.3	-8.5	-5.9
1558871_at	BC016361	Hs.549640	---	4q13.3	-3.7	-2.3
1566342_at	R34841	Hs.567557	---	6q25.3	-1.4	-2.1
1569004_at	BG541677	Hs.549563	---	19q13.32	-1.4	-2.2
212993_at	AA114166	Hs.531457	---	9q34.3	-2.0	-2.1
227620_at	AV721564	---	---	9q31.1	-2.0	-1.8
228032_s_at	AW071458	Hs.125056	---	1q31.3	-2.3	-2.6
229635_at	AW043859	Hs.235795	---	4q21.21	-5.6	-6.3
229699_at	AW237752	Hs.61558	---	3q21.1	-2.3	-2.1
229934_at	N39230	Hs.38218	---	Xq12	-12.6	-3.6
229968_at	AA504245	Hs.264347	---	4p14	-3.2	-3.9
231644_at	AW016812	Hs.200266	---	12p11.21	-6.9	-4.0
235352_at	AI270356	Hs.13500	---	1q25.3	-2.3	-2.2
235798_at	BE671123	Hs.146317	---	6p24.2	-2.6	-3.2
236065_at	BF431214	Hs.443967	---	12q12	-2.1	-2.9
238121_at	AI473796	Hs.135904	---	3q23	-2.3	-2.4
238712_at	BF801735	Hs.439558	---	3p13	-2.0	-1.5

238787_at	AA988769	Hs.125056	---	1q31.3	-2.1	-2.1
239021_at	BF512068	Hs.552072	---	4p14	-3.0	-2.6
242714_at	AW500340	---	---	6q23.3	-2.0	-2.2
232412_at	AK024690	Hs.462946	---	17q12	-2.1	-1.9

Transcript levels in PBMCs from 9 healthy control donors (Healthy) were compared with those in 7 patients with hyper-IgE recurrent infection (Job's) syndrome using Affymetrix HU133 Plus 2.0 microarrays as described in Methods. Results are the average fold-change compared with healthy control donors.

Supplemental Table 6. SIFT PolyPhen Table

STAT3 Change	SIFT probability using BLink	SIFT probability using PSI-BLAST	Polyphen score (category)
R382W	0.00	0.00	3.065 (probably damaging)
R382Q	0.04	0.00	2.165 (probably damaging)
R382L	0.00	0.00	2.840 (probably damaging)
F384L	0.11	0.00	2.551 (probably damaging)
F384S	0.13	0.00	3.001 (probably damaging)
R423Q	0.18	0.06	1.459 (benign)
S465A	0.00	0.00	1.871 (possibly damaging)
S611N	0.02	0.00	1.900 (possibly damaging)
F621V	0.06	0.02	2.292 (probably damaging)
T622I	0.01	0.00	2.165 (probably damaging)
V637M	0.01	0.00	1.721 (possibly damaging)
V637L	0.00	0.06	1.149 (benign)
P639A	0.02	0.00	2.731 (probably damaging)
N647D	0.29	0.01	1.073 (benign)
E652K	0.15	0.11	0.059 (benign)
Y657C	0.00	0.00	2.940 (probably damaging)

Bioinformatic assessment of STAT3 protein missense changes by SIFT (Ng and Henikoff 2002) and PolyPhen (Ramensky et al. 2002). These analyses take into account the replacement amino

acid (e.g., R382W and R382Q get different assessments). The main part of SIFT takes as input a query-anchored multiple alignment of putative homologous sequences. These sequences can be pre-computed using one round of BLAST and stored in NCBI's Blink and retrieved instantaneously. Alternatively, the homologous sequences can be computed using PSI-BLAST as part of the SIFT run, which is slower but more sensitive.

Figure S1. Comparison of baseline transcript levels in leukocytes from patients with HIES (Patient, n = 7) and control subjects (PMN Control, n = 10; PBMC Control, n=9).

Principal component analysis of baseline transcript levels in polymorphonuclear leukocytes (Panel A) and peripheral blood mononuclear cells (Panel B) from control subjects and patients. Panel C indicates transcripts concomitantly increased (red) or decreased (light green) in patient leukocytes. Panel D is a pathway analysis (modified from Ingenuity Pathways Analysis, Ingenuity® Systems, www.ingenuity.com) of the PMN microarray data in Panel A and Supplementary Table 1, showing relative STAT3 signal transduction in HIES leukocytes. Red nodes (shapes) indicate transcripts that are increased, and green nodes transcripts that are decreased in HIES patient PMNs. Solid lines indicate direct interactions, while dashed lines indicate indirect interactions. A line connecting two nodes indicates “binding only,” a line with an arrowhead indicates “acts on,” a line with “T” indicates “inhibits,” and a line with “T” and an arrowhead indicates “inhibits and acts on.” Square = cytokine; diamond = enzyme; horizontal oval = transcription regulator; vertical oval = transmembrane receptor; inverted triangle = kinase; vertical rectangle = G-protein coupled receptor; horizontal rectangle = ligand-dependent nuclear receptor, trapezoid = transporter; circle = other.

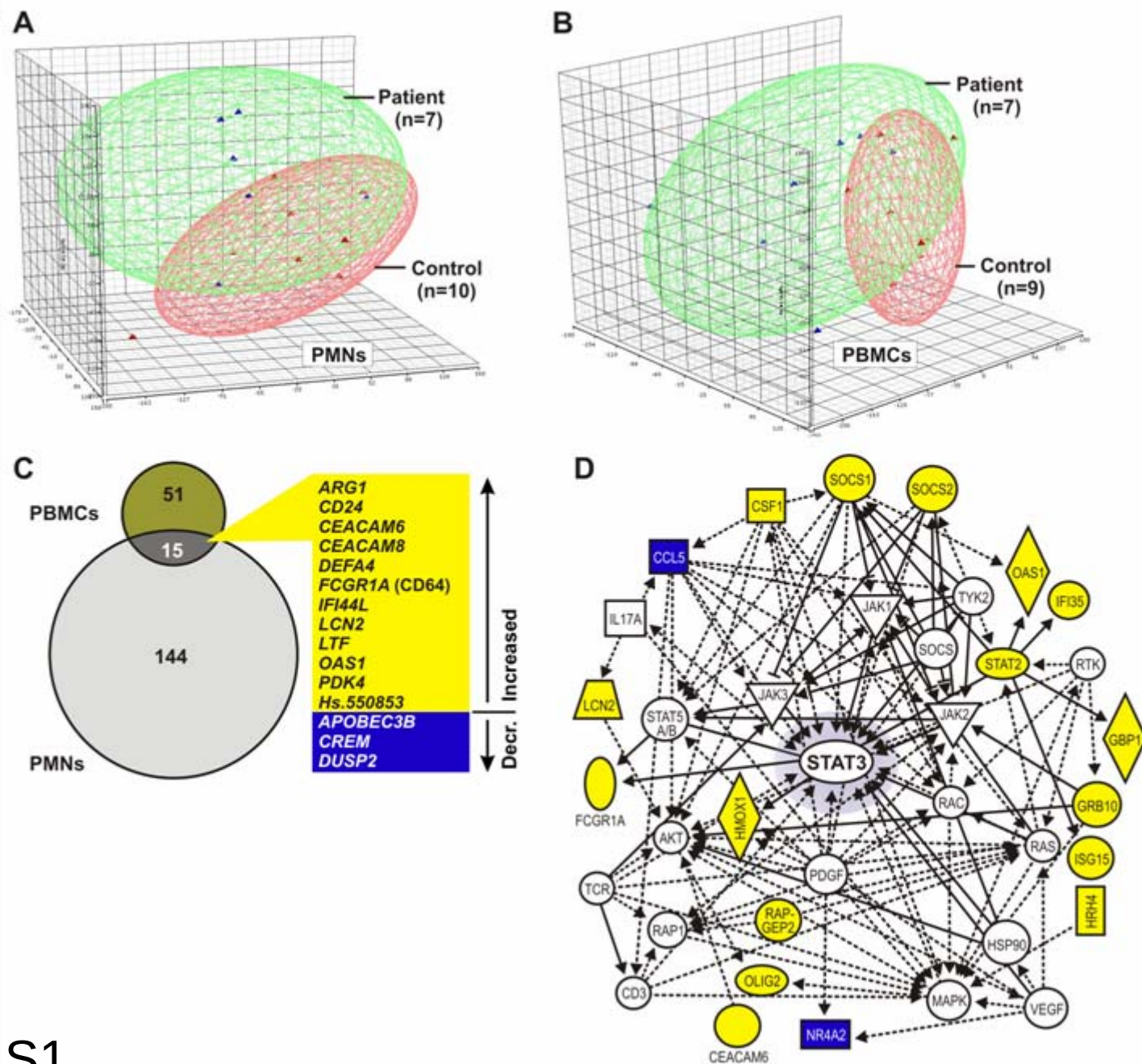
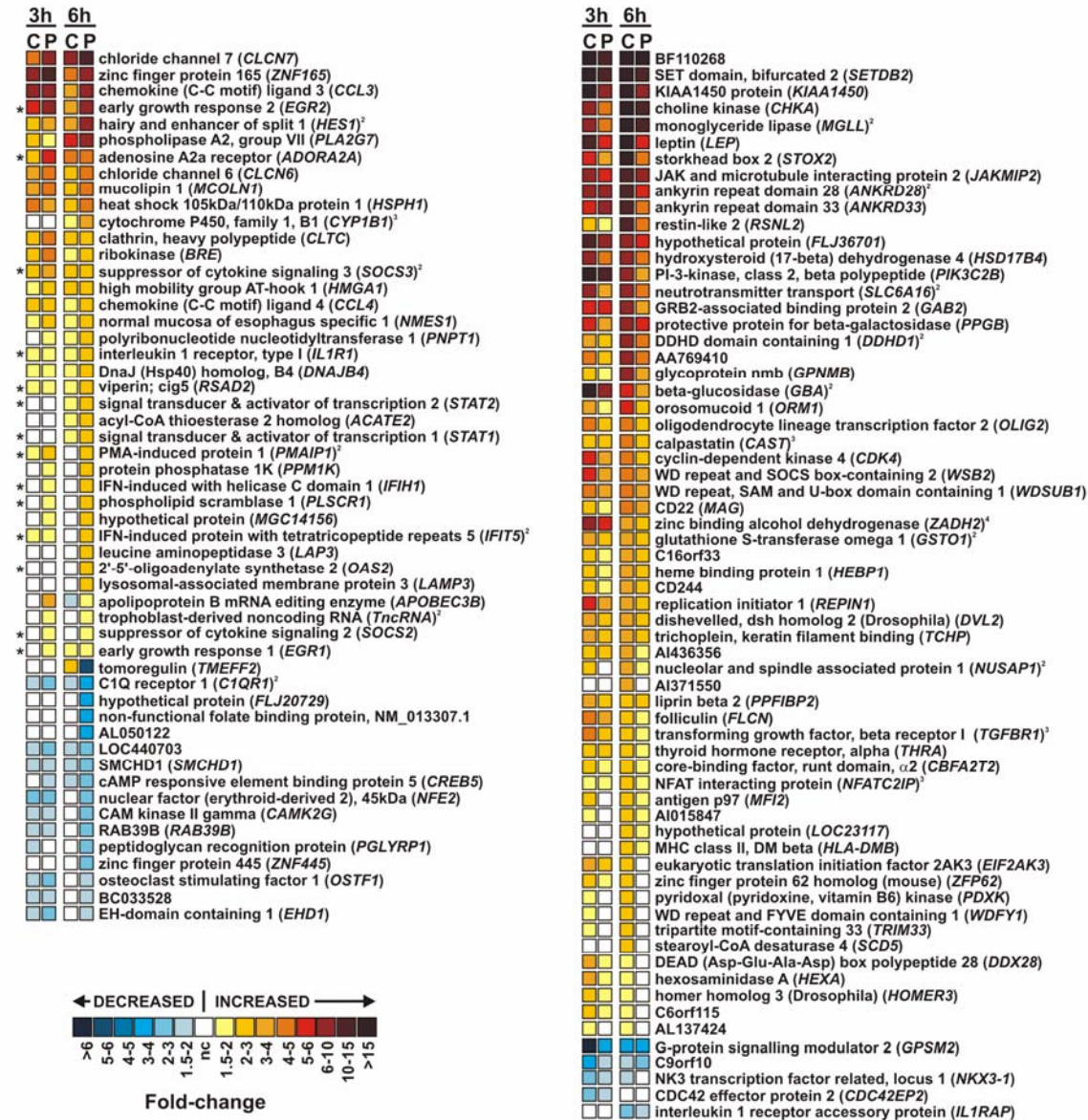


Figure S1

Supplemental Figure 2. Differential expression of selected genes in PMNs from control subjects (C) or patients with hyper-IgE recurrent infection (Job's) syndrome (P) after phagocytosis. Asterisks indicated genes regulated by IFN or involved in IFN signal transduction.

Figure S2



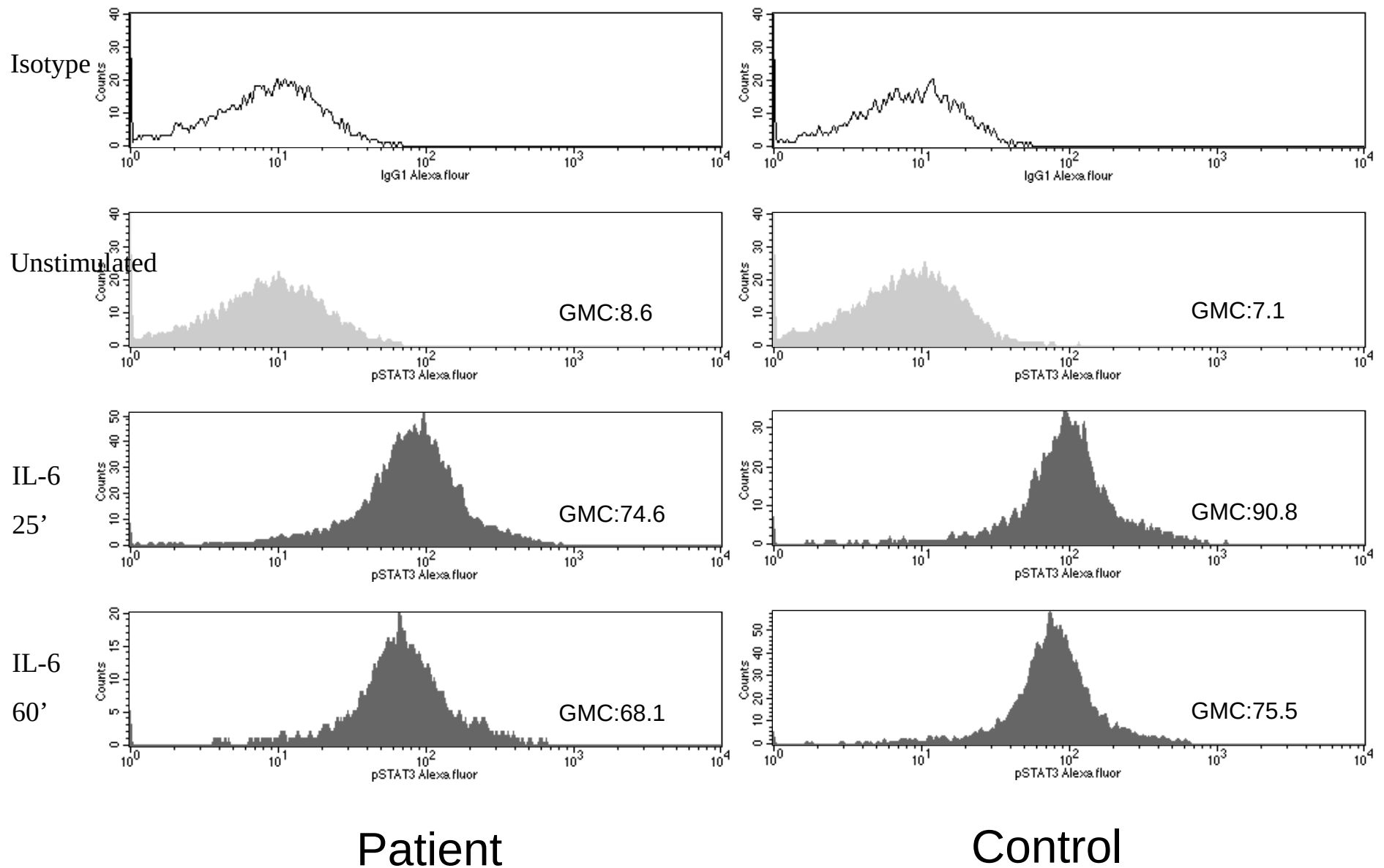


Figure S3. Flow cytometric detection of STAT3 phosphorylation. Isolated peripheral blood mononuclear cells from a healthy adult control and HIES patient J016 proband were stained for phosphorylated STAT3 (phospho-S727). Cells were unstimulated (solid histogram), or stimulated with IL-6 (10ng/ml)(lower panels) for 25 and 60 minutes, as marked and then fixed, permeabilized, and analyzed. Isotype control is shown as the broken line. Geometric mean channel (GMC) values are shown.